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INDIAN INSTITUTE OF PULSES RESEARCH भापदअस

IC PULSES 2023

International Conference on

Pulses: Smart Crops for Agricultural Sustainability and Nutritional Security

Feb. 10-12, 2023

Abstracts



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International Conference on

Pulses: Smart Crops for Agricultural Sustainability and Nutritional Security

Feb. 10-12, 2023

Abstracts

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Foreword

Pulses have now found a prominent place in common man's daily dietary basket enabling him to have a more nutritious diet. Additionally, pulses are affordable, capable of growing in marginal environments, have minimal carbon footprints and can be stored for long periods. Owing to multifarious uses, these contribute signiûcantly to achieving the goals of the 2030 agenda of Sustainable Development Goals.

This conference aims to focus on the developments on accelerating genetic gains and socio-economic upliftment of farmers through inclusion of pulses. The event has attracted international partners and is being organized by ISPRD-ICAR-IIPR in association with global organizations working for the cause of pulses like ICARDA-Morocco, WorldVeg-Taiwan, DAR-Myanmar, ICRISAT, Hyderabad, IPGA, Mumbai, etc. for a common goal of creating awareness of the beneûts of pulses as well as to drive the agenda of targeted increase in its production, productivity and consumption. The Indian Society of Pulses Research and Development works in close association with ICAR-Indian Institute of Pulses Research and both are focused to identify and work upon critical gaps in pulses research and development. In this context, the conference has been designed to encompass all researchable areas under nine concurrent sessions, including new areas of research like natural farming and data driven decision making. We have received more than 500 abstracts from universities and global and national research institutes. Each abstract has been assigned a unique ID under the relevant theme. The technical sessions are an amalgam of experienced and budding researchers who have chosen this conference as a platform to share their findings and ideas.

This publication encompasses the extended summaries shared by lead and invited speakers and abstracts submitted by researchers whose work found place as oral/rapidfire presentations or as poster presentations. In effort to go eco-friendly, we are encouraging this compilation as an e-file that will be available on the conference website as a free download. It will also be circulated to each delegate via e-mail and Whatsapp. I am happy to present this compilation and hope it finds place on the table of each pulse researcher.

The efforts made by members of the Publication committee are duly acknowledged and appreciated for successful compiling and editing of the abstracts.

(Meenal Rathore)
Chair, Publication Committee and
Co-Organizing Secretary, ICPulses2023

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Lead and Invited Lectures

Session: Farm to Fork – Planning, Policy, Perspectives

Policy initiatives for sustained pulses production

G Chandrashekhar

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That India is the world's largest producer, processor, importer and consumer of pulses is well recognized. Also, India has the world's largest acreage for pulses in two seasons, *Kharif* and *Rabi*. Pulses contribute to agricultural sustainability by improving the physical, chemical and biological properties of soil through nitrogen fixing ability. Also, pulse crops need relatively less water than many cereals.

As for nutrition, pulses are protein-rich. As the basic ingredient of diet for a vast majority of the population, pulses provide a perfect mix of biological value when used with cereals. Pulses go well with fine cereals, rice and wheat. We eat dal-roti or dal-chawal. Not only that, pulses are feed / fodder for livestock.

We have faced shortages and import dependence since early 1980s. Our imports peaked at 6.6 million tons in 2017-18. Since then domestic production has increased and our country is currently substantially self-reliant in pulses. But we cannot remain smug. A business-as-usual approach would be fraught with risks. The supply-demand fundamentals are fragile. Even one bad monsoon can lead to large shortage and largescale return to the world market scouting for import. Sustained growth in sustainable ways is the way forward. Rising incomes and demographic pressure will continue to boost demand even as less-than-satisfactory nutrition status of the country argues for increased consumption of vegetable protein that pulses provide.

The author argues that Indian pulses sector has to register sustained growth in sustainable ways in the coming years for which we need to take an ecosystem approach for its growth and development. Even as we focus on higher production, we need policies to encourage higher productivity, more efficient processing, greater value addition and more equitable consumption. Distributive trade plays a critical role in ensuring pulses are sold across the nook and corner of the country. Also, India must continue to remain as part of the global value chain.

Some key trends in the pulses sector already visible and policy action required to address some of the challenges are given below.

1. **Newer Challenges**: Land constraints, water shortage and climate change are three key challenges for Indian agriculture in general and pulses in particular. Land area for pulses cultivation, especially in Kharif season, is nearing a saturation point. Do not expect any marked increase in planted area in future as competition for acreage will only get more intense.

2. **Low Yields**: It is bane of India's pulses cultivation. Given land constraints, the only option is vertical growth through higher yields. There has been no significant breakthrough in seed technology. In a 3 to 5 year timeframe, our aim should be to reach yield of 1,000 kilograms per hectare on an average which will give us 30 million tons of raw pulses, enough to meet consumption demand of the country.

3. **MSP**: There is need to seriously review the role and effectiveness of Minimum Support Price (MSP). By itself, the MSP regime as practiced today, has failed to encourage crop shift and has not helped yield increases. MSP calculations have to take into account market realities.

4. **Consumption**: There is an uncomfortable skew in the pattern of pulses consumption. Per capita consumption number masks the reality. We need policies to promote more equitable consumption of pulses to advance nutrition security.

5. **Value Addition**: Pulses lend themselves to a lot of value-addition. There is a market for protein foods waiting to be tapped. Protein-laden pulse-based snacks – kid food, teen food, geriatric food, energy bars for sportspersons and so on – deserve support for multiple reasons.

6. **Foreign Trade**: Pulses export deserve promotion. The organoleptic profile of Indian pulses is favourable; but we have done nothing to leverage it for the export market, nor have we used our FTAs to push exports. As for import, our trade and tariff policy changes are often knee-jerk, late and unpredictable, creating huge distortions for those along the value chain.

7. **Dal mill modernization**: Several thousand dal mills across the country are small, use antiquated machinery and inefficient in operation including sub-optimal processing yields and less-satisfactory hygiene standards. There is a dire need to modernize dal mills.

For sustained growth of the pulses sector in a sustainable manner, we first have to recognize the aforesaid challenges and discuss short-term and medium-term solutions. The author's presentation during International Conference on Pulses on February 10, 2023 will focus mainly on solutions and recommended policy actions for each one of the aforesaid challenges.

***About the author**: G. Chandrashekhar, Economist, Senior Editor and Policy Commentator is a global agribusiness and commodities market specialist. For nearly forty years, he has been tracking the pulses sector and providing policy inputs for the government through his newspaper columns, business television appearances, personal interaction with senior officials and lectures in public forums. He enjoys international affiliations with global promotional bodies. He is an Independent Member of SEBI-Commodity Derivatives Advisory Committee and Consultant, U.N. International Trade Centre, Geneva. Views expressed are always personal.*

Session: Mendelian Breeding for Crop Resilience

Mendelian Breeding of Pulses: Achievements and future outlook

Pooran Gaur

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The improved varieties of pulses developed through conventional Mendelian Breeding have played pivotal role in enhancing pulses production by improving yield and expanding area of pulses. The emphasis of the breeding programs has been on development of varieties with desired crop duration and plant type, enhanced resistance/tolerance to biotic and abiotic stresses, and market preferred seed traits. During the past two decades (2001-2021), world's cowpea production increased by 134%, chickpea by 126%, pigeonpea by 76%, lentil by 71% and dry bean (includes Phaseolus bean, mungbean and urdbean) by 52%. Increase in production has resulted from both increase in area (35 to 62%) and yield (30 to 44%), except for dry beans where the increase in production is mainly due to increase in area (51%). Over 500,000 samples of genetic resources of pulses, including wild species, are conserved in different gene banks of the world (https://www.fao.org/wiews) and have been precious sources of desired genetic variability. The Global Information System of the International Treaty on Plant Genetic Resources for Food and Agriculture (PGRFA) has assigned Digital Object Identifiers (DOIs) to over 268,000 accessions of pulses genetic resources (https://ssl.fao.org/glis). These DOIs can be used as unique identifiers to unambiguously and permanently identify PGRFA being exchanged and used across organizations. Seed duplicates of over 187,000 samples of pulses genetic resources from different gene banks have been safely stored in Svalbard Global Seed Vault located on a remote island of Norway in the *Arctic Circle.* The first use of this facility is the withdrawal of samples by ICARDA as it could not operate its gene bank located in Aleppo, Syria.

We have several inspiring success stories of the conventional Mendelian Breeding of pulses from across the world. The following are some of the greatest success stories of the adoption and impact of improved pulses varieties:

1. **Chickpea in Central and Southern India:** There has been a silent chickpea revolution in central and southern India, where during the past four decades, chickpea production increased 5.3-fold (from 1.29 to 6.80 million MT) due to 136% increase in area (2.42 to 6.71 million ha) and 123% increase in yield (530 to 1185 kg/ha). Central and southern India has a share of about 43% in the global chickpea production. This success story largely remained unnoticed as bulk of this increased chickpea production went in compensating for the huge reduction in chickpea production occurred in northern India due to replacement of chickpea by wheat and

other irrigated crops in a large area (about 4 million ha). Short duration, high yielding chickpea varieties with improved adaptation to drought and heat stresses and high resistance to fusarium wilt developed though ICAR-ICRISAT collaborative research account for about 65% of the total indent of chickpea breeder seed in central and southern India and significantly contributed to increasing chickpea area and productivity in the region.

2. **Chickpea in Myanmar:** During the past 25 years, chickpea production in Myanmar increased 5.4-fold (89K to 482K MT) due to 2.7-fold increase in area (134K to 361K ha) and doubling of yield (665 to 1335 kg/ha). This is mainly because of high adoption (>90% of the chickpea area) of improved varieties having traits like early maturity, high yield potential, high resistance to fusarium wilt and tolerance to drought and heat stresses developed from ICRISAT-bred materials.

3. **Chickpea in Ethiopia:** Improved varieties developed from the breeding materials supplied by ICRISAT and ICARDA cover about 80% of the chickpea area in Ethiopia. During the past 20 years, Chickpea production in Ethiopia increased by 2.6-fold (165K to 435K MT) due to 134% increase in yield (891 to 2084 kg/ha) and marginal (13%) increase in area (185K to 209K ha).

4. **Lentil in Canada:** It was vision of Dr Alfred Slinkard, popularly known as Father of Canada's Lentil Industry, to establish lentil as a potential new crop of Canada. He introduced lentil germplasm and initiated breeding in 1970's and later developed improved varieties that triggered lentil revolution in Canada. Canada is now the world's largest producer (38%) and exporter (44%) of lentil in the world (average value of annual export US$1.3 billion during 2019-2021).

5. **Cowpea in West Africa:** West Africa accounts for 85% of the global production of cowpea. During the past 4 decades, cowpea production in West Africa increased 7.5-fold (1.0 to 7.5 million MT) because of 4.4–fold increase in area (2.9 million ha to 12.8 million ha) and 69% increase in yield (350 to 590 kg/ha). Improved cowpea varieties developed from IITA-bred materials were the major drivers for this success. The key traits include early maturity and high productivity and resistance/tolerance to major abiotic (drought, heat) and biotic stresses (aphids, thrips, parasitic weeds).

Some of the areas which need greater attention in development of pulses varieties/hybrids include improved resilience to climate change and adaptability to new niches (early maturity, heat tolerance, etc); region-specific hybrids of pigeonpea with suitable maturity duration and efficient seed production and genetic purity assessment system; labour-saving traits (suitability to machine harvesting, herbicide tolerance); further enhanced nutritional quality (protein, iron and zinc contents); and traits needed by the industries and for specialty pulses. The crop improvement programs should consider exploitation of wild species for introgression of novel genes conferring resistance/tolerance to biotic and abiotic stresses and controlling other desired traits for which genetic variability in the cultivated germplasm is not adequate.

Though the conventional Mendelian breeding of pulses has so far been very successful in developing improved varieties, there is a need to integrate novel tools and techniques (genomic tools, genetic engineering, gene editing, precision phenotyping, rapid generation advancement, data management system, etc.) to enhance efficiency of the breeding programs and increase rate of genetic gains. The integrated breeding programs will be able to develop pulses varieties in relatively shorter period and have greater capability of meeting the existing and evolving varietal requirements of farmers, consumers and the industries.

Session: Mendelian Breeding for Crop Resilience

Back to the wild - crop wild relatives as a source of adaptation

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Past domestication processes resulted in a high degree of relatedness between modern varieties of crops leading to the narrower genetic base of cultivated germplasm, prone to pests and diseases (Bohra et al. 2022, Smýkal et al. 2018). Unlike their domesticated counterparts, crop wild relatives (CWRs) have needed to adapt to the environment in order to survive. CWRs provide a key to counteract the effects of climate change on the world's food supply (Renzi et al. 2022). To fully understand and exploit this process, studies in the geographical centers of origin are needed combining ecology, physiology, and genetics. CWRs harbor genetic diversity tested by natural selection in a range of environments (Guerra-Garcia et al. 2023, Gorim et al. 2017 for lentil, Smýkal et al. 2017 for pea, von Wettberg et al. 2018 for chickpea, Berger et al. 2017, 2020 for lupine). The challenge is to incorporate such diversity of CWRs into modern crops without compromising desirable agronomical performance. With the advent of modern genomics and computation, combined with systematic phenotyping, it is feasible to revisit wild accessions and landraces and prioritize their use for breeding, providing sources of biotic and abiotic resistances and food quality traits. The establishment of hybrid populations with CWRs gives breeders a considerable benefit of a pre-breeding tool for identifying and harnessing wild alleles and provides extremely valuable long-term resources. However simple crosses between wild and cultivated germplasm is inevitably linked to a genetic drag of undesirable wild material related traits which prevented its broader use. This is time and space-consuming process that need to be repeated for every specific cross. To avoid this, the synthesis of introgression and chromosome substitution lines, containing chromosome segments from wild species in a constant genetic background of the related cultivated species defined by molecular markers has been applied to make the use of alien genomes more precise and efficient (Warshevsky et al. 2014).

As an example of CWR use, we have analyzed pea seed coat in the context of health beneficiary flavonoids and proanthocyanidins and their relation to seed defense against soil-born fungal pathogens. As result of pea domestication, the loss-of-function of polyphenol (PPO) oxidase (Balarynová et al. 2022) has been selected. There is no clear picture if this was accidental or the result of direct selection due to the presence of anti-nutritional compounds affecting digestion or

palatability of the seeds or cultural behavior favoring light color as a symbol of purity. On contrary, the functionality of PPO gene in the pea crop progenitors has been implicated in the oxidation and polymerization of phenolics providing a barrier for pathogen entry.

This talk will focus on three legume crops domesticated in the Fertile Crescent; pea, chickpea, and lentil, and summarize the current state and potential of their respective CWR taxa for crop improvement (Coyne et al. 2020). The results of advanced pea introgression lines will be discussed.

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Session: Mendelian Breeding for Crop Resilience

Recombination Breeding and Genetic Gain in Pulses: A Saga of Success

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The rediscovery of Mendel's work opened the gateway for systematic crop improvement research. The basis of improvement was hybridization followed by selection of recombinants of choice. Simultaneously, the new science of genetics evolved. It is science of study the variations among traits and their heredity. The variations present in a desired trait of interest have to be recombined through hybridization following the law of inheritance. This led in recombination breeding to develop new variety which is a path of genetic gain and basis of crop improvement. The crop improvement not only helped to understand the genetics of traits but proved to be saviour of mankind through food security. Initially the crop varieties were either a selection from mixed population or an introduction. The recombination breeding led in development of more productive varieties possessing multiple traits of economic importance introduced from diverse parents. It is a continuous process to recombine the traits of interest ensuring enhancement in genetic yield potential of new varieties. Thus, continuously recombining the useful traits/genes become a routine process irrespective of crop plants resulting in sustained improvement in production and productivity, which is an indicator of genetic gain. It is evident from the increase (6.21 times) in total food grains production from 50.82 million tonnes in 1950-51 to 315.72 million tonnes in 2021-22 as per fourth advance production estimated released by the Government of India. The average productivity over the decade for last seven decade also shows that productivity enhanced from 606.2 kg/ha (1950/51-1959/60) to 2031 kg/ha (2010/11-2019/20) which clearly indicates that over the years better recombinant varieties have been developed. Similarly, average productivity over decade of pulse crops increased from 475.1 kg/ha to 976.2 kg/ha during last seven decades. This two-fold increase in productivity is the genetic gain which is resultant of recombinant breeding. India grows more than a dozen and half pulses under varying agro-ecologies in different parts of the country during winter (rabi), rainy (kharif) and spring/summer seasons. The government of India record area, production and productivity of a few crops like chickpea, pigeonpea and lentil. Further, pulses production increased by 3.03 times during last 70 years (1950-51 to 2021-22) whereas total food grains' production increased by more than 6.11 times mainly due to research and development support for staple foodgrains like wheat, rice and maize etc. Once Government of India made investments, pulses production went up by 39.97% during last 7 years whereas in maize (33.63%), rice (19.95%) and wheat (16.13%) could not show similar growth. The productivity gains also

studied for these three crops of pulses as well. The improvement in productivity over decades in chickpea and lentil clearly speaks about the success story of recombinant breeding. However, due to various reasons success is not of that order in pigeonpea which could be observed in other pulse crops. The per day productivity of different pulse crops viz., chickpea, pea and mungbean has increased tremendously. The source of variation for recombination breeding primarily depends upon the availability of total germplasm accessions including wild and other related species. The details of germplasm and pedigree analysis also taken into account to explain the success of recombination breeding in this article.

There is need to understand the recombination breeding more precisely at molecular level. The genomic tools made to be handy to the conventional breeder to speed up breeding process for targeted advancement in genetic gain. Molecular markers are helping in reducing large segregating populations to few plants carrying genes/QTLs of interest in recombined plants. These selected segregating plants can be advanced to next generation to achieve homozygosity within 2-3 years under controlled environment following speed breeding approach which is similar to advancing segregating generations using off-seasons.

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Plant Genetic Resources Management and Utilization: Efforts of ICAR-NBPGR for Pulses

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The Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR) was established in 1976 with its headquarters at New Delhi. It is a nodal institute at the national level for the acquisition and management of indigenous and exotic plant genetic resources (PGR) for agriculture, and to carry out related research and human resources development for sustainable growth of agriculture. The activities of the bureau are plant exploration and germplasm collection, germplasm evaluation, germplasm conservation, genomic resources and germplasm exchange, plant quarantine and tissue culture and cryopreservation. It has a network of 10 Regional Stations covering different agro-climatic zones to carry out PGR activities.

India is rich in genetic diversity of major pulse crops, but the productivity and the production of pulse crops remain low compared to the world and hence, there is a need to enhance the use of diverse germplasm conserved in the National Genebank (NGB) for increasing the production. Till December 31, 2022, a total of 4,63,130 accessions belonging to over 823 genera and 2113 species in 15 crop groups. Major pulses genera for which genetic diversity is occurring in India include *Vigna, Cajanus, Cicer, Pisum, Lens, Phaseolus* and a few minor pulses such as *Macrotyloma, Canavalia, Lathyrus, Vicia, Mucuna* etc. NGB has an assemblage of <"70,000 accessions of different pulse crops through collection and introduction from India and >70 other countries in the world. Geo-referencing and mapping of diversity *vis-à-vis* germplasm collected and conserved has been completed in chickpea, pigeonpea, urdbean, mothbean, mungbean, cowpea, ricebean and accordingly, gap in collections have been identified up to the district/ taluk level. Additionally, this activity also facilitated the identification of duplicates and updation of passport data in the genebank. Trait-specific germplasm and potential sites are identified through grid mapping. *Vigna, Lathyrus* and *Cajanus* are prioritized genera for developing illustrated guides to facilitate the identification of closely related species. Two new taxa described by ICAR-NBPGR are *Vigna konkanensis* Latha, KV Bhat, IS Bisht, Scariah, KJ John & Krishnaraj and *Vigna sahyadriana* Aitawade, KV Bhat & SR Yadav. The *ex-situ* base collection at ICAR-NBPGR conserves 68,465 accessions belonging to 15 genera and 98 species of grain legumes. Of a total of 68,465 accessions, over 80% are indigenous and the remaining 20% are exotic collections. Among the indigenous collections, 3,368 accessions belong to the single state of Andhra Pradesh.

To characterize the entire grain legumes accessions conserved in the NGB, a mega programme on characterization and evaluation of germplasm was initiated in 2012-13 in which 18,775 accessions

of chickpea were characterized at three locations. These mega-characterization programmes paved the way for other prioritized crops conserved in the NGB. Under a focused strategy for enhancing germplasm utilization, ICAR-NBPGR has shifted from fragmentary work to a complete characterization approach in recent years where entire genebank accessions of certain pulses were characterized in one go using a comprehensive strategic plan. The large-scale characterization is being carried out in collaboration with varius ICAR institutes and State agricultural University partners. To facilitate enhanced germplasm utilization, core sets have been developed in chickpea, lentil, horse gram, pea, wild lentil and five species of cultivated *Vigna*. The conserved germplasm has been characterized for agro-morphological, quality and biochemical traits, biotic and abiotic stresses for identifying trait-specific reference sets and 28 crop catalogues describing 45,000 accessions of 14 pulse crops have been developed.

Near-infrared reflectance spectroscopy (NIRS) prediction models have been developed in chickpea, cowpea, mungbean, ricebean to rapidly determine biochemical parameters for a large-set of germplasm which is otherwise laborious and time-consuming with conventional methods. These prediction models would facilitate high throughput non-destructive screening of large sets of pulses germplasm and selection of desirable chemotypes in any genetic background and have a huge application in pulses improvement programmes across the world. Systematic pre-breeding activities have been initiated in *Lens, Vigna* and *Lathyrus* genera where wild species were utilized for transferring desirable traits into cultivated species of the targeted genus. Several pests of quarantine significance have been identified and salvaged from the exotic germplasm. The application of modern tools and technologies of molecular biology would accelerate the process of gene transfer for the improvement of pulses crops. The Genome-wide association studies in various pulses has accelerated the pace of identification of gene/marker-trait association, genetic dissection of important traits and thereby enhancing the utilization of germplasm collections of NGB in breeding programmes for varietal development. A total of 199 accessions of various grain legumes have been registered as unique/potential donors. Details of the registered germplasm can be accessed at http://www.nbpgr.ernet.in:8080/ircg/index.htm.

A paradigm shift is thus required to re-think and innovate processes in such a way that germplasm is used more effectively in the pulses breeding programme. Pusa Chickpea 10216, a drought-tolerant variety is a recent example of utilization of Indian germplasm. The variety has been developed after the introgression of "QTL-hotspot" containing genes for drought tolerance (germplasm collected from Jabalpur, Madhya Pradesh, India) in Pusa–372 background using molecular breeding. Hence, to unlock the full potential of pulses genetic resources conserved in NGB, there is a need for extensive phenotypic and genetic characterization via revealing the genomic regions controlling traits that are important to biotic and abiotic stress adaptation.

A PGR Portal has been hosted on ICAR-NBPGR website, which is a gateway to information on plant genetic resources conserved including pulses. The Portal contains information on about 0.4

million accessions belonging to about 1800 species. The PGR documentation is done in various forms including printing of books, crop catalogues, inventories, research papers, popular articles, pamphlets etc. In addition, ICAR-NBPGR has developed mobile apps Genebank and PGR map in PGR Informatics which can accessed through NBPGR web pages, genebank.nbpgr.ernet.in and http://pgrinformatics.nbpgr.ernet.in/pgrmap/ two mobile apps "Genebank" and "PGR Map" have been developed to enhance access to PGR information with an easy user interface. The apps have been hosted on Google Play and App Store. "Genebank App" provides a dashboard view of indigenous collections (state-wise), exotic collections (country-wise), addition of accessions to genebank, etc. The app also helps generate routine genebank reports. The app uses databases live on the backend and hence always gives updated information "PGR Map App" offers three benefits: "What's around me" helps user to obtain quickly the accessions that have been collected and conserved in the genebank from a particular location in India where the user is located at the moment; "Search the map" helps user to list the accessions that have been collected and conserved in the genebank from any selected location in India; "Search for species" helps user to map the collection sites of a crop species. Establishment of geo-informatics portal in PGR: A study to link germplasm to changing climatic regimes was earlier carried out with the funding of the CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS). A web interface named PGR CLiM was also developed to access information (www.nbpgr.ernet.in:8080/climate).

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International Mungbean Improvement Network 2 (IMIN2) - New Initiatives

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Declining crop yields increased agricultural risks, diminishing soil fertility and environmental degradation are some of the main challenges which continue to threaten societal goals of improving food, income, and nutrition security, especially in smallholder farming. There is a large demand for options for the sustainable intensification of tropical cropping systems in Africa, Asia, and Australia. The International Mungbean Improvement Network (IMIN) aims to increase farmer income, systems productivity, and food security by delivering high-yielding, disease- and pest-resistant mungbean varieties to smallholder farmers. The network will build on current ACIAR projects researching mungbean agronomy and contributing to cropping system intensification in Myanmar and Bangladesh. A wide range of useful traits including resistance to Mungbean Yellow Mosaic Disease, anthracnose, halo blight, dry root rot, powdery mildew, cowpea aphids, thrips, salt tolerance, and synchronous maturation have been identified in the mungbean mini-core collection developed by the World Vegetable Center and have been used in mungbean breeding programs by the partners of the network. Sequencing (Illumina) efforts of mungbean accessions of the WorldVeg mini-core, the Australian diversity panel, and segregating populations yielded up to now 12 Tb of sequence information that is currently used to develop a mungbean pangenome and map traits of interest for breeding. A new reference genome has been assembled for mungbean based on the popular Australian variety, Crystal. A pilot experiment on a selected germplasm set revealed the optimal planting density for automatized high throughput phenotyping of mungbean plant architecture. In Australia, the entire NAM population was sown and evaluated for key flowering traits. Data collected from this trial will enable genome-wide associated studies to dissect genomic regions associated with these traits. The further screening of the mini-core accessions/breeding lines has revealed potential genetic resources of resistance to anthracnose, powdery mildew, Fusarium wilt, cowpea

aphid, thrips, and stemfly. A set of 42 accessions from 13 *Vigna* species endemic to India was screened against three bruchid species (*Callosobruchus chinensis* L., *C. maculatus* F., and *C. analis* L.), which led to the identification of accessions with resistance. A qPCR assay has been developed by WorldVeg to detect and quantify the amount of fungal pathogen *Macrophomina phaseolina* present in stem tissue causing dry root rot. Multilocation field evaluation data of the mini-core collection and of breeding lines are available, and in parallel, high throughput phenotyping of the mungbean collection is ongoing to collect precise data on mungbean development and morphology. The project partners are actively engaged in the introgression of traits from donors identified during IMIN1 and are progressing with the testing of the high-performing lines. A new mungbean variety, Yezin-16, for the high premium sprout market segment, with green shiny bold seeds was released by the Myanmar Department of Agricultural Research. This variety is resistant to Mungbean Yellow Mosaic Disease (MYMD) as well as to Dry Root Rot disease. One of the new initiatives includes how Artificial Intelligence (AI) can be used for predictive crossing to better stack key traits. The network has a newsletter known as "Mung Central" which helps to provide updates and includes mungbean recipes from project partners. The IMIN has been extending beyond the ACIAR-funded project partners by signing of agreements and sharing germplasm with partners in different parts of the world.

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Mainstreaming Minor Grain Legumes for Enhanced Nutrition and Climate Resilience.

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Food and nutrition security vis-a-vis economic growth are going to face a stiff challenge due to population outburst especially in the developing and third world countries. By 2030 the humanity has to face challenge of feeding 9 billion people as against 5.7 billion at present. It is estimated that nearly 1.2 billion people in the world do not have enough food to meet their daily requirement and a further 2 billion people are deficient in one or more micro-nutrients. Further, it is assumed that the population growth will continue, agricultural land will be increasingly converted to non-agricultural purposes; thus, increasing competition for the remaining land area, and disorders due to malnutrition continue to kill tens of thousands of productive people. Under the circumstance, we certainly urge to exploit the alternate source of energy (food) and livelihood generation. Ethno-botanical surveys confirm that hundreds of such crops are still found in many countries representing an enormous wealth of agro biodiversity which can play a vital role to improve income, food security, nutrition and climate resilience. Agricultural development and food security depends in part on our ability to broaden the range of agricultural species in an effective and sustainable way. That means finding ways to protect and enhance the locally important species so that they can be deployed more widely in agriculture and environment management, finding ways to explore the use of local crops in order to tap the hidden potential contained in them. The benefits of minor legumes such as local importance and acceptance in consumption and production system, adaptability to specialized agro ecological niche and marginal areas, fragile environment, nutrient richness, and indigenous knowledge-based cultivation and utilization make them most potential candidate species for broadening the food basket.

Through history, mankind has met its food needs with only 5,000 plant species, representing 1% of the world flora, and big nuclei of human population depend essentially on three cereals (wheat, rice and corn) and one tuber (potato) for subsistence. Under the situation, the role of underutilized species in general and grain legumes in particular have has evolved over time and as it is today, it adds to the quality of life besides meeting needs of the rural poor in particular. Grain legumes are known for their nutritional richness especially protein and amino acids, which are largely lacking in human diets leading to malnutrition. Worldwide ~50,000 germplasm accessions of

these grain legumes are being conserved the genebanks. Although efforts have been made to harness the potential of these crops but still, they are not receiving the adequate attention in the national research programmes. An integrated gene resource management strategy to combat malnutrition, identify gene resources for their improvement and enhance their value as traditional food and medicine are needed.

This paper will cover some selected minor grain legumes such as ricebean, moth bean, horsegram, winged bean, lalblab bean, adzuki bean, faba bean, grasspea, lima bean, jack and sword bean, bambara groundnut marama bean, kersting's groundnut, African yam bean, etc. which have huge potentials to boost protein security in period of hunger and malnutrition globally but more particular in South Asia and sub-Saharan Africa. These legumes species are known for their special attributes such higher nutrient contents, resistance to biotic stresses, climate resilience and response to low input production systems but still are known by many appellations such as miscellaneous, neglected, underutilized, underexploited, and under-researched, among others.

Currently, genetic enhancement by de novo domestication of minor crops and their wild relatives using a genome editing system has been confirmed as a useful approach to explore and expand food crop resources for agricultural, food, and nutritional sustainability. The technique offers prospects for developing new crops for today and future usage. However, scientific exposition in terms of the possibility of conducting de novo domestication schemes to convert semi-domesticated minor crops and their wild relatives to fully domesticated crop species is less reported. Now following advances in molecular biological technology, which provides powerful tools for genetic study, it has become more convenient to apply genomics to the study of minor crops which further paves the way for conducting de novo domestication experiments. Therefore, the current review discusses the feasibility of applying de novo domestication for the creation of new crop species from minor legumes and their wild relatives. Some suggested requirements for conducting a successful de novo domestication of a named minor legume which is also applicable in other non-leguminous minor crop species have been provided.

We conclude that it is now beyond doubt that our crops base has shrunk to an extent that it may collapse, if the present race for growing only few crops continues. The crops, which have served the humanity for thousands of years, are facing major threat of extinction from the agricultural production system. These, in turn, provide a basis for more productive and resilient production systems that are better able to cope with various climatic changes and various stresses which agriculture in general and fragile agriculture ecosystems in particular is witnessing almost every now and then. Minor legumes provide ample opportunities to sustain their agriculture on long term basis and also to improve the nutrition of large section of societies. But we need to change our so-called modernized attitudes and policies towards these resources. As mentioned above these species offers opportunities in many ways and few could be (i) potential of underutilized plant species as risk buffers in times of climate change; (ii) improving nutrition and health; (iii) diversification of farm income.

To achieve this, we need to create and manage a database of underutilized plant species, nutritive values, successful and unsuccessful case studies, resilience to climate change and information on genetics. Involve farm communities and researchers in conservation and crop improvement, including information gathering, knowledge sharing and dissemination. There is urgent need to create awareness on their contribution to local nutrition, income, ecosystem health and farm productivity. The promotion of any new product and making it a profitable venture is not possible unless we implement and document economic and market studies of different aspects of value chains for underutilized plants, and pilot a number of global marketing initiatives in public-private partnerships. The agronomy of most of these species have not been studied and many of them are still being used from wild, thus there is need to develop guidelines of best practices for their sustainable use. Identify, publish and disseminate case studies illustrating successful approaches in sustainable use of such species to improve rural health and economies. Nothing can be achieved unless we assure funding for research and development and working together across the full spectrum of disciplines, from crop breeding to socio-political policy.

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Session: Mendelian Breeding for Crop Resilience

Tapping the Untapped: Plant Genetic Resources for Grain Legume Improvement

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Grain legumes are the primary source of protein-rich food and contribute significantly to the global food and nutritional security. Grain legumes also play an important role in improving soil health through their nitrogen fixing ability thereby leading to the environmental sustainability. Despite enormous breeding efforts, it has not been possible to enhance the production and yield of grain legumes to a satisfactory level. Narrow genetic base, which is mainly due to the bottlenecks associated with crop origin, domestication and selection, coupled with several biotic and abiotic stresses often result in low yield enhancement in grain legumes. Plant genetic resources carry many valuable and novel alleles for the improvement of cultivated crops. Development of small-sized subsets such as core and mini core collections, composite collection, reference sets and FIGS provided useful resource to identify new and diverse sources of variations for use in crop improvement programs. Crop wild relatives (CWRs) carry much needed variability for the genetic improvement of modern crops, especially for the better adaptation of grain legumes to the changing climatic conditions.

Accelerating genetic gains in chickpea (*Cicer arietinum* L.) and pigeonpea (*Cajanus cajan* (L.) Millsp.) require the exploitation of new and diverse sources of variations and use of new tools and technologies. Equipped with many useful alleles including biotic and abiotic stress resistance, CWRs provide novel genetic variations for the genetic upgradation of chickpea and pigeonpea cultivars. Precise evaluation of wild *Cicer* species following SSD at ICRISAT resulted in the identification of four accessions (belonging to *C. judaicum* and *C. bijugum*) having high levels of resistance to Ascochyta blight, 12 accessions (*C. reticulatum* and *C. echinospermum*) resistant to botrytis grey mold (BGM), four accessions (*C. reticulatum* and *C. echinospermum*) resistant to dry root rot, one accession (*C. chorassanicum*) having high seed protein, and 27 accessions for high seed Fe concentration. Enormous genetic variability has been created for various morpho-agronomic and nutrition-related traits and for BGM resistance by using *C. reticulatum* and *C. echinospermum* as donors following simple and complex cross approach. In pigeonpea, the most significant achievement of utilizing CWRs is the discovery of cytoplasmic-nuclear male sterility systems (CMS). The world's first commercial pigeonpea hybrid, ICPH 2671 was developed by using the A_4 sterility system derived from *C. cajanifolius*. Successful efforts have also been made

to introgress useful alleles from secondary genepool species, *C. cajanifolius*, *C. acutifolius*, *C. scarabaeoides*, and tertiary genepool species, *C. platycarpus*, and *C. volubilis* into popular pigeonpea cultivars, ICPL 87119 (also known as 'Asha'), ICP 8863 (also known as 'Maruti') and ICPL 85010 for the priority traits for which limited variability is present in the cultivated genepool. This includes the development and identification of introgression lines (ILs) having salinity tolerance (21 ILs), pod borer resistance (21 ILs), phytophthora blight resistance (23 ILs), and photoperiod-insensitivity (2 ILs).

The superiority of few ILs over local and/or national checks provided an opportunity to the breeders to include promising ILs in the Initial Varietal Trial of the All India Coordinated Research Project on Pigeonpea for potential release as a variety/(ies). The high-yielding, salinity and phytophthora blight tolerant ILs were shared with breeders in Myanmar and are being used in crossing program for developing new cultivars with a broad genetic base. Four pigeonpea ILs (ICP 16917 to ICP 16920) have been conserved in ICRISAT genebank and are available for sharing through the Standard Material Transfer Agreement (SMTA). There is a need to integrate modern genomics approaches and high throughput phenomics to facilitate the identification of target traits in the germplasm conserved in genebanks and their use in breeding to enhance the genetic gains in crops.

The Global Initiatives such as "Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives" (referred as the CWR Project), an 11-year project funded by the Government of Norway (via NORAD), facilitated the use of CWRs in crop breeding for food security in the new climates of the future. Total 19 pre-breeding projects including six on grain legumes (common bean, chickpea, cowpea, grasspea, lentil, pigeonpea) were implemented between 2011-2021 by involving 62 national and international partners working in 34 countries. Build on the work and achievements of the CWR Project, BOLD (Biodiversity for Opportunities, Livelihoods and Development) is a groundbreaking 10-year project to strengthen food and nutrition security worldwide by supporting the conservation and use of crop diversity. More initiatives are needed to harness the potential of plant genetic resources conserved in genebanks for developing new climate-resilient cultivars for sustainable agriculture.

Session: Enhancing the Crop Produce

Potential benefits of legume-inclusive diversification on soil health, resource conservation and ecosystem services

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Legume crops play a vital role in delivering multiple services in line with sustainability principles. Grain legumes with their intrinsic characters like biological N-fixation, deep root system, leaf litter fall, enhanced rhizospheric properties and nutrient cycling, could contribute to multiple benefits to the agro-ecosystem. Presently, there is an increased relevance of legume-inclusive diversification to address the major sustainability challenges associated with cereal-dominating production systems such as soil quality degradation [soil organic carbon (SOC) loss, secondary salinization, nutrient deficiencies], declining natural resources [groundwater, fossil fuels], ecosystem imbalances [greenhouse gas emissions, soil and water pollutions], biodiversity losses, and over-dominance of biotic stress factors. Grain legumes particularly pulses could be the potential candidate crop for diversification of several major production ecologies including rice-wheat, maize-wheat etc. Besides, inclusion of legumes in summer fallows of rice-wheat systems, rice fallow ecologies, as an intercrop in widely spaced crops (sugarcane, banana, etc.), could be strategic approaches to sustainable cropping intensification that ensures self-sufficiency in food grain production and dietary diversification. Experimental data from around the world indicate that crop diversification with legumes not only enhances production (median effect +14%), but also biodiversity (+24%) and a variety of ecosystem services, including water quality (+51%), pest and disease control (+63%). Even though there is increasing interest in legume-inclusive diversification for resource conservation, climate resilience, C-sequestration, reduced water and carbon footprint and designing conservation agriculture modules, the adoption of pulses is slow particularly in the productive agro-regions, which should be investigated and addressed by deploying regional-specific policy frameworks. Additionally, cultivars of legumes need to be developed that are more resilient to extreme climates, water and nutrient deficient environments, salinity etc. In order to realize legume's potential benefits at cropping systems level, we must strengthen systematic research, extension activities, and develop location-specific policy interventions.

Session: Enhancing the Crop Produce

Microbial inoculants as a natural resource for improving health and nutrition of pulse crops

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Current agricultural practices rely heavily on chemical inputs such as fertilizers and pesticides to meet nutritional requirements of crop plants and to combat biotic stresses. Excessive and indiscriminate use of these chemicals have resulted in food contamination, disease resistance, environmental pollution which together impacts human health. Plants obtain most of their nutrition from soils. Pulse crops require less fertilizer in comparison to cereals and oilseeds. The inbuilt mechanism of biological N_2 fixation enables pulses to meet 80-90 % of their nitrogen requirements; hence a small dose of 15 - 25 kg N ha^{-1} is sufficient to meet out the requirements of pulses. In the recent years, use of sulphur (20- 30 kg ha^{-1}) and some of the micronutrient such as Zn, B, Mo and Fe have improved productivity of pulse crops considerably in many agroecological zones.

A reliable alternative to the use of chemical inputs is microbial inoculants that can act as biofertilizers, biopesticides and biostimulants. Microorganisms are endowed with tremendous genetic and metabolic diversity. They serve multiple ecological functions in soil ecosystem from nutrient cycling to conferring biotic and abiotic stress tolerance to plants. Members of the genus *Bacillus* and *Pseudomonas* are known to have multiple beneficial traits which help the plants directly or indirectly through acquisition of nutrients, overall improvement in growth by production of phytohormones, protection from pathogens and other abiotic stressors. Some of these microbes are commercially exploited in the agro-biotechnology industry. Still the potential of microorganisms have not been realized sufficiently and requires an emphasis towards translating the relevant technologies from laboratory to land for the benefit of mankind.

Nitrogen (N) is a key component of nutrition for plants and crop production. Soils under cultivation are subjected to high annual losses of N due to leaching, which results in low levels of total and available nitrogen for plant growth. Rapid land degradation also occurs because of intense cultivation and ever shortening of fallow periods in traditional farming systems in response to increasing human population. This decline in soil quality is a serious global problem. Crop yields are often limited by N supply. Nitrogen fertilizers are used only to limited extent in high return cash crops because of their high costs and low per capita incomes of farmers in developing countries. It is in these situations that opportunities are greatest for exploitation of the capacity of legumes to symbiotically fix atmospheric nitrogen through biological nitrogen fixation (BNF), which provides N inputs into agricultural soils and helps replenish the soil N pool. Various estimates of the contribution

of BNF to soil N fall in the range of 44 - 200 Tg N y^{-1} with an average of about 140 Tg N y^{-1}. Inputs of biologically fixed N into agricultural systems are derived from symbiotic relationship between legume and *Rhizobium*, as well as due to non symbiotic associations between free living diazotrophs and plant roots. Although indigenous population of *Rhizobium* are present in soil, they are not efficient in nitrogen fixation. For this purpose, efficient and competent strains of *Rhizobium* are generally used as biofertilizers for legume crops. Legumes contribute an estimated 35 out of 75 x 10^{12} tonnes of fixed N annually. Legumes contribute to increased productivity of other crops, when incorporated into cropping systems as intercrops or in crop rotations. In intercrops, the legumes are generally contributing to maintenance and restoration of soil fertility by fixing large proportion of its own N. Decaying plant roots, nodules and above ground material when incorporated in soil also contribute to soil N.

Plants belonging to leguminosae have the ability to harness atmospheric nitrogen because of their symbiotic association with *Rhizobium.* Biological nitrogen fixation is dependent on establishment of symbiotic relationship between the legume and effective *Rhizobium* strain. When legumes are first introduced into soils, root nodule failed to develop because of low population of compatible and effective strains of *Rhizobium* in the soil. Thus addition of appropriate strains of *Rhizobium* by inoculation is generally essential where legumes have not been grown before and where there are no naturalised rhizobia. The aim of inoculation of legume seed is to coat the seed with sufficiently larger number of viable rhizobia of the correct strain to give rapid and effective nodulation of that legume in the field

Most cultivated tropical soils are assumed to have relativity large population (>100g^{-1} dry soil) of rhizobia capable of nodulating the legumes grown in such soils. However, survey of farmer's grain and fodder legume crops have shown poor nodulation in large areas and good nodulation only in few pockets in India. Presence of nodules on plant roots does not necessarily mean that sufficient N_2 is being fixed for maximum benefit to the host plant and soil. Field surveys had shown incidence of ineffective strain was as high as 40% in chickpea, 53% in green gram and 63% in groundnut. Therefore inoculation with *Rhizobium* biofertiliser is advisable in the soil which lack indigenous population of *Rhizobium* or in those soils which are high in indigenous population, but are less effective than the introduced bacteria. The subsequent survival of rhizobia in soil is influenced by environmental and soil factors. Therefore inoculation is required in each season.

Phosphorus (P) is a macronutrient required for the proper functioning of plants. Because P plays a vital role in every aspect of plant growth and development, deficiencies can reduce plant growth and development. About 74 to 80% of the P applied to the soil gets fixed in the soil by forming complexes with Ca, Fe or Al and is thus not available to the plants. Though soil possesses total P in the form of organic and inorganic compounds, most of them remain unavailable to the plants. Phosphate solubilising microbes (PSMs) are a group of beneficial microorganisms capable of solubilising inorganic insoluble phosphorus compounds to soluble P form that can easily be

assimilated by plants. PSM provides an ecofriendly and economically sound approach to overcome the P scarcity and its subsequent uptake by plants. Several studies reported that the use of PSM enhanced growth, yield, and quality of many pulse crops like chickpea, pigeonpea, mungbean and groundnut. Adequate supply of P helps in seed formation and early maturation of legume crops. It causes early ripening and stimulates young plants to produce deeper and abundant roots. *Pseudomonas striata*, *Bacillus megaterium*, *Bacillus polymyxa* and *Bacillus circulans*, *Aspergillus awamori*, *Aspergillus niger* are some of the efficient P- solubilizing microorganisms reported from India. There are substantial deposits of cheaper low grade rock phosphate (RP) in many countries of the world. Hence direct use of such RP could minimize pollution and decrease the cost of chemical treatment. Amendment of RP along with inoculation of P solubilising microorganism has been shown to be a promising alternative to chemical fertilizer application.

Potassium is an essential macronutrient required by crops. In India, 21% districts are low, 51% are medium and 28% are high in available potash due to excessive use of high yielding varieties without replenishing it and "Luxury consumption" behaviour of this macronutrient. However, there are considerable amounts of insoluble K reserves in many soils, most of which exists in alumino-silicate minerals from which K cannot be absorbed directly by plants. K solubilizing bacteria can be applied to pulse crops and can provide 10-15 kg K/ha.

Zinc is one of the eight essential trace elements or micronutrients required for the normal healthy growth and reproduction of crop plants and are required in relatively small concentrations in plant tissues (5–100 mg/kg). Zn deficiency is well reported in the soils in many parts of India. Zinc solubilising bacteria play crucial role in dissolution or insoluble source of zinc through secretion of organic acids and other metabolites. When applied to soil, it converts insoluble form of Zn to soluble form and make it available to the plant. Inoculation of Zn solubilizer helps to augment 2 to 5 kg Zn ha^{-1}. It helps in fortification of Zn in the grains.

In general, sulphur is one of the essential and indispensable nutrients for plant growth and metabolism. Naturally, sulphur is oxidized into the soil by sulphur-oxidizing bacteria promoting S uptake and plant health. Sulphur nutrition is important as it influences different metabolic pathways as a structural component of many secondary metabolites, vitamins, amino acids and enzymes. Besides influencing plant growth, the process of nitrogen fixation and nodulation is hampered due to sulphur deficiency in soil. The sulphur-containing amino acids cysteine, cysteine, and methionine are generally deficient in pulses and the adoption of chemical fertilizers is mainly responsible for the pigeon pea's capacity to fulfill the S requirement Inoculation of SOB has been reported to enhance the growth and yield of different crop plants such as groundnut by 11%. There are few reports on the coinoculation effects of *Rhizobium* and sulphur oxidizing bacteria on growth and yield of legumes. For leguminous crops, inoculation of SOB exhibit significant influence on nodulation, sulphur upake, and yield. Increased uptake of N, P and K has been recorded in pigeon pea due to sulphur nutrition. In cowpea, coinoculation of specific root nodule bacteria and SOB significantly enhanced the dry

biomass and uptake of different minerals in particular N, P, K and S. Co inoculation of SOB and *Rhizobium* enhanced the pod yield of groundnut. In another study, co-inoculation of *Thiobacillus* sp. with *Rhizobium* strain significantly enhanced the nodule number, nodule dry weight and plant biomass under field conditions. Inoculation of SOB increased the available S in soil from 7.4 to 8.43 kg ha^{-1}.

Plant diseases prevent the cultivation and growth of plants or may attack the grown plants, destroy parts or all of the plants, and reduce their produce before they can be harvested or consumed. It has been estimated that 14.1% of the crop losses are caused by the plant diseases. Use of fungicides, agricultural practices and developing resistant varieties are the major options for the management of the plant diseases. Microorganisms can be exploited and used for the ecological management of the plant diseases and soil health. Most of the work on biological or microbial control of plant diseases has focused on soil borne diseases. However, seed-borne as well as air borne diseases have also caught attention of the scientist. The microbes used are various types of bacteria (*Psuedomonas and Bacillus*) and fungi (*Trichoderma* and *Gliocladium*).

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Contribution of pulses to food and nutritional security through organic farming

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Pulses are one of the important food crops globally due to their higher protein content. The protein content of pulses, averaging about 20 to 25%, is higher than cereals, which average 5 to 10%. In addition, pulses contain other essential nutrients such as calcium, iron, and lysine that help the body fight vitamin and mineral deficiencies and disease. As on the consumer's plate, so too in the production system: pulses on average occupy only about 10 to 15% of the arable land area but contribute significantly to the value of agricultural production due to their higher prices. They are a key ingredient in dishes and cuisines globally: hummus in the Mediterranean; baked beans in English diets, or dal in south Asian cuisine. In many countries, pulses are also a part of the cultural heritage. For instance, in Nepal, Kwati, a soup made with nine varieties of pulses, is consumed during major festivals and is a central element in the diets of expectant mothers. Pulses do not include crops that are harvested green (such as green peas or green beans), or those used mainly for oil extraction or sowing purposes. Pulses are an important source of protein, especially for vegetarians or for people who do not get enough protein by eating meat, fish, or dairy. Furthermore, pulses are a healthy choice for meat-eaters, helping cut off excess fat from diets, and containing zero cholesterol. They are also a good source of dietary fibre, vitamins, and minerals, especially iron and zinc. In terms of gram-for-gram nutritional value, pulses are also far cheaper than meats or other sources of protein, offering an economical alternative. The nitrogen-fixing properties of pulses improve soil fertility, increasing and extending the productivity of the farmland. In many regions, farmers plant legumes along with other crops, a practice known as intercropping, to improve yield and promote soil biodiversity. There appears to be a widely prevalent impression, particularly among the developed countries, that there are people and nations who do not know the "incredible properties" of pulses, and believe "that their nutritional value is generally not recognized and their consumption is frequently under-appreciated" (FAO, 2016). Such a situation may be large because pulses in farming and food are essentially a third-world phenomenon. Almost 90% of the area under pulses and about 80% of the output of pulses are in developing countries and among them sub-Saharan Africa and South Asia, where the world's most poor and undernourished live, and for whom pulses are a critical source of protein, together account for about two-thirds of the area, and one-half of the output of world's pulses (Joshi and Rao, 2016). Pulse crops are also known to fight off plant disease-causing pests, thereby reducing dependency on chemical fertilizers and pesticides. Pulses also produce a smaller carbon footprint, indirectly reducing greenhouse gas emissions, and contributing

to climate action, according to the United Nations. World Pulses Day, to be commemorated annually on 10 February was established in 2018 by the UN General Assembly, which recognized the importance of pulses as well as their contributions to sustainable food production. The General Assembly also highlighted the potential of pulses "to further the achievement of the 2030 Agenda for Sustainable Development", urging efforts to heighten public awareness of the nutritional benefits of eating a variety of food, including pulses. In 2021, approximately 88.97 million metric tons of pulses were produced worldwide, a decrease of just about one million metric tons from 2020 (Statista, 2023). Pulses and cereal grains have similar total carbohydrates, fat, niacin, riboflavin, thiamine, and vitamin B_6 contents. However, pulses have higher protein, folate, iron, magnesium, potassium, and zinc content that cereals.

Pulses contain approximately 21–25% protein; however have limited amount of essential amino acids such as methionine, tryptophan, and cystine (Tiwari and Singh, 2012). The protein content and amino acid composition vary with the variety, germination, environment and application of fertilizers. The protein content in pulses is almost double than that found in cereals. Pulse proteins were classified into two major fractions *viz.* albumin and globulin. Globulins are the major storage proteins in pulse seeds constituting 35–72% of total protein and the remaining protein fraction mainly consists of albumins. Globulin proteins have a higher amount of glutamine aspartic acid, arginine, and lysine (Dahl et al., 2012). The carbohydrate content in pulses is 60–65% and starch constitutes the major fraction of the carbohydrates. Pulse starch consists of amylose and amylopectin, and wide variation in amylose content in pulse starches has been reported (Tiwari and Singh, 2012). Starches from various pulses have different physicochemical, pasting, and technological properties. Global per capita consumption of pulses started to decline in the 1960s. Slow growth in yields and the resulting rise in prices weakened demand. Furthermore, income growth and urbanization shifted preferences away from pulses as human diets became richer in animal proteins, sugar, and fats. Nonetheless, pulses have remained an important source of protein in developing countries and average global per capita consumption increased to about 8 kg/year by today. This growth was mainly driven by income gains in countries where pulses are an important source of protein, most of all India, where vegetarians account for about 30% of the population (OECD/FAO, 2020)

India is by far the largest producer of pulses accounting for about 25% of global production during the past decade. Canada (8%) and the European Union (4%) are the next largest producing countries. The Asian market accounts for more than half of all consumption, but only about 40% of the production, making it the most significant import destination. About 20% of global production is traded internationally and Canada (40% of global trade) is the by far largest exporter and India is the largest importer (30% of global trade). Africa has further expanded its production and consumption during the past decade, remaining largely self-sufficient. In 2019, the global pulses market reached a volume of 88 Mt, after an average annual growth of 2.8% p.a. during the previous decade led by Asia and Africa. This recognition is driven as part of the effort to feed the global population in an environmentally sustainable way. Pulses are protein and fiber-rich food grown as they are adapted

to semi-arid conditions and can tolerate drought stress. Daal (pulses) global consumption is currently rising at a rate of about 9% annually (Sohaib and Jamil, 2017). Pulses are an important group of crops, which is also responsible for yielding large financial gains by amounting to a large part of the exports. India is the largest producer of pulses in the world. The country has exported 410,375.89 metric tonnes (MT) of pulses to the world for the worth of Rs. 2,834.23 Crores Millions during the year 2021-22 (apeda.gov.in).

Pulse production is highly concentrated. On a global scale, beans represent the largest percentage of global pulse production (46%), followed by peas (26%), chickpeas (21%), and lentils (10%) (Pulse Canada, 2017). Currently, India is the largest importer of beans, peas, and lentils: a country where pulses are an important source of protein for a largely vegetarian population (FAO, 2016). Canada is the largest exporter of pulses, having developed a multi-billion-dollar pulse and special crops industry, followed by Australia, Myanmar, the United States, and China (FAO, 2016). Pulses encompass varieties of beans and peas usually sold dried as well as chickpeas, lentils, lupines and many more. Numbers by the FAO show that most pulses per capita are consumed in African countries, with Niger, Rwanda and Tanzania eating some of the highest daily rations. While the consumption of a high level of pulses often goes together with poverty or a lack of access to resources, regional preferences also play a role. Cuba was among the biggest consumers at 184 calories from pulses per day and capita - about the same as consumption in Haiti. Brazilians love for traditional bean dish feijoada showed in the ranking that has every Brazilian consuming 125 kcal of pulses per day. Mexicans consumed 106 kcal per capita while Indians, who often favor vegetarian fare in the form of lentil or chickpea dishes - consumed 147 kcal a day. The celebration of World Pulses Day' is an opportunity to heighten public awareness of the nutritional benefits of pulses and their contribution to sustainable food systems.

Organic farming uses nature as a model for the agricultural system

Organic Agriculture is a comprehensive agricultural production system that promotes and enhances agro-ecosystem health by sustaining the health of soils, the environment and people. It includes ecological processes, biodiversity, biological cycles, and soil biological activity. Organic farming basically combines the traditional methods of farming with the modern & innovative approach to promote non-hazardous farming techniques ensuring a healthy environment and nutrient-rich crops. An organic agricultural system consumes less energy than conventional farming methods and produces more biomass per unit of energy consumed. It includes only the use of organic additives like animal manures, organic waste, and biofertilizers. Organic farming can be effectively used to grow many vegetables & cash crops like soybeans, cotton, sugarcane, etc. Even pulses are being grown successfully through organic farming to ensure their maximum nutrients and better health of the soil. Pulse crops play a significant role in organic agriculture offering some epoch-making benefits viz. as they are able to free soil-bound phosphorous which is very important for the nutrition of plants and food we eat. Organic farming includes crop rotation, intercropping, cover

crops, ley farming, etc., and pulses can be efficiently used for all of the above. Due to their root structures, they offer efficient underground utilization of the soil. With the use of organic fertilizers for pulses in organic farming, there is no further need of using any kind of chemical fertilizers that can be harmful to the soil as well as the crops.

Pulse Production Under Organic Management

In organic farms, pulses offer a great deal of potential to diversify cropping patterns. Pulses increase soil fertility by fixing nitrogen and liberating phosphorus in organic production systems. Due to the residual nitrogen provided by the previous pulse crop, following cereal production and crude protein content in grains/seeds can therefore be enhanced in pulse-cereal crop rotations. Pulses improve soil structure, microbial activity, and water-retention capacity while lowering water erosion. They also assist to increase organic matter and microbial biomass in the soil. Leguminous crop rotations allow for ongoing production on the same plot of land in the future. Crop rotations are crucial in organic farming. Pulses can be used in organic systems in a variety of ways, including rotation, intercropping, ley farming, and as a cover crop. Legumes must occupy at least 30% of the total cropping area in order for organic production systems to achieve the full yield potential of crops at any given moment (Babu *et al.,* 2015). In NER, the use of inorganic fertilizers and chemicals is minimal, and there is very little yield difference between inorganic and organic production techniques. It has been reported that organic pea and lentil farming under NT in lowland rice fallow is a successful business in mid-altitude Meghalaya (Das *et al.,* 2014).

The basic reasons for the adoption of organically grown pulses are: (Avasthe *et al.,* 2016)

a. Most of the pulses-growing areas are marginal and rainfed, hence offer opportunities to grow under organic management condition.

b. Low requirement of nitrogen (as nitrogen-fixer) requires lesser quantities of bulky organic nutrient sources.

c. Traditional farming systems with innovative farming techniques.

d. The rainfed tribal, north-east and hilly regions of the country where negligible chemicals are used in agriculture, have been practicing subsistence agriculture for a long period.

e. Most of the north-eastern hilly areas are organic by default, utilizing very low chemicals for the cultivation of crops.

f. Soil and climatic conditions in drylands are well suited to organic agriculture. These marginal lands, with their marginal soils, do not respond well to intensive farming practices. These are actually better suited to low-input farming systems that make ample use of biodiversity.

g. Addition of organic matter will not only improve the physical condition of these dryland soils, but also greatly improve their ability to supply balanced plant nutrients. In drylands, there is an

over-exploitation of natural resources mainly because of inappropriate production-enhancing technologies.

h. Excessive groundwater pumping has drastically decreased the groundwater table in tube-well irrigated areas. In many locations of intensive-input agriculture systems, soil fertility is decreasing and certain major pests are becoming resistant to synthetic pesticides.

Need for Organic Pulse Production

The organic pulses market is at a nascent stage but offers significant growth opportunities due to an increase in consumer preference towards organic foods coupled with government support and initiatives over the past couple of years.

The following highlights key facts about the organic pulse market:

Growing demand for organic pulses from India as it produces 30–35% of the world's pulse crop, with a domestic consumption rate of 24 million tonnes per year. Currently, India consumes around 0.5 million tonne of organic pulses annually, but this quantity will likely increase in the future because of rising consumer awareness and changing consumption patterns.

Substantial increase in the production area of organic pulses under cultivation for organic pulses increased significantly over previous years as more farmers adopted organic farming practices to maximize their profits. The area under organic cultivation is expected to grow to meet the growing demand for organic food products globally.

Profitability of organic pulses farming has been increasing significantly over the last decade as more farmers adopted this practice. The profit margins for producing organically grown pulses is huge compared to conventional pulse farming. Organic food products have always commanded a price premium and this is a major reason why farmers have switched to organic pulse farming.

Higher nutritional value in organic pulses as they do not contain traces of harmful chemicals and toxins that can affect the quality of the product. In addition to this, they contain more vitamins and minerals as compared to their conventional counterparts.

Consumers prefer to buy organic pulses as compared to their conventional counterparts. The reason for this preference is that organic pulses are free from all kinds of chemicals and toxins that can severely damage human health.

The rapid growth of the pulses market include rapid urbanization and rising disposable incomes among consumers in India. In addition, increasing awareness about health benefits associated with the consumption of pulses is anticipated to boost demand for organically grown pulses over the forecast period.

Pulses importing countries are importing pulses in huge amounts. The main importing countries are Canada, the USA, China, the Philippines, UAE, Turkey, and many more. India is also importing

pulses in large quantities. The reason behind this import is that the production of pulses is not enough to fulfill the demand of the country. Hence, it needs to import from other countries having good production. Among the above countries, the United States is the world's largest importer of pulses, with a record 873,964 metric tonnes (MT) of pulse imports in the 2017/18 marketing year, up 83% from the previous year. Most US pulse imports are yellow peas, which are used for feed use and processing into split-pea soup and other products.

The organic pulses market is expected to experience a CAGR of 5.6% during the analysis period 2016–2022. There are several points outlined in the organic pulses report that can help you understand the future market trend better. So, we would conclude that the organic pulses industry is growing rapidly.

Conclusion

Organic agriculture offers the most sustainable solution for developing the agriculture sector and provides food security with the least negative environmental impacts. Along with providing premium prices to the nation's resource-poor farmers, it also offers solutions for good rural development, healthy food, and employment possibilities. To lower the risk for the nation's resource-poor farmers, it is vital to describe the numerous methods for cultivating pulses under organic conditions. A strong policy is necessary for the entire framework of the systems approach, including the inclusion of short-duration pulse variety as inter- and/or catch-crops, particularly in fallow areas, and the creation of several disease- and pest-resistant and high biological N-fixing varieties. To prepare the farmers for producing organic pulses, it is necessary to coordinate research, extension, and farmer efforts to support farmers' participation in research and broad public awareness campaigns. There is a need for crop-specific approaches that should be used in the overall framework of the systems approach to increase the area, production, and productivity of pulses in the region.

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Session: Enhancing the Crop Produce

Pulses-climate smart crops for cropping systems intensification and resource conservation

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Food legumes/pulse crops have an important role in system productivity enhancement, C-sequestration and improving the sustainability of major cereal based cropping systems through crop diversification and system intensification. Given the unique characteristics of deep root system, higher leaf fall, biological nitrogen fixation, and release of root exudates, pulses offer the potential option for improving soil health and ecosystem restoration. Presently, pulses are increasingly being advocated for diversifying cereal-cereal rotation with the objectives like minimizing the use of declining natural resources, improving soil quality, and maintaining the sustainability for long-term. Research and development on understanding on climate resilient agriculture will pave the way of ecological sustainability. Over the past few years, a range of institutions have endorsed that pulse crops are integral component of climate resilient agriculture and sustainable intensification.

Inclusion of pulses in agricultural production systems can be a key to increasing resilience to climate change. Pulses are climate smart crops as they simultaneously adapt to climate change and contribute towards mitigating its effects. It is estimated that globally, about 190 m ha of pulses contribute to 5-7 mt of nitrogen in soils (FAO, 2016). As pulses can fix their own nitrogen in the soil, they need less fertilizers (organic and synthetic), and in this way, they play a part in reducing greenhouse gas emissions. Further, multiple cropping systems, such as intercropping or crop rotations with pulses have a higher soil C-sequestration potential than monocrop systems. At present, short duration and resistance to multiple biotic and abiotic stresses tolerant varieties are available which can fit well in the existing cropping systems for diversification or intensification.

Pulses in agricultural production systems

Crop diversification/intensification

The lack of crop diversity is one of the fundamental causes for several soil, environment, and pest problems in agricultural production systems. In order to address the negative issues associated with continuous cereal-based systems, the diversification/intensification of conventional cropping systems could be a strategic option in achieving the production sustainability. Endowed with the inherent potential of deep root system, BNF, and most importantly complementary with cereals and other non-legume crops, grain legumes could essentially serve a key role in crop diversification/ intensification in different production systems. In long-term studies at ICAR-IIPR, Kanpur revealed

that inclusion of grain legumes like mungbean and chickpea in conventional rice/maize-wheat system of subtropical Indo-Gangetic plains (IGP) can improve soil health and production sustainability.

In the North Western India, the continuous practice intensively irrigated rice-wheat cropping system led to over exhaustion of ground water, developed secondary salinization, and deteriorated the soil physical conditions, which eventually made the system unsustainable and less productive over the years. To cope up with the situation short-duration pigeonpea are now being advocated in place of rice for this region to curtail the demand for irrigation water. Further, the mungbean cultivation in summer fallows of in this region offers an immense scope to practice 'ecologically intensive' cropping system.

Resource conservation

- **N-fixation/economy**: Nitrogen is the most imperative constraining elements for development of plants and yield of crops. Pulses fix 30-150 kg N/ha depending on rhizobial population, host crop, management level and ecological conditions. Soil determinants, for example, temperature, moisture and pH further decide the N-fixing limit of pulse crops. The amount of N-released by the pulse crops in the soil is adequate to make desired yield level of succeeding non-leguminous crops.
- **Nutrient recycling**: Due to its intrinsic nature of N-fixation, the N-sparing and synergistic effects of pulses are well recognized. The N-fixation by pulses enables them to meet the large proportion of their N-requirement and also helps in economizing N in non-pulse crops. Pulses can leave 18-70 kg N/ha in soil and thus considerable quantity of N can be saved in subsequent crops. The deep root systems of pulses are helping to recycle the nutrients from deeper soil layer and the decomposition of roots adds to soil C & N. Further, pulses help to solubilize the soil fixed-P and hence increased their availability.
- **Water economy**: Water requirement of pulses is lower than cereals. Further, due to deep root system, pulses are able to extract moisture from deeper soil layer thereby having ability to thrive well under rainfed situation. Thus, pulses in cropping systems could substantially reduce the irrigation water and hence reduce the production.
- **Weed smothering**: inclusion of pulses in cropping systems is one of the strategies for ecological weed management. Pulses can suppress the weeds due to breaking the prevailing crop ecology for particular weeds, act as cover crops, intercrops and through allelochemicals released after decomposition of pulse crop residues.
- Minimizes tillage operations

Ecosystem services

Inclusion of pulses in cropping systems curtails the N-fertilizers application, and thus reduces energy use and GHGs emission. Further, pulses minimize the use of fossil energy as well as reduce

the N-losses. Due to biological fixation of N, pulses have positive impacts on the ecologies. The low C:N ratio of pulses residues supports to retain more C & N in soil and hence improves soil quality. In addition, inclusion of short duration pulses during hot summer reduces C-loss from soil and enhances the C-sequestration.

Thus, inclusion of pulses in cereal dominating systems has immense value in conserving resources and enhancing productivity, profitability and sustainability of agricultural production system under changing climate.

Session: Nutri-Smart Pulses and Data-driven Decision Making

Breeding Biofortified Pulses for human health: A high-throughput phenotyping platform for quantifying nutritional traits

Dil Thavarajah, Professor

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Millions of global populations are suffering from diet-related malnutrition and obesity. Feeding the billions of people living on this planet by 2050 requires protein- and micronutrient-rich foods. In the late 1960s, the "Green Revolution" increased the production of cereals to combat global hunger. Today, millions of people worldwide suffer from obesity, overweight, and micronutrient malnutrition. Health experts are now recommending a second revolution—a "*greener*" revolution—to provide food and more nutritious foods such as *lentils, field peas, and chickpeas*. Nutritional breeding is expensive and time-consuming due to chemical phenotyping. Fourier-transform mid-infrared (FT-MIR) spectroscopy is a high-throughput, cost-effective method to quantify nutritional traits, total protein, and sulfur-containing amino acid (SAA) concentrations in plant matter. Clemson University has developed a platform to accelerate pulse biofortification using FT-MIR tools to assist breeding programs to develop pulse cultivars enriched with protein quality, prebiotic carbohydrates, and micronutrients. Models for the total protein concentration of chickpea (calibration root mean square error (RMSE) = 0.093, R^2 = 0.941, prediction RMSE = 0.103), dry pea (calibration RMSE = 0.096, R^2 = 0.845, prediction RMSE = 0.093), and lentil (calibration RMSE = 0.131, R^2 = 0.845, prediction RMSE = 0.114) utilized IR (infrared) regions associated with protein structures, namely amide bands A, I, and II. In sulfur-related models for lentil total SAA (calibration RMSE = 0.0136, R^2 = 0.827, prediction RMSE = 0.0224) and methionine (calibration RMSE = 0.0075, R^2 = 0.815, prediction RMSE = 0.0145) models utilized the C-S and S-CH_3 stretching and bending bands. This talk will summarize the positive experience of the FT-MIR platform for organic pulse breeding at Clemson University to develop protein enhance pulse cultivars.

Session: Nutri-Smart Pulses and Data-driven Decision Making

Nutrigenomics in Pulses : Way Forward

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Nutrigenomics is a rapidly evolving field that examines the relationship between nutrition, diet and the genome. It is the study of how nutrition interacts with the genetic code to affect gene expression and metabolism, with the aim of improving health and disease prevention. Nutrigenomics expands on the three omics disciplines: transcriptomic, proteomics and metabolomics. These disciplines allow us to investigate the effects of dietary components on gene expression and metabolism. Furthermore, nutrigenomics has been utilised to explore the individual variations in response to dietary components and how they alter the risk of developing chronic illnesses such as obesity, diabetes and cardiovascular disease. Additionally, nutrigenomics can be used to develop tailored dietary plans and nutritional therapies, which could help individuals to better manage their health and wellbeing. Personalized nutrition is an extension of nutrigenomics, a field of study that seeks to identify the impact of diet on individuals based on their unique genetic makeup and lifestyle. This approach is based on the idea that certain diets are better suited to certain individuals and that customizing dietary recommendations to an individual's genetic makeup and lifestyle can lead to improved health outcomes. Advances in gut microflora research have provided insight into the important role gut flora plays in human health, from digestion and immunity to mental health and chronic diseases. Through nutrigenomic testing, personalized nutrition is able to provide tailored dietary advice that can be used to maintain health and prevent disease. The potential of personalized nutrition to revolutionize the way people think about their diet and health is immense. Our research group is exploring the use of nutrigenomics to identify the health effects of various diets on animal models, including those related to obesity, diabetes, and prebiotic potential. Additionally, we are investigating ways to use bioactive components of various foods to identify universal and individual health benefits. This talk will provide an overview of the basics and applications of this rapidly emerging field.

Session: Nutri-smart Pulses and Data-driven Decision Making

Plant based food and smart proteins from pulses

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'Smart protein' (also known as 'alternative protein') are defined as products, which can reliably and predictably substitute the consumption of animal-derived meat, eggs, and dairy, because they perfectly replicate the sensory and cultural experience for consumers and offer several advantages in the supply chain for producers. Plant-based foods are one of the three categories of smart protein products, which are made from plants and can be consumed as alternatives to animal-based counterparts. These include plant-based meat, seafood, eggs, and dairy analogues. Owing to their inherently high protein content, pulses are the most promising ingredients for plant-based foods. High protein content is central to formulating perfect analogues to animal-based food products. Not limited to the protein quantity, the composition of pulse protein comprising globulins and albumins render them an apt ingredient for plant-based foods as they naturally contain the building blocks required to make the meat, dairy and egg alternatives. The functional properties of pulse proteins (water holding capacity, oil absorption capacity, emulsification, gelation, foaming) impart the right texture, taste and appearance to the plant-based foods. Due to their sustainability and ability to provide a secure global food supply, pulses open up exciting opportunities in improving the global consumption trend of plant-based foods. In turn, the increasing demand for smart protein products is creating new market opportunities for pulses and pulse-based ingredients.

Relying upon pulses as a source of alternative protein can improve the economy of developing countries that have the potential to become big players in the plant-based meat sector. This is especially relevant to India as the global leader in the production, consumption and import of pulses. As an agriculture-based economy and attributed to the continuous industrial advancements, India can potentially transform as the manufacturing hub for smart proteins and pulses are synonymous with this development. Strikingly, a 2022 research work has demonstrated the potential of proteins derived from Indian pulses such as green gram, horse gram and cowpea protein as sustainable ingredients for plant protein-based meat products. Currently, peas are the staple ingredients for the plant-based meat industry owing to their high nutrition-to-cost ratio. Leading global manufacturers of plant-based egg and meat products are using mung beans and yellow pea protein. The recent focus on indigenous crops as smart protein sources for plant-based meat applications is justified by many reasons. Mainly, cultivation of pulses is associated with lower freshwater footprint compared to animal agriculture. The water footprint per gram of protein for milk, eggs and chicken meat is 1.5 times greater relative to pulses. For 1 gram of protein, beef produces 20 times more greenhouse gas emissions than beans. More appropriately, the Good Food Institute (GFI) India's *Indigenous*

Crops Initiative aims at working across the pulse value chain and fostering research, entrepreneurship, and infrastructure development for pulse applications in the smart protein industry.

Future research opportunities pertaining to pulse-based smart protein foods span across different stages of their value chain that involve enhancing the yield and functionality of pulse proteins and transforming them into plant-based meat products. These include innovations in developing novel technologies for: (1) primary processing of pulses (dehulling, milling); (2) extraction and preparation of protein isolate/concentrate from the pulses (ex. Air classification; ultrafiltration); and (3) processing them into products that mimic the fibrous structure, cooking characteristics, texture and mouth feel of animal-derived meat products (ex. Extrusion, 3D printing, shear cell technology). With the continuous research and innovation in the Indian food processing sector, the future looks encouraging for plant-based meat products made using pulses. Consumer studies have revealed that around 63% of Indians would prefer to try plant-based meat and the unique advantages of pulses such as immunity and digestive health are expected to enhance the market opportunity of products containing pulse-based ingredients. Thus, India has the opportunity to emerge as the forerunner in nurturing product innovation in pulses. Every stakeholder in this pulse-based smart protein value chain, be it farmers, food distributors, processors, marketers, retailers, or foodservice providers, have important roles to play in inculcating pulse-based smart protein products as a nutritious, delicious, and sustainable part of the Indian diet.

Session: Nutri-Smart Pulses and Data-driven Decision Making

Enhancing farm income through storage and processing of pulses

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Indian farming is going through a vulnerable phase. Though 60% of population still depending upon agriculture and allied sectors in rural areas, but contribution of agriculture in country's GDP is just 20%. Since independence agricultural production and productivity has enhanced several manifolds, but at the cost of use of excessive chemicals, fertilizers and exploitation of ground water to cater the requirements of improved varieties, with special reference to cereals. Every effort is being made to make agriculture sustainable by adopting crop rotations and minimal usage of chemicals and fertilizers. Pulses with inherent nature of fixing the atmospheric nitrogen in root zone and survival on low inputs are the most suited crops in crop rotation. Shift towards organic and natural farming is taking place in big way, with apprehensions to match the demand of increasing population. Common perception is that by enhancing the production, the farm income can be increased, but often it is reverse. Doubling the production has chances to make the income half, instead of doubling that. Small land holdings and marginal farmers finding it difficult to generate sufficient income to support even small families. This is the main reason compelling people to leave agriculture and migrate to urban areas for livelihood. The low farm income distracts educated new generation from agriculture. Food being the preliminary requisite, probably this is right time to talk and do something concrete not only for sustainable agriculture but also about sustainable farmer. There is need to enhance farm income. The target can be achieved through several ways, namely, i) reducing cost of production, ii) increasing productivity and production, iii) storage and iv) processing and value addition.

Storage:

There was time when country was facing scarcity of foods. Thanks to the green revolution that country became self-sufficient in production of food grains. Then the focus shifted towards nutritional security. Now people want financial security and will continue agriculture when it is matching with their financial requirements. Pulses being good source of vegetarian protein will continue to be staple food for nutritional requirement. In early periods, storage and processing was done at domestic and cottage scales. With the installation of big processing units in urban areas, almost all the produce is supplied to the urban areas through vast network of aggregators, mandies and service providers. During production peaks farmers have to sell their produce at rates much

cheaper than minimum support prices. At one end farmer is market for inputs like chemicals, fertilizers, seeds, machineries etc., whereas on the other end they are supplier of cheap agricultural produce to the processing industries. In both ways monetary flow is away from rural areas, depriving rural population from quality urban life. Probably agriculture is the only industry which can provide food and income to all, provided it has to be carried out like industry. The job carried out by the middlemen need to be carried out by educated rural youth. Cleaning and grading the grains as per mandi requirement will fetch MSP to the produce. Pulses being rich in proteins, easily attract insects from the filed itself, which get carried to storage godowns. By adopting recommended storage practices, losses during storage can be minimized. Storage also enables farmers to release the grains as per their financial requirements when market is ready to fetch higher prices.

Processing and Value Addition:

Pulses are mostly consumed after dehusking and splitting, in form of dal. Dehusked cotyledons can safely be stored for longer duration as common pulse insect, bruchids, lay egg on grain surface. Pulse milling started from domestic level has become a full-fledged industry, third largest after wheat and rice milling. Premilling treatments are required to loosen the seed coat prior to milling. At cottage scale water soaking is the prevalent pretreatment, but in commercial scale milling oil and water application is most commonly adopted. Stone chakkies are used for domestic or cottage scale milling whereas abrasive carborundum rollers are used in commercial milling. Though abrasive rolls gives higher dehusking efficiency, but result into lesser dal recovery, as scouring of peripheral region of cotyledons takes place. Various research organizations have developed mini dal mill to process the whole grains at cottage or farm levels in rural areas. Thus, pulse milling can be a source of employment and income generation for rural youth. Income can further be increased by proper packaging of quality produce and it's branding. Pulses are consumed in form of various traditional cuisines and recipes. Each stage of value addition fetches the higher returns. Potential of milling byproduct of pulses, which is often utilized as low value cattle feed, have also been evaluated for food values. Being rich in proteins, phenols, antioxidants and fibers, the milling byproduct can be utilized for edible purposes and facilitate enhanced farm income.

Session: Modern Tools for Crop Improvement

Modern tools for mungbean crop improvement

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Mungbean is a warm season legume crop with short duration that fits well as rotation crop into various cropping systems. Preferred market types of mungbean vary across regions and destined use. Major breeding aims for mungbean are improving tolerance to abiotic stresses, resistance to pests and diseases, grain quality and increasing yield, while keeping the crop duration short.

Genomics assisted selection has proven merit in crop improvement. For a long time, genomic resources for marker-assisted selection were scarce for so-called minor crops like mungbean. But reduced costs for high throughput sequencing provided access to genomic resources, including whole genome sequences and high density marker systems, also for less researched legume crops such as mungbean.

The International Mungbean Improvement Network has generated multi-location evaluation data for a minicore collection of 300 accessions that represents the mungbean diversity available in the World Vegetable Center genebank collection, which currently comprises more than 10,000 accessions of this species. By combining this phenotypic information with genomic data, traits related to disease and pest resistance as well as quality traits have been mapped and markers for selection have been made available for the breeding community. For example, resistance to bruchids, an important storage pest of legume crops, was mapped to chromosome five of mungbean and markers for selecting resistant genotypes in breeding were validated. Furthermore, multilocation data were used to develop crop models to predict time to flowering of specific mungbean genotypes in response to changing temperatures.

More complex traits such as yield components or tolerance to various stresses involve multiple genes and mapping of these traits require large populations that are well phenotyped and densely genotyped. With a grant from the Illumina Agricultural Greater Good Initiative, the mungbean minicore collection and breeding materials were re-sequenced and about 200,000 SNPs were obtained. This marker resource was used for genome-wide association mapping of a large number of traits related to plant vigour, time to maturity, pod and seed quality traits, disease resistance, etc. For example, for mungbean yellow mosaic resistance, in addition to a locus on chromosome two associated with virus resistance at multiple locations, several location-specific resistance loci were mapped on chromosomes one, three nine and eleven in minicore accessions. The generated sequence information has also been used to assemble a mungbean pangenome. Pangenome construction adds presence-absence and copy number polymorphism information to sequence polymorphism data and thereby strongly improves trait mapping.

The introduction of non-destructive high throughput phenotyping methods is contributing quantitative data on traits that are difficult to access using classical phenotyping, such as biomass increase and information on plant vigour changes or progress of senescence over time. High throughput phenotyping of the minicore collection by 3D multispectral laser scanning in four wavelength channels showed genotype-specific growth curves with a few entries having very high vegetative growth rates at different seedling stages. Associations between biomass accumulation patterns at different stages and yield have been established. Green leaf index, representing the relation between the reflectance in the green channel compared to the red and blue channels was highly correlated with yield. The mungbean pangenome helps identifying genetic loci associated with these traits. Overall, access to phenomic data and genomic serves for developing genomic selection models for complex traits to increase breeding efficiency and selection accuracy in mungbean.

Session: Modern Tools for Crop Improvement

Utilizing integrated genomic approaches for dissecting the genetic and molecular basis of Seed Protein Content in chickpea (*Cicer arietinum* L)

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The seed protein content (SPC) is an important quality trait in chickpea and therefore the identification of major QTLs/genes governing the complex regulatory process would aid in the development of nutritionally enhanced chickpea varieties. Henceforth, the current study utilized the QTL-Seq approach to identify key genomic regions and genes responsible for the seed storage protein accumulation in chickpea. QTL-Seq analysis of bulked RILs from a mapping population (ICC4958 × ICC12299) contrasting for SPC identified two genomic regions (0.94 Mb on Linkage Group (LG)5 and 1.16 Mb on LG6) responsible for the seed protein trait in chickpea. Underlying these QTLs were three candidate genes that exhibited a significantly higher ÄSNP-index value. These genes were further validated in the 211 chickpea mini-core accessions that displayed a wide variation in their SPC content. Candidate gene-based association analysis revealed a tightly associated SNP affecting *ROP1 ENHANCER1* (*CaREN1*) underlying the genomic region on LG5 with a considerably higher PVE. This tightly SPC-associated SNP marker was converted into an allele-specific PCR-based marker that could be used for rapid screening of SPC for aiding in marker assisted breeding. RNAi-based downregulation of the candidate gene led to a significant reduction in the seed protein, thereby functionally validating the role of *CaREN1* in regulating the SPC trait in chickpea. The role of REN1 in chickpea SPC regulation was also illustrated using Affinity Purification-Mass Spectrometry analysis that revealed several Rab GTPases, ATP, Ca2+ binding chaperones and phosphopeptide binding proteins involved in folding and accumulation of seed storage proteins as putative interacting partners of REN1.

Session: Modern Tools for Crop Improvement

Traversing from Genomic Assisted Breeding to Genomic Selection towards Yield Resilience in Chickpea

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Chickpea saw an upward trend from 2016 where the declaration of international year of pulses catalpulted its production. The recent declaration during the pandemic by UNICEF for use of chickpea as a wholesome food for its richness in nutrients boosted its consumption too increasing further demand. The rising health awareness among people is expected to fuel the growth of the chickpeas market in the forecast period. Increasing cases of obesity, heart diseases, diabetes, and other chronic diseases are forcing people to choose healthy dietary options. Chickpeas, both canned and dried, have a low glycemic index, which helps to control blood sugar, cut cholesterol, and reduce the risk of cancer. Choline is a vitamin found in chickpeas that aids in the production of key molecules for memory, mood, muscular control, and other brain and nervous system functions. The global chickpeas market size grew from $13.93 billion in 2022 to $14.9 billion in 2023 at a compound annual growth rate (CAGR) of 7.0%. The chickpeas market size is expected to grow to $19.19 billion in 2027 at a CAGR of 6.5%. It is one of the major pulses cultivated and consumed in India. It is one of the oldest and most important sources of protein. After dry beans and peas, chickpea is the third most important pulse crop grown in the world. Chickpea accounts for 20% of the global pulse production.

Ensuring that the food production in the world is able to pace up with the burgeoning population, modern plant production technologies are the only way out. the wake of the enormous genomic advances, in chickpea and the development of a high-quality genome sequence a huge array of genomic tools and technologies have been developed in chickpea which otherwise was an genomic technology orphan crop. Simultaneouly with the advent of molecular maps and identification of a large number of market trait associations, many QTLs were identified for various traits.

GAB approaches have contributed to comprehensive characterization of allelic variation underlying important agronomic traits and their efficient incorporation in the germplasm enhancement and cultivar development processes. Development of chickpea varieties with resilience to changing climate is a challenge. Both abiotic and biotic stresses create a havoc in realising higher yields. Recent advances in genomics research has facilitated deployment of genomics tools for improving the elite varieties through genomics-assisted breeding (GAB). By following GAB approach, Ethiopia released a drought tolerant variety, called "Geletu" in 2019 (https://www.cgiar.org/news-events/news/first-ever-high-yielding-chickpea-variety-developed-using-marker-assisted-backcrossing-mabc-released-in-ethiopia/). The variety delivered the highest grain yield of 3822 kg/ha at Arsi Robe, Ethiopia, which translates into an yield advantage of 15% over the check variety 'Teketay' and 78% more than the local check. Similarly, India released drought tolerant Pusa Chickpea 10216 and FW resistant Super Annigeri 1 varieties in 2019 (https://icar.org.in/content/development-two-superior-chickpea-varieties-genomics-assisted-breeding). QTL hotspot from ICC4958 has now been introgressed into Pusa 32 (Pusa Chickepa 4005), DCP 92-3 (IPC L4-14), JG 16 (Pusa JG 16) using the MABC approach leading to the development of drought tolerant varieties. Similarly GAB has been used for pyramiding of wilt QTLs and two varieties Pusa Chickpea Manav and Shreda were developed.

In terms of translational genomics for agriculture, improved breeding lines have been developed for drought tolerance and disease resistance by using marker-assisted backcrossing (MABC) approach. For addressing complex traits such as yield under rainfed conditions that are generally governed by many small effect QTLs, MABC is not a very effective approach, whereas GS approach using genome-wide marker profile has been suggested as a potential breeding approach for developing superior lines to address such complex traits. In the GS approach, testing (prediction) population are not phenotyped but genotyped, and therefore breeding cycle time is reduced and genetic gain per unit time is enhanced. In plants, Bernardo and Yu (2007) were the first to show the utility of GS in terms of genetic gains as compared to marker assisted selection using simulated data. Since the seminal work of Meuwissen et al. (2001) on GS, a number of studies on assessing the prediction accuracy in different economically important crops, using different marker platforms and marker densities [including genotyping by sequencing, (GBS)] applying different parametric and non-parametric statistical models, have been published so far. Both, simulation and empirical studies have shown that GS has higher prediction accuracy than standard pedigree-based prediction, and most of the benefits of GS arise from obtaining accurate predictions at early stages of the breeding cycle (i.e., rapid cycling of selection). Choice of model, the size of the training population, the heritability of the trait, the span of linkage disequilibrium (LD), the marker density, and the strength of the genetic relationships between the training and validation populations, are some other majors factors known to affect genomic predictions. Majority of GS studies in crops had emphasis on estimation of prediction accuracy using simulated data and suggested up to 40% better efficiency than marker assisted selection. Based on the potential of GS for developing superior lines with

higher yield under rainfed conditions and enhancing the genetic gains ultimately in chickpea breeding, the present study was planned to identify the suitable GS models for predicting breeding values using genome wide markers on elite breeding lines in chickpea. The genomic selection technologies of identifying the superior parents for increasing breeding value (GEBV) has been initiated. It predicts breeding values of lines using genome-wide marker profiling and allows selection of lines prior to field-phenotyping, thereby shortening the breeding cycle if coupled with speed breeding or off-season advancement. A collection of 320 elite breeding lines was selected and phenotyped extensively for yield and yield related traits at two different locations (Delhi and Patancheru, India) under rainfed and irrigated conditions and genotyped. Later the advanced breeding lines from All India Testing were included in this base population. Phenotyping and genotyping data were used with six statistical GS models to estimate the prediction accuracies. GS models were tested for yield related traits *viz.,* seed yield,100 seed weight, days to 50% flowering and days to maturity. Prediction accuracy for the models tested varied from 0.138 (seed yield) to 0.912 (100 seed weight), whereas performance of models did not show any significant difference for estimating prediction accuracy within traits. Superior parents were selected on the basis of training of these models onto the test population. These were having higher GEBVs. The progeny are being genotyped for the next round of GS. Thus the chickpea breeding programmes in India are traversing from GAB to GS in partnerships.

Session: Revisiting the Roots

Multidimensional Impact of Pulses in Organic Farming

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Over the time, farmers have consciously and unconsciously manipulated the ecology of the soil by the addition or depletion of organic matter. During the green revolution era has been the major outbreak in Indian agriculture in increasing the food grain production. Soil organic reserves declined due to cereal cropping and frequent fallowing. Farming was rapidly mechanized and traditional "pulse-cereal" rotations were abandoned as relatively cheap nitrogen fertilizers became widely available and they appeared more efficient than legumes in increasing grain yields. The living components in soils require carbon as an energy source. These production changes have been detrimental to soil health and water quality, leading to an increase in plant diseases and other pest problems, all within a relatively short period of time (Pimental et al., 1991; Hoitink and Boehm, 1999). Pulses (Legume) plays a key role in improving and sustaining soil productivity on account of inherent capacity to fix atmospheric nitrogen and addition of huge amount of organic matter through roots and leaves fall. Pulses like lentil, chickpea, mungbean and blackgram may prove as ideal crops in agriculture. Continuous cultivation of cereal crops resulted in deterioration of soil, declining water tables, increasing insect pest and disease populations, and other environmental problems. Pulse crops with their unique ability of biological N2 fixation, leaf litter fall and deep root system may be a suitable option to sustain soil health. A major advantage of pulses is that they can fix atmospheric nitrogen with the help of rhizobia bacteria, thus minimizing the requirement for additional fertilizer inclusive nitrogen supplements.

Effect of pulses on soil properties and Resource Use Efficiency (RUE)

Pulses have long been recognized and valued as "soil building" crops. Growing pulses improves soil quality through their beneficial effects on soil biological, chemical and physical conditions. When properly managed, pulses benefits soil quality in the form of increasing soil organic matter, improving soil porosity, recycling nutrients, improving soil structure, decreasing soil pH, diversifying the microscopic life in the soil, and breaking disease buildup and weed problems. Apart from these, there are many other indicators which directly or indirectly related to soil quality and RUE can be used to explain advantages of pulses or pulse based system.

Improvement in soil quality

Pulses have taproots that open pathways deep into the soil which improve soil physical condition.

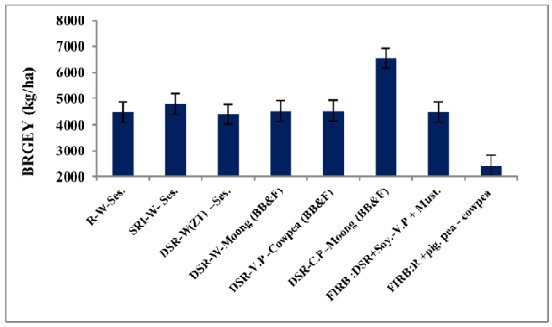
The improvements are mainly due to increase instable soil aggregates. The protein, glomalin released by roots of pulses and other plants, serves as "glue" that binds soil together into stable aggregates. This aggregate stability increases pore space and tilth, reducing both soil erodibility and crusting.

The organic farming research is going on at N. B. Crop Research Centre of Pantnagar since 2004-05 under the Network Project on Organic Farming funded by ICAR. The experimental soil was silty loam, medium in organic carbon (0.65%), available N (238 kg/ha), P (16.7 kg/ha), K (156 kg/ha) and high in available sulphur (29.3 kg/ha). *Sesbania* was incorporated as green manure prior to basmati rice only. For methane emission study, four treatments *viz.,* GM +VC, FYM + VC, SRI and chemical control were considered to quantify methane (CH_4) flux from rice field at different crop growth stages taken for study under randomized block design with three replications.

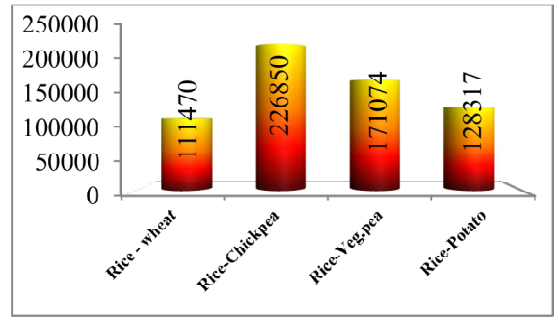
Result:

Among nutrient sources, use of Green manure (GM) + Vermicompost (VC) recorded higher dry matter production, crop growth rate as well as grain yield and system productivity of basmati rice as compared to other sources and chemical fertilizers. Among the different basmati rice crop establishment, system productivity in terms of basmati rice grain equivalent was observed higher in System of Rice Intensification (SRI) as compared to conventional planting with continuous flooding. Irrigation water applied efficiency can also be increased by adopting system of rice intensification and direct seeded rice establishment systems. Highest irrigation water use efficiency in direct seeded rice (DSR) was due to decreased number of irrigations as compared to conventional transplanting and SRI. Organic control and chemical control recorded least irrigation water use efficiency due to continuous flooding which are being adopted by the farmers. Initially methane (CH_4) emission was higher in organically fertilized plots as compared to chemical one. However, at later stages, not much variation was observed in CH_4 emission for different nutrient sources. Even with in organic system, less CH_4 was emitted from system of rice intensification field where water was maintained through alternate wetting and drying. Nitrous oxide emission and global warming potential hinger in inorganic fertilized plot as compared to organic. Bulk density of soil is decreasing under organic basmati rice based cropping system over ten years of continued crop cycles thereby decreasing the energy requirement. There has been a buildup of soil organic matter under organic farming system which is almost doubled after one decade of continuous organic farming as compared to chemical farming.

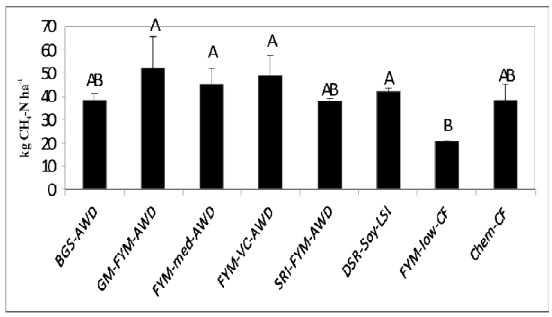
The soil quality benefits of pulses have been shown to be greater than the sum of their parts. The pulses attributes higher yield of associated cereals in combination or in rotation improved soil quality, addition of growth promoting substances, decreased disease and insect-pest pressure. Thus, inclusion of pulses in cereal based system may give the way for sustainable agriculture. Pulses can provide a multitude of benefits to both the soil and other crops grown in combination with them or following them in a rotation.



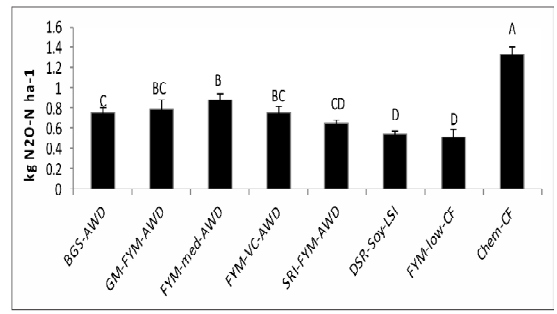
System Productivity kg/ha



Net Return kg/ha



Cumulative CH_4 emission



Cumulative N_2O emission



Vegetable pea and cowpea

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Session: Revisiting the Roots

Organic farming: harnessing traditional knowledge blended with science

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Increasing health consciousness and awareness on harmful effects of agrochemicals and environmental pollution is creating demand for chemical-free foods world-over. Consumers are becoming more health-conscious owing to the harmful effects caused by the presence of chemical pesticides in food products. According to a UN report, around 200,000 people die every year due to the toxic effects of pesticides on food products. This is causing consumers to shift their focus towards organic food products. The global organic food market grew from $259.06 billion in 2022 to $294.54 billion in 2023 at a compound annual growth rate (CAGR) of 13.7%.The organic food market is estimated to be about $512.01 billion in 2027 at a CAGR of 14.8%. India is one of the leading producer and exporter of organic products that includes cereals and pulses too. As per APEDA, the total volume of export of organic food products during 2021-22 was 460320.40 MT. The organic food export realization was around ₹ 5249.32 Crore (US$771.96 million). Organic products are exported to several countries including USA, European Union, Canada, Great Britain, Switzerland, Turkey, Australia, Ecuador, Korea Republic, Vietnam, Japan, etc. In terms of export value realization Processed foods including soya meal (61%) lead among the products followed by Oilseeds (12.85%), Cereals and millets (12.71%), Sugar (4.77%), Plantation crop products such as Tea & Coffee (2.16 %), Spices and condiments (1.72%), Pulses (1.1%) and others. Organic farming offers opportunity to developing country producers to cash upon the growing interest of consumers on organic food products. This is what emphasizes the importance of improving the productivity under organic production of cereals, fruits, pulses, spices, fiber, oilseeds etc.

The growing market for organic food products including for pulses underscores the need for improving the production and productivity of certified agricultural products which can be made available to domestic consumers and export markets. This is possible only when the traditional knowledge is effectively blended with modern science, especially when chemicals need to be substituted with natural ways and bio-inputs. At the moment, the alternatives to chemicals are not sufficient and effective enough to meet the requirement. While the need to increase food production for an increasing population is unquestionable, the focus should be not only on producing more food but also on producing better food. The research efforts need to be intensified to develop technologies which can effectively substitute chemicals like fertilizers, weedicides, and pesticides. At the same time, there is need to document, validate and popularize traditional knowledge with respect to crop

production. When there were no chemicals, farmers were still practicing agriculture with their conventional wisdom and knowledge acquired through trial & error and accumulated experience of generations. This knowledge can be utilized to help ease out chemicals from agricultural production.

Over the last 70 years, the level of vitamins and nutrients in food has drastically decreased, and it is estimated that 2 billion people worldwide suffer from lack of micronutrients, known as hidden hunger because it is difficult to detect. About 95 percent of our food nutrients come from soils, which have a natural capacity to provide nutrients to support crop growth. Soil health and fertility have a direct influence on the nutrient content of food crops. The lack of essential nutrients, including macro and micronutrients, leads to the underdevelopment of plants and a decrease in yield and in crop nutritional value. Efforts and investments focused on increasing plant nutrient uptake and balance, and ultimately, human and animal nutrition can be lost if soils are not healthy. On Earth, there are 92 naturally occurring chemical elements, 18 are essential to plants and 15 of them are supplied by soils. When soils are compacted, eroded, have their nutrient and soil organic matter (SOM) depleted, or have chemical toxicity issues due to contamination by pollutants, acids, or salts, they cannot produce food that contains the nutrients necessary for human health or even assimilate nutrients added by fertilizers application. This necessitates the focus on soil health, which can be ensured by following good soil management practices. The agronomic practices like crop rotation, fallow, flooding, deep ploughing, soil solarization-which involves a combination of physical and biological process, adjusting sowing/planting dates, irrigation, fertilization, sanitation tillage etc. Practicing good agronomic practices and paying attention to habitat management, including conserving and encouraging the spread of natural enemies can suppress and mitigate the damage created by pests. Crop rotations have been age-old traditional practices which are still promising and will continue to be important. In farming, these practices should be used more over the dependence on chemicals.

By developing efficient resource use and sustainable agronomic practices for crop-fertilization, irrigation and protection, a significant reduction in the demand for synthetic chemical fertilizers, fresh water and chemical pesticides in agriculture could be achieved without compromising yield and quality (Young et al, 2021). Application of soil-borne biocontrol agents (e.g., *Trichoderma, Beauveria, Bacillus, Pseudomonas*) may also help ensure plant protection against several diseases. Consequently, the use of chemical pesticides is significantly reduced, with potential benefits for beneficial microbes and the environment (Niu et al 2020 & Negi et al, 2021). Intercropping, organic agriculture and minimum- to no-tillage management are some of the most important sustainable agronomic practices, with applications that resulted in increased soil biodiversity and improved soil structure and health (Morugán-Coronado et al 2020). In case of pulses, N-fertilization can be effectively reduced via improved N-fixation through rhizobia inoculation to optimize crop performance and sustainable management of pulses.

In much of the farming world especially in developing countries, sowing of crops including pulses is still done following broadcast method, which leads to low productivity and hampers cultural operations. Farmers need to be educated and provided support for using seed drills for improving

productivity since it helps in distribution of seeds, placement of seeds at appropriate depths, better plant stand, and ease in performing cultural operations and improves drainage of excess water from fields. Many fruits of scientific advancements like introduction of high yielding cultivars with superior product qualities and increased tolerance to biotic and abiotic stresses, as well as application or/and encouragement of beneficial microorganisms (e.g., bacteria, algae, fungi) with the potential to increase nutrient and water uptake without compromising environment functions should also be considered as viable sustainable agronomic practices to improve plant performance and productivity (Alvares et al 2016, and Rai et al, 2020).

Finally, considering the high emphasis placed by Government of India on natural farming, the practices recommended under natural farming can be tried to see their efficacy in improving productivity. The components of natural farming *like Jeevamrit, beejamrit*, whapasa mulching etc are ancient techniques said to be sustainable (NITI Aayog, 2023, https://naturalfarming.niti.gov.in/components/). The universal principles of natural farming as propagate by NITI Aayog, need to be studied, understood and applied wherever applicable for improving the productivity without use of chemicals. For instance, *Beejamrit* is used for seeds, seedlings or any planting material. It is said to be effective in protecting young roots from fungus. *Beejamrit* is a fermented microbial solution, with loads of plant-beneficial microbes, and is applied as seed treatment. It is expected that the beneficial microbes would colonize the roots and leaves of the germinating seeds and help in the healthy growth of the plants. The research institutions including *Krishi Vigyan Kendras* are conducting trials on these techniques to see efficacies and once found efficacious may recommend for large scale adoption by farmers to replace agrochemicals.

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Session: Revisiting the Roots

Opportunity of Organic and Natural Farming in Pulses with Special Reference to North Eastern Region

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Off-late consumers' preferences are observed to be shifting towards diversified safe, hygiene & healthy food products and consciousness for environmental quality and ecosystem services are on rise. For achieving sustainable food-livelihood- environmental security, organic farming is gaining importance globally. The all India Network Project on Organic Farming recommended "towards organic" (integrated crop management) approach for intensive agricultural areas and "certified organic farming" with combination of tradition, innovation and science in the de-facto organic areas (hills) and rainfed/dry land regions. Studies also indicated that instead of individual crop based organic package of practices, farming system approach should be adopted with adequate emphasis on pulses, millets and livestock integration. India has a rich heritage of traditional environment friendly natural farming practices which are less resource intensive. Pulses are an integral part of our farming systems and inclusion of pulses in the system not only provides cheap source of protein but also contributes ~50-200 kg N/ha/year. The Government of India is also promoting natural farming and cultivation of pulses under the centrally sponsored scheme- *Paramparagat Krishi Vikas Yojana* (PKVY). Considering the potential of North Eastern Region (NER) in organic farming, the Ministry of Agriculture and Farmer Welfare, Government of India has been implementing various initiatives like **"**Mission Organic Value Chain Development for North Eastern Region (MOVCD)" to develop the North-East as an organic agricultural hub. With its proximity to south East Asian markets and home to various GI (Geographical Indicators) tags high value crops, the NER of India could emerge as a hub of agribusiness and entrepreneurship activities. The NER region is still deficient in pulses (74%) and scientific cultivation of pulses under organic and natural farming can play an important role in enhancing pulse production in the region and sustaining soil fertility. A diversity of pulses like rice bean (*Vigna umbellate*), rajmash/French bean (*Phaseolus vulgaris*), faba bean (*Vicia faba*), *sem* (*Dolichos lablab*), Cowpea (*Vigna unguiculata*) etc. are grown as component of traditional farming systems. The tree bean (*Parkia roxburghii*), rice bean (*Vigna umbellata*) and velbet bean (*Mucuna pruriens*) are also unique leguminous crops of the region. Pulses like perennial pigeon Pea (*Cajanus cajan*) are be grown in farm fences, pond dykes, field bunds etc. and soybean (*Glycine max*) & cowpea as mixed crop/intercrop with ginger/ maize. Leguminous hedge row species like *Crotialaria* sp, *Tephrosia* sp. etc. are also gown on terrace risers or in contour lines at an interval of 8 to 10 m for soil moisture conservation, improving

soil health and reducing soil erosion in steep slopes and provides a biological fencing to the farms. Since pulses fixes majority of their nitrogen demand and fits well within farming system, research and extension activities should be focused towards promotion of pulses under organic and natural farming in the NER. Such effort would enhance farmers' income and improve their livelihood in addition to promoting pulses production in the region which would certainly boost economy of the region in particular and country in general.

Session: Innovative Extension Approaches

Innovation in Transfer of Technologies for Enhancing Pulses Production in India

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India has made tremendous progress during last 10 years in terms of enhanced production and the country witnessed the "***Pulses Revolution***" recently. However, we are importing pulses (worth INR 10000 crores), particularly lentil and urdbean, to fulfill our domestic demand. Indian farmers grow 12-15 pulse crops in different parts of the country under varying agro-ecologies producing about 24-25 million tonnes of grains. It is worthwhile to mention that during 2021-22, Indian farmers are going to produce 27.69 million tonnes of pulses as per the fourth advance production estimates of the Government. of India (https://agricoop.nic.in/ sites/default/files/ Time% 20Series%20% 28English %29%20PDF.pdf.). Amongst the various pulse crops cultivated six of them viz., chickpea, pigeonpea, mungbean, urdbean lentil and pea are most common and have a sizable area under cultivation. The efforts in transfer of technology like organizing cluster frontline demonstrations, establishment of Seed-Hubs for quality seed production of newly released improved varieties, capacity development through trainings and organization of field days etc. created an environment for higher pulses production. Positive policy support from the Government of India in terms of increased import duty/tariffs on selected pulses, particularly on pea, quantitative restrictions on bulk import of pulses at cheaper rate, declaration of remunerative Minimum Support Price (MSP) well before commencement of sowing, market linkages, indicative purchase on remunerative MSP, support for micro-irrigation system for life saving irrigation, creation of Farmer Producer Organizations (FPOs), Self Help Groups (SHGs), proactive role played bydifferent Krishi Vigyan Kendra (KVKs) helped not only in sustaining production but also increased it further. Ninety seven KVKs contributed immensely in quality seed production and capacity building through Seed-Hubs which in turn ensured higher seed replacement rate in pulses. Increased adoption of quality seeds of high yielding varieties possessing diseases and insect resistance/tolerance; heat and drought tolerance; and varieties having farmers' and consumers'preferred traits besides integrated crop management practices ensured additional production of pulses to the tune of 9.35 million tonnes in 2021-22 over 2012-13 when total pulses production was 18.34 million tonnes. During the last 5 years (2017-18 to 2021-22) production (24.73 million tonnes) attained new heights and in 2021-22, 4th production estimates indicate a high time production (27.69 million tonnes) of pulses in India. In view of growing demand for protein for largely vegetarian population, there is big challenge not only to sustain current level of production but also to increase further to meet future demand.

It is also a fact that when pulses will be available at affordable price, the consumers' number will also increase leading to increase in domestic demand of the pulses in years to come. With the

availability of information technology, the time has come when we must train retailers involved in sale of agri-inputs as most of the farmers purchase these from local shops.Capacity building of farmers and other stakeholders on use of Agri-Drones for effective use of agro-chemicals and reduced cost of cultivation is going to be the major area for capacity building.Issuing of real time agro-advisories to targeted farmers for cultivation of crops using GIS, monitoring of crops' growth progression, deficiency of nutrients, abiotic stresses, diseases and insect pest incidence using artificial intelligence (AI), forewarning and forecasting using simulation models are going to be the future extension needs. Online information communication and technology based system having a pool of experts in agriculture and allied sciences i.e. 'Kisan Sarathi' is going to transform Indian agriculture very soon."

Session: Innovative Extension Approaches

Developing Ecosystems for Sustainable Legume Production

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Indian agriculture has seen a paradigm shift in the past seven decades after independence. From a state of food insufficiency to food surplus, from traditional farming to the use of high yielding varieties, from minimal input to intensive use of inputs, the farmers have come a long way. On one hand, the country has been successful in achieving food security, on the other it is far from providing nutritional security for its entire population.Pulses are high protein and as mentioned by Kumar et al (2016) they can fix atmospheric nitrogen, enables plants to utilize limited available moisture more efficiently. The opportunities innumerous with pulses having the prospect to be grown as a catch crop, cover crop, intercrop and in several crop rotations. In India, pulse productivity is much lower than other pulse producing countries. Many efforts have been made after independenceand with the success of the Technology Mission on Oilseeds (TMO) in 1986pulses were brought under it in 1991 to achieve a similar boost in production. However, the production remained almost constant at 14-15 Mt till 2014-15 and jumped to 25.72 Mt in the year 2020-21. Nonetheless, India is still not producing enough to meet the growing demands of the country. Business Line (2022) reported that India's pulses imports has been about 26.99 lakh tonnes (lt) during the financial year 2021-22 on lower domestic output and the Government's decision to keep imports open to ensure adequate supplies. Seemingly, in order to bring the imports to a minimal and raise the domestic production it is imperative to look into the problems impeding the agricultural growth. These are largely related to low productivity owing to the fragmented land, with resource poor famers having little access to latest technology or the resources to access them.

Agricultural advancement has kept pace with the need of the country but as Rai (2023) reiterated that there is no "technology fatigue"rather a "development fatigue". In a country where more than 70% farmers are small and marginal, are technology bereft, resource deprived, the need of the hour is to bring a paradigm shift in the approach and strategies. Given the opportunity farmers would be willing to change their practices and in such a scenario there is a need to build ecosystems as in any business – since at the root of it all, farming in India should look as a business enterprise and its problems need to be addressed in a similar fashion.

Ecosystems are in its very essence a concept assigned, attached and aligned to business. We need to move from the one way linear systems to have conglomerate based ecosystems that are managed at different platforms to cater to the needs of the all stakeholders' right from ensuring content, inputs, markets, partnerships and so on and so forth on hand. Ecosystem networks not only

need to be developed rather they need to be made available to the last farmer standing preserving sustainability and equity.

Legenvre et al (2022) pointed out that ecosystems were not established as a solid theoretical foundation before the years 2010s. These are distinct from industries, value chains or supply chainscharacterized by non-contractual forms of governance that brings together heterogeneous, but interdependent organizations. Recent conceptualization efforts present ecosystems as a governance mechanism where multilateral relationships cannot be reduced to a set of bilateral contracts (Autio and Thomas, 2018; Jacobides, Cennamo, & Gawer, 2018), and where non-contractual governance plays a fundamental role.

Basically the ecosystems operate in an environment that is a governance mechanism for dynamic business environments characterized by complex and rapidly evolving technical systems. It offers platforms, modular technical systems with a sizable degree of openness and its role is to offer contractual governance mechanism for access to platforms and their shared resource and non- contractual governance mechanism to attract large number of complementors within the ecosystem.

For instance in the legume seed ecosystem in order to ensure supply of good seeds to all farmers there are various players who need to be effectively mobilized in each region of the country. Right from the research organization that provide the seed and technical know- how of how to grow seeds; the seed producing companies (legume seed production majorly being in the public sector), employees who need to remain abreast with latest technologies and need skill and knowledge up gradation from time to time, the processors who are to be equipped with the processing, packaging and storage of the seeds maintaining the germination and quality, the transportation (Often neglected and transported like any other commodity, the equipment and machineries required to ensure the maintenance of thequality seed (sensors for detection of moisture, pest etc in warehouses). Similarly, such platforms need to be developed for each production, processing or marketing component and integrated in single ecosystem. Therefore, there is a need for strong linkages within and between each of these ecosystems that lacks today. For every aspect of the crop cycle it is imperative to identify the different stakeholders that will operate the ecosystems and that will thus need to be in place for production to be more remunerative and sustainable.

The onus of creating these platforms lies not only with the public sector but also with all the stakeholders and; custodians of development and progress of the country. In a largely vegetarian nation we need to stride forward in the direction of developing region based ecosystems to ensure the nutritional security of its population.

Session: Innovative Extension Approaches

Digital Extension Strategies for Future

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Digital transformation is taking place in Extension Advisory Services and organizations. While many extension organizations tried digital tools to bring incremental changes in efficiency of extension services, there is a need to increase the efforts many fold, perhaps with a full stack thinking.

Use of digital technology and appropriate implementation and investment strategies can solve diverse problems such as inadequate access to credit and information, pest infestation, crop wastage, poor price discovery, and yield forecasting etc. This is done through public and private mechanisms that rely on improving four central areas of agri-food systems: financing, production inputs, farming methods, and supply and distribution.

Extension organizations could greatly benefit from the growing number of advanced digital applications such as Artificial Intelligence, Machine Learning, Blockchain (DLTs), Unmanned Aerial Vehicles (drones), High precision remote sensing, proximity sensing devices, mobile (5G) and cloud computing etc.

In India, there's no shortage of agtech solutions deploying advanced digital solutions for increasing farmer productivity, reducing cost and opening access to larger markets. These digital innovations range from remote and proximity sensing tools to big data platforms — that can improve decision-making among farmers, suppliers and governments. Rising smartphone penetration and improving connectivity, along with improved data processing and analytics capabilities, offer us the opportunity to adapt and bring these improved solutions to smallholder farmers at a fraction of the cost of traditional extension methods.

The next generation farms and farmers are never going to be same, as we had dealt with in the past. The challenge is to contextualize the advanced digital tools such as artificial intelligence, machine learning, unmanned aerial vehicles, robotics, and internet of things. Are these just jargons? The future of digital extension could be a transformational (if not disruptive) factor in the agi-food systems, if proper strategies are in place. Accordingly, there is a need to work on structural and functional adjustments across extension organizations.

Let us talk only about the potential of mobile-based services. If 275-350 million farms gain access to time critical services, 250 million more tons of food could be produced. 20-65 million fewer tons of losses. Which is about 3-6% of total production/ market value, with substantial additional income to smallholder farmers. Precision farming technologies if extended properly will be of 1969 Billion USD proposition.

There is a potential to bring the digital dividend to the doorsteps of smallholder farmers. Empirical evidences show, with the multiplier effects of bundled services of productive capacities, market access, financial inclusion, we can increase the income to the extent of 30%, 37% and 18% respectively. For this extension organizations need to provide demand driven, personalized, accessible, affordable, applicable bundled services.

The scientific literature on digital agriculture has primarily focused on the technical aspects of applying these technologies for improving agricultural practices and productivity (Rutten et al., 2013; Wathes et al., 2008), as well as improving post-farmgate processes, such as postharvest quality monitoring in logistic process and real-time traceability (Wolfert et al., 2017). By now, there is a large body of predominantly natural and design science oriented literature on (potential) applications of digital technologies in agriculture. This is evidenced by an increasing number of review articles on topics such as precision farming, big data analysis, drones, artificial intelligence and robotics, 3D printing, artificial intelligence, IoT, and the transformative potential of these digital technologies for agricultural production systems, value chains and food systems.

The main functions of digital extension as evident from this literature are:

- sharing knowledge and experiences, and cross-learning among EAS providers, farmers and other actors, whether in the same or different location;
- improving access to information, knowledge, technologies and other innovations for EAS advisors (e.g. online access to statistics, research, information and up-to-date knowledge, mobile 'phones, monitoring and reporting systems) and for producers (e.g. call centres, access to information systems, applications and mobile 'phones, videos on agricultural practices, and exchange groups among farmers);
- providing timely and relevant information and advisory services; for market-oriented advisory services: easier and better marketing by producers, market information (prices, trader demand, etc.),
- facilitating access to certification services or direct benefit transfers;
- providing linkages to agribusiness, for information services: weather forecasts, pest outbreak news, and other disaster warnings, etc.
- improving linkages and networking to enhance collaboration and partnerships: - between farmer organizations and their grassroots members; - providing a voice to farmers; - between EAS providers at local, national and international levels; and - between actors of the agricultural innovation system.
- using data for monitoring of progress towards results planned;
- developing human resource capacities: - online training and distant learning of RAS providers, men and women farmers and youth, from which remote areas can also benefit.

Some of us are aware of how the future agri-food systems likely to be disrupted with the transformative twelve. Personalized production to nutrition, blockchain enabled traceability, IOTs for supply chains, big data analytics for crop insurance etc., are already evolving. For example; the IOTs have the potential to increase the agricultural productivity to 70% and the crop damages due to weather could be reduced to 25%. This requires future extension be futuristic and responsive and focus on technology, human behavior, economic, welfare.

Analysis of current models of digital extension in last ten years' period revealed that, the digital extension projects started from providing digital advisory, slowly incorporated procurement, e-ecommerce components. Then digital initiatives started providing financial inclusion services and currently, there is growing evidences of smart farming technologies and smart extension.

Next steps

1. From the Frontline Extension perspective, there is a need for mapping of digital innovations (across geographies, sectors, value chains, farmer profiles). ICAR/KVK system along with ATMA may conduct a series of match making workshops & innovation challenge programs to catch up with the technology pace. This will help evolving convergence of digital extension efforts at district level. In this regard, it is proposed have "1 KVK 1 Digital Consortium" mission.
2. KVK app has to be completely revamped to make it more personalized and farm specific. KVK system can work on designing the Mobile/ App Based Farm Management System. The advisories and digital services should be time scheduled, based on data driven insights. Eventually, advisories need to be linked to several time-critical service provided by other digital agriculture players.
3. Keeping in view the advancements in digital technologies, public extension systems should harness the power of drones, machine learning, AI, low cost sensor networks, blockchain/ RFID technologies for traceability, social media analytics based extension, high resolution remote sensing imageries, 3d printing etc.,
4. Based on the analysis made by Shaik N Meera (2018, 2020), there is a potential to complement the services from AgTech and FinTech startup ecosystem. It is recommended to establish ICAR/ KVK/ MANAGE led AgTech Fintech Integration Lab. This will help matchmaking of numerous digital solutions available to different contexts and strengths of public extension efforts. Medium term

5. Farms generate a huge amount of data in their daily operations, and so are fertile ground for agritech and fintech firms. Thus, in their quest to provide farmers with better services, they may end up harvesting and processing farm data without the consent of the farmer, leading to a situation where, "banks and insurance companies [know] more about the incomes and businesses of farms than the individual farmers themselves". Farmers may also be unable to adequately judge the value of their data and so may end up with compensation that is incommensurate with the same. So, there is a need for the models that leverage on the strengths of existing KVK / SDA system. They can facilitate the processes at farm level, so that farmers are not exploited.
6. Facilitate Full Stack Integration with Pluralistic Extension. Need to work on Bundled Digital Extension Modalities, Encourage Platform approaches and create a robust Agriculture Data policy.
7. The future of digital extension should focus on three levels of actions. i) Coordinated Action: Bringing multiple actors knowledge sharing and coordination ii) Digital Solutions: Products/ Services directly to farmers, consumers, businesses iii) Digital Platforms: Facilitate direct interactions between multiple users. For this immediately, the digital extension efforts should focus on Ecosystem Thinking. With this we need to design all digital initiatives as ecosystems, and NOT as systems. Ecosystems span across Centre and States, public and private, and are composed of several autonomous, interoperable, and federated systems.

Session: New Vistas in stress Resilience-Biotic Stresses

Diversity and management of *Fusarium oxysporum* f. sp. *ciceris* causing chickpea wilt

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Chickpea is one of the most important food legume crops grown throughout tropical, subtropical and temperate regions globally. India is the major chickpea producing country in the world. The crop is suffering from several biotic stresses among which wilt caused by *Fusarium oxysporum* f. sp. *ciceris* is an important factor limiting chickpea productivity. *Fusarium oxysporum* f. sp. *ciceris* is an important soil and seed- borne fungal pathogen causing wilt in chickpea globally. The disease is widely distributed in all the chickpea growing areas and causes variable losses depending upon the stages of the crop infected. Symptoms of the disease can develop at any stage of plant growth and highly susceptible cultivars can show early wilt symptoms within 25-30 days after sowing as drooping of tips followed by a dull-green discoloration, desiccation and collapse of the entire plant. The symptoms are usually more visible at flowering stage (late wilting).

The populations of *F. oxysporum* f. sp. *ciceris* collected from major chickpea growing areas of the country were highly variable in their growth rate and pattern, size of macroconida and colony characters. During our preliminary study, three new races of the pathogen were established in India based on the reactions on a set of differential cultivars of chickpea used by earlier workers in 1982. Further, based on the reactions of 64 isolates of *F. oxysporum* f. sp. *ciceris* representing five states of India on a set of earlier differentials, more than one race was found to be present in each state. Most of the isolates did not match the race specific reactions, therefore, it was suggested that the chickpea cultivars, namely, KWR108, GPF2 and DCP92-3 that had shown clear cut differential reactions for Indian populations should be incorporated into the earlier reported set of differentials. A new set of 10 differential cultivars of chickpea namely, C104, JG74, CPS1, BG212, WR315, KWR108, GPF2, DCP92-3, Chaffa and JG62 were identified for race profiling of Indian populations of the pathogen. The pathogenic populations collected from entire country were characterized into 8 races. The distribution pattern of the races in India was mapped. Genetic diversity of the Indian populations was analysed using various molecular markers namely, RAPD, URP, ISSR and SSR. The populations proved to be highly variable and the molecular groups partially corresponded to the states of origin/chickpea-growing region of the isolates as well as races of the pathogen. Different gene regions such as TEF-1á, *â*-tubulin, and ITS were also used to determine the genetic diversity and about 90% populations showed more or less similar grouping pattern. The groups did not correspond to the state of origin and races of the pathogen. High level of similarity among the populations in respect of these gene sequences was observed.

Various bio-agents were evaluated against the pathogen, amongst which *Trichoderma harzianum* and *T. viride* were found effective to some extent. Novel seed dressing and soil application formulations were developed from these bio-agents. Soil application of PBP 4G (*T. viride*) along with seed treatment with Pusa 5SD (*T. harzianum*) together with a fungicide, carboxin provided the highest seed germination, shoot and root lengths and grain yield with the lowest incidence of wilt in chickpea under field conditions. The efficacy of seed treatment with Pusa 5SD has been validated at different locations in India. The efficacy of the developed module enhanced by combination of bacterial antagonist. A combination of seeds treated with Pusa 5SD (*T. harzianum*) + *Pseudomonas fluorescens* 80 + *Mesorhizobium ciceri* + Vitavax power also provided the highest germination, grain yield and the lowest wilt incidence at field level.

Session: New Vistas in Stress Resilience- Biotic Stresses

Nematode Diseases of pulses, their current status and management options

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Pulses provide protein of high biological value in vegetarian diet aiding to overcome malnutrition in masses. This led to the pulse crops becoming an essential component of cropping systems in the past. However, with the adoption of wheat rice cropping system using high yielding cultivars, the area under pulses was not increasing. And thus productivity of pulses had to be enhanced through various means to meet the growing demands. At present the average productivity of 995 kg/ha of these crops is far below the potential yield of over 2000 kg/ha. Several factors are responsible for poor and unstable yield of pulse crops, the most important being biotic and abiotic stresses. Biotic stresses include insect pests, diseases and nematodes. Stresses due to nematodes are important and go many times unnoticed due to lack of clear-cut symptoms causing huge losses. Managing nematode diseases can be one of the important means to increase productivity of pulses. The crop plants under increased stress of climate change may further be affected by nematode infection. In general, losses due to nematodes range from 5-60% depending upon the nematode species and their population densities coupled with environmental conditions. Important nematode pests causing losses in pulses are roo-knot nematodes (*Meloidogyne incognita* and *M. javanica*), pigeonpea cyst nematode (*Heterodera cajani*), root lesion nematode (*Pratylenchus thornei*) and reniform nematode (*Rotylenchulus reniformis*), Based on the literature available on the distribution of important nematodes in pulses, root knot nematodes are most widely distributed nematodes. Two species are important in pulses which are *Meloidogyne incognita* and *M. javanica*. *Meloidogyne incognita* is more widely distributed compared *M. javanica*. *Meloidogyne javanica* had been reported on pulses mainly in Haryana, UP, Rajasthan and Gujarat while *M. incognita* is infecting pulses in many states wherever they are grown. *Heterodera cajani* is serious on pigeonpea and is distributed in Haryana, UP, Gujarata, Karnataka and Tamil Nadu. *Pratylenchus thornei* is mainly pest of chickpea and is reported from UP and MP. Once the nematodes infestation is found in standing crops, there is no immediate control method to overcome nematode problem at that point of time. Strategic approach is required to manage the nematode problems for future crops to be grown in nematode infested fields. Many cultural practices have been very effective in managing the nematode populations. Deep summer ploughing after light irrigation in areas of hot summer, several cropping sequences have been worked out which are effective in reducing nematode populations. Trap crops and bio-fumigation can also play important role in reducing nematode infestation. Improving

the soil health through organic amendments, FYM, green manuring, etc. can reduce the nematode losses. Many biocontrol agents are effective against plant parasitic nematodes. Use of these biocontrol agents could be one of the components of nematode management strategy. Exploitation of resistant sources against nematodes can play important role in reducing the losses due to nematodes. New techniques based on RNAi and biotechnology may also help in combating nematode problems in pulses. Chemical options for nematode management in pulses are limited. Only one chemical carbofuran 3G is available as nematicide for nematode management and for using in pulses label claim is required. Managing the nematode problems by any means will definitely play important role in increasing the productivity of the pulses thereby contributing towards the nutritional security of the masses.

Session: New Vistas in stress Resilience - Biotic Stresses

Pest Management in Pulse Crops with Climate Change Perspective

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India is world's largest consumer and importer of pulses. Pulses are important source of dietary protein for predominantly vegetarian populace of our country. The country's pulse production has recorded commendable boost from 2016-17 onwards with the production ranging between 22.4mt in 2016-17 to 25.5mt in 2021-22 due to the concerted efforts scientist, farmers and policy makers. The pulse production is estimated at 26.96mt during 2022-23 that will help to diminish the demand for pulse import to a greater extent. The productivity of pulses in India (<1000 kg/ha) is lower than other countries. Crop pests including pod borers, pod fly, defoliators, sucking pests and bruchid inflict about 20% yield loss in grain legumes and their effective management thus becomes imperative for ensuring good harves. Several outbreaks of pod borer and spotted pod borer have been recorded on grain legumes in India. The scale insect, in pigeon pea and beet armyworm, mealy bug and white fly in chickpea have emerged as new pests, while leaf miner and mealy bugs are some of the emerging pest problems in pigeon pea in India.

Integrated Pest Management (IPM) has been adopted as "Cardinal Policy" In India for crop protection since 1985. The algorithm *i.e.* stepwise procedure for implementing IPM thus involves, crop loss assessment, pest risk analysis, development of pest surveillance & forewarning methodology and decision support tools, harmonious integration of IPM tactics and convergence of various crop protection agencies. Climate change is also projected to influence effectiveness of pest management tactics that requires effective climate change mitigation and adaptive measures.

Assessment and extrapolation of yield losses are mandatory at both the strategic and tactical decision levels. Empirical approach has generally been used for establishing regression damage functions between pest damage and crop yield that however behave in a location specific manner. On the other hand, the assessment of crop losses due to pests with mechanistic approach through simulation models is based on the concept of pest damage mechanisms that specify plant physiological processed affected by the pest injury. Mechanistic insect population simulation models could be developed and linked to crop simulation model, InfoCrop that facilitated climate change impact assessment both on pest dynamics as well as crop-pest interactions. Pest surveillance facilitates timely decision making in regard to interventions based on the existing pest and natural enemy densities. Mostly it has been done in physical inspection mode and with the help of various types of

traps, light traps, sex pheromone traps, and yellow and blue sticky traps. The ICT and geo-spatial techniques such as "remote sensing" can be taken advantage of for e-surveillance in large areas. In the recent past, ICT-based surveillance and advisory has facilitated wide area pest management and is currently being implemented in about 180 lakh hectare in Maharashtra and Haryana in collaboration with State Agriculture Departments.

Preference needs to be given to the cultivation of resistant cultivars as their use greatly reduces need for other pest control methods. Agronomic practices, such as manipulation of sowing time, crop intercropping and balanced fertilizer application, and mechanical removal of infested plant parts and conspicuous pest stages helps to reduce pest incidence. There is rich diversity of predators and parasitoids that needs to be conserved and enhanced against harmful effects of pesticides. Consideration of natural enemy population in decision making could help in avoiding unwarranted pesticide applications and in conserving natural enemy populations. Ecological engineering can be practiced through planting of flowering plants on field bunds to create favourable environment for useful organisms. Likewise, suitable intercropping can be used to discourage pests and encourage natural enemies. Besides, bio pesticides such as neem, *Bt*, NPV and *Trichoderma* are to be used to minimize pesticide use.

Pesticides have definite role to play in pest management, however, their application should be need-based and in a judicious manner. Insecticide resistance management (IRM) should form an integral part of IPM programmes. Creation of awareness regarding IPM among various stakeholders, strengthening pest surveillance, ensuring availability of IPM inputs and climate resilient IPM adaptations will enable effective pest suppression and realization of higher productivity in an eco-friendly manner thereby enhancing farmers' income, promoting exports and preventing environmental degradation.

Session: New vistas in Stress Resilience-Biotic Stresses

Translational genomics for disease resistance pigeonpea breeding

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Pigeonpea remains the major source of protein in India specially for the vegetarian consumers. Its productivity has often been challenged by the diseases such as sterility mosaic disease (SMD), fusarium wilt (FW), pod borer and more recently by phytopthora blight (PB). This crop has acquired optimum genomic resources such as high-quality reference genome, gene expression atlas, high-mid-low density genotyping assays, SNP based quality control panels and diagnostic markers for SMD and FW resistance. While efficiency and impact of associated genomic regions for FW and SMD resistance are being assessed; the parallel efforts are intensified to identify better sources of resistance and associated genomic regions for key diseases such as SMD, FW, PB and pod borer. Sequencing-based trait mapping approaches are already been optimized for speedy discovery of candidate genes and superior haplotypes. Integration of genomic breeding (marker-assisted selection, haplotype based breeding and genomic selection) in combination with recently optimized technologies such as rapid generation advancement and single seed-chipping based genotyping provides further opportunities to infuse more precision in addition to saving resources and time. More focussed and long-term research strategy needs to be implemented by integrating the genomics in understanding and utilizing the genebank diversity to make the pigeonpea more resilient to existing and emerging disease threats to ensure sustained production in farmers field.

Session: New Vistas in stress Resilience - Biotic Stresses

Strategies for biotic stress management in pulses under changing climate

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Globally, 30-40% of crop produce is lost to pests and diseases annually, with overall losses in yield far greater in Asia and Africa. This temporal disruption of ecosystem pest and disease distribution and severity combined with the geographical synchronization of pests and beneficial insects calls for new and more urgent ways such as accelerating crop research and developing climate smart agriculture services to tackle challenges that threaten to dislocate livelihoods of farmers, the poor and vulnerable. Projections of future pathogen/disease dynamics and ranges have not included several climatic factors and several pathogen/disease life cycle stages to be more reliable. Such approaches are particularly valuable because they comprise future options to manage disease risks and minimise potentially adverse effects on crop yield. Lack of preparedness, inadequate knowledge on pest risks and the paucity of timely crop protection advice have hampered progress in this area. In lieu of the above there is an urgent need to conduct pest and disease model input experiments under climate change scenarios and use them for producing a tool or an application for farmers in a palatable form.

Under the DST funded center of excellence on climate change research for plant protection, ICRISAT alongwith NARS have developed weather-based prediction models to significantly important pests and diseases in cereals, pulses, cotton that can forecast the first appearance and peak severity of pest and diseases in a crop season. These models have been linked with weather based agro advisory for real time management of pests and diseases (http://ccrpp.iari.res.in/coe-pest). Model have also been developed to predict the risk vulnerability maps with spatial and temporal distribution of emerging pests and diseases under future climate scenarios in a specific crop/district/ block. Under the state-of-the-art climate change research facility at ICRISAT equipped with facilities like OTC (open top chamber), FACE (Free Air CO2 enrichment Facility), CTGT (CO2 and Temperature Gradient Tunnels) have generated strategic knowledge on the impact of elevated temperature and CO2 on primary productivity parameters of dry land cereals and legumes, pests and diseases, yield and nutrition.

Adequate knowledge and tailored awareness of pest and disease outbreaks alongwith reliable, consistent access to new tools and technologies with a seamless decision support system are indispensable among stakeholders to improve the management strategies and promotion of plant health under changing climate. Effective plant health management is critical for improving the productivity, profitablity, sustainability and resilience of agrifood systems.

Session: New Vistas in Stress Resilience- Abiotic Stresses

Integrated multi-omics for unravelling candidate genes associated with drought stress tolerance in chickpea

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Drought stress limits plant growth and productivity significantly in chickpea. An integrated multi-omics analysis can provide a better molecular-level understanding of drought stress tolerance. We performed comparative transcriptome, proteome and metabolome analyses of two chickpea genotypes with contrasting responses (drought-sensitive and drought-tolerant) to drought stress to gain insights into the molecular mechanisms underlying drought stress response/tolerance. The differential expression analyses identified the differentially regulated genes, proteins and metabolites under control and/or drought stress conditions in/between the chickpea genotypes. The pathway enrichment analysis of differentially expressed genes and proteins suggested the involvement of glycolysis/gluconeogenesis, galactose metabolism, and starch and sucrose metabolism in the drought-tolerant genotype. The integrated multi-omics analysis revealed co-expressed genes, proteins and metabolites involved in phosphatidylinositol signaling, glutathione metabolism and glycolysis/ gluconeogenesis pathways, specifically in the drought-tolerant genotype under drought. These stress-responsive pathways were coordinately regulated by the differentially expressed genes, proteins and metabolites to circumvent the drought stress response/tolerance in the drought-tolerant genotype. The co-expressed genes/modules were further investigated for the identification of transcription factor encoding genes, and those located within the known *QTL-hotspot* region for drought tolerance in chickpea. The *QTL-hotspot* associated genes, proteins and transcription factors may further contribute to improved drought tolerance in the drought-tolerant genotype.

Further, we investigated DNA polymorphisms between the sets of chickpea genotypes with contrasting drought stress response (drought-sensitive vs drought-tolerant) via whole genome resequencing. In total, 36,406 single nucleotide polymorphisms (SNPs) and 3,407 insertions or deletions (InDels) differentiating drought-sensitive and drought-tolerant chickpea genotypes were identified. The genes harboring DNA polymorphisms in their promoter and/or coding regions and exhibiting differential expression under control and/or drought stress conditions between/within the drought-sensitive and tolerant genotypes were found implicated in stress response. We identified DNA polymorphisms within the *cis*-regulatory motifs representing the transcription factor binding sites in the promoter region of abiotic stress related and QTL-associated genes, which might contribute to the differential expression of the candidate drought-responsive genes. In addition, we revealed

the effect of non-synonymous SNPs on mutational sensitivity and stability of the encoded proteins, which suggested their plausible roles in determining differential drought stress response in the chickpea genotypes.

Next, we analyzed the DNA methylation profiles in the chickpea genotypes at single base resolution to analyze the epigenetic regulation of drought stress response. The analysis suggested differential methylation dynamics and suggested the regulation of differential gene expression via DNA methylation in the chickpea genotypes under drought stress. Altogether, the multi-omics analyses provided new insights into the drought tolerance mechanism in chickpea and the prioritization of candidate genes for functional analysis.

Session: New vistas for Stress resilience- Abiotic stresses

Plant available silicon and abiotic stress mitigation - progress and perspectives

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Frequent abiotic stresses due to unpredictable climate conditions have challenged agricultural production globally. Among many limiting factors, deteriorating soil health, declining agrobiodiversity, unusual weather patterns, and biotic and abiotic stresses can lead up to 70% decline in crop yield to complete crop failure. Various abiotic stresses (such as drought, heat, cold, flood, high light intensity, metal toxicity, low nutrient availability, and salinity) alone or in combination mediate physiological and biochemical damage affecting plant growth and productivity throughout crop cycle. At cellular level, these stresses result in overproduction of reactive oxygen species (ROS), leading to oxidative damage, ultimately disrupting cellular homeostasis. Excessive ROS production overwhelms the antioxidant defense leading to oxidative damage to biomolecules such as DNA, pigments, proteins, and lipids, which can eventually lead to apoptosis or programmed cell death.

Essential elements are necessary to complete plant's growth and life cycle however, some of the non-essential elements can benefit plant especially under a stressful environment. Among these non-essential elements, positive effects of plant available silicon in enhancing plant's ability to tolerate various biotic and abiotic stresses and ultimately improving crop yield and quality are widely known. Silicon (Si) is the second most abundant element in Earth's crust after oxygen. However, silica (SiO2), the most common form of Si, is unavailable to the plants. Silicon does exist in the plant available form in a much smaller fraction, as an uncharged monomeric molecule as silicic acid or mono silicic acid ($Si(OH)_4$ or H_4SiO_4). Plant available silicon is taken up by plant roots at soil pH less than nine. Root uptake of plant available Si is facilitated by Si specific influx and efflux transporters. Once taken up by the roots, other influx transporters assist and regulate root to shoot Si transport, facilitated via xylem up to leaf tissues. However, plant available Si's positive effects on the plant growth depend on plant's absorption ability which is affected by species and genotypic differences. Based on Si % on the dry weight basis to Si absorption, plants are high (>5%), intermediate (1%), and low (<0.1%) accumulators. Various studies have shown that monocots are high Si accumulators compared with dicots/eudicots. In addition to plant available Si's uptake via plant roots, it can also be applied directly to areal plant parts as foliar application and mainly taken up through stomata, trichomes and cuticles. Recently, Si foliar application is becoming a popular mode of choice in agriculture, firstly due to the ease of application. More importantly, foliar application is a viable option to increase Si accumulation of Si intermediate and non-accumulator plants, leading to improved plant functions.

Recent research has demonstrated that when plant is under abiotic stress, and simultaneously when plant available Si is available in the cytosol, there is enhanced production of various antioxidants (enzymatic and non-enzymatic), phytohormones and upregulation of related genes. At the cellular level, plant available Si mitigate abiotic stresses by scavenging ROS and normalizing the cellular metabolic pathways. In nutshell, under stressful environments, Si mediates various plant processes, including redox homeostasis, hormone regulation and signaling, osmotic balance, assimilation of nutrients including nitrogen, photosynthesis, transpiration, and carbohydrate metabolism.

Future research, at the fundamental level should focus on better understanding the cellular and molecular mechanisms responsible for Si mediated stress tolerance, driven by the omic technologies especially transcriptomics and proteomics. However, at applied field level, efficacy of various Si products, relevant modes of its application, interactions with different soil and plant types require further attention for the success of Si mediated abiotic stress tolerance and enhancing crop yields.

ABSTRACTS

Farm to Fork: Planning, Policy, Perspectives

S1.1: Public Private Partnership for effective marketing of agricultural produce

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Public-Private Partnership is a contractual agreement between a public agency and a private sector entity. Through this agreement, the skills and assets of each sector are shared in delivering a service or facility for the use of the general public. In addition to the sharing of resources, each party shares the risks and potential rewards. India enjoys a distinct position in the world when it comes to pulses production. Several private sector companies are active in field of agriculture and agri-business that are directly engaging with the farmers for technology transfer and entire value chain. The cases of Rallis India-Tamil Nadu Govt. partnership for enhancing black gram cultivation in Pudukkottai district of Tamil Nadu, Tata Chemicals Ltd.-Punjab State Govt. Partnership for promotion of summer moong in Punjab are some of its examples. Public-Private partnership in India are mostly involved in contract farming models undertaken by agri-business companies which usually takes care of pre-agreed price, quality assurance, quantity and time of delivery, and as per the contract, farmers are required to plant the contractor's crop on his land and to harvest and deliver it to the contractor based upon anticipated yield and contracted acreage mostly at a pre-agreed price. PPP has made positive changes in market linkage of farm produce and some of them are: capacity building of farm families, reduction of risk and uncertainties, social mobilization and economic empowerment of farmers, knowledge management, development of high end technologies, productivity enhancement, economic empowerment of farm women, gender mainstreaming in agriculture, and many more.

S1.2: Effectiveness of price policy for pulses in India: Present status and way forward

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A conducive price policy is vital for the sustainable development of any crop sector, especially for pulses which are risk-prone owing to cultivation on marginal landsunder harsh-rainfed conditions. To ensure remunerative prices, the Indian Government announces Minimum Support Prices (MSPs),based on the recommendations of Commission for Costs and Prices (CACP), New Delhi, for three *kharif* pulses (pigeonpea, greengram & blackgram) and two *rabi* pulses (chickpea & lentil). Along with MSP, procurement support when farm prices fall below MSP and increase in MSP over the years are also needed. To find out how far these criteria were achieved, requisite data for all five pulses for the last ten years were collected from multiple sources (CACP, New Delhi, Ministry of Agriculture and Farmers Welfare, Ministry of Commerce & Industry, Govt of India). Price series were deflated using Wholesale Price Indices to arrive at real prices and then growth analysis was performed. Results indicated that for the overall period (2013-14 to 2022-23), compound growth rates in MSPs for all five pulses were significant: ranging from 1.9% (5.1% in nominal terms) in pigeonpea to 4.98% (8.28% in nominal terms) in case of lentil. Besides the increasing MSPs, procurement of pulses at MSP also improved during recent years: pulses procured increased from 1.52 lakh tonnes during 2009-2013 to 112.63 lakh tonnes during 2016-2020 (74 times increase). During the latest period (2016-17 to 2020-21), chickpea accounted for 51% of the pulses procured while pigeonpea accounted for 29%. Though for the overall period, growth rates in MSPs in real terms were positive and significant, for the latest five-year period (2018-19 to 2022-23), growth rates were either not significant (-2.43%^{NS} for pigeonpea, -2.00%^{NS} for urd;-2.69%^{NS} for chickpea & 0.92%^{NS} for lentil) or declined significantly (-3.8%** for mung) indicating that MSPs in real terms were not increasing. Further, to understand the impact of MSPs on farm prices, monthly data on all India average farm prices for whole pulses were collected from November 2021 to October 2022. In lentil (whole), farm prices were 20% higher than the MSP and in urd (whole), farm prices were 5% higher than the MSP - differences were statistically significant in both these cases. In chickpea (whole), difference between MSP and farm prices were not statistically significant. While, in case of pigeonpea, farm prices were 7% lower than the MSP and in mung, it was 9% lower. Hence, despite the substantial growth in the procurement of pulses recently, there is still scope for improvement to ensure remunerative pulses farming.

S1.3: Seed Hubs for increasing production of indigenous pulses: A success story

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Seed is most vital input to harvest the good commercial yield. Use of quality seed enhances the productivity up to 15-25%, hence seed production of pulse crops through farmers participatory approach is days need. Department of Agriculture and Farmers welfare, Govt. of India sanctioned "Creation of Seed Hubs for Increasing Indigenous Production of Pulses in India', under NFSM, Pulses" at Pulses Improvement Project, MPKV, Rahuri from 2016-17. The certified seed production programme of improved varieties of pulses i.e. Pigeonpea var. Phule Rajeshwari, green gram var. BM 2003-2 and Chickpea var. Phule Vikram was implemented involving seed growers in Ahmenagar district. Total 4827.36 qtls of quality seed produced on 80 farmers field and amount refunded to farmers for their produce as per the buy-back policy of MPKV Rahuri. The total quantity of 3260 qtls certified seed of chickpea variety Phule Vikram was produced in this project. This programme generated employment opportunities for rural youths, farm workers and womens as seed production is skill oriented work. Farmers are also getting the benefit of subsidy of under National Food Security Mission (NFSM) and 10-15 % higher price to their produce as compare to prevailing local market price. Socio-economic status of farmers gets improved due to generation of additional income through seed production, this helped farmer to start the other enterprises and further development of farming community. It also helped in crop diversification and improvement of seed replacement ratio of Chickpea and other pulses.

S1.4: Climate Change: Potential impact on pulse production in India

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Increasing climate variability with change in climate is recognized unequivocally. Temperature, moisture and green house gases are the major variables of climate change. The most obvious effect of climate change is on global mean temperature which is expected to rise between 0.9 to 3.5^0C by the year 2100. Pulses are very sensitive to weather fluctuations. Productivity of most pulse crops will decrease by 10-15% by 2100 due to increase in temperature and rainfall variability. Since 87% of pulse acreage is rainfed, the crops are likely to be hit substantially. About 77% of Chickpea, 90% of Pigeonpea, 90% of Mungbean and Urdbean, 94% of Lentil and 100% of Horse gram cultivation is rainfed. More than 80% of pulse farmers are small/marginal, thus having less capacity to cope with climate change impact. Pulses are the climate smart crops as they simultaneously adapt to climate change and contribute towards mitigating its effects. In order to develop climate ready pulse crops we need to develop high yielding varieties with multiple resistance to abiotic stresses, improvement in water and nutrient use efficiency, genetic engineering for gene pyramiding, broadening the genetic base and development of short duration varieties.

S1.5: Deciphering pigeonpea [*Cajanus cajan* L. (Millisp.)] yield gap in India shows scope for improvement

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Pigeonpea is an important pulse crop of rainfed agricultural system for ensuring food and nutritional security to the majority of the vegetarian population in India. Pigeonpea thrives well under harsh environment, nevertheless very responsive to intensive cultivation practices. The present study on the pigeonpea yield gap analysis between potential, achievable and farmers yield have been estimated based on the data recorded over 16 years (2005-2020). During this period the average potential and achievable yields of pigeonpea were 3313 and 1860 kg/ha, respectively. However, the realized farm level yield (776 kg/ha) is just 23.43% and 41.73% of the potential and achievable yields, respectively. The potential (-5.45%) and achievable (-3.24%) yields have showed the decreasing trend of Compound Annual Growth Rate (CAGR) over the period considered in the current study. Whereas, the average farmers yield has recorded a steady and positively increased (13.75 kg/ha/year) trend with the constant of 659.48 kg/ha over 16 years. Notably, the increase in farm yields is 47.7% (950 kg/ha in 2019-20) as compared to 2005 (650 kg/ha). The enhanced farmer yield could be attributed to the availability of high yielding pigeonpea varieties coupled with adoption of optimum management practices. However, the gap between the potential and the realized yields is more due to up-scaling of technology coupled with erratic field managed by the farmer and vagaries of the climate. Sustaining the achieved self-sufficiency in pulses requires addressing aforementioned issue and diversifying the cropping systems with climate resilient varieties, encouraging large-scale on-farm trials and a strong policy support.

S1.6: Global pulses production, consumption and trade scenario

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Pulse crops play an important role in the cropping systems and contribute to food as well as nutritional security of the vegetarian population of the world. These crops are being grown in 93.18 million hectares area, contributing 89.82 million tons of pulses in the global food basket with productivity level of 964 kg per ha. India, Canada, China, Myanmar, Brazil, United States of America, Australia, Pakistan and Bangladesh are the major pulses producing countries. Dry beans are the most important pulse crops contributing 30.67 percent to the total pulses production of the world followed by chickpea (16.79%), dry peas (16.30%), cowpea (9.91%), lentil (7.28%) and pigeonpea (5.58%). Dry beans cover 37.35 percent of total area under pulses followed by cowpea (16.16%), chickpea (15.93%), dry peas (7.72%), pigeonpea (6.54%) and lentil (5.38%). Canada (28.4%), USA (9.2%), Myanmar (8.1%), Australia (5.6%), Argentina (5.0%), China (4.5%), Russia (3.8%), Turkey (2.5%), Tanzania (2.3%), India (2.2%), Mexico (1.8%), Mozambique (1.8%), Ethiopia (1.6%), France (1.6%) and UAE (1.5%) are the major pulses exporting countries of the world, as per value of the product. While, India, China, Pakistan, Turkey, USA, UAE, Egypt, Italy, United Kingdom, Spain are the top ten pulses importing countries of the world. The consumption of pulses, which was around 11 kg per capita per year during 1990, has come down to almost 7.7 kg per capita per year, at present.

S1.7: Production, trade, and key policies considerations for pulses in India

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Pulses are nutrient-dense plants that guarantee food and nutritional security and can significantly aid in achieving several Sustainable Development Goals (SDGs). India has been recognized as a significant producer of research output globally. It is the largest producer of pulses (27.69 mt, or 26%), consumer of pulses (27%), and importer (15%). Cereals were the focus of agricultural policy during the green revolution since it was intended to encourage the production of cereal crops to fulfill food demand. After adopting the MSP, a critical aspect of the agricultural pricing policy for pulses, the country saw an increase in output that resulted in a decrease in imports. India has implemented several policy initiatives and research priorities for the overall pulses sector development to increase pulses production and bridge the gap between demand and supply. Government policy's influence on pulses production suggests a paradigm shift in strategy through short-, medium- and long-term plans to achieve self-sufficiency in pulses production and ensure nutritional security for the population. Further, Mission-mode approach to increase the production in regions wherein demand is more than the supply. Policies like 'cluster frontline demonstrations' shall be implemented to increase the production.

S1.8: Sustaining pulses revolution in India: Policy perspectives

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India has witnessed a revolution in pulses production recording an all-time high of 27.69 MT in 2021-22. During last decade, there has been a 53% increment in productivity (630 kg/ha to 965 kg/ha) and 23% increase in area (23.28 Mha to 28.69 Mha) resulting in more than 88% increase in total pulses production (14.66 MT to 27.69 MT). This quantum jump has been possible due to synergy among availability of improved technologies, quality seeds and enabling government policies. Major policy decisions like increase in MSP (30-55%), procurement through FCI, NAFED and SFAC, creation of 20 lakh tonnes buffer stocks in pulses, creation of seed hubs, increasing import duties by 30-60% on chickpea, pea, lentil and pigeonpea, revoking restrictions on exports, organizing more than 80,000 cluster demonstrations each year through KVK's, RKVY, PMKSY, market integration through e-NAM etc have stabilised production and price of pulses and lead to more than 60% decline in import of pulses from 6.6 MT (2016-17) to 2.46 MT (2020-21). Pulse production required an annual growth rate of 1.23% to achieve the target of 39 MT by 2050. With increasing pressure for land by competing millets and oilseeds and various biotic and abiotic stresses adversely affecting crop yields, long term policy support is required for sustaining the pulses production through NFSM Pulses supporting breeder seed production, distribution of seed mini-kits of new varieties, scheme on Inter-cropping of pulses with sugarcane, TRFA programme, buffer target of 23 lakh tonnes of pulses under price stabilization fund etc in India.

S1.9: Deciphering the constraints and opportunities for improving value chain system in pulses

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India leads in terms of total pulses area under cultivation (33Mha), production (27.64 Mt) and consumption. While highlighting the strategies to maintain the increased production trend (16.32 Mt in 2015 to 27.69 Mt in 2021, MoAFW, DAC, 2022) of pulses we need to think about its affordability to mass. To achieve such targets the cultivation of high yielding shorter-duration pulse varieties and varieties that are resistant to biotic and abiotic stresses should be encouraged. Along with the improved crop husbandry intensive extension efforts are also compelling in bolstering the production pace. Commonly in India, farmers sell their produce to the buyers or markets to make money in order to buy inputs for his subsequent crop and this will increase the supply chain price. Inflated price of pulses in the retail market is creating a concern for nutrition availability in the rural India. Case study 2016; Tamil Nadu, farmers' realisation increased from 47% to 63% of the retail price of white lentil once the growers organised themselves into a producer company. Therefore, an urge to trim long supply chain, omitting such bulk buyers and transportation from farmers to farmers can make pulses an attractive and healthier food in India. Establishing processing units at the panchayat/ block level will add income, opportunity employment for rural women and youths. These multi-dimensional approaches maintaining a unified supply chain without middle mans, value addition facilities along with hygienic packaging facilities, diversification across exporters to overcome the deficit will surely be a win-win strategy.

S1.10: Economic valuation of ecosystem services from pulses in India: A meta-analysis

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Besides health and nutritional benefits, pulses provide many ecosystem services (ES). However, their contribution to enhancing ecosystem services, particularly regulating and supporting services, is undervalued or not estimated. Therefore, the economic valuation of key ecosystem services viz., biological nitrogen fixation (BNF), carbon sequestration, and soil fertility from major pulses, including gram, pigeon pea, green gram, and black gram, was carried out using direct and indirect valuation methods in a meta-analysis framework. A total of 252 observations from 75 studies were used to quantify the ecosystem services from pulses. The farm-level impacts indicated that pulses crops derived about 40 kg/ha of nitrogen from the atmosphere through BNF, ranging from 27 kg/ha for gram to 64 kg/ha for green gram and black gram. Furthermore, significant environmental benefits such as improved carbon sequestration (0.5/ton/ha/year) and additional nutrient availability (57kg NPK/ha/year) were observed. The economic value of non-marketed services from pulses is estimated at Rs. 10,135/ha/year, which is 20% of the total value of ES including market value of production. At the country level, pulses crops provided additional Rs. crores 56031 to the society in terms of non-marketed services. The study results will sensitize the stakeholders and policymakers about ES provided by pulses and develop the mechanism for payment of ecosystem services.

S1.11: Enhancing breeder seed production for achieving seed security in pulses

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Quality seed production is a vital input for sustaining any crop production system. Realizing the importance of quality seed in enhancing indigenous pulse production and ensuring self-sufficiency in the country, the Government of India conceived and executed a noble programme by strengthening/ reinforcing the existing breeder seed production programme in the country. DAC&FW, New Delhi, GoI initiated mega programme on "Enhancing breeder seed production for increasing indigenous production of pulses in India" during 2016. To execute and monitor the project for desired goal/ output ICAR-Indian Institute of Pulses Research, kanpur has been assigned the major responsibility to implement this project. Following approval of this novel project on 28th june 2016 by involving 12 centres covering 8 states viz., Bihar, Uttar Pradesh, Madhya Pradesh, Maharashtra, Rajasthan, Odisha, Andhra Pradesh and Karnataka, a total budgetary allocation of INR 203.9 million was provided as one time grant. These centre come under the gamut of National Agricultural Research System involving ICAR-institutes, AICRP centres located in SAUs and central Agricultural universities in some states. Since this project has also provision of creating infra-structure including works (INR 112.5 million). establishing seed processing unit (INR 27.9 million) and purchase of farm implements (INR 63.5 million), It helped the centre in developing necessary infra-structures(s) for meeting post harvest needs of the quality seed produced. Since the commencement of this programme in 2016, substantial quantity of additional breeder seed (19705.09) of different pulse crops were produced. Durning 2016-2022, additional breeder seed of 2955.94q of pigeonpea, 2245.25q of mungbean, 2161.07 q of urdbean, 8650.99 q of chickpea, 1958.51 q of lentil and 1733.24 q of fieldpea were produced by these different national agricultural research centres across the country. This has resulted in raising substantially quality seed supply in the country, to boost both productivity and production in pulses, which in turn has made the country self-reliance in pulses seed sector.

S1.12: Technologies and policy interventions towards achieving self sufficiency *(Atmanirbharata)* in pulses

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India is the largest producer, consumer and importer of pulses in the world. Pulses are one of the major food crops in India due to higher protein content. Pulses form an integral part of the Indian diet, providing much-needed protein to the carbohydrate-rich diet. Major pulses grown in India are chickpea, pigeonpea, mungbean, urdbean, lentil and peas and minor pulses such as cowpea, horsegram, moth bean and cluster bean. Recently Government has initiated various measures and policies for boosting pulse production in the country such as exponential rise in Minimum support price (MSP) for major pulses coupled with multi-fold increase in procurement of crops at MSP. Various initiatives were undertaken in the NFSM-Pulses in all the states and Union Territories of India. Support for breeder seed production, creation of 150 Seed Hubs at ICAR institutes and state agriculture universities and krishi Vigyan Kendras. To produce the certified seed of latest high yielding varieties of pulses assistance is provided to Central Seed Agencies. A new scheme "Intercropping of pulses with sugarcane implemented in several states and launched targeting rice fallow area (TRFA) which is one of the potential area could be exploited to achieve targeted production of pulses. Technological measures include distribution of certified seeds of high yielding varieties of pulses, farm machineries, plant protection chemicals, nutrient management soil ameliorants and cluster demonstrations on improved package of practices. As a result, the pulse production in the country has increased to a record production of 26.96 Million Metric Tonnes during 2021-22 and reduce the dependence on imports.

S1.13: Success of seed hub model in pulses through contract seed production programme

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Pulses are cheap sources of quality protein and offer the great scope for nutritional security. The pulses production is revamping in India from last decade. As of 2020, India had 28.3 million hectares under pulse cultivation. During 2005-06, the total production of pulses in India was 13.38 million MT, which increased to 25.58 million MT during 2020-21. In Tamil Nadu, total production of pulses in 2020-21 is 0.664 million MT in an area of 8.03 lakhs ha. It is encouraging to note that new programs, government support, and collaborations between research institutes, farmers and various other stakeholders are boosting the production of pulses and helping the farmers immensely. One such programme is implementation of seed hub scheme which is operated in different centres in India to increase the pulses production. In National Pulses Research Centre, TNAU, Vamban, Tamil Nadu. Seed hub was implemented from 2016-2017 onwards. Every year 300 quintals of certified seeds of pulses were produced both in foundation and certified class under contract seed production programme in farmers field of nearby villages apart from breeder seeds and truthfully labelled seeds. It involves nearly 50 farmers per year as seed growers. This 300 quintals of quality seeds have been distributed to 3750 acres commercial cultivation. It contributes to 1125 MT of pulses in food grain production with the monetization value of 6.75 crores. The Implementation of seed hub is one of the successful model which not only contributes in increasing pulse production but also it develop the seed entrepreneurs.

S1.14: Towards scaling indigenous production of pulses in India: Role of seed hubs

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Lack of quality seed continued to be one of the greatest impediments in bridging up the vast yield gap(s) between the realizable and realized productivity of crop(s) in the farmer's fields. It is demonstrated that pulse productivity can be increased many-folds by simply making available the quality seeds of right crop/variety at right time/place. Analyzing the importance of quality seeds in agricultural production, Department of Agriculture, Cooperation and Farmers Welfare, GoI, has taken a novel initiative to ensure quality seed availability locally through creation of seed hubs through a dedicated project "Creation of seed hubs for increasing indigenous production of pulses in India" with total outlay of INR 2253.108 millions. This project is aimed at establishing 150 seed-hubs located mainly in ICAR Institute/State Agricultural Universities/Krishi Vigyan Kendraa (Agriculture science Centres) belonging to non Governmental Organizations and public funded institution in different pulses producing areas covering 24 states of the country. ICAR-Indian Institute of Pulses Research, Kanpur, at the helm of affairs (Nodal agency) for implementing the project for creation of seed hubs and providing the technical support for quality seed production, has taken adequate steps in both formation and functioning of these seed at National level. Accordingly, 150 seed hubs have been created in ICAR Institutes/State Agricultural Universities, AICRP centres and Krishi Vigyan Kendras keeping ICAR-ATARIs in loop so that quality seed sale activities can be coordinated in a better way linking other KVKs (not involving directly with the seed hub projects). The project has novel provision for one time grant of INR 5.0 million in the first year per seed hub for creating infrastructure (seed processing plant and seed storage facilities), In addition to this, INR 10 million has been allocated to each seed hub as a revolving fund to meet various expanses for production, procurement and processing of seeds. The profit generated out of the seed sale has been utilized by seed-hub for development of other facilities/manpower as per need for scaling quality seed production of pulses. Each seed hub was given a target of producing approximately 100 tonnes every year. A total of 52421.61, 111801.02, 123784.31, 109614.77, 110706.50 and 97849q of quality seed of different pulses were produced during 2016-17, 2017-18, 2018-19, 2020-21and 2021-22 respectively. Overall, quality seed to the tune of 103335.68q mungbean, 78405.24q urdbean, 109996.32q pigeonpea, 225511.89q chickpea, 53290.36q lentil, 29661.03q fieldpea, 2030.86q mothbean, 3472.96q cowpea, 2017.40q horsegram, 6967.36q rajmash and 1488.11q lathyrus were produced through different seed hubs during 2016-2022. Production and making available the quality seed of different improved latest varieties of various pulses has increased the seed replacement rate, varietal replacement rate and the production of pulses in the country. .

S1.15: Quarantine weed seeds in lentil consignments imported from different countries

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India is the world's largest producer, consumer, and importer of pulses. India's pulses imports rose 9.44 per cent to about 26.99 lakh tonnes during the financial year 2021-22 over 24.66 lakh tonnes in 2020-21 on lower domestic output and the Government's decision to keep imports open to ensure adequate supplies. The bulk shipments of pulses known to contain exotic weed seeds as contaminants. A total of 709 lentils shipments weighing 109,598 tons were imported to India through different ports during the period of 2018-2020. Imported lentil shipments were inspected as per provisions of Plant Quarantine (Regulation of Import into India) Order (2003) issued under Destructive Insects & Pests Act, 1914. A total of 50 Weed species representing 13 families were observed contaminating imported lentil shipments. Of these, four weed species i.e., *Raphanus raphanistrum*, *Thlaspi arvense*, *Polygonum lapathifolium* and *Echinochloa crus-pavonis* are exotic to India. Indigenous weeds of 46 species representing 13 plant families were intercepted. Shipments from Canada contaminated with maximum number of indigenous species (30) followed by USA (23) and Australia (7). On the basis of the study it is concluded that plant quarantine officials at the port of entry should ensure proper inspection of imported pulse consignments and mitigate the associated risk prior to release of consignments for use.

S1.16: Potent role of pulses to enhance immunity modulators

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Once we are supposed to protect ourselves from the virus from outside, we need to protect ourselves beginning right from our body by strengthening the immune system. The immune system is indeed complex and is to a great extent impacted by the environment around us. Our immune system has a rather complex structure, with two arms – innate immunity and adaptive immunity. The innate immune system comprises many different kinds of cells, each that perform a different role. These are macrophages, neutrophils, eosinophils, basophils, mast cells, natural killer cells and dendritic cells. The adaptive immune system has the B-cells and T-cells. For the coordinated functioning of so many different cells, a regular and balanced supply of nutrients is crucial. Minerals and vitamins play a pre dominant role in combating immunity. Pulses are good source of potassium, calcium, iron, magnesium, zinc, selenium, vitamins A, B, C and E, Omega 3 and dietary fibres. Vitamins A is associated in development of immune system and plays a regulatory role in cellular immune responses and humeral immune process. Vitamin C has one of the highest antioxidant and helps in building the cell needed for immunity functions. Blackgram contains adequate quantity of vitamin A & C. Vitamin B (foliate) provides a vital role in DNA and protein synthesis and hence directly affects immunity functions. All pulses are good source of vitamin B. Vitamin E directly works with the immune cell function and helps in building immunity. It is a potent antioxidant and has the ability to modulate host immune function. Good source of vitamin E are the peanuts. Iron (Fe) plays an essential role in immune cells proliferation and maturation especially lymphocytes. Good source of Fe are whole pulses. Selenium reduces oxidative stress and reduces inflammation. It also helps in enhancing immunity. Pigeonpea and chickpea dal contains adequate selenium. Zinc (Zn) helps in keeping the immune system healthy. Source is the lentil and urdbean. Omega 3 fat also plays a vital role in building immunity. Rajmash, cowpea, blackgram and soybean are the rich source of omega 3. Greengram is heaped with dense nutrients including manganese, magnesium, phosphorous, copper, potassium, zinc, vitamin B and is an excellent source of protein and dietary fibre. Chickpea is super rich in protein, foliate, zinc, calcium and dietary fibre. It is, therefore, recommended that the pulses must be a part of our daily diet as it will strengthen our immunity system and protect us from virus and other numerous medical conditions. Pulses can be included in a big way in community kitchen run by various social organization now a days, enhancing the pulse components in mid-day meal and inclusion in the Public Distribution System (PDS).

S1.17: India towards *'Atmanirbharta'* in pulses

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Pulses production in India has reached a record 26.96 MMT in 2021-22 from 18.24 MMT in 2010-11. As a result, India's import dependency of pulses came down from 19% in 2013-14 to around 9% in 2021-22; which is projected to drop down further to around 3% by 2030-31. An integrated approach through the scientific innovations and government schemes for farmer's has helped India reach this milestone in order to meet the domestic requirement of pulses. New high yielding varieties and the establishment of seed hubs for quality seeds availability has further helped to enhance the yield from 656 kg/ha to 888 kg/ha. Record increase in MSP of the pulses is further encouraging farmers to enhance acreage under pulses production, as a result the area under pulses has increased from 24.91 Mha in 2015-16 to 30.37 Mha in 2021-22. Pulses procurement has increased more than 74 times during 2016-21 in comparison to 2009-14. Implementation of NFSM (Pulses) scheme across the nation has brought revolutionary change by providing quality inputs and training to the farmers. Import policy and price stabilization fund has further supported farmers in realizing the potential price for their produce and availability of pulses as a major source of protein for the Indian population at affordable cost. Further, promoting and strengthening the pulses FPO's, favourable government policies and innovative scientific innovations will lead to surplus production of pulses in India.

S1.18: Genome edited crops and plant variety protection in US and India – An technolegal review

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India holds the record for second-largest agricultural land in the world, with around 60% of rural Indian households living from agriculture. In India, the agriculture sector employs half of the country's population, and we depend significantly on the farmers to provide sustenance. The legal conceptualization of farmers' rights is globally reflected in the adoption of the International Undertaking on Plant Genetic Resources 1983 by the Food and Agricultural Organisation. The Protection of Plant Varieties and Farmers' Rights (*PPV&FR*) *Act*, 2001, aims to recognize and protect the rights of farmers in respect of their contribution toward conserving, improving, and making available plant genetic resources for the development of new plant varieties. The Bill aimed to bring harmony between the conflicting rights of farmers and plant breeders and to equate farmers' rights with those of breeders. Since 1998, The United States Department of Agriculture, USDA has granted not less than 1,952 granted Plant Variety Protection / PVPs covering transgenic plant varieties. In addition to PVPs on transgenic varieties containing foreign DNA by definition, the USDA has recently begun granting PVPs on gene-edited plant varieties. The PPV&FR Act is nascent and needs to enhance the scope to accommodate Genome edited crops and Transgenic plants.

S1.19: A profitable venture for resource poor farmers of Tiruchirappalli District

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Pulses are the important sources of proteins, vitamins and minerals and are popularly known as “Poor man’s meat” and “rich man’s vegetable”, contribute significantly to the nutritional security of the country. Currently, we are in the mid-way of self-sustaining in pulses production as we are world leader in production, consumption and import as well. India import 2-3 million tons (MT) of pulses during 2010-11, causing huge hard foreign earning. By the 2050 we will able to sustain our production and we turned to net importer to net exporter for pulses if every things goes as per plan. Another unique feature is its source of livelihood and still not a commercial business.

S1.20: Global Pulses Scenario: trend, marketing and policy initiatives for enhanced nutritional security

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Between 1961 and 2021, global dry pulses production increased over 48.67 Mt(127.16%) compare to 38.27 Mt in 1961, this is still insufficient, compared to demand at global level. In the last one decade (2012-2021) the total pulses production rose by 19.45% vis-à-vis the total pulses marketing rose by 52.73% at global market. The increased demand for pulses was evident by announcement of UNGA, 2016 as International Year of Pulses and 10th February as World Pulses Day, acknowledging benefits of pulses for human health and soil rejuvenation. India is lead producer (27.69 Mt) and consumer (29.96 Mt) of pulses in the world. India requires 39 Mt of total pulses by 2050. The productivity of pulses in India (950 kg/ha) is less than USA (1266 kg/ha) and Canada (1429 kg/ha), because of cultivating pulses in rainfed marginal lands. In recent years, India has initiated a number of measures for boosting pulses production, with the aim of reducing the dependence on imports. Procurement of pulses, regulated import, accelerated MSP and the global promotion of pulses brought dramatic transformation in total production. To meet the future pulses domestic need, growth rate of 2.2% till 2050 is required which is possible by bringing rice-fallow land into pulses production, infrastructure investment for storage and finance facility for warehouse development and value addition in pulses. Today, at least 2 billion people lack sufficient nutrients; paradoxically, there are >2 billion people are overweight/obese. This burden of malnutrition can be addresses by adding pulses rich diet for healthier world.

S1.21: Legume: The futures of sustainable plant-based food systems in India

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With the intensification of agriculture, the simplification of crop rotations, and the rise in demand for meat, dairy and cereal products, legume production and consumption are low in India. But as the environmental consequences of agriculture (biodiversity loss, high greenhouse gas emissions, water pollution) and the health outcomes of modern diets (heart disease, cancer, diabetes, obesity) become better known, so great and varied hopes are being expressed about the future role of legumes in the food system. This paper reviews these hopes, mapping the promissory narratives now orbiting around legumes. It identifies six food futures, each of which is made possible through the greater use of legumes in various production, processing, marketing and consumption contexts. These promissory narratives are theorized as contrasting responses to three major areas of contestation in the food systems literature. Namely i) the sustainability of livestock management, ii) the role of technology in different visions of the 'good diet', and iii) the merits of different models for how to make agricultural management more sustainable. It identifies the promiscuity of legumes – in terms of the range of food futures they permit – before distilling three points of consensus amongst advocates of the potential of legumes. These points of consensus relate to their nitrogen fixing capacity, their high protein content, and their long-standing historical role in the context of Indian food and farming. This map of legume dreams serves to guide deliberations amongst researchers, policymakers and industry stakeholders about the futures of plant-based food in India.

Mendelian Breeding for Crop Resilience

S2.1 Bean diversity of hills: An informal genetic reservoir

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Common beans being a very important protein source across five continents. In emerging and pressing concerns, such as climate change, beans play a crucial role in the diversification and sustainable intensification of agriculture. A better characterization and utilization in breeding is provided by knowledge about the degree of genetic diversity, identification, differentiation, and characterization of genotypes and populations. The physical parameters of seed color, shape, and size, as well as 100-seed weight ranging from 17 to 55.9 g, showed a significant genetic variation among the 172 accessions that were collected. Maize being the prominent companion crop for pole type beans across the Jammu and Kashmir . A combination of seeds is put in the fields here to prevent a total crop failure and guarantee a healthy harvest of dry beans because, according to numerous farmers in these regions, red colored beans are more susceptible to environmental uncertainties than the beans of other colors. On the other hand, to produce green pods and shell beans, improved early maturing bushy seed is sown in the fields situated in conveniently located sections of the state.However, over the past 3-4 decades, a sizable percentage of land in many regions, particularly in the province of kashmir, has been turned to apple orchards, which were formerly well-known for their maize-bean intercropping .It has led to a reduction in the production of common beans. Crop failures are increasingly occurring frequently in the area due to unusually long drought spells.Severe rains is also damaging and washing down the crop produced on the steep slopes that are common in that region. Keeping in view the sustainability of this crop and livelihood options associated with it, strong emphasis is required to safeguard this legendary crop of hills.

S2.2:A new high yielding variety "gt-104" for gujarat conditions

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a versatile, stress-tolerant, and nutritious grain legume, possessing traits of value for enhancing the sustainability of dry sub-tropical and tropical agricultural systems.The present study was conducted to develop high yielding, SMD (Sterility Mosaic Disease) and wilt resistant selections with bigger seed size and longer pod length traits in pigeon pea. The experiment involved a cross made between GNP-357 x BSMR-853 ('Vaishali') during *rabi* 2009-10 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. The segregating material was bulked till 2014 for having medium maturity, red flower, spreading type, indeterminate growth habit and SMD resistance, and was evaluated along with checks *viz.*, 'Vaishali', AGT-2, GJP-1 and BDN-2 from 2015 to 2017. The results for grain yield of this variety were found to be superior to checks, which was tested at 17 locations in Gujarat and found to be have high yield advantage of 21.9%, 21.2%, 12.5% and 27.6% over the checks 'Vaishali', GJP-1, AGT-2 and BDN-2, respectively. It was found have average yield of 1873 kg/ha which exceeded the checks. The performance of this variety was also found to be superior under AICRP network in central zone when tested with checks ICPL-87119, BDN-2 and JKM-189. Moreover, this variety was found to be resistant to SMD disease and wilt resistant. With an objective of replacing the old varieties and giving an improved variety with high yield potential along with resistant to diseases to farmers of Gujarat, a new variety GT-104 was developed.

S2.3: Impact of dormancy on seed quality of mungbean in *in-situ* germination

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Quality seeds are inevitable to meet the challenges of ever increasing population and food security.The most efficient task is to examine the seed quality of various pulse crops, particularly in mungbean and how it relates to dormancy. The aforementioned factor has taken into consideration and conducted the experiment entitled "Dormancy studies in *in-situ* Germination in Mungbean (*Vigna radiata* L.)" at Department of Agricultural Botany, VNMKV, Parbhani during *Kharif* 2020 and *Kharif* 2021. The experiment arranged in Randomized Block Design with two replications and 34 treatments has four rows of 4.5 meter long with 45 cm distance in between rows. The experimental materials included in the present study were 34 entries including 9 checks. Morphological, yield contributing and seed quality characters were recorded on field and laboratory of Seed Technology, Department of Agricultural Botany, VNMKV, Parbhani. The statistical analysis of data was carried out as per the standard method. The seed quality parameters *i.e.* germination percentage, vigour index I and II were studied among all the tested genotypes after harvest. Among the genotypes Phule M 818-8 recorded high followed by AKM-1605 and Phule M 817-13 while TBM-6 recorded low seed quality of aforementioned parameters. The dormancy has evaluated by measuring the time of opening the pods in *in-situ* germination. The genotypes *viz.* AKM-1603, AKM-1602 and TBM-4 has taken very short time to open the pods means these were found favorable in *in-situ* germination which indicates that these are less dormant genotypes. This study revealed that the dormancy of the mungbean can assess by the method of measuring the time of opening the pods by *in-situ* germination.

S2.4: Generation mean analysis for yield and its component traits in pigeon pea(*Cajanus cajan* L. Mill Sp.)

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Pigeonpea (*Cajanus cajan* (L) millsp) is the sixth most important grain legumes of tropics and sub-tropics. It is rich soure of protein ,carbobydrate and certain minerals. The present investigation, entitled "Generation mean analysis for yield & it's component traits in pigeonpea" (*Cajanus cajan* L.Mill Sp.) was undertaking during *kharif* 2018. The experimental material comprised of six generation (P_1, P_2, F_1, F_2, BC_1, BC_2) derived from three crosses *viz;* BDN 708 × BDN 2014-1, BDN 711 × BDN 2010-1 and BSMR 853 × PUSA 2001 along with standard check BDN 716. The material was evaluated during kharif 2018 in a RBD with two replications. The data was generated on yield and related traits. Analysis of variance showed highly significant differences & were present among the crosses studies for all the character. Analysis of variance was carried out to test the significance among generation studied. However, the crosses BDN 708 × BDN 2014-1 and BDN 711 × BDN 2010-1 was found superior for various trait.All characters under study showed duplicate type of gene action for two or more crosses such as transgressive segregants can be obtained in these characters. Complimentary type of gene action was observed to play an important role in the inheritance of the days to 50% Flowering, 100 seeds weight in the cross BDN 711 × BDN 2010-1 and number of pods per plant in the cross BSMR 853 × PUSA 2001.

S2.5: Heterosis studies in short duration hybrids of pigeon pea

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Pigeon pea (Cajanus cajan (L) Millsp) is the sixth most important grain legumes of tropics and subtropics. Pulses are important for sustainable agriculture, enriching the soil through biological nitrogen fixation. Presence of heterosis is an important for development of hybrid varieties in breeding program. Extent of heterosis decides the fate of the hybrid variety. The present investigation, entitled "Heterosis studies in short duration hybrids of pigeonpea (Cajanus cajan (L) Mill sp.)" was undertaking during kharif 2018. The experimental material was developed through L x T fashion using four lines and seven testers along with standard check BDN 716. The material was evaluated in RBD with two replications. The character studied were 50% flowering, days to maturity, plant height(cm), number of primary branches, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length(cm), 100-seed weight, seed yield per plant.The heterosis is the genetic expression of the beneficial effects of hybridization. In the present investigation, heterosis is estimated for all the crosses for ten yield and yield contributing characters and expressed as percent increase or decrease over better parent (BP) and over standard check BDN 716.The crosses BDN 708 x BDN2014-1, BDN 711 x BDN 2010-1, BSMR 853 x PUSA 2001 showed significant heterosis over better parent and standard check for various traits which was undertaken for study.The exploitation of heterosis for developing high yielding commercial hybrids in pigeonpea has been found highly fruitful in spite of its often-cross pollinated nature because significant heterosis is encounter F1 hybrid for successful and economical technology for commercial hybrid seed production is available.

S2.6: Genetic variability and association studies for yield and yield contributing traits in pre-breeding lines of greengram (*Vigna radiata* (L.) wilczek)

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Greengram is third most important pulse crop which is widely adapted and can improve soil fertility. The genetic variability and association studies help in selection which would increase the yield potential of greengram. Two hundred stabilized lines (F_9) obtained from the cross VBN (Gg) 2 and *Vigna radiata* var. *sublobata/2* were evaluated. The yield and yield contributing traits were recorded to evaluate genetic variability, heritability, genetic advance as % of mean and correlation among the yield and its component traits. Analysis of variance exhibited significant differences among the lines for all the ten quantitative traits indicating the presence of genetic variability. The high GCV values were found for the traits *viz*., single plant yield (30.18) and the number of pods per plant (26.80). High heritability combined with high genetic advance as per cent of mean was observed for the number of pods per plant (90.19, 52.43), single plant yield (89.58, 58.84), the number of pods per cluster (79.28, 22.70) and the number of clusters per plant (69.50, 30.22) which indicates additive gene effects. In the present study, the number of pods per plant had a high positive direct effect (0.919) on a single plant yield. Therefore, the selection for these characters would improve yield in greengram.

S2.7: Gene action and combining ability analysis for yield associated traits in blackgram (*Vigna mungo* (L.) hepper)

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Blackgram is the grain legume crop mainly grown in variable edaphic and weather conditions in India results in low productivity. However, the yield of blackgram can be improved by breeding methods involving potential parents by analysing the combining ability. A set of three female parents (CO 5, CO 6 and ADT 5) and six male parents (MASH 1008, VBN 6, VBN 8, VBN 9, VBN 10 and VBN 11) were crossed in Line × Tester mating design. The crosses along with parents were evaluated for ten quantitative characters. The gene action for all the traits and combining ability of the parents and crosses were analysed. The predominance of non-additive gene action was observed for all the traits studied. The parents, CO 5 and VBN 11 were found to have significant positive general combining ability effect (*gca*) for yield and its component traits. The crosses, CO 5 × VBN 8, CO 5 × VBN 11 and ADT 5 × VBN 10 showed significant specific combining ability effect (*sca*) for single plant yield. Among the crosses, CO 5 × VBN 8 was identified as the best cross based on *sca*, *per se* performance, *gca* of parents and heterosis for yield and yield component traits. For single plant yield, CO 5 × VBN 11 was performed well for all the above parameters. Hence, these two crosses could be utilized for recombination breeding to improve yield in blackgram.

S2.8: A new high yielding and MYMV resistant mung bean variety "gm-6" for gujarat conditions

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Mung bean (*Vigna radiate* L.) Wilczek is an important short duration pulse crop of Gujarat and it grows in all three seasons of year. The present study was conducted to develop high yielding, an early maturing, compact (non-viny), bunchy pod bearing, MYMV resistance in mung bean. The experiment involved a cross made between Meha x GM-4 during 2010 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. The segregating material was handled upto summer 2013 and bulks were derived which were evaluated along with checks *viz.,* Meha, GM-4 and GAM-5 from 2014 to 2016. In overall performance for all summer season trials, GM-6 was found to be superior with 7.65%, 41.12% and 15.58 % against the checks Meha, GM-4 and GAM-5 while considering all kharif trials it exhibited 13.85 % and 10.03 % increase over Meha and GAM-5, respectively. So considering both seasons for overall performances of 29 tests in Gujarat it was found promising where it recorded 11.1 %, 11.7 % and 13.7 % increase over check varieties Meha, GM-4 and GAM-5. While under AICRP network in kharif-16 in central zone (ten locations) it has proved superiority with 64.6 %, 8.2 %, 22.6 % and 3.1 % increment against GAM-5, BM-49, AKM-8802 and PKV AKM-4 respectively. Therefore, a new variety GM-6 was developed, which has high yield potential, earliness, short stature, bold seeded and long pod, synchronous maturity along with MYMY resistance which is suitable in the existing cropping system.

S2.9: Gene action and combining ability for yield related traits in greengram (*vigna radiata* (l.) wilczek)

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Narrow genetic base and lack of exploitable variation have become a major constraints for yield improvement in greengram. Identifying genetically superior parents and breeding scheme to be adopted becomes a pre-requisite for the development of elite cultivar. Thereby, blending the knowledge on gene action and combining ability plays a key role. In the present study, combining ability analysis was carried out in twenty-five crosses derived out of Line × Tester mating design (5 x 5) using the parents with the bruchid resistant lines (V 2709 and V 2802) and bold seeded testers (VGG 16 - 058, VGG18-002, WGG42, BGS 9 and GAM 5) In addition to the above parents, three high yielding lines were also used. The hybrids, parents and the check variety were evaluated in RBD with two replications and ten quantitative characters were recorded. Non-additive gene action was found to be prevalent for the quantitative traits observed. Exploring the *per se* and *gca* effects, COGG 13-39 and VGG 18-002 were adjudged as the best parents and the crosses involving above parents will be productive for synthesizing a dynamic population with superior recombinants. Considering the *per se, sca* and heterosis, the best crosses identified for single plant yield and pods per plant were, V 2709 × GAM 5 and COGG 13-39 × VGG 16-058. These crosses can be further exploited to obtain transgressive segregants for higher yield, bold seeds and bruchid resistance through appropriate breeding strategy.

S2.10: Genetic analysis of greengram (*vigna radiata* (l.) wilczek) genotypes on the basis of yield and yield attributing characters during summer season

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In the present investigation ten genotypes of greengram were evaluated for six characters at the Instructional Farm, Sasya Shyamala KVK ,RKM Vivekananda Educational & Research Institute, Arapanch, Sonarpur Kolkata during summer season. The experiment was carried out in RBD with three replications. The genotypes showed significant all the characters like days to 50% flowering, days to maturity, seeds per pod, pods per plant, 100 seed weight and yield/ha. The genotype RSM-51 (933.33 Kg/ha) recorded highest yield per ha and pods per plant whereas highest 100 seed weight (g) and seeds per pod was recorded by the genotype Utkarsha (4.81g). The phenotypic coefficients of variation (PCV) for all the traits were higher than the corresponding genotypic coefficients of variation (GCV) which indicated that these characters are influenced by the environment. The high heritability in broad sense coupled with high genetic advance percentage of mean were recorded by the characters seed per pod, pods per plant, 100 seed weight and yield per ha indicating that the heritability of these characters were most likely due to additive gene effects for controlling these traits. The yield per ha showed significantly positive correlated with days to 50% flowering, pods per plant, seeds per pod and 100 seed weight while days to maturity showed positive but non-significant with seed yield per ha both genotypically as well as phenotypically.

S2.11: Pdkv Ashlesha : A High Yielding, Moderately Resistant, Medium Duration Pigeonpea Variety For Central Zone of India

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Pigeonpea is one of the important pulse crops of Maharashtra, Gujrat, Chattisgarh, Madhya Pradesh, grown either as sole or mostly as intercrop. Most of the pigeonpea varieties under cultivation are from mid-early and medium maturity group. Hence, the breeding work is more concentrated to develop high yielding, multiple disease resistant genotype from medium and mid-early group. Accordingly, a medium duration genotype, AKTM 1637 was developed by Dr. PDKV, Akola and found promising in station trails. Hence, it was entered in Initial Varietal Trial-(Medium) in which it performed well and promoted to Advanced Varietal Trial-1 and AVT-2 (Medium) subsequently in CZ. Based on the mean performance of three years, AKTM 1637 (1933 kg/ha), has recorded 15.26 %, 29.73 % and 13.97 % superior yield performance over checks in CZ. In Agronomic trials it was found to be fertilizer responsive up to 125% and yielded better than check BDN 716. Further, AKTM 1637 has shown moderately resistant reaction to wilt and SMD, *Phytophthora* blight, *Macrophomina* blight and *Cercospora* leafspot and also shown similar reaction to pod borer and *maruca* as in case of check varieties. It has red medium to large size seeds with 19.50 % protein and 73.30 % *dal* recovery. AKTM 1637 was found promising in all respect and accordingly, it has been identified and released for CZ in the name of "PDKV Ashlesha" and further notified by CVRC. It is expected that "PDKV Ashlesha" will contribute to enhance the production and productivity of pigeonpea crop in CZ of India.

S2.12: New Cowpea Genotype PGCP-63 for summer rice - fallow cultivation in kerala

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Cow pea (*Vigna unguiculata (*L.Walp.) cultivated in Kerala State for both vegetable and grain purpose during rabi and summer rice fallows. In order to test the yield performance of new cow pea genotype PGCP-63, frontline demonstrations were conducted at five different locations of Palakkad district in Kerala State during 2021-22. Based on the yield data received from farmers, PGCP-63 recorded the yield performance of 2535kg/ha where as the local check Kanakamony recorded the yield performance of 1792 kg/ha. The new cow pea genotype matures in 72 days. With regard to quality characters, it is having crude protein of 24.29 per cent, tannin (mg/g) content of 0.71 and with 84 per cent digestibility. The cooking time is 42 minutes. The young pods are light green and highly tasty. The new genotype is highly preferred by the farmers due to its dual nature. It can be promoted to cultivation to farmers in Kerala in large scale in summer rice fallows.

S2.13: Identification, characterization of dry root rot resistant lines and development of mapping population in chickpea

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Dry root rot (DRR) caused by *Rhizoctonia bataticola* [(Taub.) Butler] is a serious constraint to chickpea production in warm and arid regions. Under changed scenario of climate the disease is becoming more prevalent in central and southern zone of India. Therefore, identification of resistant source and its utilization in breeding programme is very much important. In the present study, 55 genotypes were screened in sick-pots against DRR. Six genotypes (K 850, KAK 2, H 208, BG 14-4, BG 12-119 ICC 14395) showed no wilting symptoms in sick pots are categorized as resistant. The two genotypes; ICC 14395 and Pusa 212 resistant and susceptible to DRR respectively were chosen for further study. The paper towel method of screening categorically differentiated these two genotypes for DRR. The endophytes isolated from these two genotypes were characterized and studied for their antagonistic effect. The fungal endophytes isolated from ICC 14395 showed antagonistic response against the pathogen. The mapping population was developed by hybridization between these two genotypes and F_2 lines were advanced by single seed descent method. Phenotyping of mapping population in sick pots was carried out at F_6 generation. Twenty lines found resistant, 40 were moderately resistant. 51 were susceptible and 46 were highly susceptible to DRR. The two parents were also screened for 154 SSR markers to identify the polymorphic markers. 15 markers were found polymorphic between the parental lines. The mapping population will be screened these markers for construction of molecular map and identification markers linked to DRR resistance in chickpea.

S2.14: Development of pre-breeding lines through interspecific hybridization between greengram and ricebean

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Ricebean (*Vigna umbellata)* is cultivated mainly in eastern and northeastern India as a grain and fodder crop. The minor pulse has been little studied but its prolific growth and abundant pods suggest that it has a potential for high grain and fodder yield. Studies revealed that this species has high level of resistance to the bruchid beetles, powdery mildew, yellow mosaic virus, cercospora and bacterial leaf spot from which all of the other species of this genus suffer greatly. Hence, an attempt was made to cross *Vigna radiata* and *V. umbellata* to transfer the important traits and to develop pre-breeding lines. Four female parents of greengram and six accessions of ricebean were crossed and F_1's were evaluated. The hybrids of the crosses *viz*., CO6 × CORB9, CO(Gg)7 × RRB18 and CO(Gg)7 × LRB576 were confirmed by using a dominant morphological marker *viz.*, hypogeal germination and followed by SSR marker CEDG115. Two hybrids *viz.*, CO6 × CORB9 and CO(Gg)7 × RRB18 were found to be sterile. The partial fertility and poor pod set was observed in the hybrid CO(Gg)7 × LRB576 (17–21 per cent pollen fertility).The seeds collected from the above cross were forwarded to F_2 generation. The progenies were advanced and evaluated from F_3 to F_8 generation. The segregation of greengram type plants were observed from F_6 generation along with ricebean type progenies. The pre- breeding lines thus developed were evaluated for biotic stresses. This study will be useful for the improvement of greengram.

S2.15: Status and Strategies of Moth bean (*Vigna aconitifolia*) Improvement in Arid Region

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Moth bean [*Vigna aconitifolia* (Jacq.) Marechal] is important pulse crop of Indian arid zone receiving erratic and less rainfall. Since, last three decades it is being cultivated over an area of 1.0 to 1.5 million hectares with productivity hovering around 300 kg per hectare. One of the main region of low productivity is its cultivation exclusively under rainfed conditions where other crops hardly produce biomass. It has been cultivated in moisture scarce situations for decades resulting in need based evolution to such hostile situations providing elasticity and plasticity in it genome by synthesizing adaptive proteins. The crop has, therefore, survived with much needed morphological modifications like, prostrate growth behaviour, broad leaves with dense canopy, higher biomass but poor partitioning, slow growth, indeterminate growth habit, fast penetrating tap root system converting carbohydrate to newer leaves compared to pods even at maturity. Thus, there is need to increase productivity of moth in the genetic background of drought avoidance. Manipulation of avoidance to escape mechanism would be therefore, expected to pay rich dividends for increasing grain yield. Thus, first approach in moth bean must be induction of early maturing mutants having 25-28 days flowering and 55-58 days maturity. The second approach would be to attempt crossing programme between traditional varieties with drought avoidance and varieties showing drought escape tendency. The idea is to combine genes for both escape and avoidance phenomena with altered plant type having profuse bearing on main stem supported by sprawling branches for adaptation under long range of ecological niches.

S2.16: Effect of mutagens on seedling parameters and induced variability in Cluster bean (*Cyamopsis tetragonoloba*)

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Cluster bean, an annual legume cultivated in north western parts of Indian arid zone covering states of Rajasthan (> 80 % area), Gujarat, Haryana and parts of Punjab over an area of 5.0 million hectares. Exploitation of available diversity for inducing earliness and yield improvement through hybridization is cumbersome due to small flower size and very poor seed setting in manually hybridized buds. Therefore, seeds of two distinct varieties (RGC-936 & RGC-1066) treated with graded doses of gamma rays (100, 200, 300, 400, 500, 600, 700, 800. 900 & 1000 Gy) and EMS (0.1, 0.2, 0.3 & 0.4 %) were sown in field as well as in pots. No significant differences were observed in germination among the treatments but after 15 days of sowing yellowing of leaf tips started and severe mortality observed beyond 700 Gy. Only few plants survived in 1000 Gy treatment that too with stunted growth. A gradual reduction in seedling parameters were recorded in both the varieties in M_1 however differential behaviour of varieties was conspicuous. Besides seedling parameters a clear-cut reduction in number of pods, pod length, seeds per pod and seed yield per plant were recorded beyond 500 Gy showing the effectivity of gamma rays. Further, a wide range of variability was observed for yield and yield contributing traits in M_2 generation. On the basis of per se performance 35 M_3 progenies identified for further evaluation and selection of promising mutants for earliness and yield suitable for arid zone.

S2.17: Combining ability and heterotic response for yield and its components in faba bean (*Vicia faba* L.)

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A line x tester set of 45 F_1's and their 18 parents (15 lines and 3 testers) alongwith two checks were evaluated for twelve characters. The variances due to lines were found non-significant for all the characters except plant height, number of pods per plant, biological yield per plant and grain yield per plant. This indicated less importance of general combining ability and additive gene effects in expression of 8 out of 12 characters. The mean squares due to lines x testers' interactions, indicating importance of specific combining ability and non-additive gene effects, were found highly significant for all the characters. The five best crosses were EC 243626 x HB 9-16, HB 30 x HB 9-15, EC 329627 x HB 9-15, EC 263620 x HB 9-16 and EC 301470 x DFB 14-1 which showed significant and positive *sca* effects for grain yield per plant as well as some other yield components. In case of grain yield per plant, heterobeltiosis varied from -35.75 to 100.74 per cent and standard heterosis ranged from -35.10 to 46.30 per cent over SV_1 *i.e.* HFB 1 and from -33.26 to 50.46 per cent over SV_2 *i.e.* Vikrant. The most desirable crosses showing high mean performance alongwith high heterosis for grain yield per plant were EC 243626 x HB 9-16, HB 30 x HB 9-15, HB 50 x HB 9-15, HB 10 x HB 9-16 and HB 10 x HB 9-15.

S2.18: Variability, correlation and path coefficient analyses for yield and yield contributing characters in faba bean (*Vicia faba* L.).

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An experiment was carried out at A.N.D.U.A.T, Kumargang, Ayodhya during *Rabi* season of 2018-19. Experimental material is comprised of 44 genotypes including 4 checks i.e. Vikrant, ET- 218787, ET- 218751, ET- HFB- 1, which were sown in augmented block design. The entry ET-218781 produced highest seed yield per plant (12.46 g) and also showed highest mean performance for 100- seed weight, harvest index. The most promising line showing highest seed yield with mean performance for other yield contributing characters were identified as ET- 218721, ET- 218766, ET- 218767, ET- 218745, ET- 218765.Pods per plant, number of seeds per pod, 100-seed weight and harvest index showed significant and positive correlation with seed yield per plant. Path analysis identified harvest index, pods per plant and biological yield per plant as important components having high order of direct effect; and the maximum indirect effects on seed yield per plant was exerted by pods per plant via harvest index; seeds per plant (0.19656), plant height, pods per plant and 100 seed weight via biological yield per plant; harvest index, seeds per pod, biological yield per plant and days to maturity via pods per plant. The result of the present investigation suggested that the entry ET- 218721 showed highest mean yield performance and therefore can be used as a parent in breeding varieties for high yield. The characters showing significant positive correlation and direct effect on yield would be highly effective and efficient in improving yield.

S2.19: Phule Kaveri (Phule Tur 11-4) : The new mid early duration pigeonpea variety for south India.

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Pigeonpea [*Cajanus cajan* (L.) Millsp] is an important grain legume crop in the semi-arid tropics of Asia and Africa due to its high protein (20-22%) content. The diseases like wilt, sterility mosaic and occurrence of mid-season and terminal droughts during reproductive phase were limiting factors in production of late maturing pigeonpea varieties. The efforts were made to develop the mid early maturing pigeonpea varieties(<165 days) with high yield and tolerance to sterility mosaic and wilt diseases by using pedigree breeding. Phule Kaveri (PT 11-4) the mid-early duration high yielding pigeonpea variety was developed at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth Rahuri and was released by Central Variety Release Committee during 2022. It matures in 164-165 days, suitable for *kharif* sowing. The variety has light brown color and bold seed with 100 seed weight of 11.52 g with a protein content of 20.17 per cent. It is moderately resistant to *fusarium* wilt (25.90%), sterility mosaic (27.82%) diseases and tolerant to pod fly. In AICRP trials (20 locations in 2019-20 to 2021-22) this variety recorded yield on an average of 1591 kg/ha which is 22.86 , 37.87 and 21.64 percent higher over the national checks Phule Rajeshwari, PRG 176 and TS-3R respectively. The yield potential of this variety was 2441 kg/ha. The variety Phule Kaveri (PT-11-4) is suitable for south zone of India which includes Tamilnadu, Karnataka, Andhra Pradesh, Telangana and Odisha states.

S2.20: Phule Trupti (Phule Tur 10-1) : The new mid early duration pigeonpea variety for central India

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Pigeonpea [*Cajanus cajan* (L.) *Milllsp.*] is an important often-cross pollinated grain legume crop of semi-arid tropics grown under rainfed condition. Pigeonpea crop is sensitive to biotic and abiotic stresses such as wilt, sterility mosaic diseases and terminal drought, which reduces the productivity in late maturing (>185 Days) varieties. Hence, efforts were made to develop the mid early maturing pigeonpea varieties(<165 days) with high yield and tolerance to sterility mosaic and wilt diseases by using pedigree breeding. Phule Trupti(PT 10-1) the mid-early duration high yielding pigeonpea variety was developed at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth Rahuri and was released by Central Variety Release Committee during 2022. It matures in 162-165 days, suitable for *kharif* sowing. The variety has 100 seed weight of 10.81 g with a protein content of 19.25 per cent. It is moderately resistant to *fusarium* wilt (19.89%), sterility mosaic (18.37%) diseases and tolerant to pod fly. In AICRP trials (25 locations in 2019-20 to 2021-22) this variety recorded yield on an average of 2266 kg/ha which is 26.03, 33.45 and 42.97 percent higher than the national checks TJT 501, Phule Rajeshwari and BDN 711 respectively. The yield potential of this variety was 3203 kg/ha. The variety Phule Trupti (PT-10-1) is suitable for central zone of India which includes Maharashtra, Madhya Pradesh, Gujarat and Chhattisgarh states of the country.

S2.21: Estimation of genetic variability, character association and path analysis for yield and its contributing traits in chickpea (*C. arietinum* L.)

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The present investigation entitled "Estimation of genetic variability, Character association and path analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.)" was carried out with forty four genotypes. The experiment was conducted in Randomized Block Design with three replications at Pulses Research Unit, Dr, Panjabrao Deshmukh Krishi Vidyapeeth, Akola during Rabi 2020-21.The observations were recorded on eight characters. Analysis of variance indicated significant differences among the genotypes for different morphological characters. The phenotypic coefficient of variation was higher than genotypic coefficient of variation. The high values of GCV and PCV observed, in eight characters. The highest estimates of heritability coupled with higher genetic advance as per cent of mean was observed for characters number of secondary branches per plant followed by seed yield per plant, number of pods per plant, seed yield per plot, and 100 seed weight. The seed yield per plant was significant and positively correlated with number of primary branches per plant, number of secondary branches per plant and number of pods per plant. Path coefficient analysis indicated that number of pods per plant, 100 seed weight, plant height, and number of primary branches per plant showed high positive direct effects as the major yield contributing traits for enhancing the yield in chickpea.

S2.22: Pattern of variations in chickpea landraces collected from Singrauli, Sidhi and Rewa Districts of Madhya Pradesh

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Chickpea is a leguminous crop that offers good nutrition to people across the world. A set total of 16 chickpea accession were collected and deposited in gene bank at NBPGR-New Delhi. During *rabi* 2021; 16 chickpea accessions were grown for seed multiplication and characterization at Indian Institute of Pulses Research (IIPR)-Regional Station- Bhopal. Variation was observed for 6 qualitative and 10 quantitative traits and among qualitative traits; purple flower colour, erect and semi-spreading plant type, normal and serrated leaf type, one flower/peduncle and presence of stem pigmentation and medium leaflet size were predominant in all 16 accessions whereas, quantitative traits in ranged; 44.4 to 64.8 cm for plant height; 60 to 79 days for 50 percent flowering; 123 to 136 days for maturity; 4.66 to 7.33 for primary branches; 9.33 to 12 for number of secondary branches; 39.5 to 100.5 for pods/plant; 21.9 to 32.8 cm for 1st pod bearing length; 13.9 to 29.0 grams for 100 seed weight and 1.73 to 3.84 kg grain for plot (4.8 m^2 area). IC 637049 (3.84 kg) was the highest yielder followed by IC 637076 (3.83 kg) whereas, lowest yield was recorded for IC 637071 (1.73 kg). High variability for 100 seed weight was also observed where IC 637077 (29.0 grams) showed maximum seed weight followed by IC 637076 (26.4 grams) whereas, lowest was observed in IC 637031 (13.9 grams).

S2.23: BAUPP16-30 : A promising genotype of Pigeonpea (*Cajanus Cajan*) for Jharkhand state

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Pigeonpea is one of the most important pulse crops grown in many states of India including Jharkhand and plays an important role in sustainable food and nutritional security. Increased pigeonpea production is possible with high yielding varieties suitable for different agro-climatic conditions.In recent year pigeonpea production has enhanced in Jharkhand manifold due to favourable climatic condition. Production and productivity is primarily depends on availability of suitable varieties among the farmers. To extend the better of choices of pigeon variety, a new genotype of – BAUPP16-30 has been identified for farmers of the state. Pedigree/SSD selection method of breeding was used to develop the genotype form the crossed material of CORG 9701 X AL 1571. The genotype has been tested in various trials like station trial, coordinated trial and multiplication trial during 2017 to 2020 against the checks BDN – 2 , JKM 189, BA – 1 and found stable over the location in terms of yield and other agronomic traits. The Average grain yield was 19-20 q/ha with maturity 184-186 days (medium maturity group). In coordinated trial it yielded 15.3 q/ha at Ranchi with an average of 17 q/ha over 12 location of central zone. The average plant height of the variety is 200-210 cm. The genotype was found to be resistant to wilt (9.2%) and tolerant to Pod borer complex (1.4%). Performed good under moisture stress condition. High heritability combined with high genetic advance was recorded for number of pods per plant, clusters per plant and plant height indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

S2.24: Introgression profiling and evaluation for productivity traits of chickpea derivatives from *Cicer reticulatum* and *C. echinospermum*

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Chickpea (*Cicer arietinum* L.) is the world's second most important food legume crop species. Genus '*Cicer*', includes 36 perennial and 10 annual species; of which, *Cicer arietinum* is the only species domesticated and under cultivation. The major constraints affecting chickpea productivity are its narrow genetic base, higher self-fertilization rate and 'single domestication' event. Sustained efforts are required to increase the yield potential of chickpea by introducing un-adapted genes from distantly related *Cicer* sp. A total of 90 interspecific derivatives derived from four different crosses viz., I: PBG5 × ILWC229; II: BGD72 × ILWC229; III: PBG5 × ILWC246 and IV:BGD72 × ILWC246 were evaluated for productivity traits during 2020-21 and 2021-22 at PAU, Ludhiana. Significant differences were revealed among the derivatives for all the productivity traits. Seed yield per plot had a positive and highly significant correlation with biological yield per plot along with positive direct effect of biological yield per plot on seed yield. Around 450 SSR markers were used for introgression profiling. The per cent introgressions in the derivatives of four crosses, ranged from 0.00 to 38.89 %. Overall, out of 90 derivatives; in cross I: PAU21-1, crossII: PAU21-34, cross III: PAU21-69 and cross IV: PAU21-74 recorded maximum seed yield per plot with 31.49%, 11.77%, 29.32% and 7.15% introgressions, respectively and can serve as potential donors in the ongoing chickpea breeding programs.

S2.25: Mapping of genes for efficient Chickpea-*rhizobia* symbiosis using inter-specific population of *Cicer*

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Chickpea (*Cicer arietinum* L.) is a cool season food legume, originated from Turkey. There is an increasing concern for the sustainability of agriculture due to the depletion in soil fertility status, area, productivity along with the nutritional value of food crops. With this view, an inter-specific RIL population of a cross between GPF 2 (released cultivar having moderate nodulation and N-fixation traits) and ILWC 141 (*C. reticulatum*; having high nodulation and N-fixation traits) was utilized for the mapping of biological nitrogen fixation (BNF) traits. Phenotypic evaluation was done for BNF traits such as nodule number, leghaemoglobin content, chlorophyll content and nodule dry weight. For analysis, genotypic data were generated using genotyping by sequencing (GBS-ddRAD) approach. A total of 25,233 filtered SNPs were obtained based on 2X genomic coverage but post filtering, 520 SNPs were eventually used for linkage map generation and bi-parental QTL mapping using QTL ICi mapping software. For nodule number, QTLs were mapped on linkage groups (LG) 1, 4, 5 and 6, while for leghaemoglobin content on LG 1, 3, 6 and 7. Out of 140 RILs, RIL number 122 exhibited high nodule number and leghemoglobin content, while RIL number 104 and 9 had high nodule number and chlorophyll content. Significant SNPs underlying the QTLs were identified for the traits which will act as template for development of molecular markers. These markers along with potential donor RILs identified can be used in marker-assisted selection (MAS) based chickpea breeding programme.

S2.26: DUS Characterization of Chickpea Varieties based on Plant and Seed morphological traits

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Chickpea (*Cicer arietinum* L.) is an important leguminous crop rich in protein (20 - 26%), carbohydrates (62%), fats (4%), and trace elements, and is also a vital source of minerals such as calcium, copper, and iron and niacin. Protection of Plant Variety and Farmers Right Authority started PVP legislation Phase II to conduct the DUS testing of different crops to give them protection under PPV & FRA act 2001. The varietal Stability, Uniformity and Distinctness depend on varietal characterization, identification and genetic purity assessment. This is important for Plant breeders, Farmers, Certification Officers, Seed Production Officers and Seed Growers, for maintaining quality of the seed. To conduct a DUS testing of chickpea it is grown in two independent season and location.Rahuri is one of the DUS testing Centre in case of Chickpea. During the *Rabi* 2021-22 DUS trial conducted for Two Candidates varieties along with Twenty Reference varieties evaluated for various plant and seed morphological traits at Pulses Improvement Project, MPKV, Rahuri. Characterization was done as per the DUS guidelines received from PPV & FRA authority. The results of the present study clearly indicated that the genotypes of chickpea can be distinguished and identified on plant and seed morphological characters. These differences in morphological traits were useful in identification of individual chickpea genotypes. It was helpful to the plant breeders and Farmers to get a protection for their innovation.

S2.27: Screening of chickpea germplasm lines for drought tolerance based on Relative water content (RWC) and Membrane stability index (MSI) under rainfed condition

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Chickpea is one of the most important legume crop in India. It is mostly grown under rainfed conditions. Biotic and abiotic stresses are the major constraints in chickpea production. Among them drought stress is one of the major limiting factor in chickpea production. In present study of chickpea five hundred germplasm lines along with four checks were evaluated under moisture stress in Augmented Design at Pulses Improvement Project, MPKV, Rahuri-413 722, Dist.: Ahmednagar (M.S.), India during *Rabi* 2021-22. The observations on Relative Water Content (RWC) (%), Membrane Stability Index (MSI)(%), Canopy Temperature (^{0}C), Days to 50% flowering, Days to maturity, Number of pods per plant, 100 seed weight (g) and Harvest index (%) were recorded. The germplasm lines having the higher RWC and MSI values reflecting the higher capability to tolerate the drought stress. From the present investigation the germplasm lines ICC 181, ICC 595, ICC 1016, ICC 5929, ICC 6363, ICC 6367, ICC 6372, ICC 6395 and ICC 6788 exhibited higher values of Relative Water Content (RWC) and Membrane Stability Index (MSI) which are drought tolerant. Therefore molecular analysis of these germplasm lines should be done to confirm drought tolerance and these line can be used in crossing programme so as to develop drought tolerant varieties as well as can be screened one more year and the lines which having common over the years can be identified and registered as a drought tolerant donor.

S2.28: Development of YMD resistant and dual season photo insensitive mungbean genotypes through interspecific hybridization

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Development of YMD resistant mungbean breeding lines for dual season cultivation can help in improving its adoption at large scale. A set of 22 mungbean interspecific derivatives lines derived from mungbean (*Vigna radiata*) x urdbean (*V. mungo*) and mungbean (*V. radiata*) x ricebean (*V. umbellata*) developed at PAU were evaluated for suitability to dual season cultivation and Yellow Mosaic Disease resistance. In summer season, the interspecific derivatives SML 2301 (10.69 g), SML 2388 (10.11 g) and SML 2399 (11.6 g) were found to have significantly higher values of seed yield per plant than mean value. In the *kharif* season, SML 2315 (8.45 g), SML 2375 (6.93 g) and SML 2388 (7.27 g) yielded significantly higher than the trial mean. All the interspecific derivatives were highly resistant to YMD. The interspecific derivatives *viz*; SML 2388 and SML 2399 out-yielded the respective best checks in both the seasons and hence showed immense potential as dual-season YMD resistant lines for cultivation. In both the seasons, pods per plant, biological yield and harvest index were significantly and positively correlated with economical yield. Similarly, biological yield and harvest index chipped in positively and directly towards economic yield in both the seasons. Molecular analysis of the parents and the derivatives revealed that the SSR-9 could be linked with the segment governing YMD resistance in these lines. Thus, upon validation, SSR 9 could serve as a linked marker for use in marker assisted resistance breeding programmes.

S2.29: Transgressive Segregation studies in F_2 Generation in Mungbean (*Vigna radiata* (L.) *Wilczek*)

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An experiment was conducted to identify the transgressive segregants for yield and yield contributing characters in F_2 population of three crosses in mungbean. In most of the tansgressive segregants, in each of the three crosses, better parent yield was transgressed with transgression of one or several other characters. In general, the highest proportion of transgressive segregants were recorded for number of pods per plant, followed by number of pods per cluster, 100 seed weight, yield per plant, number of seeds per pod. In most of the transgressive segregants, in each of the three crosses, better parent yield was transgressed simultaneously with transgression of one or several other characters. Simultaneous transgression of grain yield per plant in association with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant and 100-seed weight was observed more frequently. It was concluded that either grain yield per plant is dependent on this character or there may be linkage drag, so that genes responsible for these characters move together. The most promising transgressive segregants observed in F_2 generation were Plant No.104 of Cross 1, Plant No.11 of Cross 2 and Plant No. 112 of Cross 3.

S2.30: A New Lentil Variety for North Western Plain Zones of India

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Lentil is an important *rabi* season legume crop of global significance. It is a nutritionally rich crop having the biomolecules vital for human health viz., proteins, carbohydrates, vitamins, minerals and fibre. Not only it improves the health patterns, but also enriches the organic carbon content of soil, thereby improving its fertility status. Punjab Agricultural University, Ludhiana has developed a new variety LL 1613 which has been recommended for cultivation under timely sown irrigated conditions in the North Western Plain Zone of India during 2022. The candidate variety developed from the cross LL 1112 × PL 02-6 exhibited distinct yield superiority over best check Pant L 063 and it was moderately resistant to rust and wilt along with good culinary properties. Hence, the variety was identified for the North West Plain Zone comprising states of western Uttar Pradesh, northern Rajasthan, Delhi, plains of Uttarakhand, Punjab, Haryana and part of Jammu and Kashmir. The variety possesses green stem with very light purple tinge. It has an average plant height of 37 cm. The variety flowers in 96 days and matures in 131 days. The 100-seed weight of this variety is 2.3 g. It has a protein content of 23.29 %. The variety recorded an average seed yield of 1617 kg/ha with a yield superiority of 23.72 % and 14.28 % over the check varieties L 4147 and Pant L 063, respectively on the basis of 17 research trials conducted in the zone during 2019-20 to 2021-22.

S2.31: Assessment of GCV, PCV, heritability and genetic advance for seed yield and its attributing traits in Lentil (*Lens culinaris* Medik)

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The present investigation was carried out with 40 genotypes of lentil laid out in randomized block design with three replications during rabi 2021-22. The material was employed for the assessment of genetic variability, heritability and genetic advance for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of peduncles per plant, number of pods per plant, biological yield per plant, hundred seed weight, harvest index and seed yield per plant. Analysis of variance revealed significant differences among the genotypes indicating presence of good amount of genetic variability in the genotypes for all the characters studied. Relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the character's expression. High estimate of GCV, heritability coupled with high genetic advance as per cent of mean was found for the characters like number of pods per plant, biological yield per plant, number of branches per plant, number of peduncles per plant indicating the contribution of additive gene action in the inheritance of these traits hence direct selection would be rewarding. Genotype RKL 22-69, RKL 22-30, RKL 20-26, RKL 22-41 and RKL 22-75 were superior for seed yield per plant and component traits, hence can be used in further breeding programme. Seed yield per plant was significantly correlated with biological yield per plant, harvest index, number of pods per plant, number of peduncles per plant, number of branches per plant and plant height.

S2.32: Genetic variability, heritability and genetic advance in pigeon pea [*Cajanus cajan* (L.) Millspaugh] genotypes for seed yieldand agronomic traits

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Nineteen elite pigeonpea genotypes were evaluated to estimate the genetic variability and heritability for grain yield and yield contributing characters during *Kharif,* 2021 at RARS, Warangal, Telangana state. The analysis of variance revealed significant differences among the genotypes for the traits studied indicating that a large amount of variability was present in the genotypes. Yield ranges from 774 kg/ha to 1575 kg/ha among genotypes with a mean of 1071kg/ha. The values of genotypic and phenotypic coefficients of variation (GCV and PCV) were low for days to 50% flowering (GCV: 4.44; PCV: 4.44) and 100seed weight (GCV: 9.32; PCV: 9.59), while genetic variability moderate for plant height (PCV:12.55) and is high for grain yield (kg/ha) (PCV :21.29). The character *viz.,* pods per plant (H(%): 71.00; GA as % of mean: 27.56) showed high heritability with high genetic advance indicating the preponderance of additive type of gene action and selection may be effective. The characters like days to 50% flowering (H(%): 97.14; GA as % of mean: 8.94), days maturity (H(%): 97.14; GA as % of mean: 6.71) recorded high heritability and low genetic advance,while,100seed weight (H(%): 94.47; GA as % of mean: 18.66) exhibited high heritability with moderate genetic advance and grain yield (H(%): 58.71; GA as % of mean: 25.75) recorded low heritability and high genetic advance indicating the non-additive gene action and selection may not effective and heterosis breeding and identification transgressive segregants is the effective way to improve these traits.

S2.33: Morphological characterization of aluminium tolerance in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Al toxicity is the major limiting factor in acidic soils. The management approaches for soil amelioration by application of lime to raise soil pH does not improve subsoil acidity and are economically not feasible. Under acidic soils (pH <5.5), Al gets solubilized into toxic mononuclear (Al^{3+}) which induces phytotoxicity in crop plants. Therefore, in the present study, seventy diverse genotypes of pigeonpea were evaluated for aluminum tolerance under induced acidic conditions in hydroponics. Al stress responses of these genotypes on various morphological attributes were observed on the basis of different relevant parameters viz. shoot and root length and biomass accumulation (Fresh weight and dry weight) for comparative evaluation of all the genotypes taken under study. The major and earliest visible symptom of Al toxicity is inhibition of normal root growth which appears in few minutes to hours. The root system architecture was studied in detail using root image analyzer. Al accumulation in root tips was examined using Morin stain and the regrowth of roots was studied with Hematoxylin staining. Significant genotypic variation for Al stress tolerance was observed among the genotypes screened under hydroponic conditions. The highly tolerant genotypes for Al stress induced under acidic condition were selected and used in breeding programme.

S2.34: Climate resilient new genotype of Kabuli chickpea HK 13-114 identified for High seed yield

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Pulses are climate smart and mitigate the effects of climate change but their narrow genetic diversity has been always a major constraint to their improvement for wider adaptation. The changing climate scenario has made it more challenging to breed and develop climate-resilient genotype for high seed yield along-with high seed index in kabuli chickpea. In Haryana area under chickpea is decreasing from 125, 000 hectare (2001-2002) to 36, 000 hectare only (2020-2021). Among the total chickpea area in Haryana, kabuli chickpea is less than 5 % area only. Advanced farmers adopt to cultivate only kabuli chickpea due to its high market price i.e. double price than desi chickpea. In late sown condition (after 15th November), there is less germination percent in kabuli chickpea. To overcome this problem, new genotype HK 13-114 identified having very good germination and seed vigor during vegetative stage. Station trials conducted during Rabi 2018 to Rabi 2022 reported 2206 kg/ha seed yield which is 10.03 percent higher over check variety HK-02 (2004 kg/ha). The four years result indicates that this genotype has stable performance over the location and years. In co-ordinated trial conducted during Rabi 2018-2020 recorded 1994 kg/ha seed yield (12.84 % increase) compare with check variety BG 3022 (1767 kg/ha). It implies that new genotype HK 13-114 has wide adaptation to climate change. Genotype HK 13-114 is included as a parent in the crossing block during Rabi 2022-23 for further exploitation in Kabuli chickpea breeding programme.

S2.35: Physiological basis of yield variation in field pea (*P. Sativum* l.)

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A field experiment was conducted during rabi 2021 at UAS, Dharwad to study the "Physiological basis of yield variation in field pea (Pisum sativum L.) genotypes". Significant differences were observed for various morpho- physiological, growth, biochemical parameters, yield and yield components between the genotypes. Among 16 genotypes, IPFD6-3, HUP-2, P-725 possessed significantly higher plant height and number of primary branches per plant, leaf area, leaf area index when compared to other genotypes. The genotypes IC381455, IPFD6-3, Rachana having higher value for specific leaf weight (SLW), net assimilation rate (NAR), absolute growth rate (AGR) and crop growth rate (CGR) and , SPAD (soil plant analysis development) values. The highest test weight was observed in the genotype IPF9925 followed by P-725 and KMPR-400 and lowest in genotype Nippani local-2. The genotype IC381455 was superior as well as efficient with respect to production and partitioning to total dry matter, particularly in reproductive parts. Significantly higher total chlorophyll was observed in IC381455. The seed yield exhibited a significant and positive correlation with plant height, number of primary branches per plant, total dry matter, leaf area, leaf area index and growth parameters. However, seed yield had negative correlation with days to 50% flowering and days to physiological maturity. Significant differences were observed with respect to yield and yield components within the genotypes and were highest in IC381455 followed by IPFD6-3 and Rachana.

S2.36: Morphological characterization and evaluation of pigeon pea germplasm under rainfed conditions

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Pigeon pea [*Cajanus cajan* (L.) Millsp.] is an important grain legume grown for its protein-rich seeds for human consumption. Characterization and evaluation of germplasm is the pre-requisite of any crop improvement program. 72 pigeon pea germplasm accessions were characterized and preliminary evaluation was carried out with the help of pigeon pea descriptor. Based on branching patterns, the accessions were grouped into 61 spreading and 12 compact types. 73 genotypes were divided into 53 indeterminate, 11 determinate and 9 semi-determinate types based on growth habit. Fourteen genotypes were extra short, 26 short, 9 short medium, 19 medium, 2 medium long and 3 long maturity groups. Out of 73 genotypes. 40 genotypes had lanceolate, 20 narrow elliptic and 13 broad elliptic leaves. Flower color was yellow in 36 genotypes, light yellow in 27, orange yellow in 8 and ivory in 2 genotypes. Pod color was mixed green and purple in 50 genotypes, purple in 13 and green in 10 genotypes. Number of pods ranged from 110 to 1094.5. Pod weight ranged from 48 to 661 g. Hundred seed weight ranged from 6.5 to 20.97 gm. Seed yield ranged from 28 to 409 gm. Large amount of variability and diversity was observed in morpho-physiological and biometrical characters. Diversity in plant genotypes provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics.

S2.37: Identification of stable lentil (Lens culinaris Medik) cultivars in Rice-Fallow agro-ecology to enhance cropping intensity and productivity

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In rice-fallow eco-system, lentil is the most favourable choice among the farmers to be grown as a rabi crop. To tap the rice fallow area of the state, selection of variety is always concerned in terms of stability. Genotype x environment interaction (GEI) analysis is fundamental in crop improvement programs to guide selection and for a recommendation of high-performing and stable genotypes for breeding or production. Assessment of the GEI effects and determining grain yield stability among diverse lentil genotypes are two major objectives of the present study. Thirteen lentil genotypes of lentil were tested continuously for three years (2019-20 to 2021-22) using RBD with three replications. Data collected were subjected to additive main effects and multiplicative interaction (AMMI) analysis. The analysis revealed that the first primary component of interaction (IPC1) factor was responsible for 69.2 % variation due to G × E interaction. On other hand, the second primary component (PC2) factor accounted for 30.8% variation in the G × E interaction. Genotype, environment and GEI accounted for 16.4, 33.5, and 49.6%, respectively, of the total variation for grain yield. The AMMI analyses indicated that genotypes HUL 57, RLG 272, WBL 77, PLEE 1902, RVL 18-4 and RKL 16-304 recorded yields higher than the mean yield over three environments. Genotypes PLEE 1901, RKL 14-49, WBL 77, HUL 57 were identified as the most stable ones across the seasons and may be recommended for general cultivation among the farmers to choose from under rice fallow cultivation of lentil.

S2.38: Assessment of Genetic Variability in Chickpea (*C. arietinum* L.)

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The present investigation has been carried out to study the variability in Chickpea **(***Cicer arietinum* L.). The magnitude of genotypic variance was highest for number of pods per plant followed by days to maturity, Harvest index and days to 50% flowering. The pods per plant recorded highest phenotypic variance followed by days to maturity and harvest index. Genotypic coefficient of variation (GCV) was highest for harvest index. Phenotypic coefficient of variation (PCV) was also highest for harvest index. Maximum heritability was observed for 100 seed weight (95.00%) and that of the estimates of genetic advance was ranged from 0.33 to 22.53% at 5% level of significance and 0.42- 28.87% at 1% level of significance with the highest estimate in case of number of pods per plant (22.53%) and (28.87%). Thus considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as per cent of mean, the characters like seed yield per plant, 100 seed weight, number of pods per plant, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod are the most important characters in chickpea improvement.

S2.39: Study on Genetic Divergence in Desi Chickpea (*C-arietinum* L.)

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Generally plant breeders select the parents on the basis of phenotypic divergence, but for effective breeding, the knowledge of genetic diversity among the parents with respect to the characters which are to be improved is essential. The present investigation entitled, "Genetic Divergence Studies in Chickpea **(***Cicer arietinum* L.)" has been carried out in forty three genotypes of chickpea along with three standard checks. It was observed that, 100 seed weight (30.90 %) contributed highest for divergence. It was followed by days to maturity (19.38 %). The genotypes under study fall into seven clusters. The cluster III was with the highest number of genotypes (11) followed by cluster II (10), clusters V (09), cluster VI (06) and IV and VII had one genotype. The maximum inter cluster distance (D =309.50) was observed between cluster VII and cluster V, while the minimum inter cluster distance (D = 41.46) was observed between clusters IV and II. Crossing between the genotypes belonging to the same clusters will not give desired improvement hence; the parents selected for crossing should be from different clusters. Considering all the characters, it was suggested that the genotypes in clusters VII and cluster V are suitable for further breeding programme.

S2.40: Long or short, Straight or curved, String or stringless: What makes the bean (*Phaseolus vulgaris* L.) pods shatter

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Pods are important in terms of the reproductive fitness of legumes. Shattering as a process is the dispersal of a crop's seeds upon their ripening . Under domesticated system, it is generally an undesirable process as it leads to loss of harvestable yields. In the present study, we sought to undertake the first comprehensive phenotyping in 254 common bean genotypes pod-shattering including the various mechanistic aspects as well as assess natural variation in the available germplasm set for 16 seed physical traits including shattering score. There was substantial variability in 16 pod physical traits in 254 genotypes of common bean indicating significant diversity of the material in respect of pod traits as indicated by the broader range and CV values. Using Random Impact Assessment (RIA), we found substantial variability in pod shattering score in 254 genotypes of common bean indicating significant diversity of the material Shattering score had a mean value of 6.098 with a range of 1.07 to 9.13. Highest shattering score was recorded in case WB-6, WB-20-247 and N-7 while as lowest value for shattering score was recorded in WB-1129 and WB-216. Shattering score was negatively correlated pod thickness (r = - 0.698) followed by ventral/dorsal length ratio (r = -0.468) and positively correlated with various other pod physical traits including breadth/thickness ratio (r = 0.599) and string percent (r = 0.590). The PCA concentrated 86.91 % variability in the first five principal components, and the first PCs accounted for 55.62 % of the total variation.

S2.41: Identification of fertility restorers for A_2 CMS lines and exploitation of heterosis in early maturing pigeonpea

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Pigeonpea is the most important legume crop grown in India next to chickpea. India is the largest producer of pigeonpea in the world. However, the productivity of pigeonpea in India remained stagnant over the years. The productivity of pigeonpea can be improved through exploitation of heterosis. The cytoplasmic genetic male sterility is the predominant method employed in hybrid development in pigeonpea during the recent days owing to the advantages involved. The present study involved identification fertility restorers for three *Cajanus scarabaeoides* (A_2) based early maturing (120-130 days) male sterile lines *viz.,* CORG 990047A, CORG 990052A and CORG 7A. A total of 77 inbreds were involved in the hybridization program and 186 hybrids were synthesized and evaluated. The pollen fertility of the hybrids ranged from 0.00 to 94.89 per cent. The independent confirmation of pollen fertility and pod set by selfing showed that, the hybrids *viz.,* CORG 990047A × AK 261322, CORG 990052A × AK 261322 and CORG 7A × AK 261322 were identified as fertile. The inbred AK 261322 was identified the potential restorer of fertility in A_2 male sterile lines. The hybrids *viz.,* CORG 990047A × AK 261322 (35.19 %), CORG 990052A × AK 261322 (12.75 %) and CORG 7A × AK 261322 (19.77 %) showed high standard heterosis for single plant yield over CO(Rg)7, a commercial check variety. Polymorphic SSR markers were identified among the parents of the respective hybrids and can be utilized in future to assess the genetic purity of the hybrids. The hybrids identified in the present study can be exploited for commercial cultivation after evaluation under various yield trials to estimate its performance.

S2.42: Phenotypic characterization and identification of multiple disease resistant sources in horsegram

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Horsegram (*Macrotyloma uniflorum* (Lam) Verdc) is known for its nutritional as well as medicinal properties as it contains 23% protein and is rich in lysine content when compared to pigeonpea and chickpea. It is an under-utilized pulse crop with great potential in sustainable agriculture as it enriches soil considerably by fixing atmospheric nitrogen and increasing the organic matter of soil.One of the main reasons for low productivity of horsegram may be attributed due to diseases ,as the crop is susceptible to various diseases . Among the various diseases powdery mildew causes greater yield losses in horsegram. About 100 accessions of horse gram were phenotypically characterized for various qualitative and quantitative traits and screened for powdery mildew, cercospora leaf spot and yellow mosaic virus disease under natural field condition during the years 2020-21 and 2021-22 at IIPR Regional Research Centre, Dharwad. Phenotypic variation was observed among the accessions with respect to various morphological characters studied. The entries such as TCR-1740 (82 days), IC-341310 (86), IC71776 (87 days), IC-342973 (89 days), and TCR-1758 (89 days) were identified as early maturing genotypes of horsegram. Most of the accessions had semi-spreading growth habit and in-determinate growth pattern. Most of the genotypes revealed highly susceptible reaction to powdery mildew disease, moderately susceptible to *Cercospora* leaf spot and yellow mosaic virus. The accessions such as TCR-1746, GPM-22, TCR-1418, GPM-03 and GPM-65 exhibited multiple disease resistance reaction under natural field condition. The identified multiple resistant genotypes of horsegram could be utilized in breeding programme to develop the multiple disease resistant cultivar of horsegram.

S2.43: Genetic variability in pigeonpea (*Cajanus cajan* L. Millspaugh)

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Fifty germplasm lines were evaluated for variation in morphological and agronomic traits for selection of cultivar potentially suitable for higher yield and nutritious quality. A wide range of variation was found in twelve quantitative and qualitative traits. The most important correlations corresponded to number of pod per plant, test weight and biological yield per plant at genotypic level. These yield components exhibited varying trends of association among themselves. The interrelationship among yield components would help in increasing the yield levels and, therefore, more emphasis should be given to yield components, while selecting better plant types in pigeonpea. Path coefficient analysis indicated the highest positive direct effect on seed yield per plant by biological yield per plant followed by harvest index, days to maturity and number of pod per plant, thereby indicating a true relationship between them. Studies pertaining to genetic divergence were also carried out using Mahalanobis's D^2 statistics for 50 pigeonpea genotypes which resulted in the formation of six clusters. On the basis of inter cluster distances, cluster III and cluster IV were found to be more divergent. Therefore, it was concluded that the genotypes belonging to these cluster should be intercrossed to generate more variability. Based on the mean performance, five genotypes *viz.,* IC 274103, TJT 501, IC 323233, IC 274087, RAJIV LOCHAN were found elite genotypes.

S2.44: A novel high yielding mid-early maturing pigeonpea variety GT 107 (Banas Abhay) for Gujarat

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The new mid-early maturing pigeonpea variety GT 107 (Banas Abhay) breed through pedigree selection method from the cross between GT 404B x GTR 40 during *kharif* 2008-09 at Pulses Research Station, SDAU, Sardarkrushinagar, Gujarat. The variety GT 107 was tested in a preliminary evaluation trial (PET) in *kharif* 2016. It was found promising and further it was tested in state multilocation trials from *kharif* 2017 to 2019. It was also tested under the AICRP-Pigeonpea IVT trial in *kharif* 2018 as SKNP 1608 at sixteen locations (Central and South zone)) across the nation. The pigeonpea variety GT 107 was tested under a total of 13 state trials against various checks viz., GT 101, GT 103 and BDN 711. The mean performance of GT 107 for grain yield over locations, including the preliminary trial was 1879 kg/ha. It exhibited overall yield advantage of 32.23%, 14.71 and 36.38 per cent over the checks GT 101, GT 103 and BDN 711, respectively. GT 107 found superior over 9 locations in central zone against check TJT 501and BDN 711 by 9.26 and 3.50 per cent, respectively. While under south zone at 7 location GT 107 had proved its superiority with 5.63 and 18.68 per cent increment against check PT 0012 and PRG 176, respectively. The variety GT 107 matures within 160 days (145-165 days) (mid-early group) with indeterminate plant type, having yellow colour flower, straight green pod with brown streak, 3-5 seeds per pod and cream colour seed. It has resistant against wilt, moderately resistant to sterility mosaic and root knot nematode. Having better quality and high yield potential will likely to make it widely adopted as versatile variety. The pigeonpea variety GT107 is recommended for *kharif* season in Gujarat.

S2.45: Exploitation of obscured concealed allelic diversity of wild Cajanus to hasten Genomics-assisted breeding for heightening crop improvement in pigeonpea (*Cajanus cajan*)

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Pigeonpea, commonly called Red gram or Arhar, faces a productivity crisis around the globe due to numerous biotic and abiotic stresses.In this scenario, the crop wild relatives (CWR) of pigeonpea, give a ray of hope to improve the genetic background of the cultivated Cajanus gene pool. To extrapolate these unearthed genomic diversities of wild, we require a thorough understanding of the pre-historic domestication episodes that are changing their shape with the expansion of the available scientific evidence. Keeping aforesaid in view, Interspecific hybridization between seven *Canajus cajan* genotypes viz., ICPL 88039, ICPL 11253, ICPL 11256, ICPL 11265, ICPL 11333, ICPL 11300 and ICPL 11306 with the wild species C. scareboides, *Rhyconsia rothi, C. acutifolius* and *C. cajanifolius* were attempted during *kharif* 2018. Successful pod set was observed in direct crosses involving C. cajan as ovule parent and *C. scareboides* as pollen parent while the reciprocal crosses were failed to set pods. The only surviving F_1 of ICPL 88039 × *C. scareboides* , ICPL 11253 × *C. scareboides*, ICPL 11306 × *C. scareboides* and ICPL 11300 × *C. scareboides* were vigorous in growth and exhibited variation in flowering, leaf, flower, pollen fertility, plant habit, pod colour and seed morphology with predominance of *C. scareboides* plant type. Seed size variation was observed in all crosses. With respect to test weight, cross ICPL 88039 × *C. scareboides* have 4.80 g seed weight while its parents have 2.33 g and 10.10 g, male and female respectively. The partial homology coupled with seed set suggested the possibility of incorporating traits of economic importance such as pest resistance from *C. scareboides* into *C. cajan*. It encapsulates various stress-resilient CWR of pigeonpea and their use in several pre-breeding programs to develop numerous breeding populations for crop genetic enhancement. We expect the newly explored genetic variations may be used in the breeding programs for re-wilding the cultigens' genomic background to open a new avenue for genetic gain and crop improvement capacity of pigeonpea.

S2.46: Colour diversity in Kidney bean (*Phaseolus vulgaris* L.): A Potential source for crop improvement

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Kidney bean (*Phaseolus vulgaris* L.) is one of the globally important legume crop and an important component of human nutrition because of high protein content (20%–25%), complex carbohydrates (50%–60%) and a good source of vitamins, minerals, poly-unsaturated fatty acids and appreciable amount of folate and fiber. Kidney bean are nutritious and their consumption is associated with many health benefits that can fight against protein malnutrition. The adequate amount of variability was observed in seed color, shape and size. Differences in colors of bean seeds such as Reddish, Dark red, Brownish, Cream white, Black, Black speckled and Brown mottled were observed with high predominance of red colored seeds. Conservation of this remarkable genetic diversity is obligatory for future dissemination, breeding and the investigation of the genetic relationships. Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat. The present work was to study the relation between seed colour diversity, their morphological, biochemical and molecular characterization in twenty different genotypes of kidney bean.

S2.47: Wild kindred of pigeonpea [*Cajanus cajan* (L.) Millsp.]: Forth coming source of CMS and abiotic stress tolerance

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a versatile, stress-tolerant, and nutritious grain legume, possessing traits of value for enhancing the sustainability of dry sub-tropical and tropical agricultural systems. The use of crop wild relatives (CWR) in pigeonpea breeding has been successful in providing resistance, quality, and breeding efficiency traits to the crop. Potentiality of pigeonpea CWR to be further employed in crop improvement by compiling wild species occurrence and ex situ conservation.The seventeen prioritized relatives of pigeonpea have been established at Pulses Research Station, SDAU, Sardarkrushinagar. Initially, breeders looked for the CMS system in cultivated germplasm, but their efforts were fruitless. Following that, they created other CMS systems using wild pigeonpea relatives. These are (i) A_1 cytoplasm from *Cajanus sericeus*, (ii) A_2 cytoplasm from *Cajanus scarabaeoides*, (iii) A_3 cytoplasm from *Cajanus volubilis*, (iv) A_4 cytoplasm from *Cajanus cajanifolius*, and (v) A_5 cytoplasm from cytoplasm of cultivated species, *C. cajan*. (vi) A_6 cytoplasm from *Cajanus lineatus* (vii) A_7 cytoplasm from *Cajanus platycarpus* (viii) A_8 cytoplasm from *Cajanus reticulates*. These taxa differ considerably among themselves and in comparison to the crop in their adaptations to temperature, precipitation and edaphic conditions.These wild genetic resources are broadly under-represented in ex situ conservation systems, with 80% of species assessed as high priority for collecting, thus their availability to plant breeders is insufficient. Identification of species and highlighting their geographic locations for further collection in order to improve the completeness of pigeonpea CWR germplasm collections, with particular emphasis on potential traits for CMS source and abiotic stress tolerance

S2.48: Genomic resources in *Vigna radiata*: An important legume of India

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Mungbean (*Vigna radiata*) is amongst the most popular legume crops of India. Seeds and sprouts of this plant are great source of carbohydrates and proteins. In addition to these macro-elements, mungbeans are also good source of flavonoids such as vitexin and polyphenols that protect the plant against stress. However, these measures still fall short of protecting the plant against some major abiotic and biotic stresses, which lead to considerable loss in crop yield. Stress response in plants is a highly regulated process with much yet to be discovered regarding the molecular mechanisms involved. We believe that much of this information is embedded in the genome and many such regulatory mechanisms could be deciphered by understanding the genome. Therefore, we have assembled a high-quality chromosome-level assembly of the mung bean genome for *V.radiata* cv. IPM02-3. We have annotated the genome to identify ~27,000 protein coding genes. Long-reads based sequencing of transcripts has helped generate full-length transcripts which were analysed to identify long non-coding RNA sequences. Besides, we have also identified molecular markers like simple sequence repeats in the genic and genomic regions of the mungbean genome. This data also helped us develop a differential gene expression profile for drought response based on the publicly available short read data for mungbean in well-watered and drought conditions. The high-quality genome assembly will also act as a reference to identify other structural variants. Therefore, this study will prove to be a credible addition to the repertoire of genomic resources for important pulses of India.

S2.49: Prospects of chickpea varieties bred at Regional Agricultural Research Station, Nandyal, Andhra Pradesh

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Chickpea is an important pulse crop of India with a lion's share of 47% (11.91 mt) of total pulses produced in India (25.46 mt). South Indian states contribute nearly 28 per cent of the chickpea area. Unlike traditional chickpea area of North India, these south Indian states had unique climate and are characterised by short and warm winters. During growing season, crop is exposed to moisture stress and soil borne diseases. To address these constraints, Acharya NG Ranga Agricultural University of Andhra Pradesh has initiated chickpea research at Regional Agricultural Research Station, Nandyal during 2004 and in a while the ICAR strengthened it as main centre for southern India. The inexorable efforts of research have led to the development and notification of seven chickpea varieties. Nandyal Gram 857 (high yielding *desi* chickpea with tolerance to wilt) and Nandyal Gram 119 (high yielding large seeded, short duration *kabuli*) were notified for Southern India. Nandyal Gram 3 and Nandyal Gram 49 with drought tolerance; NBeG 47 (Dheera) and Nandyal Gram 776 amenable to machine harvesting; and Nandyal Gram 452 with high yield and desirable seed quality are spreading in Andhra Pradesh, Karnataka and Telangana. NBeG 779 *desi* chickpea amenable for mechanical harvest and extra large seeded *kabulis* for export (NBeG 833 and NBeG 844) will be released shortly. Large scale farm trials with these varieties demonstrated genetic gains in farmers' fields with immense prospects for nourishing the chickpea revolution in southern India.

S2.50: Nandyal Gram 776, a high yielding machine harvestable desi chickpea variety released for Andhra Pradesh

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Development of varieties suitable for machine harvest is the foremost research priority in chickpea as the existing popular varieties grown in India are not suitable for machine harvest due to their growth habit.Research efforts from 2013 to 2022 at Regional Agricultural Research Station (RARS), Nandyal have led to the development of a desi chickpea variety Nandyal Gram 776 (NBeG 776) which was notified during October, 2022 for commercial cultivation in Andhra Pradesh state. NBeG 776 is a high yielding variety with upright growth habit, tolerant to wilt and is very well suited for machine harvesting. The plant grows to a height of 45-48 cm with pod bearing zone 22-25 cm above ground level. It has a yield potential of 2500-2800 kg/ ha with a duration of 90-105 days. It has attractive brown coloured seeds with test weight of 25g and protein content of 20.9%. Its performance in yield trials at RARS, Nandyal from 2013 to 2016 showed the yield advantage of 17.8% over check JG 11. In multi location trials of Andhra Pradesh conducted during 2017-18 and 2018-19, NBeG 776 exhibited 11.0% and 15.0% yield increase, respectively over JG 11 and NBeG 49. As a minikit in farmers' holdings (2017-18 to 2020-21), a yield gain of 16.1% over JG 11 was demonstrated. High yield potential of the variety coupled with saving in labour due to machine harvesting has resulted in economic returns and is being preferred by farmers as a better alternative to the existing *desi* varieties in Andhra Pradesh.

S2.51: Genotype × Environment interaction and stability analysis for earliness and yield in pigeonpea (*Cajanus cajan* L. Millsp.) mutants.

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In pigeonpea, earliness is directly related to photoinsensitivity.The responses to photoperiod and flowering time in pigeonpea were strongly linked and controlled by same genetic system. Development of high yielding, early and stable cultivars helps to cope with climatic adversities. Stable genotypes show low degree of fluctuation in their performance across the diverse environments. In the present study, 55 TS-3R derived mutants (treated with gamma irradiation of 250Gy along with 0.2 per cent EMS) were evaluated for stability analysis across Vijayapur, Dharwad and ICRISAT during *kharif* 2021. Two stage combined analysis using mixed model, revealed the presence of significant genotype × environment interaction for days to fifty per cent flowering (earliness), plant height, seed yield per plant, hundred seed weight and yield per hectare. Biplot analysis was employed to explicate the stability and adaptability of pigeonpea mutants. Dharwad environment found highly discriminative for mutants with respect to both earliness and yield per hectare. Vijayapura and ICRISAT formed a mega environment for earliness by the virtue of their positive correlation. The mutant entries, TS-M_5-39, TS-M_5-5 and TS-M_5-40 appeared site specific with promising yield in Dharwad, ICRISAT and Vijayapura, respectively. However, TS-M_5-1, TS-M_5-41 and TS-M_5-17 were found early and specifically adaptable in Dharwad, ICRISAT and Vijayapura, respectively. TS-M_5-41 and TS-M_5-33 were found to be stable with high mean performance for both earliness and yield per hectare. Reliability of these mutants can be explicated in upcoming years.

S2.52: Karan guar 14: A new high-yielding and quality gum content variety of cluster bean for NWPZ areas of India

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Guar [*Cyamopsis tetragonoloba* (L.) Taubert] is an important annual arid legume mainly cultivated under resource-poor conditions in the arid and semi-arid regions of India. The industrial potentialities of guar seed are based on a complex polysaccharide called galactomannan (gum). To fulfill the demands of guar gum industries, there is a dire need to upgrade the cultivation of guar, mainly for seed (gum) purposes. In this view, the new guar variety Karan Guar 14 is a high-yielding with good quality gum content developed by RARI Durgapura and *recommended for different guar producing areas of India.* It was developed by crossing between RGC 1038 and RGC 1017 and further maintained by pedigree breeding method. In the four years coordinated yield trials (2018-19 to 2021-22), it was out yielded (1222 kg/ha) with the superiority of 16.71 % over the check RGC 1066 (1047 kg/ha) followed by 14.53 % over the check HG 2-20 (1067 kg/ha) and 14.31 % over the check RGC 1033 (1069 kg/ha). Plants are erect and branched type, mature in 90–95 days. The flowers of the variety are pink and leaf with a serrated margin. Seeds are light grey to black brown and medium bold (2.74-3.34 g/100 seeds). The variety recorded good quality traits like protein(28%), carbohydrate (43 %), endosperm (32.26 %) and gum (29 %) with a high viscosity profile (3412 cp) indicating better gum quality in the international market. The variety also posses resistance towards key diseases like bacterial leaf blight (BLB), root rot and alternaria blight. Moreover, a lower incidence of whitefly, leafhopper, and aphid was observed as compared to the check varieties.

S2.53: Induction of early maturing, high yielding, and anthracnose resistant mutant lines of local land races with gamma rays and ethyl methane sulphonate of Rajmash (*Phaseolus vulgaris* L.) of Union Territory of Jammu and Kashmir

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Rajmash (*Phaseolus vulgaris* L.) is mainly cultivated in hilly areas of Union Territory of Jammu and Kashmir during *kharif.* It is grown both for vegetables and dry grains. Land races *i.e.,* Bhaderwah Local (BL) and Poonch Local (PL) were used for induction of anthracnose resistant and high yielding lines. The present study was undertaken in *kharif* 2021 and 2022. In the light of present investigation, mutant line induced by gamma rays *viz.* R-BL-M_3-12 showed resistance against anthracnose along with earliness in maturity by 26.14 days and superiority in seed yield by 6.77g/plant over controls followed by R-BL-M_3-14 exhibited resistance against anthracnose along with 25.12 days earlier in maturity with 7.63g/plant higher in seed yield and R-BL-M_3-13 indicated 21.98 earlier in maturity along with superior in seed yield 7.98 g/plant over controls (BL & PL) and another induced mutant line with EMS *i.e.,* R-PL-M_3-22 showed moderate resistance against anthracnose along with earliness in maturity by 17.83 days but at par in seed yield(g/pl) over controls. However, both the controls (BL & PL) matured in 119 and 133 days, respectively and seed yield/plant (BL-5.6g/plant and PL-4.49g/plant). But all these induced mutant lines showed at par in Iron (mg/100g), Zinc(mg/100g) and Protein content as compared to both the local land races and such lines may be carried forward for development of mutant's genetic stocks / varietal development programme of Rajmash for North Western Himalayan region.

S2.54: Development of extra early field pea (*Pisum sativum* L.) genotypes and their assessment using GGE biplot

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Extra earliness in terms of flowering and maturity coupled with higher grain yield is an ultimate strategy for field pea promotion in short-season environments and to escape prevailing terminal stresses. Therefore, the development of stable, extra early and high-yielding genotypes has been the objective of the field pea breeding program. Consequently, at the outset, extra early field pea material was generated following hybridization between available early type genotypes and subsequent generations were advanced using pedigree method in succeeding winter season during 2012-13 to 2016-17. Lastly, 44 extra early field pea genotypes were developed and to understand the role of genotype, environment, and their interaction in the performance of extra-early genotypes these genotypes were evaluated during winter season of 2017-18 and 2018-19. The integration of GGE biplot analysis and multiple comparison tests detected that a higher proportion of variation in studied traits was due to genotypes as an interactive factor followed by genotype x environment interaction, justifying the requisite of multi-environment testing. The present study effectively recognized "Mega environment" for environment-specific breeding. The GGE biplot identified genotypes IPFD 18-15 (11) for DF and IPFD 18-17 (13), IPFD 18-13 for DM were considered as desirable genotypes. In case of GY, genotype IPFD 18-20 (16) was the most ideal genotype and IPFD 18-24 (20), IPFD 18-28 (24) and IPFD 18-39 (35) were considered as most desirable. These ideal and desirable genotypes would be valuable genetic resources for comprehensive breeding programme of field pea for developing high yielding varieties with earliness.

S2.55: Genetic Diversity studies in spring planted Blackgram (*Vigna mungo* L.) Germplasm

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Blackgram is an important pulse grown across India. In the present study which included 36 genotypes of blackgram cultivated during the *Zaid* season, 2021, a genetic diversity analysis was done. Analysis of variance showed significant differences among genotypes for all characters. High PCV and GCV were observed for the harvest index and number of pods per plant. High heritability and genetic advance as percent mean recorded by 100 seed weight, harvest index and biological yield per plant. Genetic Advance as percent mean for harvest index. It is estimated that high GCV, PCV, heritability, genetic advance and genetic advance as percent mean was performed by harvest index, number of pods per plant and 100 seed weight. which implies effective selection in this studied population. Thirty-six genotypes were grouped by six clusters. Maximum inter-cluster distance between III and V was maximum followed by III and VI, IV and V, IV and VI, V and II. Maximum contribution to genetic divergence was shown by 100 seed weight followed by biological yield per plant, number of primary branches. Therefore, the characters contributing to maximum divergence needs greater emphasis for deciding the clusters for the purpose of selection of parents for further hybridization.

S2.56: An extra early germplasm source identified for dry bean improvement in India

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We assessed the phenotypic diversity of twenty-nine exotic common bean germplasm and three elite cultivars (Arun, Uday, and Utkarsh) in three winter seasons and one rainy season in two bean production environments (Kanpur & Shimla). The genetic variability parameter estimation revealed that the exotic bean germplasm has sufficient variability for all the studied traits. Further, the most heritable and genetically advanced quantitative trait was seed yield, followed by hundred seed weight, pod length, and pods per plant. According to a trait association study, phenological traits' days to maturity have a high positive correlation with days to initial flowering and days to 50% flowering. Pods per plant and seeds per pod have the most significant influence on increased grain yield. The principal component analysis (PCA) depicted that the first two PC components accounted for 63.3% of the variation and demonstrated substantial diversity among exotic bean lines for the traits studied. The hierarchical clustering analysis exhibited that twenty-nine accessions and three cultivars were clustered into three groups. The early flowering and maturing accessions are grouped in cluster I, high pods per plant, and high grain yield accessions are grouped in cluster III. Choosing parents from these two clusters improves the high seed yield with early maturity. The mean value of phenological growth traits and grain yield in selected accessions was also determined and compared. Temperature is the primary cause of phenological variations in both environmental conditions. In this study, we identified four genetically divergent and stable performance accessions, including EC932021, EC932189 (earliness), and EC931452, EC931971 (high grain yield), which may help in designing new breeding programs for common bean improvement.

S2.57: High yielding desi chickpea genotypes for combine harvesting with special reference to Andhra Pradesh state

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Sixty six advanced breeding lines of desi type chickpea developed at Regional Agricultural Research Station, Nandyal were evaluated during Rabi 2021-22. Seven yield attributing characters including yield were measured in Nandyal Gram entries. Performance of the advance genotypes was tested against popular variety JG 11 and also recently released high yielding variety NBeG 452. Nineteen advanced lines recorded higher yield with the yield advantage of 10-28% over the best check NBeG 452 (2535 kg/ha). Twenty seven genotypes had semi erect plant type with more than 45 cm plant height coupled with higher yield than the check. The most promising genotypes *viz*., NBeG 1871, NBeG 1879, NBeG 1864, NBeG 1874, NBeG 1920 and NBeG 1912 recorded more than 20% yield advantage with desirable characters like plant height, higher number of pods per plant, test weight and seed yield (3070-3246 kg/ha). Thus these promising genotypes can be considered for further testing in yield trials for assessing their yield stability and suitability to mechanization in large holdings.

S2.58: Insights into regulation of organ size using genetic, physiological and molecular characterization of a chickpea (*Cicer arietinum* L.) mutant

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Chickpea, grown worldwide has a narrow genetic base. Mutation breeding helps creating genetic variability and isolating desirable mutants. We isolated a novel chickpea mutant through gamma irradiation of cultivar 'Vijay' (400 Gy). It showed elongation phenotype in all the organs. The mutant also has higher aerial biomass and seed weight than Vijay without any yield penalty. A higher early vigor in the mutant as compared to the parent cultivar contributes towards its better early establishment under salt (NaCl) stress, with a higher LC_{50} (249±2.5 mM) & GR_{50} (138±3.2 mM) than Vijay (226±4.8 mM & 108±4.6 mM resp.). Malondialdehyde, proline, Na^+, K^+ content, higher shoot biomass and late appearance of salt toxicity symptoms in the mutant indicates its better performance than 'Vijay' under salt stress in early vegetative phase. F_2 population (n=280) was developed by crossing the mutant with cultivar RSG888. 1:2:1 segregation ratio ($\div^2$=4.886, p=0.086 at p<0.05) indicated incomplete dominance. Bulked segregant analysis identified 6 putatively linked markers to the elongation phenotype. Presently, these markers are being mapped using linkage mapping. A comparative transcriptome of Vijay and mutant at early seedling stage identified 474 DEGs (302 down- & 172 up-regulated transcripts). GO and KEGG analysis mapped the DEGs to the pathways regulating cell division, elongation, cell wall biogenesis, and carbohydrate metabolism. The study indicated that coordinated regulation of these pathways regulate organ size development and early vigor that contributes to a better seedling establishment under salt stress. The study will help identifying genes regulating these pathways and understanding regulatory mechanisms.

S2.59: New Desi type chickpea variety for highlands of West Iran

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Chickpea is the most important plant from the group of crops known as grain legumes, which is divided into two groups, Desi and Kabuli, based on the size, shape and weight of the seeds. The introduction of the latest Desi type chickpea variety in the country dates back to more than five decades ago. In this direction and in order to achieve a new variety with desirable characteristics, during two research projects, during the years 2013 to 2019, local masses of chickpeas from the three provinces of Kurdistan, West Azerbaijan and East Azerbaijan were collected, purified and were improved by mass selection method. Then the seed yield and other traits of the selected genotypes were compared with the control cultivars (Pirouz and Kaka) and based on the results of the initial tests, 18 selected lines with superior yield and agricultural traits were selected in four stations of Kurdistan, West Azerbaijan, East Azerbaijan and Zandjan underwent adaptability and stability trials. The results revealed that the IDDUR-2012-12 line originating from Bukan (West Azerbaijan) had high grain yield, stability and good marketability characteristics and was identified as the superior genotype. After passing the necessary evaluations, this line was approved and named "Kani" at the variety introduction session of the Seed and Plant certification and Registration Research Institute.

S2.60: Characterization of entire mungbean collections of Indian National Genebank and development of core set

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Mungbean also popularly known as greengram [Vigna radiata (L.) R. Wilczek] is one of the important legume crops of India. Mungbean is known for its nutrient rich grains, and plays an important role in nutritional and food security particularly in South, East and Southeast Asia. Poor genetic base in mungbean cultivars is a major hinderance in improving grain yield and resistance against biotic and abiotic stresses. However, a substantial amount of genetic diversity is conserved in seed genebanks, which may help in identification and utilization of useful diversity for the crop improvement.Therefore, we have characterized 4,100 accessions of mungbean conserved in Indian National Genebank, New Delhi using important agro-morphological traits (17 quantitative and 8 qualitative) at two locations i.e., Jodhpur and Badnapur which are two different agro-climatic zones having contrasting climatic and soil conditions. Entire accessions were grown during kharif 2019 and 2020 following standard agronomic practices. Statistical analysis of characterization data revealed a substantial amount of phenotypic variability traits such as plant biomass, no. of pods/plant, no. of pods/cluster, total pod weight/plant, grain yield/plant and 100 seed weight. Based on passport information, principal component score (PCS), Core Hunter-3 statical program, and some biased selections, a diverse set of 400 accessions was designated as core set. Quality check of the core using summary statics, Shannon's Diversity Index, Shannon' Equitability Index, PCS, hierarchical clustering, and trait correlation indicated excellent representation of diversity in the derived core set of the entire mungbean collections. This core set was further validated using 43 agro-morphological traits. We hope that this core and the variability revealed from this study will accelerate the mungbean germplasm utilization and the mungbean improvement.

S2.61: The Indian national genebank cowpea core set: a valuable resource for research, breeding and improvement

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Increasing demand of cowpea as a staple pulse under climate changing regime has led to the unlocking of diverse germplasm collections conserved in the gene banks to develop its superior varieties. Incorporation of new sources of genetic diversity into breeding programs is crucial for continuing to improve yield, quality, as well as tolerance to abiotic and biotic stresses.The National Bureau of Plant Genetic Resources Gene bank, India, currently has 3,720 accessions comprising 2,156 indigenous and 1,564 exotic collections. The entire set of germplasm was characterized for two years over two locations i.e., Delhi and Bengaluru. High phenotypic variability was observed for 12 quantitative and 15 qualitative traits. A core set comprising 425 accessions (230 Indian and 195 exotic) was derived based on the characterization data as well as geographical origin using a Core Hunter 3 software. We found this core set to be sufficiently diverse and representative of the entire collection based on the comparison made using Shannon–Weaver diversity indices and $\div^2$ test. These results were further validated by summary statistics. The core set displayed high genetic diversity as evident from a higher coefficient of variance in comparison to the entire set for individual traits and overall, Shannon–Weaver diversity indices. Trait specific germplasm (TSG) were identified for earliness (EC244108, IC276936), erect, bold type (IC202774, IC202931), stay green, pubescent type (EC762384), pod length and yield. The cowpea core set completely represents the entire collection and constitutes a potential TSG that can be utilized in accelerating cowpea improvement programs.

S2.62: Assessment of Seed Characteristics in common bean (*Phaseolus vulgaris* L.)

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An experiment was conducted at Agricultural Research Farm, Banaras Hindu University, Varanasi during winter-2021 to study the six seed characteristics (seed length (mm), seed width (mm), seed thickness (mm), 25-seed weight (g), length/width ratio and width/thickness ratio) among 50 common bean (*Phaseolus vulgaris* L.) genotypes. The various variability parameters such as ANOVA, descriptive statistics, correlation, principle component analysis and cluster analysis were carried out. ANOVA showed significant difference for genotypes which indicated presence of sufficient genetic variability among genotypes. Mean performance of 50 genotypes revealed the presence of variation in the traits studied *viz*., Seed length varies from 9.33 (HUR- 331) to 16.00 mm (HUR- 332 and HUR- 201) with a mean value of 12.98 mm. Similarly, mean for seed weight was 7.52 g and varied from 3.47 (HUR-351) to 11.17 g (HUR- 52). The association study showed the significant positive relationship between traits (0.68 to 0.86; $p<0.01$) except, seed thickness with width/thickness (-0.67; $p<0.01$). The first 3 principle components (PCs) explained 97.96% of the total variation. First PC explained 55.40% of the total variation and governed by seed weight (g) and seed length (mm). PC2 was positively defined by width/thickness and seed thickness (mm). 3 clusters were obtained from cluster analysis, the highest intracluster distance recorded by cluster I (7.33) whereas highest intercluster distance recorded between cluster II and III (8.38). Genotypes HUR-415, HUR-52, HUR-342 and HUR-275 had good seed characteristics and they are recommended to be used in breeding program for improvement of seed characteristics of common bean.

S2.63: Assessment of Genetic Diversity in Cowpea

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Cowpea is an important annual legume crop grown in subtropical and tropical regions. It is mainly grown for their edible seeds which are rich in protein, vitamins, and minerals. In this regard, an experiment was conducted during spring-summer of 2020-21 at ICAR-IIPR Regional Research Station, Dharwad to study the genetic diversity, genetic variability, heritability, correlation and path analysis, along with an objective to characterize the qualitative traits, among the selected 62 genotypes of cowpea. The analysis of variance revealed significant differences due to genotypes for all the traits, Among the qualitative traits, a wide range of variations were observed for flower color, seed coat color, seed eye color, and seed shape. Genetic variability analysis revealed very high PCV and GCV for the number of clusters per plant followed by the number of pods per plant, test weight, and seed yield per plant. High heritability coupled with high GAM was observed for test weight followed by the number of pods per plant and seed yield per plant. Mahalanobis D2 analysis showed considerable genetic diversity and grouped the 62 genotypes into five clusters. The maximum inter-cluster distance was recorded between clusters III and V. Characters like seed yield per plant, test weight and the number of pods per plant contributed maximum towards genetic divergence. Clusters III and V were most diverse in nature and the genotypes constituted in these clusters could be utilized as parents for the hybridization program. The identified superior genotypes viz., PL-5, V-578-1, CO-7, and GP-40 for traits such as seed yield per plant, test weight, pod length, number of seeds per pod, and days to physiological maturity could be used in cowpea breeding programs for its genetic improvement.

S2.64: Genotypic variation for tolerance to preharvest sprouting in mungbean germplasm

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Seeds of mungbean (*Vigna radiata* [L.] R. Wilczek) are being protected inside the pods, uncertain rain at the time of physiological maturity makes them vulnerable to pre-harvest sprouting (PHS) that causes loss in grain quantity and quality. PHS is a phenomenon of germinating the seeds inside the pod while still attached to the mother plant and the leading cause of PHS is lack of fresh seeds dormancy (FSD). Consequently, development of mungbean cultivars with short period of FSD has become vital to curtail the losses caused by PHS. To determine the amount of genotypic variation for tolerance to PHS, we analysed diverse mungbean accessions (110 accessions) for variations in PHS, fresh seed germination (FSG) and activity of á-amylase enzyme. Wide variation for PHS tolerance and FSG among accessions were observed, and nine genotypes were found to be tolerant to PHS. Seed germination in a pod, a measure used to evaluate PHS, varied from 4.18% in IC314347 (highly tolerant to PHS) to 95.13% in IC488879 (highly susceptible to PHS). Tolerance to PHS was also associated with slower water uptake by seed. The á-amylase activity at 48 and 72 h after germination was positively correlated with the FSG and PHS. Therefore, á-amylase can serve as a useful marker to screen a large number of mungbean genotypes for FSD and PHS.

S2.65: Identification of Extra-large seeded kabuli chickpea genotypes with better physical culinary properties

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Chickpea (*Cicer arietinum* L.) is an important dietary source of protein and carbohydrate. Kabuli chickpea which is essentially used as culinary should have superior physical and cooking traits. In a study, sixty one extra-large seeded (100 seed weight> 40g) kabuli chickpea genotypes were evaluated for their superior culinary properties based on their physical and hydration properties. Physical dimensions viz, length, width and thickness were measured and Seed volume, surface area, sphericity, shape aspect ratio, true density, bulk density and porosity were derived from them. Hydration parameters such as hydration capacity, swelling capacity, hydration index, swelling index, seed coat content and thickness were also measured after soaking seeds overnight. The study indicated that 100 SW ranged between 65.29 g (ELSKP 55) to 40.09 g (ELSKP 21) while seed volume was between 571.42 mm^3 (ELSKP 55) and 308.14 mm^3 (ELSKP 31). ELSKP 52 had maximum sphericity (88.37%) and shape aspect ratio (86.08%) and ELSKP 17 showed least values for both traits (78.43% and 71.41% respectively). Lowest seed coat content was observed in ELSKP 24 (3.51%) and thinnest seed coat was found in ELSKP 27 (0.12 mm). Maximum values for true and bulk density were observed in ELSKP 27 (1.41 g/cc and 1.30 g/cc respectively) and ELSKP 56 showed minimum values for both densities (1.14 g/cc and 1.06 g/cc respectively). Hydration capacity ranged from 0.706 g/seed (ELSKP 50) to 0.356 g/seed (ELSKP 37) meanwhile Swelling capacity ranged from 0.960 ml/seed (ELSKP 49) to 0.480 ml/seed (ELSKP 15).

S2.66: Phenotypic characterization and identification of trait specific donors in Cowpea

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Cowpea is an important multipurpose food legume used as a source of nutritious food, vegetable, and fodder in the tropics and sub-tropics. Cowpea can be grown as sole or mix-crop/ intercrop with a number of cereals. To utilize the variation available in the germplasm in a breeding program, germplasm evaluation, and characterization are essential, to identify the trait-specific donors. With these objectives, a diverse set of 300 cowpea germplasm lines were evaluated for various quantitative and qualitative traits. Field evaluation was conducted during the years 2020-21 and 2021-22 at ICAR-IIPR RRS, Dharwad. Wide range of variations was observed in the germplasm lines for the traits under study. The entries such as IC-97767 and IC724303 (75 days), EC-724284 (79 days), and EC-738194 PL-4, (80 days) were identified as early maturing genotypes of cowpea. The entries such as Goa cowpea-3 and MP-2 (110 days) were late maturing in nature. More than 3 pods/peduncle were observed in the genotypes, RC 101, PL-4, EC 472252, and GC-3. Genotypes Goa cowpea, TPTC 29, PL-1, IC-202718 had Pod Length (>14cm). The genotypes EC-528457, GC3, EC724751, RC-19, GC-4, IC-19786 and EC-390277 had >20 number of pods per plant. Erect plant stature (PH<60cm) were observed in genotypes PL-1, EC-528393, PL-4, GP-40 Test weight (>16gm) was observed in KBC-9, EC724454, EC724824 genotypes. Cowpea germplasm was also evaluated for 9 different qualitative traits to understand the variation available in the germplasm. Identification of trait-specific donors will help in the introgression breeding for the genetic improvement of cowpea.

S2.67: Stability of restorer lines developed from interspecific crosses for yield and yield components in pigeonpea [*Cajanus cajan* (L.) Millsp)]

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The five cytoplasmic genetic male sterile lines based on A_2 cytoplasm and twenty restorers from diverse source were evaluated at three different locations *viz.* Parbhani (L_1), Badnapur (L_2) and Ambajogai (L_3) during *Kharif* 2020-21. The fifteen restorers *viz*. BDNHR 1, BDNHR 21-2, BDNHR 22-1-2, BDNHR 24-1-2, BDNHR 41-2, BDNHR 43-1, BDNHR 44-5, BDNHR 46-3, BDNHR 47-2, BDNHR 49-3, BDNHR 52-1, BDNHR 53-4, BDNHR 55-2, BDNHR 57-3, BDNHR 58-4 were identified and developed from segregating materials of interspecific cross involving *C. scarabaeoides* wild species, however two restorer *viz*. BDNHR 31-1 and BDNHR 60-2 identified and developed from segregating materials of interspecific cross involving *C. albicans* wild species. The female parent BDN 2004-3A showed average stability for seed yield per plant and most of the important traits *viz.* days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and protein content. Among male parents (restorers), BDNHR 1, BDNHR 24-1-2 and BDNHR 60-2 exhibited highest seed yield per plant with regression coefficient near to unity and least deviation from regression lines which also exhibited average stability for most of important traits such as number of primary branches per plant, number of secondary branches per plant, number of pods per plant and pod length. Hence, these parents appeared to hold great promise for development of high yielding and widely adaptable pigeonpea hybrids.

S2.68: Registration of Six Bruchid Resistant Germplasm in *Vigna*

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Bruchid is a serious pest of stored pulses and causes tremendous losses to grains deteriorating their quality rendering them unfit for human consumption. *Vigna* group of pulses are attacked by several species of bruchids and not many cultivated sources are known till date which have a high degree of resistance to these species. Wild *Vigna* accessions are a repository of useful genes for several traits including resistance to biotic and abiotic stresses and therefore could be a valuable genetic resource for bruchid resistance as well. Keeping this in view, 42 wild accessions from 13 *Vigna* species were rigorously screened against three cosmopolitan bruchid species *viz., Callosobruchus maculatus* (F.), *C. chinensis* L. and *C. analis* (F.) on the basis of free choice (FC), no choice (NC) and confirmatory no choice (CNC) tests. As a result, 17 wild accessions were identified as resistant/highly resistant against two species viz., *C. chinensis* and *C. maculatus*. Among these, the accessions rated as highly resistant against the two species were proposed for registration as unique germplasm realizing their importance in transfer of this trait in elite backgrounds via introgression breeding. Based on the merits of the germplasm, two accessions of *V. umbellata* (IC 251439 and IC251442) and one of *V. vexillata* (C248326 (INGR22039) were registered as useful genetic resource against *C. maculatus (*F.). On the other hand, two accessions of *V. mungo* var. *mungo* (acc. IC251385, IC 251387) and one of of *V. vexillata* (IC248326) were registered as unique germplasm for resistance against *C. chinensis* L. All these registered accessions will be deployed in introgression breeding programmes in mungbean and urdbean across the country to develop bruchid resistant superior cultivars. Further, these lines could also be further subjected to biochemical as well as molecular analysis to identify the specific components imparting resistance to bruchids.

S2.69: Genetics of fertility restoring genes in CGMS based hybrids in pigeonpea [*Cajanus cajan* (L.) Millsp)]

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A precise understanding of the genetics of fertility restoration, pollen fertility (%) and amount of viable pollens produced by particular hybrid are important traits and had a basic need for the successful production of high yielding cytoplasmic genetic male sterility based hybrids in pigeonpea. The present investigation comprising of parents (P_1 and P_2), F_1's, F_2's and BC_1F_1's progenies of four selected hybrids involving four cytoplasmic genetic male sterile lines based on *Cajanus scarabaeoides* (A_2) cytoplasm and four restorers from diverse sources. Among these restorers, three restorers *viz*. BDNHR 1, BDNHR 21-2 and BDNHR 22-1-2 were identified and developed from segregating materials of interspecific cross involving *C. scarabaeoides,* however one restorer *viz.* BDNHR 60-2 from interspecific cross involving *C. albicans* wild species. The results revealed that the hybrids *viz.* BDN 2004-1 A x BDNHR 1, BDN 2004-4 A x BDNHR22-1-2 and BSMR 736A x BDNHR 21-2 which involving the restorer gene identified from *C. scarabaeoides* source showed the monogenic dominant gene action (3:1) with single fertility restoring gene. However, only one hybrid *viz.* BDN 2004-2A x BDNHR 60-2 which involving the restorer gene identified from *C. albicans* source showed digenic duplicate gene action with complete dominance for fertility restoration in Pigeonpea hybrids. The information generated on genetics of fertility restoration will help in knowing the selection of breeding methods and further transfer of fertility restorer genes in to elite backgrounds.

S2.70: Studies on heterosis for quality traits in pigeonpea

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The present investigation was carried out to study the heterosis for quality traits in pigeonpea [(*Cajanus cajan* L. Millsp.)]. The experimental material comprised of thirteen parents and their thirty F_1's produced in line × tester mating design with one standard check PAU-881 were grown in randomized block design replicated thrice during *Kharif* 2020-21 at Field of AICRP on Pigeonpea Agricultural Research Station, Ummedganj, Kota. The perusal of the whole heterosis study revealed that the cross combinations RKPV 901-2 × PA 291, RKPV 1013 × ICPL 88039 and RKPV 918-1 × PA 291, RKPV 1015-1 × PA 291, RKPV 1013 × UPAS 120, RKPV 1011-1 × UPAS 120, RKPV 904-1 × PA 291, RKPV 904-1 × ICPL 88039 and RKPV 0527 × PA 291 were identified as promising crosses with significant heterosis in desired direction as well as high *per se* performance for quality traits in pigeonpea. The by and large results of heterosis studies revealed that the cross combinations, RKPV 918-1 × ICPL 88039, RKPV 916-1 × ICPL 88039, RKPV 904-1 × ICPL 88039, RKPV 1013 × ICPL 88039, RKPV 0527 × PA 291 and RKPV 912-1 × ICPL 88039 were identified as promising hybrids having significant heterosis with high *per se* performance in desired direction for seed yield per plant in pigeonpea.

S2.71: Utilization of wide hybridization technique for development of *In-situ* germination resistant breeding lines in Mungbean (*Vigna radiata* L. Wilczek)

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Mungbean (*Vigna radiata* L. Wilczek) is a hepatoprotective agent in dietary supplements with 25% protein content. Mungbean seeds, being protected inside the pod, but susceptible to pre-harvest sprouting following rainfall in the month of September which drastically reduces the quality of seed. The ultimate goal of this study was to develope the resistant breeding lines to *in-situ* germination. An attempt was made possible to produce interspecific crosses between wild *Vigna radiata var. sublobata* (Accession No. BWM-29) with the cultivated mungbean *Vigna radiata* (BM-4). Further, three-way (BM 4 x BWM 29) x BM 2003-2) and four-way cross ([(BM 4 x BWM 29) x BM 2003-2] x BM 2002-1) were made to increase pod length and seed size. Observations of advanced generations *viz.* F_6 and F_5 were recorded at the interval of 5 days, 10 days and 15 days access the resistance level for dormancy. Obtained data from 979 pods and 13083 seeds from 293 single plant selection (SPS) tested for dormancy showed dormancy in 526 pods and 9087 seeds. The SPS of three-way cross for 60 pods and 599 seeds from 15 SPS recorded 44 pods and 314 seeds with no germination. However, in four way cross, among 61 SPS, number of pods and seeds found resistant to *in-situ* germination were 142 and 1027 respectively. As a result, the dormancy was transferred from wild source of mungbean BWM-29 to cultivated mungbean. While newly developed *in-situ* resistant mungbean lines will also facilitate an opportunity to be used in future breeding programme.

S2.72: Combining ability analysis for quality traits in pigeonpea

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The present experiment was undertaken to study the combining ability for quality traits in pigeonpea. The experimental material consisted of thirteen parents and their thirty F_1's produced in line × tester mating design. The estimates of general combining ability (GCA) effects for quality traits revealed that the lines, RKPV 1013, RKPV 916-1, RKPV 1011-1, RKPV 904-1, RKPV 0527 and testers UPAS 120 and PA 291 were identified as promising parents for protein, carbohydrate and phenol content whereas the lines RKPV 916-1, RKPV 918-1, RKPV 0527 and tester ICPL 88039 were observed as good general combiner with high *per se* performance for seed yield per plant in pigeonpea. The specific combining ability (SCA) effects revealed that the cross combinations, RKPV 1011-1 × UPAS 120, RKPV 901-2 × PA 291, RKPV 1013-1 × ICPL 88039, RKPV 912-1 × ICPL 88039, RKPV 904-1 × PA 291, RKPV 1015-1 × PA 291, RKPV 1013 × UPAS 120 and RKPV 918-1 × ICPL 88039, RKPV 904-1 × ICPL 88039 and RKPV 0527 × PA 291 were observed as promising hybrids with significant *sca* effects as well as high *per se* performance for quality traits in pigeonpea. The crosses RKPV 1015-1 × UPAS 120, RKPV 0527 × PA 291, RKPV 912-1 × ICPL 88039, RKPV 1013 × ICPL 88039, RKPV 918-1 × ICPL 88039, RKPV 904-1 × ICPL 88039 and RKPV 916-1 × ICPL 88039 were observed as promising hybrids with desirable *sca* effects as well as high *per se* performance for seed yield per plant in pigeonpea. Therefore, theses crosses may be utilized for heterosis breeding as well as for isolating the promising segregates in advanced generation.

S2.73: Inheritance study for branching pattern in Pigeonpea

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Types of branching pattern in pigeonpea plants are recorded qualitatively. Plant branching pattern further grouped into three classes *viz*., erect, semi spreading and spreading type, which contribute directly or indirectly in the source-sink relationship, its harvesting methodology and ultimately contributing to yield of a plant. In parents (P1 and P2) semi –spreading class of plant branching patterns was observed whereas in all the four crosses under study F_1's generations/ population were exhibits semi-spreading types of plant branching patterns.In cross, GRG-152 X Rajeevlochan and it's reciprocal cross plant branching pattern was observed and the finding for this trait in segregating generations. In studies of F_2 population segregation was found with 12,7 plants were erect type, 275, 214 plants were semi- spreading type and spreading type were 50, 52 plants observed in both crosses. It resembles well with expected ratio of 12:3:1 (Masking gene effect). This masking gene action occur due to dominant allele of both are together present , one of the two dominant gene mask the effect on another and give semi spreading branching pattern. When both the gene presents in recessive state gives spreading type. The calculated chi-square value of the cross GRG-152 X Rajeevlochan and it's reciprocal cross is 8.27 and 6.36 which was less than the table value at 0.025% to 0.005% respectively. The ratio obtain is valid.

S2.74: Divergence and cause effect analysis under drought condition in chickpea (*Cicer arietinum* L.)

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An investigation was carried out with thirty five genotypes including check in RBD in three replication at rainout shelter in experimental farm of RPCAU, Pusa, Samastipur. The observations were recorded on five randomly selected plants from each plot and data subjected to standard statistical analysis for eighteen characters viz. days to 50% flowering, plant height, number of primary branch per plant, number of secondary branch per plant, number of pods per plant, number of seeds per pod, harvest index, yield per plant, number of nodules per plant, nodule weight per plant, nodule dry weight per plant, root length, root volume, root dry weight, peroxidase, catalase, protease and proline content. The analysis of variance revealed the significant differences among the genotypes for all characters under study. Pods per plant and peroxidase exhibited positive and significant correlation with the grain yield along with their high and positive direct effect as harvest index, catalase, protease and proline content also exhibited positive and significant correlation with yield owing to the positive and high indirect effect via pod per plant suggesting that these traits may be considered during the course of selection for enhancement of yield in chickpea. Maximum inter cluster distance was observed between cluster III and cluster VII suggesting that the genotypes placed in these clusters are most divergent and suitable for producing heterotic recombinant in crossing program. DC 17-1111 in cluster VI had higher cluster mean for most of the yield attributing traits may be used as suitable donor to incorporate the respective traits in the recipient parent. Maximum contribution towards divergence was shown by Proline content followed by protease content, catalase content and nodule weight per plant.

S2.75: Distribution of pigeonpea wild species in selected districts of West Bengal and Jharkhand

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In India, wild species of pigeonpea (*Cajanus cajan* (L.) Millsp.) are distributed mainly along the Deccan plateau, Chota Nagpur plateau, western ghats, eastern ghats, vindhya region, north eastern ghats, Himaliyan foot hills and isolated places of northern plains. Crop wild species contribute to the gene pool and, hence, there is need to map their distribution and diversity in their habitat ecologies. *Cajanus scarabaeoides* is the predominant species reported from Jharkhand and Wes Bengal. Explorations of pigeonpea was organized by ICAR-NBPGR in collaboration with ICAR-IIPR during 29th January to 13th February, 2022 in Seraikela Kharsawan and East Singhbhum districts of Jharkhand and Puruliya district of West Bengal. Two species of wild pigeonpea viz. *Cajanus scarabaoides*, *C. crassus* were found in explored areas of Jharkhand, whereas only *Cajanus scarabaoides* was observed in the surveyed tracts of West Bengal. *Cajanus scarabaoides* was distributed on the ghats, highlands, open grassland, open forest throughout the explored areas. The occurrence varied from few to abundant depending on the habitat invasion by human encroachment, grazing, type of vegetation, topography and edaphic factors. It was also growing freely in higher frequency in Dalma forest of Jharkhand and Ayodhya Hills of West Bengal on rocky soil along the open sunny drenches. *Cajanus crassus* was observed at one site in Dalma forest and four locations on the hillock of Chandil range. *C. scarabaeoides* and *C. crassus* are potentially endangered primarily due to habitat loss in the surveyed regions of West Bengal and Jharkhand.

S2.76: Evaluation of pigeonpea *(Cajanus cajan)* genetic diversity using Principal Component Analysis

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A collection of 45 redgram genotypes were evaluated for nine morphological and phenological characters by principal component analysis for determining pattern of genetic diversity and relationship among individuals. The largest variation was observed for seed yield per plant with coefficient of variation of 76.65% followed by number of pods per plant (74.98 %), number of branches (30.27%) and plant height (26.93%). The least variation was observed in days to maturity with coefficient of variation of 11.17%. Principal component analysis was used to assess the variation and relative contribution of various traits towards total variability. In this study, principal component 1 had the contribution from the traits such as days to 50 % flowering, plant height, seed yield per plant and number of pods per plant which accounted to 36.47 % of the total variability. The principal component 2 explained 24.36 % of total variability from number of seeds per pod, pod length, number of branches and 100 seed weight. Number of pod per plant, days to maturity and seed yield per plant had contributed 15.72% of total variability in principal component 3. The cumulative variance of 76.55 % of total variation among nine characters was explained by first three axes. Thus the results of principal component analysis used in the study had revealed the high level of genetic variation and the traits controlling for the variation were identified. Hence, these entries can be utilized for trait improvement in breeding programs for the traits contributing for major variation.

S2.77: Pre-breeding for incorporation of biotic and abiotic stress tolerance in pigeonpea

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Cultivated pigeonpea genotypes are often vulnerable to biotic and abiotic stresses. Wild relatives and land races are important sources of genes for economic traits. It is difficult to utilize these genes because they are present in the pile of unfavourable genes and causes linkage drag in the derived lines. Pre-breeding interventions were applied to incorporate useful genes into agronomically superior genotypes. Inter-specific and intra-specific crosses, involving *Cajanus scarabaeoides*, *C. cajanifolius* and trait specific germplasm were generated with an aim to incorporate useful genes in adapted genotypes. The cultivated genotypes were used as female parent whereas, *C. scarabaeoides* and *C. cajanifolius* were used as pollen source. *Fusarium* wilt resistance, drought tolerance, nematode resistance and pod borer tolerance were target traits. Selection pressure was applied for specific donor trait and desirable background agronomic attributes. *Fusarium* wilt resistance was tested in the wilt sick plot. Resistance against pod borer was evaluated in field trials and confirmed under no choice assay. The drought tolerant lines were evaluated at Kanpur and Bhopal under rainfed condition and rain out shelter. Waterlogging tolerance was evaluated in artificially waterlogged plots. The improved breeding lines were also evaluated for yield and other agronomic traits. The donors possessing traits of economic importance were identified and submitted in the gene bank. Among the putative test entries, IPAD-5 exhibited drought tolerance over the year and location, whereas WDBCE 6-3-4-6 and WDBCE 6-3-4-7 were identified as tolerant to pod borer on the basis of field trial and no choice assay.

S2.78: Breaking seed coat imposed dormancy in wild relatives of pigeonpea (*Cajanus cajan* L)

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Pigeonpea is an important nutritious grain legume for enhancing the sustainability of dry sub-tropical/tropical agricultural systems. Wild pigeonpea species possess large variability and are an important source of germplasm for research and crop improvement activities like resistance, quality, and breeding efficiency traits to the crop. Occurrence of physical dormancy in the form of hard seed coat prevents proper utilisation and conservation of wild species of pigeonpea, Hence, in the present investigation attempt has been made to understand the variability in hardseededness and the pre-treatments to overcome it in 44 accessions comprising of 10 wild pigeonpea species (*Cajanus scarabaeoides, C. crassus*, *C. platycarpus*, *C. cajanifolius, C. lineatus*, *Rynchosia minima*, *R. bracteata*, *R* rothii, *R rufescens* and *R. aurea*). The level of hardseededness varied from 36-100%, with an average of 76.5%. Likewise, the time to initiate germination (T1), achieve 50% germination (T50) and mean germination time (MGT) varied between 16.18-249.9h, 94.7-607.7h and 37.5-153.2h, respectively. Overall, all the treatments reduced hardseededness and improved germination over the control, with partial incision on seed coat (PSCI) being the best treatment for all the species recording 70-98% germination, except for *R. aurea* (30%) and *C. cajanifolius* (59%). The hot water treatment (HWT) for 30 and 60 minutes was the best treatment for *C. cajanifolius* recording germination of 66-70% as compare to 11% in control. The sulphuric acid scarification (SAT) for 2 m was the best pre-treatment for overcoming dormancy and improving germination in *R. bracteata*, *R. rothii* and *R. rufescens*. The result indicated a significant inter and intra species variation in the effectiveness of pre-treatments in overcoming physical dormancy, suggesting that the optimum pre-treatment for overcoming hardseededness should be standardised for each accession. Also the dormancy breaking pre-treatments not only reduced hardseededness and improved final germination percent but it also reduced time for T1, T50 and MGT, suggesting that use of such pre-treatments before sowing could result into higher, uniform and rapid germination.

S2.79: Genetic variability studies for yield, yield components and disease resistance in advanced breeding lines of green gram

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In the investigation carried out at AICRP on MULLaRP, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka,. during *Kharif*-2020 and rabi 2020-21, a set of one hundred and thirty-four (F_7) genotypes of green gram were used to assess genetic variability for yield, and yield components. During summer-2021, a set of one hundred and twelve genotypes (F_6) were screened against MYMV under natural field conditions. In *kharif*-2021, forty advanced breeding lines (F_7) were screened against anthracnose disease resistance. Highest seed yield per plant was observed in DGGV-189 (12.41g per plant), DGGV-182-2 (12.02g per plant) and DGGV-241 (11.24g per plant). The genotypes DGGV-79, DGGV-195, and DGGV-125 showed tolerance to pre-harvest sprouting. The traits, number of pods per plant, number of and number of branches per pod recorded high GCV, PCV and shown significant positive correlation with yield and exhibited high direct positive effect on yield. Among the sixteen F_6 progenies derived from the cross DGGV-2 × WGG-42, 12 genotypes DGG-81, DGG-63, DGG-100, DGG-177, DGG-182-2, DGG-189, DGG-191, DGG-197, DGG-79-2, DGG-241, DGG-242 and DGGV-122 recorded moderately resistant reactions to MYMV. Further mutation breeding of LGG-460, which is susceptible to anthracnose and shattering, yielded DGGV-73, a genotype that was shattering tolerant and moderately resistant to anthracnose. These genotypes can be used in breeding anthracnose resistant genotypes.

S2.80: Development of Mungbean [*Vigna radiata* L. (Wilczek)] Genotypes for Foliar Disease Resistance

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A series of field experiments spanned over seven years (2014-2021) were conducted at AICRP on MULLaRP, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka,. In the first set of experiments, the material was comprised of eight varieties of green gram which were treated with 20kR gamma radiation.M_1 was planted in *Kharif* 2014 and each variety was bulk harvested. M_2 was planted in summer 2014 and individual plant selection was carried out. Mutant families were advanced to the further generation in *Kharif* 2015 and *Rabi 2015* The M_2 mutants were scored for their reaction to anthracnose , cercospora leaf spot and powdery mildew diseases with respective susceptible and resistant checks. In another set of experiments aimed at developing MYMV tolerant genotypes, an investigation was carried out with 168 F_2 individuals derived from crossing *vigna trilobata* and DGGV2. The promising entries were stabilized through a series of selfing generations. Evaluation of advanced breeding lines for their reaction to various foliar diseases revealed that the breeding lines DGG-67 (Mutant of Sona mung), DGG-59 (Mutant of DGG-7), DGG-95 (Mutant of TARM-1), DGG-377 (Mutant of IPM-2-03) showed resistant reaction to powdery mildew. The lines DGG-61, DGG-188, DGG-65, DGG-104 derived from mutant of Sona mung showed moderately resistant reaction with PDI of 25. 16.6, 13.33 and 16.66 percent to Cercospora leafspot. Powderymildew and MYMV respectively. These superior genotypes can be used in further breeding programmes by introgressing all the desirable traits.

S2.81: Enhancement in crop produce *via* Characterization of Cowpea (*Vigna ungiculata* (L.) Walp)

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Hundred germplasm accessions including 68 exotic and 32 indigenous local cultivars procured from NBPGR New Delhi, were sown in augmented design for the study. Characterization of germplasm collections is needed in pre-breeding activities, therefore to characterize and preliminary selection of cowpea collections through DUS characterization as per the Bioversity International, Rome, Italy (1983) made accordingly. Experiment was carried out at College of Agriculture, IGKV, Raipur, Chhattisgarh, India. Plant growth habit noted that out of 100 genotypes studied 38, 53 and 6 were found to be erect, semi-erect and prostrate respectively. Plant pigmentation trait showed classes with; no pigmentation for 70, very slight pigmentation for 19 and extensive pigmentation for 11 genotypes. When plant hairiness was examined, 94 glabrescent and 6 short appraised hairs out of 100 genotypes. Terminal leaflet shape offered that 5 globose, 51 sub-globose, 34 Sub-hastate and 10 hastate were found out of 100 gemplasm. Flower colour displayed that out of total genotypes 3 white, 78 violet and 19 mauve-pink coloured flowers accession. Leaf texture was studied 61 carcarious, 24 intermediate and 15 membranous type of classes for genotypes. Seed colour was exhibits 8, 28, 22, 15, 9 and 22 genotypes in different colour classes *viz*., white, brown, black, red, grey and mottled respectively. The purpose of characterization is to identify accessions that have superior character so that they can be used as parents in the breeding program. In present study which dealt with the assessment of qualitative traits of cowpea accessions revealed substantial amount of genetic variability among them. therefore that they can be developed in breeding activities.

S2.82: Variation in tolerance to pre-harvest sprouting in mungbean

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Mungbean (*Vigna radiata*), is one of the important pulse crops of Asia. Mungbean seeds lack fresh seed dormancy (FSD) and are susceptible to pre-harvest sprouting (PHS). PHS deteriorates the quality of the grains produced and reduces yield. Mungbean varieties having short duration of FSD could help overcome the losses imposed by PHS. We screened forty mungbean genotypes to study variations in fresh seed dormancy and tolerance to PHS. Water imbibition capacity of pods (WICP) was also recorded in three replications of fifteen pods each. Pre-weighed pods were placed in growth chamber maintained at 25°C following between paper method of germination to evaluate WICP and PHS. After incubation of 24 h in growth chamber, the pods were taken out, blotted dry, weighed and were immediately placed back for evaluation of FSD and tolerance to PHS. Water imbibed by the pods was calculated as gain in weight after 24 h of incubation. Number of sprouted pods (%) and seeds germinated per pod (%) was recorded after 4 days of incubation. There was a wide variation in FSD and tolerance to PHS among the examined genotypes. Out of forty lines, genotype M 1255 was found to be least susceptible (< 30%) to PHS. WICP varied from 45.85 to 53.44 %. PHS in these genotypes varied from 28.33% in genotype M 1255 to 93.33% in genotype M 1378. The variation in PHS among genotypes found in this study could be further utilized in mungbean improvement programme.

S2.83: Characterization of chickpea genotypes based on morphological and seed traits

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Chickpea is one of the important pulse crops of India. Varietal characterization, identification and genetic purity assessment is very important not only for field functionaries but also in crop improvement. Understandings of morphological and seed traits facilitate the identification and selection of desirable traits, designing new populations and transferring their desirable genes. The present investigation was carried out at RARS, College of Agriculture, Vijayapur involving 150 genotypes (117 *desi* & 33 *kabuli*) and 9 checks. Observations were recorded as per DUS guidelines and found large variation for different morphological traits. These genotypes were characterized and grouped into different classes. In that 8 different qualitative and 13 quantitative descriptors. The *desi* type are characterized by pinkish flowers, small plant stature, small leaflets with growth habit of spreading and semi erect and usually 1-2 seeds per pod. The *kabuli* type have long plant stature, white flowers, bigger leaflets and usually 2-3 seeds per pod. Seed characters of *desi* type are small, irregularly shaped seeds of various colours (light brown, green, black or variegated colours) having thick and rough seed coat. The *kabuli* type have large owl's head shape, beige and creamy beige colour, larger seed with smooth and rough seed coat. The results clearly indicated that the genotypes of chickpea can be distinguished and identified by plant and seed morphological characters. These differences in morphological traits were useful in identification of individual chickpea genotypes and superior lines will be used for the future breeding programme.

S2.84: Evaluation of combining ability and heterosis among Full Diallel population for yield and its attributing traits in Pigeonpea [*Cajanus cajan* (L.)]

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Pigeonpea [*Cajanus cajan* (L.) Mill sp] seed yield is a complex and multiplicative character, which is highly influenced by environmental variations. Heterosis and combining ability which recognizes the hybrids with high yields are the most important standards in a breeding programme. Experimental material consisted 5 parents, 10 direct and 10 reciprocal crosses of Pigeonpea. The parents were crossed during *Kharif* 2020-2021 on 5 x 5 diallel fashion. Parent and F_1's in all combinations were evaluated by utilizing Full Diallel Analysis, Method- I, Model- I, (Griffing's Approach) in CRBD Design using 3 replications during *Kharif* 2021-2022. Observations were taken on nine different characters. A high degree of heterosis was observed for different trait in different crosses of pigeonpea (direct & reciprocals). Cross Vipula x GRG 152 showed maximum value for all the three types of heterosis for days to 50% flowering, Vipula x BDN 716 reported maximum value for all the three types of heterosis for plant height and Vipula x CG Arhar-2 reported maximum value for all the three types of heterosis for shelling %. High significant heterobeltiosis was exhibited by hybrid CG Arhar-2 x Vipula.Combining ability analysis reported the predominance of non-additive gene action for all the characters as ratio of gca effect to sca effect was found less than unity. Parent BDN 716 reported to be a good general combiner for days to 50% flowering and number of pods/plant. Hybrids GRG 152 x Rajeevlochan and CG Arhar-2 x Vipula were found to be superior for different traits.

S2.85: Genetic variability for agro-morphological and yield traits as related to phosphorus status in mungbean

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Phosphorus (P) is an essential macromolecule critical for crop productivity of mungbean and other grain legumes across the world especially under acidic soil conditions. Plants respond to phosphorus scarcity by activating a range of mechanisms exhibiting a remarkable variation in root and other agromorphological traits for higher uptake of phosphorus from soil. The study was designed to characterize such variations in 139 mungbean genotypes under two different soil conditions (Field I: pH-5.13 to 5.79 and available P-12.86 to 61.12 kg/ha; Field II: pH-5.08 to 5.61 and available P-5.51 to 8.29). observations were recorded on plant count, days to 50% podding, plant height, no. of clusters per plant, no. of pods per cluster, grain yield, 100 seed weight, root volume, root length and no. of root tips. Analysis of variance revealed significant variation for all the traits under individual as well as across the environment. The principal component analysis (PCA) revealed that first two principal components (PC1 and PC2) contributed almost 43% and 42% under red soil and neutral soil, respectively. Inter-trait associations and contribution of traits under studied soil conditions were shown in PCA biplots. Based on grain yield under both the soils, the test genotypes were grouped in three categories *viz.,* high, medium and low yielders. In field I, seven genotypes were found to be high yielder while in field II only one genotype was reported to be high yielding and those could be used in future breeding programme to develop promising mungbean cultivars for the specific soil condition.

S2.86: Unveiling the Genetic Potential of Horsegram Germplasm of National genebank under Tropical Humid Climate of Kerala, India

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Horsegram a minor legume of Indian origin has immense potential as a food, forage and medicinal value crop. Considering its worthiness as a future crop, an attempt was made to evaluate a large-scale genetic resource of horsegram maintained in National Genebank, ICAR-NBPGR, New Delhi. A total of 2148 accessions of horsegram germplasm collected from different regions of India were evaluated for two years during 2019-21 at NBPGR Regional Station, Thrissur in an augmented block design. The genotypes were assessed based on 19 morphological traits and *Mungbean Yellow Mosaic Virus* (YMV) susceptibility. Among the germplasm, 89 accessions exhibited erect growth habit, which is suitable for mechanical harvest. The early flowering nature (<40days) was noticed in 1510 accessions while 70 were late (>70 days) to flower. Highest number of pods per plant was recorded in accessions IC553492 (251), IC320969 (201), IC055062 (184), IC470167 (181) and IC139423 (180). A total of 47 genotypes out yielded the best check PHG9 with 12g/plant and the highest yielding accessions included IC553492 (27.11g), IC342125 (20.84g), IC139423 (20.45g), IC470170 (19.79g) and IC470167 (19.67g). Twenty-one accessions excelled over the check AK 21 with highest hundred seed weight of 5g. Polymorphism seed coat colour has been noticed and the whole germplasm were grouped into 16 seed colour categories. The genotypes were also screened against YMV resistance in the field epiphytotic condition and seven genotypes *viz.,* IC043515, IC123026, IC123027, IC123028, IC139371, IC139374 and IC139392 were found free of any symptom even at pod maturation stage indicating high resistance against YMV.

S2.87: Identification of extra early and mechanical harvestable chickpea (*Cicer arietinum* L.) genotypes under rainfed conditions

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Chickpea is an important rabi pulse crop in India and Karnataka. At present, the existing chickpea varieties are either semi-erect or semi spreading, with medium height and branches close to the ground, and the first pod height is less. These characters pose difficulties for mechanical harvesting. Hence, there is a need to develop a tall, non-spreading plant type with pods borne considerably above the ground level. This, in turn, will be amenable to mechanical harvesting at a low cost. Therefore, the present study was planned at the Zonal Agricultural Research Station, Kalaburagi, Karnataka, 96 Bengal gram genotypes were evaluated in preliminary yield trails along with four national checks (JG 14, RVG 204, Phule Vikram and NBeG 47) under rainfed conditions during Rabi 2021 by following a lattice square design with two replications. One genotype KCMH96EE-2 (1204 kg/ha) recorded higher yield compare with four checks (Phule Vikram (1193 kg/ha), RVG 204 (1104 kg/ha), JG 14 (889 kg/ha), and NBeG 47 (661 kg/ha)), the three entries *Viz.,* KCMH96EE-24, (1182 kg/ha), KCMH96EE-42 (1150 kg/ha) and KCMH96EE-84 (1125 kg/ha) were recorded higher yield compare with one check (RVG 204 (1104 kg/ha) and plant height in genotypes ranged from 41.75 cm 60.00 cm with an overall mean of 51.40 cm and among standard checks, 46.00 cm (JG 14) to 56.75 cm (Phule Vikram). Five genotypes have the highest height compared to the control (56.75 cm), as well as other important traits such as days to 50% flowering, days to maturity, and test weight. These will be further evaluated in advanced yield trails for confirmation of yield potential and can be used as parents in hybridization programmes or released as varieties after testing in advance trials.

S2.88: Identification of Large-Seeded High-Yielding Stable Kabuli Chickpea genotypes

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Chickpea is one of the earliest food legumes cultivated. India is the largest chickpea producer and consumer in the world. Among desi and kabuli, large seeded kabuli types have more consumer preference and hence fetch premium price to the farmers. Fortunately, the trading of extra-large seeded Kabuli types is dominating the international market. Approximately one million tons of chickpea were imported by Government, private organizations and other agencies. But the large seeded kabuli chickpea with high yields is a rare combination so far. Hence, the present research work was carried out at Zonal Agricultural Research Station, Kalaburagi, Karnataka, 21 Bengal gram genotypes were evaluated in preliminary yield trails along with four checks (ICCV 92311, NBeG 119, ICCV 95311 and ICCV 16309) under rainfed condition during Rabi 2021 by adopting randomized block design (RCBD) with three replications.12 genotypes recorded higher yield compare with four checks (ICCV 92311 (589 kg/ha), NBeG 119 (519 kg/ha), ICCV 95311 (589 kg/ha) and ICCV 16309 (833 kg/ha)), out of 12 genotypes top five genotypes viz., KCEK21-101 (942 kg/ha), KCEK21-112 (933 kg/ha), KCEK21-115 (928 kg/ha), KCEK21-117 (911 kg/ha) and KCEK21-120 (875 kg/ha) along with yield these genotypes showed extra-large traits.

S2.89: Genetic variation for traits related to phosphorus use efficiency in *Vigna* species

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Phosphorus (P) is major limiting nutrient reducing crop yields especially in weathered soils of subtropics and tropics. P exhibits poor mobility and availability to plants in soil. To overcome P deficiency in soil phosphatic fertilizers are added to soil. Global phosphate rock reserves are finite and the addition of phosphatic fertilizers is not financially and ecologically sustainable. Mungbean (*Vigna radiata* (L.) Wilczek) is important grain legume for nutritional security. Attempts are being made to develop mungbean varieties with better P use efficiency through enhanced P uptake and utilization. In the present study 327 accessions of 18 *Vigna* species were examined for inter and intra specific variation for traits related to phosphorus uptake and utilization efficiency under hydroponic conditions at two levels of phosphorus. Significant species specific variation was recorded for studied traits. Among the studied *Vigna* species mungbean exhibited higher phosphorus use efficiency. Seven mungbean genotypes (IC 251950, IC 585931, V1002532AG, IC 371653, IC 331615, V1001400AG and V1000532BG) were found promising for both PupE and PutiE. Using mean and standard deviation as criteria, mungbean genotypes identified with high phosphorus use efficiency include IC 25950 and IC 583664. Mungbean genotypes KPS 1546, IC 277060, IC 697141, IC 343440, and Pusa 0831 were identified based on stress tolerance index as genotypes that performed better under P stress. Cultivated species revealed higher PUE in comparison to wild forms. The most promising genotype identified from this study for PUE can be used as parent for development of mapping population of mungbean for understanding genetics of PUE under low phosphorus environment.

S2.90: Studies on genetic variability of some quantitative characters in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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In pigeonpea assessment of genetic variability present in the population and the extent to which it is heritable are important factors to have effective selection in breeding programme. This experiment on pigeonpea was conducted under rainfed conditions at Agricultural Research Station, Ummedganj, Agriculture University, Kota, Rajasthan, during *Kharif*, 2020-21. The genotypes were grown in 6 rows of 3.6m length spaced 60 cm apart with the plant to plant distance of 20 cm. Each genotype was planted in three replications in Randomized Block Design. Observations were recorded on seed yield per plot, days to 50% flowering, days to 80% maturity, plant height, branches per plant, pods per plant and 100-seed weight. Mean squares due to genotypes revealed that genotypes had significant differences for the all the characters in pigeonpea. In the present study, high heritability accompanied along with high genetic gain (GG) was recorded for important yield contributing traits. The characters showing high heritability estimates coupled with high genetic gain (GG) indicates the preponderance of additive gene action and greater scope for improvement in these traits through selection.

S2.91: Genetic interrelationship among yield and its contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Diverse genotypes of pigeonpea were evaluated for association studies through correlation and path analysis under rainfed conditions at Agricultural Research Station, Ummedganj, Agriculture University, Kota, Rajasthan, during *Kharif*, 2020-21. The genotypes were grown in 6 rows of 3.6m length spaced 60 cm apart with the plant to plant distance of 20 cm. Each genotype was planted in three replications in Randomized Block Design. Observations were recorded on seed yield per plot, days to 50% flowering, days to 80% maturity, plant height, branches per plant, pods per plant and 100-seed weight. In the present investigation, grain yield was found to be highly significant and positively correlated with important yield contributing traits in pigeonpea. In path analysis highest positive direct effect on grain yield was recorded for different traits which were also positively correlated with grain yield. Over all study showed that selection may effective for the pods per plant, branches par plant, test weight, and days to maturity for genetic improvement in pigeonpea.

S2.92: Generation mean analysis for yield and its components in mungbean

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The analysis of gene effects for some yield characters and detection of epistasis in mungbean [*Vigna radiata* (L.) Wilczek] was studied in three crosses, namely; Pusa 0871 x ML 818, Pusa0672 x IPM 02-14, and 818x RMG991 involving five parents and evaluated in randomized block design for days to maturity, number of seeds per pod, 100-seed weight and grain yield per plant under timely and late sown conditions through generation mean analysis during *kharif* 2015 at Rajasthan Agriculture Research Institute, Durgapura Jaipur. Six populations, viz. P1, P2, F1, F2, BC1 and BC2 of three crosses involving five parents were evaluated. The nature and magnitude of gene effects for yield and its components in mungbean were studied using six parameter models of generation mean analysis. A joint scaling test detected the presence of epistasis, and the inadequacy of the additive-dominance model was established. Additive (*d*) and dominance (*h*) gene effects, along with one or more types of non-allelic interactions (i, j, l), contributed significantly towards the inheritance of all the quantitative characters in the majority of the crosses. Duplicate type of epistasis and predominant dominance effects was also prevalent in most of the cases. Thus, postponement of selection in later generations may be suggested to obtain transgressive segregates to improve mungbean populations.

S2.93: Evaluation and identification of extra early and early mechanical chickpea genotypes

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Chickpea remains as an important cool season global grain legume crop, offering plant based dietary protein and essential micro nutrients to human population across the globe. Chickpea yield is seriously challenged by various biotic and abiotic stresses. In parallel, given the current deleterious effects of global climate change, increasing event of heat stress (HS) is appearing as one of the important abiotic stresses, causing detrimental effects on various crops including cool season grain legumes. The present study was carried out at Zonal Agricultural Research Station, Kalaburagi, 57 Bengal gram genotypes were evaluated in preliminary yield trails along with three checks (NBeG 47, Phule Vikram and RVG 204) under rainfed condition during Rabi 2021 by adopting lattice square design with two replications.four genotypes *viz.,* KCMH57EE-42 (1242 kg/ha), KCMH57EE-08 (1242 kg/ha), KCMH57EE-27 (1221 kg/ha) and KCMH57EE-36 (1162 kg/ha) recorded higher yield compare with three checks (NBeG 47 (571 kg/ha), Phule Vikram (1158 kg/ha) and RVG 204 (675 kg/ha)) and days to maturity in genotypes ranged from 45.00 days to 101.00 days with an overall mean of 98.39 days and among standard checks, 98.00 days (Phule Vikram) to 101.00 days (RVG 204). 25 genotypes showed early as compare to three checks, these genotypes have other additional features like acceptable plant height for mechanical harvest and test weight. These genotypes will be further evaluated in advanced yield trails for confirmation.

S2.94: Genotype x Environment Interaction and Yield Stability in Mungbean [*Vigna radiata* (L.) Wilczek]

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The present investigation was conducted during *kharif* 2020 & 2021 as well as summer 2021 & 2022 crop seasons. The experimental material consisted of 40 mungbean genotypes, planted in R.B.D design with three replications. The AMMI model was used to identify most stable genotype over all the four growing seasons for all the 10 characters. The analysis of variance for AMMI model revealed that the main effects (genotype and environment) and interaction effects (genotype x environment) were significant for all the 10 studied characters indicating that based on the mean value as well as ASV scores, stable genotypes were identified for different characters. On the basis of IPCA I scores, biplots, mean values and ASV score, genotype PM 15-17 for number of days to maturity; genotype HUM 12 for plant height; genotype PM 15-19 for number of primary branches per plant; genotype PM 15-15 for number of clusters per plant; genotype PM 15-6 for number of pods per cluster; genotype PM 15-18 for pod length; genotype SML 1815 for number of seeds per plant; genotype PM 15-21 for total pods per plant; genotype PM 15-12 for 100-seed weight and genotype IPM 02-3 for seed yield per plant were considered as most stable genotypes in all four consecutive seasons in mungbean. Another stability index, *i.e*., YSi (Yield Stability Index) was also calculated and genotype IPM 02-3 was identified as the best performing genotypes in terms of yield/plant which followed by genotype PM 15-20.

S2.95: Correlation and Path Coefficient Analysis of Yield and Yield Components in Chickpea (*Cicer arietinum* L.).

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The present investigation was carried out for, "Correlation and Path Coefficient Analysis of Yield and Yield Components in Chickpea **(***Cicer arietinum* L.)". Correlation studies showed that the traits *viz.* harvest index, number of pods per plant, number of secondary branches per plant, days to 50% flowering, plant height, days to maturity, number of primary branches per plant and number of seeds per pod exhibited positive and highly significant genotypic correlation with seed yield. This indicates that the simultaneous improvement of these characters through selection. In other words, an increase in the magnitude of these characters would lead to an increase in the magnitude of grain yield. In path coefficient analysis the characters, harvest index, number of pods per plant, number of secondary branches per plant, days to maturity and days to 50 % flowering had positive direct effect on seed yield in decreasing order of magnitude *viz.* plant height and number of primary branches per plant exhibited negative direct effect on seed yield per plant. Among all the components character harvest index exhibited the highest direct effect (p=0.4663) on seed yield. Hence, the selection of genotypes based on these characters as selection criteria would be helpful in improving the seed yield potential of chickpea.

S2.96: Identification of extra earliness in segregating populations of Urdbean (*Vigna mungo*)

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Urdbean is an important pulse crop in Indian sub-continent, cultivated during kharif season in northern India and rabi season in southern part of the country. Breeding short duration urdbean varieties is of thoughtful importance to tackle terminal moisture stress and reap impressive yields by breaking the yield level. Hence, in the present study it was aimed to identify desirable segregating populations for earliness from a set of advanced breeding lines of urdbean. During kharif 2021 a total of 523 single plant selections from F_4 segregating generations were obtained from a group of 31 crosses for its advancement for yield and its component traits including earliness. Four advanced breeding lines (SPS) *viz*. IPU 182-21 derived from cross of IPU 94-1 x IPU 99-31 were identified for its earliness. The next best advanced breeding lines IPU 182-161 derived from a cross using IPU 02-43 X CoBG 653, IPU 182-22 derived from a cross using IPU 94-1 X IPU 99-31 and IPU 182-164 derived from cross using IPU 02-43 x CoBG 653 were also identified for earliness. High frequency of such favourable segregants indicates that the parents possess diverse alleles and genes governing respective characters from which it could be inferred that there is an ample scope to bring them in a single genetic background through careful selection in further generations. Meticulous selection schemes along with proper pedigree maintenance can aid in successful development of short duration urdbean varieties from these segregants.

S2.97: Studies on genetic diversity in blackgram (*Vigna Mungo* L. Hepper) germplasm in Bastar region

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Among pulses, black gram (*Vigna mungo* L.) is an important short duration crop widely cultivated in India. Blackgram Germplasm is collected from Bastar region which was used in this experiment. The present investigation was conducted to examine the genetic diversity existing among 82 genotypes of blackgram with two check verity (Indira Urd Pratham and T.U. 94-2) during *kharif* 2020 under randomized block design with three replications. The data was recorded for thirteen quantitative characters to obtain estimates of variability, heritability, genetic advance and divergence. Analysis of variance showed significant differences between genotypes for all the 13 characters studied. High estimates of GCV and PCV were observed for seed yield per plant, plant height (cm), number of primary branches per plant and test weight of thousand seeds. High heritability and genetic advances indicated least influenced of environment on the expression of character and characters governed by additive genes respectively. High heritability accompanied with high Genetic Advance as percent of mean observed for the traits plant height (cm), Test weight of thousand seeds, seed yield per plant(g), harvest index(%) and petiole length (cm) due to additive gene effect abundant sources provided for improving the traits though section.

S2.98: Characterization of Morphological Traits and Genetic Divergence of Exotic *Kabuli* Chickpea Lines

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Chickpea one of the major *rabi* pulse crop in M.P sharing 35–40% of the land under cultivation and production. During the *rabi* season 2020–21 at Seed Breeding Farm, JNKVV, Jabalpur, 64 exotic *kabuli* chickpea lines including local check JGK 5 and national check PUSA3022 were grown in RCBD with two replications. The variation was shown by morphological traits comprising foliage colour, leaflet size, pod length, seed size and the phenological traits *viz*., days to flower initiation and maturity. There was a significant variation for number of effective pods per plant, total number of pods per plant, number of primary and secondary branches per plant, stem thickness, height of the first fruiting node and plant height. Genetic divergence analysis, *kabuli* chickpea lines were grouped into 8 clusters. The trait stem thickness had highest percentage of contribution to total divergence. These clusters were liable for expressing maximum diversity among the clusters. Cluster II has the largest among all the clusters consisting 17 exotic lines followed by cluster I had 13 lines, cluster V had 12, cluster IV had 11 and cluster III had 8 genotypes. Cluster VI, VII and VIII were monogenotypic having genotype X013TR46-IFC-S4, FLIP09-250C-IFC-S3 and FLIP82-150C-IFC-S2 respectively. The highest inter cluster divergence was observed between genotypes of cluster VI and cluster VII, followed by cluster V and cluster VI, cluster VI and cluster VII, cluster VI and cluster VII, cluster II and cluster III. Inter cluster distance was lowest between cluster VI and cluster I.

S2.99: Correlation and path coefficeint analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.)

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The present investigation was carried out for correlation studies and path coefficient analysis in Pigeonpea (*Cajanus cajan*) at College of Agriculure, Badnapur, during *kharif* 2019-20. The characters number of pods per plant, test weight, number of secondary branches per plant, number of seeds per pod exhibited positive and highly significant genotypic correlation with seed yield. This indicates that the simultaneous improvement of these characters through selection. Path coefficient analysis indicated that the characters *viz.* days to 50 % flowering and plant height exhibited negative direct effect on seed yield per plant. Hence, the selection of genotypes based on these characters as selection criterion would be helpful in improving the seed yield potential of pigoenpea.

S2.100: Genetic base of lentil cultivars developed in India as revealed by pedigree analysis

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Lentil is among the oldest domesticated crops in the world. It is a cool season food legume playing a significant role in human and animal nutrition as well as soil fertility. . To develop new varieties compatible for facing logarithmic climate change, the new gene pool of varieties must be broadened by introducing wild species, land races and exotic germplasm into breeding practices. The present study quantifies the genetic base of released varieties that provide indirect information about the relatedness of the varieties. In lentil, pedigree analysis of the varieties bred for over 70 years in India covering 81 varieties was performed. Ludhiana local, was most frequently used as a parent in more than 20% of the released cultivar followed by Bihar local (> 17%), LG171 (> 14%) and JLS1 (>12%).Ancestor Ludhiana local collected from Punjab was used in the development of L 9-12 variety in 1972. Similarly, Bihar local parent was used in the development of T 8 variety in 1967. Both these ancestors have wider adaptability. The relative genetic contribution (RGC) from ancestors was found maximum of Ludhiana local (0.087), Bihar local (0.070), LG171 (0.054) and JLS1 (0.041). However, 36 out of total 60 parents used only once in the pedigree. Extensive and repetitive use of superior genotypes in lentil improvement programme of India led to genetic erosion and narrowing of genetic base as evident from significantly low superiority of the recently released varieties of lentil. Hence, the integration of new germplasm is of paramount importance for broadening the genetic base of lentil cultivars.

S2.101: Breeding tactics Accelerating Pulses Gains

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Pulses provide high biological value protein in vegetarian diets overcoming malnutrition in masses. In rotation with cereal crops, pulses serve in the nitrogen economy, enrich soil health, and are a primary source of high-quality dietary/vegetarian protein of high biological value, contributing significantly to global food and nutritional security. Primarily pulses in India are cultivated in low fertility, troublesome soils, and unpredictable environments, offering little scope for area expansion, their productivity has to be elevated by developing high-yielding, input-responsive, and stable cultivars to meet the requirement & reduce import, saving valuable foreign exchange. Plant breeders can readily use conventional breeding involving new and diverse sources of variation via wild types to develop genotypes with a broad genetic base for climate resilience. The new methodologies involve developing new plant types to reduce maturity duration, induce more synchronized development in pod formation, and repartition the dry matter used for seed formation. Genomics enabled crop improvement involving developing population mapping for targeted traits, mapping and tagging of genes, MAS for insulating against major diseases, and identifying QTLs; allele mining of genes will be of greater importance towards pulse improvement. The post-genomic era involving RNAi technology can be fruitfully utilized to improve grain legumes' nutritional traits and suppress anti-nutritional chemicals/compounds. Diverting efforts in basic and strategic research will ultimately give improved high-yielding varieties/breeding lines/enhanced methodologies and a better understanding of mechanisms provided by climate change. Although the slow pace of grain legume research, it is moving and is a long way ahead.

S2:102: Evaluation of pigeonpea genotypes for Sterility Mosaic Disease

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Pigeonpea (*Cajanus cajan* (L.) Millsp is an important legume crop with high protein and nutritional triats. The crop is affected by many biotic and abiotic stresses. Among biotic stresses sterility mosaic disease (SMD) is the most important constraint on pigeonpea production. In the present investigation, seventy two pigeonpea entries from AICRP centers were screened along with susceptible check ICP 8863 and resistant check ICP 2376 for Sterility Mosaic Disease (SMD) under field condition by leaf stapling method during *kharif* 2020-21 and 2021-22 at RARS, Vijayapur, UAS, Dharwad to identify the resistant sources. Based on the Percent Disease Incidence (PDI), the genotypes were classified into resistant, moderately resistant and susceptible. Out of seventy two entries screened against sterility mosaic disease, eighteen entries *viz.*, BDN 2013-45, LRG 471, TDRG 323, DA 2020-1, BDN 2013-2, MAL 52, BSMR 253, BSMR 528, BSMR 553, BSMR 853, BWR 164, MAL 13, PAH 05, BRG 1, BRG 2, BRG 3, BRG 4 and BRG 5 showed resistant reaction, and thirteen entries *viz*., PT 11-4-4-1, PT 2017-1, AKTM 1644, CRG 16-002, GJP 1904, PT 11-16, WRGE 367, IPA 19-55, KA 18-1, PUSA 195, PT10-1-1-2, KA 17-2, BRG 4 were found to be moderately resistant to sterility mosaic disease.

S2.103: Effect of Genotype by Environmental Interactions on Grain Iron (Fe) and Zinc (Zn) Concentration of Biofortified Lentils in Nepal

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Billions of people are directly affected by the micronutrient malnutrition called "hidden hunger". Lentils are rich in proteins and micronutrients (Fe, Zn) which is good for human health, and excellent as animal feed. Twenty-five lentil genotypes were evaluated at three locations to determine the effect of genotype x environment (GE) interaction on iron and zinc concentrations in grains. Analysis of variance showed significant genotypic variation for grain Fe and Zn concentrations at each location. Pooled analysis of variance revealed highly significant effects of genotypes and environments for Fe and Zn concentrations but GE interaction only for Zn concentration. The range for seed Fe concentration across the locations was 82.53 to 133.49 ppm with a mean value of 101.04 ppm. The range for seed Zn concentration across the locations was 54.03 to 75.34 ppm with a mean value of 64.22 ppm. Although both the micronutrients were influenced by the environment, seed Fe was more sensitive to environmental fluctuations in comparison to seed Zn concentration. The study revealed that genotypes Sagun, RL-6, and LG-12 were more stable for Fe concentration and WBL-77, ILL-7164, and RL-11 for Zn concentration. In the AMMI analysis employing Gollob's test, the first two PC explained 100% of the GE variation. PC 1 and PC 2 explained 87.19% and 12.81% of total GE interactions for Fe concentration and likely for Zn concentration, respectively.

S2.104: Estimation of Genetic Diversity, Heritability and Association of Characters in *Glycine Max* (L.) Merril. for Yield and its Contributing Traits.

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Soybean [*Glycine max* (L.) Merr.] is one of the non-conventional seed crops and is profitably grown throughout each spring and fall season.To assess genetic component characters , the yield and the contributing traits were recorded. Leaf area (55.02%), plant height (43.27), harvest index (5.64%), seed per pod, biological yield, physiological maturity, and hundred seed weight were found to have the highest per cent contribution to genetic divergence. Heritability along with genetic advance estimates illustrated higher for some traits due to additive gene action and higher heritability with moderate genetic advance indicated the presence of some heritable traits. Leaf area had the highest PCV and GCV content (39.98, 39.94), followed by plant height, pod/plant, and in contrast lowest is physiological maturity and 50% maturity. Higher heritability along with high genetic advance as a percentage of mean was observed for plant height and leaf area. On the other hand moderate genetic advance with higher heritability were observed for numbers of seed/pod which indicated the presence of both additive and non-additive gene actions for these traits. Numbers of seed per pod is positively and significantly correlated with biological yield (r = 0.277) while biological yield was negatively and significantly correlated with harvest index (r = -0.278) at 5% level of significance. The most divergent and promising genotypes were identified viz., Shivalika and JS 97-52 of cluster 5, RVS 2011-77, JS 20-90 and JS 21-17 of cluster 6, and RVS 2011-32 of cluster 12. These genotypes can be used as parents in further hybridization programmes.

S2.105: Screening and diversity analysis of moth bean (*Vigna aconitifolia* (Jacq.) Maréchal) accessions in the arid region of western India

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An experiment was conducted with 300 moth bean accessions in augmented design to estimate the presence of genetic variability and to identify suitable donors under the hot and arid climatic conditions of Bikaner, Rajasthan. The data were recorded on different agro-morphological traits at different growth stages of the crop. Out of eight quantitative traits the most significant quantitative traits for arid regions are days to 50% flowering and yield per plant. IC-8851, IC-329051, IC-370508, IC-415116, IC-415127, IC-415134, IC-415138, IC-120963 were identified as early flowering types; therefore, these accessions can be used as a donor for the development of short-duration varieties. Accessions IC-11368, IC-34715, IC-39709, IC-39741, IC-35942, IC-11352, IC-52152, IC-39835, IC-39659, IC-10185, IC-10530, IC-11344, IC-11463, IC-10880 were identified high yielding over the check varieties. Accessions IC-121065, IC-311396, IC-36616, IC-39816, IC-311450 were identified with > 6 seeds per pod; Therefore, these accessions with more seeds per pod can be utilised as a donor in the breeding programme. Further, this study will help the researchers to select potential genotypes most suited to extreme conditions and can be utilised in developing new varieties.

S2.106: Promising YMD resistant Blackgram varieties for rice fallow conditions

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VBN 9 is a blackgram variety, a derivative of Vamban 1 x UH 04-04 and suitable for rice fallow cultivation in south zone states of India viz., Andra Pradesh, Tamil Nadu, Kamataka and Odhisa. This variety matures in 74 days. Average seed yield is 1126 kg/ha which is 9.43, 16.20, 22.00 and 28.69 per cent increase in yield over LBG 7 (1029 kg/ha), LBG 752 (969 kg/ha), LBG 645 (923 kg/ha) and COBG 653 (875 kg/ha) respectively. Another variety, ADT 7, a mutant of ADT 3, semi erect and determinate plant type with broad to narrow lanceolate terminal leaflet. Light purple wash on the basal portion of plant and purple petiole. It matures in 65 to 70 days and average yield of the variety is 724 kg/ha, which is a 19.69 percent increase in yield over ADT 3 (606 kg/ha) and a 10.53 percent increase over ADT 6 (655 kg/ha). Both the varieties showed resistance to YMD, leaf crinkle, and stem necrosis; resistant to stem fly with moderate resistance to pod borer and pod bug.

S2.107: Distinctness, Uniformity and Stability (DUS) testing of Mungbean and Urdbean

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During *kharif* 2019 to 2022 at ICAR-IIPR,Kanpur a total of 37 candidate varieties urdbean (25) and mungbean (12) were tested along with reference varieties in each crops for distinctness, uniformity, stability (DUS) of traits in order to protect under the act on protection of plant Varieties and Farmer Right Act (PPV&FRA) 2001. DUS test generates official description of a variety which is to be used for assessing varietal purity (in crop inspection and grow out test), to identify one or more specific phenotypic characters having least environment influence for certification and registration purpose of a new variety. In present investigation out of twenty five candidate varieties of urdbean in which twenty four were farmers varieties (FV) and one was new variety(NV). Of them, in nine varieties viz. 2883/2129,2886/2054,22KHU-1,22KHU-4,22KHU-5,22KHU-6,22KHU-8,22KHU-9 and22KHU-10 different observation related to DUS testing could not recorded due to severe incidence of Yellow Mosaic Virus (YMV) disease. Furthermore, in the case of urdbean among the twelve Farmers Varieties two varieties viz. 2883/2462, 22KHMF-1different observation related to DUS testing could not recorded due to severe incidence of YMVand redmites'. In one farmer variety of mungbean which was very late type DUS testing could not recorded.Over all 25 varieties were characterized for plant growth habit, leaflet terminal shape and other morphological traits in both the crops during testing. Interestingly, it was observed that two farmers varieties of mung bean '2883/2482, 22KHM-4' were showed resemblance as urdbean type plant. The above finding indicate the necessities of execution of DUS testing for mapping the character profile of candidate varieties which is submitted by the applicant for the purpose of deciding on granting registration to a new variety.

S2.108: Genetic variability, character association and path coefficient analysis in chickpea (*Cicer arietinum* L.) grown under heat stress conditions.

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Genetic variability, correlation and path coefficient analysis was studied for seed yield and its component traits among 113 breeding lines of chickpea sown under non-heat stress and heat stress conditions at Kanpur. The analysis of variance exhibited significant differences among genotypes for all traits under study indicating presence of sufficient amount of variability among the genotypes for various traits. High GCV and PCV were observed for seed yield per plant, 100-seed weight, harvest index, effective pods number per plant, total number of pods per plant and secondary branches number. High heritability coupled with high genetic advance as percentage of mean was noted for seed yield per plant followed by 100–seed weight, harvest index, effective pods number per plant and total number of pods per plant indicated that selection may be effective for this character. Seed yield per plant was positively and significantly correlated with plant height, primary branches number, secondary branches number, pods number per plant, effective pods number per plant and 100-seed weight indicating that these three traits were main yield attributing traits. Path analysis indicated that number of effective pods per plant and 100- seed weight had maximum direct effect on seed yield. Based on seed yield ICC15614, ICC1205, ICCV06108, IPC2018-168, JG130, JG14 and GNG1958 have been identified as heat tolerant lines. The potential for indirect selection for heat stress tolerance using these associated characters may be useful to the breeder to formulate appropriate breeding plans for selection of the genotype which tolerate high temperature conditions

S2.109: Genetic enhancement of desi chickpea under late sown conditions of North Eastern Plain Zone of India

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Conventional breeding for desi chickpea under under late sown conditions of North Eastern Plain Zone (NEPZ) or rice fallow ecosystem of India targets an ideotype with early flowering, maturity by 120 days, high biomass and higher yield than the checks (BG372, KPG59). The Doubling Farmers Income by 2022 has been reported by Directorate of Pulses Development, Bhopal, and endorsed the area expansion of chickpea under late sown conditions of NEPZ. Collar rot disease has been posing major impediment for novel breeding materials under this ecosystem but some potential responses have been observed in the tall advanced breeding lines (ABLs) with plant height of >65cm and erect growth habit. Total 24 chickpea ABLs with checks (BG372, KPG59, IPC06-77) were evaluated under late sown conditions (sowing on 10th December) at Kanpur. Entry IPC17-373 (3088kg/ha) was found top yielder followed by IPC17-16 (2988kg/ha), IPC17-139 (2811kg/ha), IPC14-133 (2800kg/ha), IPC15-185 (2788kg/ha), IPC17-377 (2766kg/ha) and best check IPC06-77 (2661kg/ha) with the 100-seed weight ranging from 15 to 20g. Check varieties for late sown have bushy spreading-semi spreading growth with height of 40cm, whereas, the highest yielding entry IPC17-373 (3088 kg/ha) had a height of 69.51cm which was higher than national check (HC5, height 65cm) for mechanical harvesting type varieties. High yielding entries, IPC17-373 & IPC17-377 had their heights above 62cm. Those entries had comparatively short internodes with erect-semi erect plant type and higher yield with respect to check can be bred for late sown conditions which may pave the way for machine harvesting in such ecosystem.

S2.110: A high yielding and MYMV disease resistant Greengram variety VBN 5

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The high yielding Greengram variety VBN 5 is derived from the cross VBN (Gg) 2 x ML 1451 and matures in 70 - 75 days. This variety was release during 2022. The average yield of VBN 5 is 878 kg/ha which is about 10.2 and 13.2 *%* increased yield over the two check varieties *viz.,* VBN 4 (797 kg/ha) and CO 8 (775 kg/ha) respectively. In station trials, it recorded a mean yield of 1002 kg/ha in *kharif* season and 1191 kg/ha in *rabi* season which is about 18.3 (847 kg/ha) and 10.48 (1078 kg/ha) *per cent* increased yield over the check variety VBN (Gg) 3 and 35.5 and 21.4 *per cent* increased yield over CO 8. In multi location trials, it recorded an average yield of 746 and 977 kg/ha during *kharif* and *rabi* seasons respectively. Which is 31.7 and 16.2 *percen*t yield increment over check CO 8 and VBN 4 In Adaptive Research Trial during *kharif* season over 46 locations, it recorded an average yield of 847 kg/ha with 9.0 *per cent* (777 kg/ha) and 7.8 *per cent* (786 kg/ha) increased yield over the check varieties. In *rabi* seasons (44 locations), this variety recorded an average yield of 852 kg/ha, which is 10.5 (771 kg/ha) and 13.8 (749kg/ha) *per cent* increased yield over the check varieties. In OFT trial conducted over 16 locations in Virudhunagar and Thoothukudi districts, this variety recorded grain yield of 941 kg/ha which is 10.6 *per cent* increased yield over VBN 4 (851 kg/ha). It is determinate plant type, medium duration with multiple blooming nature, resistance to Mungbean Yellow Mosaic Virus (MYMV) and Urdbean Leaf Crinkle (ULCV) diseases. This variety contains 22.85 % protein and 100-seed weight ranging from 3.5 - 4.0 g.This variety is suitable for cultivation during *kharif, rabi and summer* seasons of Tamil Nadu.

S2.111: Evaluation of chickpea genotypes for yield and mechanical harvesting traits

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Mechanization of farm operations is essential for improving efficiency of agriculture and reducing cost of cultivation. Chickpea genotypes with upright and tall growth habit having fruiting zone starting at about 30 cm from the ground are considered suitable for combine harvesting. The experiment consisted of 270 genotypes and 8 checks sown in augmented design with 10 blocks. Each genotype was sown in a single row with 4 meter row length and spacing 30x10 cm during *rabi* 2019-20 at Regional Agricultural Research Station, Vijayapura. Among 270 genotypes, 25 genotypes were found to be superior in yield and mechanical harvesting traits compare to the checks NBeG 47 and GBM 2. The mean sum of squares due to various sources of variation for quantitative characters was studied, out of 11 characters 10 characters showed significant differences, indicating that the variability among the chickpea genotypes accessions was significant. Among the desi types the genotype ICCV 191618 and ICCV 191115 with plant height of 62 cm, 61 cm respectively and the height of the first pod from ground of 43 cm, 40 cm respectively in comparison to checks NBeG 47 and GBM 2. In kabuli types, the genotypes ICCV 191301 and ICCV 191308 were found to be superior with plant height of 52 cm, 51 cm respectively and height of first pod from ground of 35cm, 38cm respectively compared to the checks MNK 1 and KAK 2. New breeding lines suited to mechanical harvesting are developed for strengthening the breeding programs.

S2.112: Greengram VGG 18 002 - A new high yielding bold seeded Greengram culture suitable for value addition

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The Greengram culture VGG 18 - 002 is a derivative of EC 496839 x IPM 409-4 and matures in 65 - 75 days. It is a bold seeded culture recorded 100 seed weight ranging from 5.5 - 6.0 grams and suitable for sprouting. Sprouted seeds of VGG 18-002 synthesize high quantity of Vitamin C (18.17 mg/100) than the check variety CO 7 (12.25 (mg/100g). The yield of VGG 18-002 is 900 kg/ha which is 13.92, 16.42 and 14.79 *per cent* increased yield over the check varieties CO8 (790 kg/ha) CO7 (773 kg/ha) and VBN 4 (784 kg/ha) respectively. In station trials at NPRC, Vamban, it recorded a mean yield of 1397 kg/ha and 1505 kg/ha during *kharif* and *rabi* seasons respectively which is 20.2 (1162 kg/ha) and 33.8 (1124 kg/ha) *per cent* increased yield over the check variety CO 8. In multi location trials, the culture VGG 18-002 recorded the yield of 984 kg/ha and 949 kg/ha during *kharif* and *rabi* seasons respectively. It is 7.1 and 30.3 *per cent* increased yield over the check variety CO 8. In Adaptive Research Trials conducted during *kharif* season (67 locations), the culture VGG 18-002 recorded an average yield of 838 kg/ha. It was 13.2 (740 kg/ha), 13.7 (737 kg/ha) and 13.4 (739 kg/ha) *per cent* increased yield over the check varieties CO 8, CO 7 and VBN 4 respectively. In *rabi* season trials (41 - locations), this culture recorded an average yield of 885 kg/ha, which is 7.9 (820 kg/ha), 11.3 (795 kg/ha) 7.1 (826 kg/ha), *per cent* increased yield over the check varieties CO 8, CO 7 and VBN 4. It is also highly suitable for making sprouts, prepare roasted seeds, snacks and savories. It has also manifested high yield and moderately resistant to Mungbean Yellow Mosaic Virus (MYMV) and powdery mildew diseases and resistant to urdbean leaf crinkle virus disease. At present, this culture is being under testing in OFT. Considering the superior quality along with yield this culture may be approved to release as a variety for savories.

S2.113: Cowpea VCP 14 001 - A new high yielding determinate type Cowpea culture

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The cowpea culture VCP 14-001 is a cross derivative of VBN 1 x VCP 10-001developed at National Pulses Research Centre, Vamban and tested in station yield evaluation trials at NPRC from 2014 to 2017. In *kharif* seasons the culture VCP 14-001 has registered 826 kg/ha which is 4.6 percent increases yield over VBN1 and in *rabi* seasons the culture 14-001 has registered 2582 kg/ha which is 69.1 and 46.78 per cent increased yield over the check VBN 1 (1527 kg/ha) and CO(Cp) 7 (1759 kg/ha) respectively. In Multi-location trials, in *kharif* season the culture VCP 14-001 has registered 791 kg/ha from 12 locations, which is 4.7 per cent increased yield over the check variety VBN 3 (755 kg/ha) and 2.59 per cent over CO(Cp)7 (771kg/ha). However during rabi season the culture registered the average grain yield of 1054 kg/ha which is 18.01 per cent increased yield over the check variety VBN 3 (893 kg/ha) and 19.78 percent increased yield over CO (Cp7) (905 kg/ha). In Adaptive Research Trials conducted during 2020- 21 & 2021-22. In kharif season (63 locations) the culture VCP 14-001 has registered the average grain yield of 998 kg/ha, which is 8.8 per cent increased yield over the check variety VBN 3. In rabi season (39 locations) it has registered an average yield of 1114 kg/ha which is 13.09 per cent increased yield over the check variety VBN 3 (985 kg/ha). The maximum yield of 2160 kg/ha was recorded in Vadamadurai in Dindigal district. The overall average yield of VCP 14-001 is 1072 kg/ha which is 15.9 percent increased yield over VBN 3(925 kg/ha). The culture possesses special advantages of determinate plant type, synchronized maturity, resistance to Bean Common Mosaic Virus and moderately resistant to pod borer. The cowpea culture VCP 14-001 is having preferable seed colour with acceptable cooking quality with high protein (18.61 %) and fibre (5.6 %).

S2.114: Agro-morphological characterization of blackgram (*Vigna mungo* L. Hepper) germplasm collection conserved in the Indian National Genebank and development of a core set

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Blackgram/Urdbean/Mash (*Vigna mungo* L. Hepper) is one of the most important pulse crops in Asian countries. The Indian National Genebank (INGB) conserves ~2266 accessions of blackgram from the diversity rich areas. These genetic resources are crucial for genetic enhancement and crop improvement of blackgram. In order to facilitate the efficient utilization of blackgram genetic resources, a core set of blackgram collection at INGB has been developed. Towards this, characterization, and preliminary evaluation of total 2,266 blackgram accessions from INGB were undertaken during *kharif* season 2019 and 2020 at Hyderabad, India. Data were recorded on 16 qualitative and 14 quantitative traits. A wide range of variability was observed for important traits such as days to maturity, plant height, primary branching, pod number per plant, test seed weight, grain yield per plant etc. Core Hunter 3 was used to develop five different core sets following optimisation of average genetic distances and representativeness. These five core-sets were then evaluated on different indices such as genetic distance, mean difference percentage, variance difference percentage, coincidence rate of range, and variable rate of coefficient of variance in comparison to threshold values of these indicators. Accordingly, the best core set comprising 218 accessions was selected which could capture maximum diversity as shown by increased Shannon Weaver diversity index as well as similar trait distribution pattern as that of the entire collection, PCA and other indices. The blackgram core set of INGB is expected to accelerate utilization of diverse germplasm in blackgram breeding and crop improvement.

S2.115: Pre-breeding techniques to develop new genetic resources in major food legumes crops

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The major difficulties limiting grain legume production and yield globally are the limited genetic base of cultivars and the inadequate exploitation of genetic resources. The genetic manipulation of grain legumes requires the exploitation of fresh and interesting sources of variation. Important sources of genetic diversity for crop development can be found in wild relatives with increased levels of resilience or tolerance of various stressors. However, linkage drags and cross-incompatibility barriers restrict their use for cultivar development. Pre-breeding offers a special opportunity to get around this by introducing desirable genes from wild germplasm into genetic backgrounds that are easily exploited by the breeders with minimum linkage drag. In order to develop new gene pools for chickpea, pigeon pea, and groundnut with a high frequency of useful genes, wider adaptability, and a broad genetic base, pre-breeding activities using promising landraces, wild relatives, and good well cultivars have been started in National and International. In pre-breeding programmes, the availability of molecular markers will greatly assist in reducing linkage drags and improving the effectiveness of introgression.

S2.116: Studies on seed dormancy induction and release in green gram (*Vigna radiata* L. Wilczek)

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Precocious germination, whilst the seed is still attached to the mother plant, known as preharvest sprouting (PHS), occurs when the seeds got exposed to high humidity or rain just before harvesting in crops that lack dormancy. PHS results in substantial production losses to the tune of $1 billion US dollars worldwide annually, apart from reducing grain quality. Green gram, the third most important legume in the country, is highly susceptible to PHS, with a yield loss of up to 60-70% when harvesting coincides with rains. Interestingly, green gram requires both dormancy (hard seeds) and easy imbibition due to its susceptibility to PHS and its usage as a dietary sprout, respectively. We studied a total of 132 genotypes of green gram for dormancy patterns at different time intervals from freshly harvested seeds (FHS) up to eight months of storage under ambient conditions. We find a significant difference in seed hardness among the genotypes at FHS. The maximum and minimum seed hardness were 53.64% and 0%, respectively, while the average seed hardness among the genotypes was 19.85% at FHS. The release of seed hardness was increased with the enhancement of storage time, but the pattern of release in seed hardness among the genotypes differed at different intervals. After eight months of storage, the maximum and minimum seed hardness was 8.75% and 0%, while the average was 0.83%. These studies help the breeder choose genotypes resistant to PHS and lose their dormancy in a shorter period to be used for dietary sprouts.

S2.117: Genetic Variability and Divergence Analysis For Yield And It's Component in Pigeon pea [*Cajanus cajan* (L.) Millsp.]

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The present investigation in Pigeon pea [Cajanus cajan (L.) Millsp.]" was conducted at Oilseed Research Farm, Kalyanpur, C. S. Azad University of Agriculture and Technology, Kanpur- 208 002 (U.P.) during kharif season 2021-22. The research has been investigation on selection viz. genetic variability, heritability and genetic advance, correlation coefficient and path analysis were carried out for thirty four genotypes to identify the traits directly or indirectly assist in seed yield improvement. Days to maturity, plant height, number of secondary branches, days of 50% flowering, 100 seed weight, number of primary branches, biological yield, seed yield per plant, harvest index, number of pods per plant and number of seeds per pod have identified as high heritability value. Seed yield per plant showed positive and high significant genotypic and phenotypic correlation to harvest index, days to maturity, biological yield, 100 seed weight, number of pods per plant, positive and significant correlation with plant height, days to 50% flowering and positive correlation with number of secondary branches while negative correlation with number of primary branches and number of seeds per pod. The analysis of path emphasized that the characters viz., plant height, days to 50% flowering, days to maturity, number of secondary branches, number of pods per plant, biological yield, harvest index and 100 seed weight showed positive and direct effect on seed yield at genotypic level and phenotypic level, should be taken into consideration for formulating selection breeding programme in order to bring about improvement in the populations.

S2.118: Evaluation of yield and yield attributing traits in high yielding cowpea mutant lines developed using gamma rays and sodium azide

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Continuous demand for cowpea is prevalent to meet the food and nutrition demands of the rapidly growing human population that is expected to increase to 9.6 billion by 2050. Cowpea is a warm-season grain legume often categorized as an orphan crop with immense scope of yield improvement. Compared to other primary pulse crops, the average annual yield of cowpea is less due to low yielding potential of existing cultivars. For improving yield, two widely consumed cowpea varieties, viz., Gomati VU-89 and Pusa-578 were treated with different doses of gamma rays and sodium azide. According to the experimental results lower and higher doses of gamma rays and sodium azide induced a proportional increase and decrease increase in the mean values of traits. Data on ten quantitative and three biophysiological traits were subjected to one-way analysis of variance and post hoc Duncan's multiple range test. Correlation analysis revealed highly significant and positive association of yield with pods per plant, seeds per pod and seed weight. Path analysis revealed maximum direct impact of seeds per pod upon plant yield. This indicated that increasing these attributes could invariably increase the total plant yield. Cluster analysis grouped mutagen treated and untreated population into separate clusters with cluster size ranging from 1 to 4. Principal component (PC) analysis of quantitative traits depicted first two PCs with Eigen-value higher than 1 cumulatively contributed 40.46 and 33.47% of total variation for varieties Gomati VU-89 and Pusa-578, respectively.

S2.119: Variation in Seed Developmental Pattern in Different Varieties of Greengram (*Vigna radiata* L.)

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Greengram (*Vigna radiata* L.) is the third most important pulse crop of India. An attempt was made to identify the stage of physiological maturity in different varieties of mung bean for achieving highest vigour and quality in the seed which permits an accurate measure of the duration of the seed filling period preventing early or delayed harvesting of seed ensuring good seed quality. Five green gram cultivars namely Nyagarh Local Green, Nayagarh Local Black, GV-3, OBGG-101 and OBGG-102 were sown in rabi 2018-19. The seed developmental pattern was studied using morphological, physiological and biochemical parameters and seeds were harvested at different stages i.e. from 7 to 35DAA (Days After Anthesis). The results showed an enhancement in pod length, weight, number of seeds/pod and 1000 seed weight up to 28 DAA in most of the genotypes under study. For understanding the stage of physiological maturity, dry matter accumulation, moisture content germination and vigour index was of prime importance. Average moisture content of seed was recorded to be maximum at 14DAA (69.00%). Seed moisture content was minimum at 35 DAA in all the genotypes. Maximum dry matter accumulation and loss of seed moisture was recorded between 28 to 35 DAA. Initiation of germination was recorded at 14 DAA. Maximum germination was recorded at 28DAA (71.30%). Protein accumulation continued up to 28 DAA where it was maximum (highest in GV-3 i.e. 29.50%). Vigour index-I with highest magnitude was recorded in GV-3, OBGG-102 and OBGG-101 (2184.98, 1911.43, 1770.45 respectively) at 35DAA. Enhancement in above parameters was maximum from 7 DAA to 21 DAA. Germination and vigour index decreased after 28 DAA for Nayagarh Local Green and Nayagarh Local Black indicating attainment of physiological maturity at 28 DAA. For OBGG-101, OBGG-102 and GV-3 physiological maturity was attained at 35 DAA.

S2.120: Development of superior breeding material of urdbean and lentil and its harnessing in organic and Natural farming and traditional cropping system under hill ecology

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Subhash Palekar Natural Farming (SPNF), aims at reducing the use of toxic chemical fertilizers and pesticides. In SPNF many crops are cultivated in the same area with pulses as an inter crop. Pulses have virtues of efficient utilization of limited soil moisture and nutrients like N and P_2O_5, fix atmospheric nitrogen and reduce soil erosion. These help in crop diversification, intensification and sustainability. Pulses create a congenial and diverse environment in the field which supports beneficial insects, wildlife and micro-organisms providing a resilient ecosystem to curtail insect-pests and pathogens attack, help in accumulation of soil carbon thus pulses inclusive crop rotations have a higher soil carbon (C) sequestration potential than of the mono crop systems. In HP, active breeding program of pulses viz. urdbean has resulted in development high yielding urdbean lines viz. DKU82, 87, 90, 92, 98, 102, 116, 118 etc. with stable resistance to MYMV, anthracnose, Cercospora leaf spot and/or powdery mildew. These were found promising under different agro-climatic zones under AICRP (MULLaRP) both in Kharif, summer and rabi seasons. In lentil, high yielding and rust resistant genotypes viz. DKL 37, 50, 55, 80 etc. were promising under AICRP MULLaRP trials. The genotypes were also suitable under organic agriculture and natural farming and will be registered with NBPGR. Urdbean genotypes DKU 87, 90, DKU 98, and and DKU 116 are being tested at farmers for their release as varieties in HP.

S2.121: Conventional and molecular breeding for disease resistance in chickpea: status and strategies

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Chickpea (*Cicer arietinum* L.) is an important grain legume at the global level. Among different biotic stresses, diseases are the most important factor limiting its production, causing yield losses up to 100% in severe condition. The major diseases that adversely affect yield of chickpea include Fusarium wilt, Ascochyta blight and Botrytis gray mold. However, dry root rot, collar rot, Sclerotinia stem rot, rust, stunt disease and phyllody have been noted as emerging biotic threats to chickpea production in many production regions. Identification and incorporation of different morphological and biochemical traits are required through breeding to enhance genetic gain for disease resistance. Various studies have clearly indicated the possibility of transferring resistance genes and desirable co-adapted gene complexes from unexploited wild annual species to the cultivated species. At this juncture, the valuable genetic resources present in the primary gene pool can be successfully utilized in plant breeding programmes for genetic enhancement of chickpea. However, most of the wild species possessing high degree of resistance to multiple stresses are present in the secondary and tertiary gene pools where hybridization with the cultivated species is often limited by reproductive barriers. Gene introgression from the wild species can be monitored effectively with the use of molecular markers, which will expedite the transfer of agronomically important traits into desirable genetic backgrounds for the development of varieties with durable resistance through marker assisted selection.

S2.122: Dissecting the anther development stages by quantifying flower morphological traits in chickpea (*Cicer arietinum* L.)

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Cold stress induces flower abortion in chickpea (*Cicer arietinum* L.), a winter sown crop well known for its higher protein content. For completion of its life cycle, chickpea plants undergo different phases of development starting from vegetative phase which is further transformed to reproductive phase. Both, early and late flower developmental stages are well known for its sensitivity to cold stress resulting in yield and productivity losses in chickpea. However, exact causes of floral abortion are largely unknown. Elucidation of floral development is important to understand the development of flowers and mechanisms underlying flower initiation and development including genes involved in transition of vegetative stage to reproductive stage or transition from one flower stage to another. We have developed a user friendly criterion based on flower morphological traits to estimate anther stages. It was proved that flower length has direct correlation with anther/flower development stages and hence, flower length can be used to estimate anther development/flower development stages in chickpea. Thus, a simple method of flower length measurement will eliminate the use of complex process of transverse sectioning followed by microscopy for identification of anther development stages. Since, flower length varies among genotypes especially at later stages of flower development, a combination of flower length and flower stage can be appropriate criteria to identify the anther stages in chickpea. Understanding of reproductive development and its correlations will pave the way for dissection of molecular mechanisms including gene regulation leading to floral organ development in chickpea.

S2.123: Study on seed quality enhancement, storability and field performance of Kabuli chickpea varieties

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The field and laboratory experiments were conducted at Regional Agricultural Research Station, Vijayapur during 2018-19. The experimental design was Factorial Randomised Block design with two *kabuli* varieties (KAK 2 and MNK 1) and seven treatments involving polymer (10 and 20 ml/kg), vitavax (3 g/kg) and their combinations along with castor oil (10 ml/kg). Among the treatments, combination of vitavax powder (3 g/kg) + polymer coat (20 ml/kg) has recorded significantly higher seed quality parameters, protein content, dehydrogenase activity, reducing and non-reducing sugar content followed by vitavax powder (3 g/kg) + polymer coat (10 ml/kg) combination throughout the storage. MNK 1 *kabuli* variety has better storability due to its bold seed nature providing more food reserves.Further, the stored seeds were treated with bioagent *Pseudomonas flurescence* (30 g/kg) to study the field performance. The treatment combination of vitavax powder (3 g/kg) + polymer coat (3 ml/kg) + *Pseudomonas flurescence* (30 g/kg) has recorded higher seed yield (21.95 q/ha) compared to control. Among the varieties, MNK 1 has responded better compared to KAK 2 (28.26 q/ha) for the best treatment combination with 34% and 24% increase in seed yield over their control (13.04 and 22.70 q/ha, respectively) due to the inherent difference in their yield potential.

S2.124: Elucidating the root architecture development under differential tillage systems of rice fallow in lentil (*Lens culinaris* Medik.)

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Lentil (*Lens culinaris* Medik.) is a treasure of easily digestible protein and other minerals. Poor production potential of this crop can be addressed by increase in area of lentil cultivation under rice fallows. Besides all the potentials of lentil cultivation in rice fallow, this system is characterized by restricted root growth and poor nutrients availability. Dearth of findings regarding the detection of suitable lentil genotypes with preferable root architecture facilitating better nutrients uptake warrant immediate interventions by researchers. Present research findings integrated the objectives of detection of lentil genotypes with favourable root architecture that promote better nutrients uptake followed by unravelling the expression profile of some genes governing root development in lentil. A set of 24 lentil genotypes with variable yield performance under "with till" and "no till" rice-fallow system was appraised for their root architectural study. Genotypes with high yield and better nutrient uptake efficiency exhibited more root volume and lateral roots in contrasting tillage system with better root morphology in "with till" system. ILL-7978, 2011S 56234-1, L-1112-19, IC-281600 for "no till" along with ILL-8006, IC-559996 for "with till" rice fallow could be recommended for having apposite root architectural traits to uptake more nutrients. Expression profiling of *LcTTM3* (*Lens culinaris* triphosphate tunnel metalloenzyme 3) and *LcATP5* (*L. culinaris* auxin transporter like protein 5) genes exhibited multiple fold increase in four lentil genotypes when sown in "with till" compared to "no till" system with higher expression in genotypes having better yield.

S2.125: Developing legume cultivars suitable for Sudanese farming systems

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Faba bean, chickpea and lentils are important food legume crops grown as cool season crops under diverse agroeclogies in Sudan. These crops play an impotyant role in increasing soil fertility through atmospheric nitrogen fixation. These crops are considered as cash crops contributing to the rural livelihood in the country. Still, the current productivity of these crops remain low as the current varieties are old and become susceptible to major diseases and facing different climatic challenges. In order to develop appropriate varieties, ICARDA has developed breeding product profiles for these crops with a priority to introgress heat tolerance genes into the current grown varieties. More than 500 segragating populations emanating from targeted crosses in these crops were shared and with ARC-Sudan which resulted in the identification of high yielding with heat tolerant faba bean, chickpea and lentils lines through direct selection from ICARDA materials. ARC is currently expanding areas under chickpea and faba bean in new areas at Gezira-Scheme and introducing lentil as new crop in the Gezira cropping system to enhance food legumes production and productivity in Sudan. Legume nurseries introduced from ICARDA were evaluated for five seasons (2018-2022) in new production areas resulting in zeroing down on nine faba bean and seven chickpea lines as promising genotypes that require large-scale on-farm evaluation in farmers' fields. Five promising lines of lentil were currently submitted to the National System for Evaluation and Release as varieties. These new materials will allow to expand area under legume production in new production regions and address the demand of these pulses in Sudan.

S2.126: Identification of photothermo-insensitive with climate-smart early maturing chickpea genotypes

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Chickpea is a photothermal-sensitive crop that greatly suffer from low temperature (<15 p C) and high temperatures (>35 p C). It is a long-day crop, whose flowering is promoted by >12h. The photothermal-sensitive of crop prevents horizontal crop spread under a variety of agro-climatic conditions and the development of insensitive genotypes that perform well in all seasons requires donors that provide genes that confer this trait. Therefore, a study was conducted to identify genotypes that are mature early and insensitive to photoperiod and temperature. The set of 74 genotypes was evaluated in *Kharif* 2021 to select eight promising early maturing genotypes with high-yielding capacity. Then further investigations were conducted under natural open field conditions in different seasons viz., Late *Kharif* 2021, Rabi 2021, Summer 2022, Early *Kharif* 2022 and *Kharif* 2022 to identify the genotypes with photothermo-insensitivity among the selected eight genotypes. All genotypes flowered and produced yields at all seasons of the year, although some flowered later and others earlier, and produced variable yields. Among these, the genotypes which are performed better especially under summer seasons are considered as a photothermo-insensitive, such as IPC 06-11, ICCV 92944, JG-14 and ICE 15654-A are able to flower and set pods with higher seed yield with 41.4/9.3 °C range of temperature and 10.8/9.3 h photoperiods and also these genotypes proved to be early maturing genotypes capable of early flowering, resulting in shorter days to achieve physiological maturity. These genotypes can be used as donor aids in the development of early maturing and photothermo-insensitive chickpea.

S2.127: Novel tools for improving faba bean productivity in diverse agroclimatic conditions

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Faba bean (*Vicia faba* L.) is an important cool season legume crop grown globally on 2.94 million ha with total production of 5.66 million tonnes in 2019-21. The global faba bean productivity increased from less than 1.0 tons/ha in 1961 to 2.1 tons in 2021 indicating the impact of research efforts made over last five decades. However, this crop is currently affected by several biotic (fungal diseases, parasitic weeds) and abiotic (heat and drought) stresses. Resistance/tolerance to biotic and abiotic stresses are mainly controlled by polygenic genes in faba bean. Phenotypic selection is cumbersome, remains a number game, and requires multi-environment evaluation. Recent developoment in rapid generation advancement through speed breeding and use of genomic tools will allow to shorten breeding cycle and increase the selection accuracy. Molecular markers associated with resistance to biotic stresses were identified over last three decades. Recently, ICARDA has developed speed breeding facilities which will allow to advance three generations per year. The genotyping by sequencing (GBS) yield 10,794 high quality single nucleotide polymorphisms (SNPs). A total of 130 SNPs highly associated with phenological and yield related traits under herbicide and heat stresses were identified using Single-trait and Multi-trait GWAS, respectively. KASP markers will be designed to implement genomic selection in faba bean. The makers will facilitate and fasten the efficient and effective development of high yielding and tolerant faba bean breeding lines to biotic and abiotic stresses.

S2.128: Breeding Strategies for abiotic stress tolerance in pulses

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Pulses, being rich in protein, minerals and vitamins, play a significant role in the nutritional security of Indian people, especially those below poverty lineEnvironmental stresses such as erratic and insufficient rainfall, extreme temperatures, salinity, alkalinity and aluminum toxicity limit the yield and productivity of many cultivated crops including pulses. Pulses are leguminous plants whose grains are used exclusively for food and are generally grown in harsh environments. Therefore, pulses encounter a number of abiotic stresses during various stages of their life cycle. Each type of stress hampers the growth of the plant and decrease the crop production by disturbing the normal physiology and morphology.The narrow genetic base has to be dealt in proper perspective specially to bring together high yielding genes from wild relatives and land races. It will also help in minimizing vulnerability of pulses to different biotic and abiotic stresses.So, there is a need to take care about these stresses/challenges and combat against them *i.e.,* development of genotypes tolerant to heat, drought and waterlogging, management of abiotic stresses and coping up mechanism against the challenges. For this, conventionalplant breeding techniques supplemented with novel plant breeding techniques should be maintained to put forth for the development of pulses varieties resistant to stress factors. Further, these techniques help thegrowers/producers to obtain higher yielding varieties of various pulse cropsunder environmental stress conditions.

S2.129 Estimation of Genetic Diversity, Heritability and Association of Characters in *Glycine Max* (L.) Merril. for Yield and its Contributing Traits

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Soybean [*Glycine max* (L.) Merr.] is one of the non-conventional seed crops and is profitably grown throughout each spring and fall season.To assess genetic component characters , the yield and the contributing traits were recorded. Leaf area (55.02%), plant height (43.27), harvest index (5.64%), seed per pod, biological yield, physiological maturity, and hundred seed weight were found to have the highest per cent contribution to genetic divergence. Heritability along with genetic advance estimates illustrated higher for some traits due to additive gene action and higher heritability with moderate genetic advance indicated the presence of some heritable traits. Leaf area had the highest PCV and GCV content (39.98, 39.94), followed by plant height, pod/plant, and in contrast lowest is physiological maturity and 50% maturity. Higher heritability along with high genetic advance as a percentage of mean was observed for plant height and leaf area. On the other hand moderate genetic advance with higher heritability were observed for numbers of seed/pod which indicated the presence of both additive and non-additive gene actions for these traits. Numbers of seed per pod is positively and significantly correlated with biological yield (r = 0.277) while biological yield was negatively and significantly correlated with harvest index (r = -0.278) at 5% level of significance. The most divergent and promising genotypes were identified viz., Shivalika and JS 97-52 of cluster 5, RVS 2011-77, JS 20-90 and JS 21-17 of cluster 6, and RVS 2011-32 of cluster 12. These genotypes can be used as parents in further hybridization programmes.

S2.130 Screening and development of yellow mosaic disease resistant lines in soybean (*Glycine maxx*. L. Merill)

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Soybean is grain a legume recognized for its two-fold use as vegetable and oilseed giving both quality consumable protein (38-44 %) and oil (18-22 %). However the widespread occurrence of yellow mosaic disease influence its production negatively. Therefore, the study was conducted at College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India during kharif 2019-20 to identify diverse YMD resistance soybean genotypes. After phenotyping under field condition, molecular screening was performed by using 25 microsetellite markers to analyse the YMD resistant lines in soybean. A set of five gene-based markers were hand-picked for screening all the 60 soybean genotypes for Yellow Vein Mosaic Virus disease. A total of 17 alleles were discovered with a mean of 3.40 alleles per locus for different markers. The gene diversity varied from (0.5044 to 0.6128) Satt305 and Satt308 with a mean value of 0.5628 and Polymorphic Information Content (PIC) values varied from (0.4279 to 0.5359) with an average value of 0.4756, respectively. The primer which showed highest gene diversity and PIC values was Satt308 while the lowest gene diversity and PIC values was observed from the primer Satt305. The major allele frequency varied from Satt305 (0.6333 to 0.4667) Satt308, respectively, with a mean value of 0.5200. The SSR molecular markers with higher PIC worth might be utilized for screening of enormous quantities of germplasm line(s). which decrease the use of resources and the time resulted in high yielding soybean varieties with a low incidence of YMD.

S2.131 Phule Vasu (PU0609-43) - A New High Yielding Black gram Variety for Maharashtra

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Black gram is one of the important pulse crop requires low inputs. The productivity of kharif Black gram is very low. The present improved varieties have lower yield potential and disease susceptibility. There is need to develop high yielding variety combined with early maturity, better quality and resistance/tolerance to major pests and diseases. The Black gram *var.* Phule Vasu is developed by pedigree selection method from a cross between TAU-1 X BDU-1 at Oilseeds Research Station, MPKV, Jalgaon. It was tested for several locations and environments for its stability performance. The variety Phule Vasu and existing released varieties were evaluated for their yield performance under field conditions. The results indicated a significant improvement in yield level under field conditions. The new variety Phule Vasu reported average yield of 859 kg/ha which is 16.39%, 12.88%, 17.92%, 22.04% and 6.19 percent higher than the checks TPU-4, TAU-1, AKU-15,BDU-1and PDKV Black Gold respectively. It is bold seeded having early maturity, moderately resistance to major diseases like powdery mildew, mungbean yellow mosaic virus under field conditions. Considering consistent performance, the Urdbean genotype Phule Vasu (PU-0609-43) has been accepted for released for cultivation in the *kharif* season for Maharashtra state under the name of Phule Vasu in center seed subcommittee on crop standards and notification and release of varieties 2022.

Enhancing the Crop Produce

S3.1: Stability assessment for seed yield of mechanical harvestedchickpea genotypes through AMMI and bi plot analysis

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Genotype × Environment interaction for grain yield were investigated using mechanical harvested 10 Chickpea genotypes in five environments *viz.,* Bidar (E1), Kalaburagi (E2), Bheemarayanagudi (E3), Raichur (E4) and Hagari (E5).The ANOVA for grain yield revealed highly significant (p<0.01) for trials, environments and PCA I and significant (p<0.05) for genotypes, PCA II and PCA III. The significant interaction indicated that the genotypes respond differently across the different environments.GBM-2×WR315 (F7)-118 (1365 kg/ha) (G4) and ICCV191612 (1169 kg/ha) (G3) were recorded the highest and ICCV191608 (956 kg/ha) (G1) lowest mean seed yield (kg/ha) value of the genotypes averaged over environments. As a result, an inconsistent performance of the genotypes across the environments was recorded. Further, the environment's mean seed yield was ranged between 560.07 (kg/ha) for E2 to 1852.20 (kg/ha) for E1, while average seed yield over environments and genotypes was 1101.17 kg/ha. Such that the locations, E2 and E5 are poor, while E1, E4 and E3 were found to be rich according to the environmental index value. Among the genotypes, GBM-2×WR315(F7)-118 (G4), ICCV191612 (G3), RVG-204 (G2)and PHULE VIKRAM (G5) have higher average yields and adaptable to favorable environments, while genotypes KCMH-20-17 (G8), GBM-2 (G7), DCMH-20-11 (G10), GBM-2×WR315(F7)-104 (G9), NBeG-47 (G6) and ICCV191608 (G3) adapted to poor environments. Hence, these genotypes can be used directly as a variety or choice of parent for hybridization programme.

S3.2: Identification and evaluation of chickpea genotypes for root nodule and high yield

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The ability of chickpea genotypes to obtain sufficient nitrogen via its root nodulation is of critical important in supporting growth and grain production. The knowledge and identification of highly responsive chickpea genotypes towards root nodules could be helpful for the breeder in choosing desirable parents to utilize in the breeding programme. Hence, the present study was proposed with a set of 30 chickpea genotypes with 3 checks (Sabour Chana2, PG 186, and Pusa 256) using randomized block design with three replications under natural field condition. All chickpea genotypes were evaluated for root nodule and yield parameters were found statistically significant. Nodule assessment were done at 4 different stages such as pre-flowering (45 days), flowering (65 days), podding (95 days) and at maturation (105 days) stages. Out of the total genotypes studied, significantly high number of nodules were observed duringflowering and podding stages. The number of nodules ranged from 2.25 (pre-flowering) to 26.5 (podding). Maximum number of root nodules was observed on primary roots at the pre-flowering stage, however in the later stages, it was shifted to the secondary root. All root nodule were found effective/ fertile (pink colour) till podding stages later on color changed to blackish brown and was waned. Seed yield showed a positive and significant correlation with number of secondary root nodules/plant, number of effective root nodules, chlorophyll content, dry weight of root nodules/plant, number of nodules per plant, number of pods per plant and harvesting index. In nutshell, the genotypes namely BRHT-8, Sabour chana-2, BRHT-12, JG-218, ICC-67, BRHT-1, and BRHT-6 exhibited considerably high nodulation and seed yield. The findings of this study showed that root nodules played significant role in enhancing the seed yield by improving soil fertility through atmospheric nitrogen fixation.

S3.3: Sustaining crop productivity in maize-chickpea cropping system through integrated nutrient management in vertisols of southern peninsular India

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Maintenance and improving soil fertility with production of nutritionally fortified quality foods play an important role in meeting the needs of growing population is a challenging task for the farmers in the Vertisols of southern Peninsular India. Use of microbes with organic amendments and inorganic fertilizers sustains crop yields of maize and chickpea in this region. Hence, a field experiment was conducted during *Kharif-Rabi* season of 2021-2022 to know the effect of Integrated Nutrient Management in Maize-Chickpea cropping system on crop yield and Economics in Vertisols of southern India. In T_8 treatment, application of 100% Recommended Rate of Fertilizer (RRF) (100:50:50 kg N:P_2O_5:K_2O with Microbial Consortia and $ZnSO_4$ at 25 kg ha^{-1} and $FeSO_4$ at 25 kg ha^{-1})produced 21% higher grain yield (8224 kg ha^{-1}) and water use efficiency (23.2 kg ha^{-1} mm^{-1}) in maize. Higher yields in maize are attributed to greater values of yield components i.e. grain weight per plant (81.00 g $plant^{-1}$) and 100 grain weight (32.84 g $plant^{-1}$) over farmers' practice of cultivation. Similarly, during winter season, application of 100%Recommended Rate of Fertilizeri.e. 25:50 kg N:P_2O_5 with *Rhizobium,*Microbial Consortia and $ZnS0_4$ and $FeSO_4$ at 0.5% spray at flowering (T_8**)** producedgreater chickpea grain yield (2798 kg ha^{-1}) and 35% higher water use efficiency (6.92 kg ha^{-1} mm^{-1}) over farmers practice of application of 75% RRF in chickpea cultivation. This was attributed to higher pods weight (12.57g $plant^{-1}$), seeds weight per plant (11.30g $plant^{-1}$) and 100 seeds weight 24.51 g. Even better root growth i.e. 15.2 cm root length, root weight (0.78 g $plant^{-1}$), higher number of nodules (29.2), nodule weight (0.90 g $plant^{-1}$) produced better growth with higher yields in chickpea in T_8 treatment. In maize, net returns were higher by 12% with T_8 treatment over farmer's practice of cultivation.

S3.4: Adoption of improved conservation and production technologies for higher Pulse production through watershed management in the SAT of South India

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Watershed development projects are viewed as multipronged approach to bring sustainability in overall production and livelihood of a hydrogeological unit. Adaptions of c**onservation** measures, improved crop production technologies and increased area under protective irrigation (during Post-Project period)are tend to contribute towards stabilization of crop productivity. However, the studies evaluating impact of watershed projects particularly on pulse crops production and productivity are scarce. Therefore, the impact of six watersheds namely GR Halli,Chinnatekur,Joladarasi,PC Pyapli, Netranahalliand Ramasagarawere studied to segregate the changes occurred in pulse crop production and practices adopted. Overall, cropping intensity in the studied watersheds increased up to 16.8%, crop yield increase varied from 34% to 65% over the outside watershed. In Joladarasi watershed, redgram and greengram yields increased from 15.7 to 19.4% during *kharif* season, whereas, during *rabi* season the yields of chickpea increased by 28% over outside watershed due to adoption of rainwater conservation practices. Similarly, the increase in yields due to improved technologies ranged from 12% to 33% in chickpea and 29 and 36% in groundnut + redgram intercropping system over traditional farmers technology in P.C. Pypili watershed in Andhra Pradesh. In Netranahalli watershed intercropping of groundnut (TMV-2) with redgram (BRG-2) and cowpea (C-152) increased groundnut pod equivalent (GPE) by 27%, netreturnswerehigherby102%and B:C ratio increased from 1.21 to 1.41over control. Intercropping of groundnut (K-6)withredgram(BRG-2)andcowpea(C-152)increasedGPEby 36%, net returnsby85%and B:Cratio increased by 21% (1.48 to 1.76)withimprovedcultivarsoverlocalcultivars. In Ramasagara watershed Groundnut+redgram yield increased by 35%+47% (TMV-2+BRG-2) to 45%+58% (K-6+BRG-2) over local varieties cultivated by the farmers.

S3.5: Effect of preceding maize crop herbicidal residues on germination and growth of succeeding blackgram (*Vigna mungo* (L.) Hepper)

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Maize is one of the most important food crops in India and more than 80% of maize is grown in *kharif* season. Weeds are the most critical pest, which causes the highest yield reduction in food grain crops. Unavailability of skilled labour in time necessitated the use of herbicides in maize. Each herbicide has somesignificant half shelf-life on the soil and it has a significant impact on the succeeding crop. Shrinking in land areaforce intensive cultivation, which shorten thewaiting period of succeeding crop and fertility restoration is a major reason for inclusion of cereals-pulses cropping system. Residual impact of herbicides caused significant influence on germination and growth of succeeding crops.The field experiment was conducted at Agricultural College and Research Institute, TNAU, Madurai to evaluatethe residual effect of herbicides used in preceding maize on succeeding blackgram. Treatments were application of pre-emergence atrazine 0.25 kg/ha or pendimethalin 1 kg/ha applied singly on 3 DAS and in combination with postemergence tembotrione 120 g/ha or halosulfuron methyl 90 g/ha on 25 DAS, weed-free check and unweeded check in maize. Herbicides applied in maize did not cause any phytotoxicity and residual impact on succeeding blackgram. However, the treatments influenced succeeding blackgram growth. The highest plant height (29.5cm), shoot length (9.99cm), root length (8.0cm), dry matter production (1.17g/plant), number of nodules (9.64/plant) and seedling vigour index (1473) of succeeding blackgram was recorded in pre-emergence atrazine 0.25 kg/ha at 3 DAS followed by post-emergence tembotrione 120 g/ha at 25 DAS.

S3.6: Effect of agronomic management strategies on growth and yield of rainfed redgram (*Cajanus cajan* (L.) Millsp)

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Redgram is an important food legume which is largely cultivated under rainfed conditions. India reported about 4.46millionhectare area under redgram cultivation with a production of 4.18 million tons at 937kg/ha productivity. Underrainfed condition, improper crop management practices lead to low productivity of redgram. With the adoption of suitable agronomic management strategies, productivity could be increased to meet our demand and achieve self-sufficiency in production.The field experiment was conducted in Tamil Nadu during North East Monsoon season of 2019 and laid out in randomized block design with three replications. Agronomic management approaches *viz*., high density planting at 30 cm × 30 cm in addition to the recommended spacing of 60 cm × 30 cm, nipping of primary branches at 45 and 60 days after receipt of soaking rain and foliar application of 1% Pink-Pigmented Facultative Methylotrophs (PPFM) spray was compared with farmer's practice in redgram variety Co(Rg) 7. Pre-monsoon sowing has been taken up and the rainfall received during the cropping period was 521.7 mm on 31 rainy days. The results revealed that sowing at 60 × 30 cm + nipping at 45 days after receipt of soaking rain showed a higher level of relative water content (51.6%) associated with a lower level of proline (26.61 mg g^{-1}). Further nipping at 45 days recorded significantly increased the total number of productive branches, number of pods $plant^{-1}$, grain yield (1512 kg ha^{-1}), net return and benefit-cost ratio under rainfed conditions.

S3.7: Manipulation of planting dates for the management of pod fly, *Melanagromyzaobtusa* Malloch (Diptera: Agromyzidae) in pigeonpea

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Manipulation of date of sowing of crops is an important cultural practice to avoid the peak infestation of insect pests on the crop. Hence, present investigation was carried for three years (2019-20, 2020-21 and 2021-22) during *Kharif* at Zonal Agricultural Research Station, Kalaburagi, UAS, Raichur to assess the effect of date of sowing chosenfour sowing dates*viz.,* 1st and 20th July, 5thand 20th August and three varieties *viz*., TS 3R (mid early duration),GRG 811 (medium duration) andBSMR 736 (long duration)on the incidence of pod fly, *Melanagromyzaobtuse* in pigeonpea. The study revealed that the crop sown on 1stJuly recorded significantly lower pod damage (12.14 %) and seed damage (13.51 %) followed by 20th July sown crop. The incidence was in increasing in delayed sown crop as compare to early sown. The crop sown on 20th August which recorded significantly highest pod (42.40 %) and seed damage (35.09 %). Among varieties studied (TS3-R, GRG 811 and BSMR 736), the pod damage (15.80 %) and seed damage (16.47 %) was significantly lower in TS 3R variety while it was higher in long duration variety BSMR 736 which recorded 43.87 and 39.51 per cent pod and seed damage respectively.Thus this study showed that, advancing the sowing date and growing early maturing varieties escape the incidence or if noticed only at lower level of infestation.

S3.8: Evaluation of foliar application of liquid fertilizers with Unmanned Aerial Vehicle (UAV) mounted sprayer in blackgram (*Vigna mungo* L)

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Field research trial was conducted at J farm research centre, Tractors and Farm Equipment Limited to assess the feasibility drone-based spraying in blackgram during the year of (2019-20 and 2020-21) in *Rabi* season. Application of agrochemicals is one of the decisive operations in agriculture to meet ever demanding food production. The rapid development of unmanned aerial vehicles (UAV) technology as a new method of nutrient / herbicide/pesticide application using low spray volumes demands scientific evaluation compared to conventional practices. The drone mounted sprayer mainly consists of spray fluid tank (10 & 16 l capacity), four fine spray nozzles and GPS enabled chip. The maximum capacity of 10-16 l to cover upto one acre of land within 8 minutes.The spraying with the UAV was found best option as compared to Conventional/farmers practice. The highest yield (1429 kg/acre) was recorded with (T7) followed by T3 (1351 kg/acre), T2 (1254 kg/ acre), T5 (1073 kg/acre), T6 (994 kg/acre) & T1 (887 kg/acre). The UAV spraying with 25 lit of spray fluid + 100% of agrochemical dose per ha (T7-J farm drone-based practices – Seed to Seed) is the best remunerative option to the farmers. This option has recorded increases in yield by 81.57 % and gross income INR 40446/ha as compared to Farmers/Conventional practice.The spraying with 25 l spray fluid has also saved water (345 l water/ha) as compared to 370 l of spray fluid in conventional method. It saves Ca. 90% of total water requirement.

S3.9: Effect of conservation tillage practices effect on crop productivity and resource use efficiency under pigeonpea-wheat cropping system in the Western Indo- Gangetic Plains

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In search of a suitable resource conservation technology under pigeonpea (*Cajanus cajan*) –wheat (*Triticum aestivum*) system in the Indo-Gangetic Plains, the effects of conservation agriculture (CA) on crop productivity and resource-use efficiency were evaluated during a twoyear study. The treatments were: conventional tillage (CT), permanent narrow-bed (PNB), permanent narrow-bed with residue (PNB+R), permanent broad-bed (PBB), permanent broad-bed with residue (PBB+R), zero tilled flatbed (ZT), zero tilled flat bed with residue (ZT+R). Layout of experiment was randomized block design with three replications. Soil moisture found more value under residue treatments (13-22%) because they reflect solar radiation, and improve water holding capacity of soil. PNB, PBB treatments had 10-20% lower soil moisture as compared to CT treatment but it was sufficient to fulfil crop water demand resulting saving of irrigation water. Soil temperature on the bed remained always 0.5–3.7^{0}C higher than flat surface thus planting on beds is preferred in winters, as seed germination, growth of the seedlings improved in the conservation treatments. Yield attributes and yields were found maximum in PBB+R followed by ZT+R treatment in both the crops. Lowest yield was found under CT treatment. Water and radiation use efficiency also found higher in CA practices as compared to CT. These positive impacts under PBB+R over CT plots were perceived to be due to no tillage and significantly higher amount of residue retention. Thus PBB + R and ZT+R technologies would be very useful under a pigeonpea–wheat cropping system in this region.

S3.10: Impact of foliar application of nano nitrogen and nano zinc on nutrient content and uptake by mustard (*brassica junceaL.*)

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The aim of this present investigation is to study the effect of foliar application of nano n and zn on nutrient content and uptake by mustard (*Brassica juncea*L.) crop. the field experiment was carried out during october to march 2022 season at instructional farm, rajasthan college of agriculture, MPUATudaipur which lies in agro-climatic zone iv-a of rajasthan, India. the field was designed in a randomized block design having 10 treatments which were replicated thrice. the treatments include the various combination RDF and nano fertilizers of N and ZN. the application treatment t6 (100% NPKZN +1st spray of nano nitrogen and zinc at 30 das +2nd spray of nano nitrogen and zinc at 45 das) has significantly increased nutrient content and uptake (nitrogen, phosphorus and potassium) by seed and stover of mustard.

S3.11: Response of soybean to varied levels and methods of molybdenum application on chlorophyll and root growth

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World agriculture research is revolving around sustainable food production with environmental stability. Indian agriculture is facing challenges from multiple fronts *viz.,* climate change, multi-nutrient deficiency and lower factor productivity*etc*. India imports the highest edible oil in the world, although it produces the highest food grains. Soybean is a dual crop grown for oil and protein content, it's a potential crop for food and nutritional security. Molybdenum (Mo) is an essential ultra-micro plant-nutrient required for growth and development and increasing yield. The quality of soybean is known to improve with Mo application through enzyme-mediated oxidation-reduction reactions, especially in the reduction of nitrates to ammonia before amino acids and protein synthesis. Thus, a field experiment was conducted at AHRS, Bavikere, Shivamogga, during the *Kharif*seasons of 2021 and 2022 to assess the effect of Mo on Soybean. The ten treatments comprised seed treatment with Mo @ 2, 4 and 6 g kg^{-1} of seeds, foliar application of Mo at 0.025, 0.05, 0.1%, and soil application of Mo @ 500, 1000and 1500 g ha^{-1}, and control (Zero Mo). The experiment revealed, the application of Mo @ 6gkg^{-1} of seeds improved total chlorophyll and SPAD and had a positive correlation with N-uptake (r=0.89), besides improving root nodules $plant^{-1}$ (63.5) at 45DAS, total nutrient uptake (N:176.04, P:18.2, K:104.2 kg ha^{-1}) and (Mo: 246.6 g ha^{-1}). It also resulted in higher seed and haulm yield(1695.02 and 2520.02 kg ha^{-1}), oil (20.6) and protein (41.1), followed by soil application of Mo @ 1000g ha^{-1}.

S3.12: Evaluation of dual cropping sequences involving pulses and oilseeds under conserved moisture in Bundelkhand region of Uttar Pradesh

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In search of a suitable cropping sequence(s) in Bundelkhand region under conserved moisture, a trial was carried out during kharif 2021-22 at Crop Research Centre, Gursarai (Jhansi) with the objective to reduce the area under kharif fallow through dual cropping for better livelihood of the farmers. The study area is under rainfed with black cotton soil (Mar). There were 15 treatments, viz. 3 kharif situations viz., fallow, urdbean and *Sesbania* for green manuaring and five rabi crops viz., chickpea, fieldpea lentil, mustard and linseed. Urdbean plots had higher system productivity (2155 kg/ha), followed by Sesbania (1656 kg/ha). Fallow plots had minimum system productivity (1586 kg/ha), which was almost similar to that of Sesbania plots. Further, fieldpea yielded the highest grain yield (2547 kg/ha), followed by chickpea (2106 kg/ha) and lentil (1769 kg/ha). The lowest yield was registered under linseed (1082 kg/ha). Interactions of kharif situations and cropping sequences revealed that urdbean based sequences involving pulses and oilseeds in rabi season established its superiority over the other two sequences i.e. Sesbania and fallow based sequences. Urdbean – fieldpea recorded the highest productivity (2841 kg/ha), followed by urdbean – chickpea (2493 kg/ha) cropping sequences. Urdbean – linseed sequence recorded the lowest crop productivity (1369 kg/ha). Thus, on first year results basis, invention of urdbean in kharif fallow would be found more productive in this area.

S3.13: Enhancement of farmer's income via urd-bean intercropping in sugarcane during summer in western region of Indo-Gangetic Plain/Zone-V

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Sugarcane is the prominent cash crop in the western portion of theUpper Gangetic Plains Region of larger part of Indo-Gangetic plain. Farmers of this region are well versed in innovative agro-technologies thereby presently extensively adopting trench method for sugarcane planting on large scale. Since, urd-bean is the widely consumed pulse of this region therefore, wide space available in form of ridges between two rows of sugarcane can easily be utilize for cultivation of urd-bean crop as an extra intercrop during the summer season *i.e*., between March-June. Hence, to establish the economic viability of the technique an adaptive field trial was conducted at farmer's field in the Muzaffarnagar district of Uttar Pradesh. Under this trial, a single row of urd-bean was sown on the ridges during 1 to 10 March immediately after transplanting of sugarcane and finally the crop was harvested between 10-15 June. All intercultural operations *viz.*, weeding, disease and pest management *etc*. were done as per requirement. Urdbean intercropping in no way penalized sugarcane yield rather increased it to the tune of 4-5 ton/ha and this may be due to the incorporation of urd-bean residues in rows during earthing-up in sugarcane. An additional benefit of nearly 0.8-ton urd-bean grains/ha was achieved from the same field. Moreover, the trial also discouraged the weed infestation that caused a monetary benefit to the farmers by saving huge expenses and time incurred in managing weeds during this period. Therefore, intercropping of urd-bean in sugarcane not only proved to be a successful practice but also enhanced farmer's income besides improving the soil health.

S3.14: Resource use and economic potential of chickpea cultivation in Haryana

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A study was conducted in Bhiwani, Dadri and Mahendragarh districts of Haryana during the year 2021-22 with the objective to work out the economics and resource use efficiency of chickpea. Budgeting technique was employed to draw practical implications and production function was used for measure the extent of resource use in chickpea cultivation for taking policy decisions to encourage its cultivation in Haryana. The Negative growth rates of area and production of chickpea was observed in Haryana during last two decades (2000-20) in same period owing large replacement of area towards mustard and wheat. The gross and net returns of Chickpea cultivation in Haryana worked out were Rs. 78003 ha^{-1} and Rs. 23388 $ha^{-1.}$ The value of B: C ratio was 1.43 over total cost. The marginal value productivity (MVP) of chemical fertilizer, plant protection chemicals, machinery and irrigation was greater than unity for Bhiwani, Dadri, Mahendragarh and overall Haryana which indicates that these inputs were underutilized in the respective district. On the other side, the value of MVP were less than unity for human labour and seed in all districts indicating that these resources were over utilized and needs to be curtailed for higher returns. The major Constraints faced by Chickpea growers were unavailability of improved varieties in local market (85.83%), Price realization less than M.S.P./under pricing their produce (80.83%), non-adoption of package of practice/ low input used (75.83%) and high incidence of insect-pest infestation (64.17%).

S3.15: Influence of sowing date on performance of mungbean varieties

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A field experiment was conducted at Research farm of CCSHAU Regional Research Station; Rohtak during kharif 2021.The objective of the experiment was to study the effect of different date of sowing on phenology, growth and yield of mungbean varieties.The soil of the experimental field was sandy loam in texture, neutral in reaction, low in organic carbon and available nitrogen, medium in available phosphorus and high in available potassium.The experiment was laid out in split plot design with three dates of sowingviz.25th June, 10th July and 25th July in main plot and four varieties viz. MH1142, MH 318, MH 421and MH 1703 in sub plot replicated thrice. Overall results depicted that mungbean sown on 25th June took significantly higher number of days to attain flowering and maturity as compared to delayed sowing of 25th July. Mungbean sown on 25th June produced taller plants with higher no. of branches /plant, no. of pods /plant and no. of seeds/ pod. The crop sown on 25th June being at par with 10th July produced 8.95 % higher seed yield than 25th July sown mungbean.Various mungbean varieties failed to influence days taken to flowering. But Mungbean varieties MH 1703 and MH 1142 took higher no. of days to attain maturity while MH 318 took least no. of days to attain maturity. Among all the mungbean variety tallest plants were recorded in MH 1142 (51 cm) which was significantly taller than rest three varieties. The number of pods/plant was recorded highest in mungbean variety MH 1142 which was significantly higher than MH 1703 but at par with mungbean variety MH 318. However number of branches /plant, yield attributes (No. of seeds/ pod and 100 seed wt) and seed yield were significantly higher in mungbean variety MH 1703 followed MH 1142. Mungbean variety MH 318 recorded lowest seed yield which was 10.97 % and 7.05 % lower than MH 1703 and MH 1142 respectively.

S3.16: Performance of newly released Jammu Lentil-144 in different sowing environmentsunder rainfed conditions of low altitude sub-tropical region of N-W Himalayas

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Lentil is an important *rabi* season crop of rainfed areas, but under changing climatic conditions, the crop is suffering a lot due to high temperature especially during reproductive stages.Among the various production technologies, time of sowing and varieties plays the most important role which affects the productivity of crops. An experiment was conducted during *rabi* 2017-18 and 2018-19 to evaluate the performance of Jammu Lentil-144 along with L 4147, L 699 and PL 406 varieties sown under 3 dates of sowing (*viz*., 20th October, 4th and 19th November) thus creating three different sowing environments in factorial RBD with 3 replications. Jammu lentil-144 observed significantly higher seed yield values as compared to the other varieties. However, variety L4147 registered significantly minimum seed yield values, whereas varieties PL 406 and L 699 were statistically at par. Variety Jammu Lentil 144 observed 114.8, 14.7 and 17.2 per cent higher seed yield over L 4147, L 699 and PL 406, respectively. Jammu Lentil 144 took mean 83 and 128 days to 50% flowering and physiological maturity, respectively. Significantly higher seed yield of lentil observed in 20th October sowing, followed by 4th and 19th November sowings. The early sown crop (20th October) also took more days to 50% flowering (98.2) and physiological maturity (139.0) as compared to the later sowings.

S3.17: Agronomical performance of newly released Jammu Lobia Super 60 variety under sub-tropical areas of Jammu and Kashmir UT

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Cowpea is an important *kharif* season crop grown under rainfed areas of Jammu region of J&K UT. Under the current circumstances, new modern varieties can never be fully exploited with the existing fertilizer practice and fails to show its full potential unless these are providedwith adequate doses of fertilizers.An experiment was conducted during *kharif* 2018 and 2019 to evaluate the performance of Jammu Lobia Super 60 (JLS-60) along with Local Dhiansar (LDH-1) as check with 4 nutrients level control (no fertilizer), 25% less than Rec. NP, Rec. NP and 25% higher than Rec. NP in factorial randomized block design with three replications. JLS-60 observed significantly higher seed yield values as compared to the local variety LDH-1. However, JLS-60 registered about 40-50 per cent higher seed yield values than LDH-1. JLS-60 took mean 40.2 and 62.3 days to 50% flowering and physiological maturity, respectively. However, LDH-1 variety had taken 60.4 and 81.5 days to complete the reproductive stages.Significantly higher seed yield of cowpea observed in 25% higher rec. NP followed by rec NP and 25% less rec NP; however, the minimum yield was recorded in control. Cowpea fertilized with higher (25%) NP dose also took more days to 50% flowering (53.7) and physiological maturity (73.9) as compared to the other fertilizer doses. However, the minimum days to flowering and physiological maturity were envisaged by the control.

S3.18: Achieving sustainability in production in India through tech-innovations is crucial in realizing self-reliance in the pulses sector

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Pulses are smart food and play the very important role in achieving Sustainable Development Goals (SDG) of the United Nations. Being cultivated in wide environmental conditions, season and niches, these have proved as an essential source of dietary protein and energy for a large population of the country. Besides protein, these are an excellent source of carbohydrates, dietary fibres, vitamins, minerals and phytochemicals. Supplementation of pulses with cereals in diets also helps in amino acid balance. Therefore, with greater food value of pulses, these have played a crucial role in food and nutritional security by alleviating protein hunger and malnutrition prevalent amongst the poor. The importance of pulses is further highlighted from the fact that their contribution accounts for nearly 703 billion Indian rupees to the Indian economy in fiscal year 2020 which is significantly higher compared to the previous fiscal year. Thus, this sector contributed about five percent to the GVA (gross value added from pulses) of crops that same year, an increase from a little over 4% in fiscal year 2012. Contrary to their enormous food values/energy content, these crops are still grown on marginal lands, with minimal inputs, mainly under stress-prone/constrained environments (rainfed/dryland ecosystems receiving meager inputs etc.) resulting in under-exploitation of their productivity-potential and optimal-spread compared to many competing crops(s). Pulses do have a unique ability to fix atmospheric N (40-60 kg of N/ha) in their root nodules (and leaf falls and rhizospheric contribution), thereby improving fertility of soil/site through its carry-over effects. Thus, inclusion of pulses in the cropping system(s) (as a candidate crop) is regarded as a BOON that reduces the need for synthetic fertilizers, consequently decreasing greenhouse gas emissions and raising carbon sequestrations.

S3.19: Salicylic acid and biochareffect on productivity of rainfed chickpea (*cicer arietinum* l.) in South-Western Rajasthan

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The field experiment was conducted at Rajasthan College of Agriculture, MPUAT, Udaipur during *rabi* 2021-22 in factorial randomized block design with twelve treatments comprising of four doses of salicylic acid viz., water spray, 50, 100 and 150 ppm and three doses of biochar *viz*., control, 1 and 2 t ha^{-1} and replicated thrice. Chickpea variety JAKI-9218 was sown on 1st November, 2021 at seed rate of 80 kg ha^{-1}. The foliar application of 100 ppm salicylic acid at flower initiation and pod filling to chickpea significantly improved growth parameters *i.e.,* dry matter $plant^{-1}$, effective nodulesand chlorophyll content over application of salicylic acid at 50 ppm and water spray, respectively.The chickpea raised with foliar application of salicylic acid upto 100 ppm significantly improved yield attributes *viz*., pods $plant^{-1}$, yield $plant^{-1}$ and test weight thereby enhanced seedyield by 10 and 26%, respectively over foliar spray of salicylic acid at 50 ppm and water spray. Application of biochar @ 2 t ha^{-1}recorded significantly maximum dry matter $plant^{-1}$, number of effective nodules and chlorophyll contentover application of biochar @ 1 t ha^{-1} and control, respectively. The increasing levels of biochar up to 2 t ha^{-1} significantly increased yield attributes *viz*., pods $plant^{-1}$, seeds pod^{-1}, yield $plant^{-1}$ and test weight with concomitant increase in seed yield 16 and 38%, respectively over application of biochar at 1 t $ha^{-1}$and control.

S3.20: Evaluation of pigeonpea (*cajanuscajan* L.) based intercropping systems under semi-arid zone of Gujarat

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A field experiment was conducted during *kharif* of the year 2018-19, 2019-20 and 2020-21 at Pulses Research Station, S. D. Agricultural University, Sardarkrushinagar,Gujarat to evaluate pigeonpea (*Cajanus cajan L.*) based Intercropping systems under semi-arid zone of Gujarat. The treatments were T1 = pigeonpea + blackgram (1:2), T2 = pigeonpea + greengram (1:2), T3 = pigeonpea + maize (1:2), T4 = pigeonpea + groundnut (1:2), T5 = pigeonpea + blackgram (1:3), T6 = pigeonpea + greengram (1:3), T7 = pigeonpea + maize (1:3),T8 = pigeonpea + groundnut (1:3),, T9 = sole pigeonpea, T10 = sole blackgram, T11 = sole greengram, T12 = sole maize, T13 = sole groundnut and T14 = sole pearl millet. Among pigeonpea based intercropping systems, pigeonpea + groundnut (1:3) was found superior with mean maximum pigeonpea equivalent yield 2699 kg/ha and also gave mean maximum net returns of Rs. 1,24,077/ha. Further, this intercropping system also recorded relatively higher land equivalent ratio of 1.55 indicating yield advantage of 55% compared to sole crops.

S3.21: Effect of nutrient management practices and foliar nutrition for sustainable production of fieldpea (*Pisum sativum L.*)

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A field experiment was conducted during Rabi season of the year 2016-17, 2017-18 and 2018-19 at Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar, Gujarat to find out the best nutrient management practices and foliar nutrition for higher nutrient use efficiency and yield of fieldpea under North Gujarat condition. The experiment was carried out in Factorial randomized block design with four replications. The experiment consist of fifteen treatment combinations involving three levels of nutrient (fertilizer) application (N1: 75 % RDF, N2: 100 % RDF and N3: 125 % RDF) and five levels of foliar application (F1: Water spray (control), F2: Neem coated urea 2 % at pre flowering and pod initiation stage, F3: NPK (19:19:19) 0.5 % at pre flowering and pod initiation stage, F4: NPK (17:44:00) 0.5 % at pre flowering and pod initiation stage, F5: NPK (0:0:50) 0.5 % at pre flowering and pod initiation stage. The results of three years data indicated that differences due to different rate of fertilizers were found non-significant during individual as well as pooled data, while the foliar application of nutrients were found significant in pooled results. The treatment T3 (NPK 19:19:19) spray at pre flowering and pod initiation stage recorded significantly higher seed yield (3009 kg/ha) as compare to all the reaming treatments and also secured the highest net returns of Rs. 70196 /ha with highest B:C ratio of 2.24.

S3.22: Foliar nutrition on growth and yield attributes of black gram (*Vigna mungo* L.) in the Grid Region of Gwalior

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A field experiment to study the effect of foliar nutrition on growth and yield attributes of black gram (*Vigna mungo* L.)was conducted at the crop research center, School of Agriculture, ITM University, Gwalior, (M, P.) during the Kharif season of 2020-21. The treatments under study included Absolute control [T_1], Recommended dose of fertilizers (RDF)[T_2],RDF+DAP @ 2% at pre-flowering stage [T_3],RDF+Urea @ 2% at pre-flowering stage [T_4],RDF+KNO_3 3% at pre flowering stage [T_5],RDF+19:19:19(N :P: K) 1% at pre flowering stage [T_6],RDF+Urea 1% at pre flowering stage+KNO_3 1% at pod formation stage [T_7],RDF+DAP 1% at pre flowering stage+KNO_3 1% at pod formation stage [T_8], and RDF+19:19:19 (N:P: K) 1%at pre flowering stage + $KNO_3$1% [T_9] at pod formation stage in a randomized block design.Crop is sown following recommended agronomical practices.[T_9] attained the significantly higher plant growth and yield at all growth stages of the plant.The significantly higher plant height, number of leaves, as well as number of branches, number of root nodules, nodules dry weight, grain (1259kaha^{-1}) and stover yield (2030 kgha^{-1}) at maximum crop growth stages recorded in this treatment.The economic traits i.e., net gain and B-C ratio in [T_9]was at par with [T_8]and significantly superior over other treatments.The application of RDF +19:19:19 (N:P: K) 1%at pre flowering stage +KNO_3 1% at pod formation stage in black gram is suggested for the farmers of the Grid Region of Gwalior.

S3.23: Nano-fertilizer based nutrient management in chickpea

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With more than 40% of all pulse acreage and production going to chickpea, it is the most significant pulse crop in India. When compared to other nations, India has extremely low average chickpea productivity. One of the causes of such low productivity is the growing of crops in marginal to sub-marginal land where the soils are deficient in micronutrients, especially zinc and iron. Leguminous crops like chickpea need a lot of phosphorus, zinc, and iron to grow. Phosphorus is crucial for the development of roots, nodules, and the transformation of energy in nodules during nitrogen fixation, zinc for production of nodules, and iron for leghemoglobin and nitrogenase enzymes. Therefore, a deficiency of any of these nutrients has a major impact on seed quality and crop output. The majority of farmers rely on traditional types of fertilizers to supply the crop's nutrient needs. Because a large portion of these traditional fertilizers is lost to the soil-plant-atmosphere system, their nutrient use efficiency is quite low. In this case, using nano-fertilizers might be a sustainable choice to increase chickpea production and nutrient use efficiency. Therefore, in order to determine how nano-fertilizers affect chickpea growth and seed yield, a study was conducted. Results showed that compared to other treatments, 100% RDF + Nano Zn+Fe seed coating @ 62.5 ml ha^{-1} + Nano Zn+Fe foliar spray @ 250 ml ha^{-1} (50% seed coating + 50% foliar) recorded better emergence, plant growth, yield attributes, and seed yield.

S3.24: Response of mung bean (*vigna radiata* l.) genotypes to induced water stress

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An experiment was carried out to study the effect of induced water stress in mung bean germplasm consisting of 124 genotypes at SKUAST-Kashmir under controlled (polyhouse) and laboratory (PEG-6000 mediated screening) conditions respectively. The experiment was laid out in completely randomiseddesign (CRD). Under polyhouse conditions the traits *viz.* rooting depth, fresh weight of roots, dry weight of roots, root volume, no. of leaves, shoot length and shoot weight were recorded, whereas under laboratory conditions the traits *viz.* primary root length, seedling length, no. of laterals and root biomass were recorded. Under polyhouse conditions the seeds were sown in polybags in two sets one for drought tolerance and other as well watered. Initially four seeds of each genotype were sown and after the plants reached at three leaf stage, only two opposite competitive plants were allowed to grow and other two were discarded. The drought was imposed after 21 days after sowing. The roots were extracted after 45 days from sowing of seeds and were analyzed for various root and shoot traits. The mean rooting depth under drought and well-watered conditions was 41.64 cm and 18.66 cm respectively. Mean fresh weight and dry weight of roots under drought and well watered conditions were 0.369 g, 0.279 g and 0.138, 0.077 g respectively. Mean root volume was also higher under drought conditions (3.64) as compared to well-watered conditions (1.50). The shoot traits *viz.* mean shoot length and mean shoot weight was higher in well-watered conditions (37.72 cm and 9.44 g) as compared to drought conditions (24.59 cm and 5.78g) respectively. However, no. of leaves was found to be non-significant in both drought and well-watered conditions. The different concentrations of PEG-6000 (0%, 10% and 20%) were used to induce water stress in seeds and were analyzed for various root and shoot traits. The results concluded that on increasing the concentration of PEG-6000 from 0-20% all the recorded traits showed the decreasing trend.

S3.25: Influence of foliar nutrition on growth and yield of pigeonpea(*Cajanus cajan* (L.) Millsp.)

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Pulses are commonly known as food legumes which are an important source of dietary protein, energy, minerals and vitamins for the mankind. In pigeonpeafoliar nutrition reduces the cost of cultivation which in turn reduces the amount of fertilizer thereby reducing the loss and also economizing crop production. A field experiment was conducted to evaluate the influence of foliar nutrition on growth and yield of Pigeonpea during *kharif*, 2019-20 at Regional Agricultural Research Station, Warangal, Telangana. The experiment was laid out in randomized block design with three replications having eight treatments namely T_1: RDF only, T_2: RDF + 19: 19: 19 @ 0.5 %, T_3: RDF + Mono Ammonium Phosphate (MAP) @ 1%, T_4: RDF + Pulse magic @ 1%, T_5: RDF + Urea, 2%T_6: RDF + $ZnSO_4$ @ 0.5 %, T_7: RDF + $FeSO_4$ @ 0.5 %, T_8: RDF + $ZnSO_4$ @ 0.5 % + $FeSO_4$ @ 0.5 %. Pulse magic @ 10 g/l (Product developed and released by UAS, Raichur for enhancing the yield of pulse crops. It contains 10 percent nitrogen, 40 percent phosphorous, 3 percent micronutrient and 20 PPM plant growth regulator. Significantly higher grain yield (1486 kg/ha) was recorded with RDF+ Pulse magic @ 1% but, which was statically on par with RDF + Urea spray@ 2% (1453 kg/ha) and RDF + 19: 19: 19 @ 0.5 % (1416 kg/ha).

S3.26: Crop diversification: ways for sustainability under changing climate scenario

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Indian agriculture is currently dealing with second-generation issues of declining water table, nutritional imbalances, salinity and soil degradation, a rise in pests, etc. Crop diversification holds out a lot of promise for addressing these issues because it meets basic needs, improve farm incomes, withstands weather anomalies, manages price fluctuations, ensures a balanced food supply, uses less fertilizer and pesticides and generates employment opportunities.In order to increase agricultural productivity on a specific farm while taking into account the various returns from value-added crops with complementary marketing potential, crop diversification helps by inclusion of new crops or cropping systems. It can boost resilience in a number of ways, including enhancing the capacity to control pest outbreaks and slow the spread of pathogens both of which could get worse under future climate scenarios and by protecting crop production from the negative effects of increased climatic variability.Crop diversification has produced a number of significant benefits, including knowledge creation, improved farming methods, improved dietary variety, use of new technologies and practices (such as soil and water conservation), new energy sources (fuel), the development and release of new plant varieties, the introduction of new plants (for food, fuel, fodderand forage) and women farmer empowerment. But, the absence of markets for a variety of agricultural products, farmer investments that have been lost in specialized machinery and infrastructure, and farmer "path dependency" as a result of government policies are a few examples of its sluggish growth.

S3.27: Evaluation of different herbicides against complex weed flora in black gram (*Vigna mungo* (L.) Hepper)

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A field experiment was conducted at MPUAT, Udaipur during *kharif* 2021in RBD design with 13 treatments consisting of pendimethalin 750 g/ha pre-emergence (pe), pendimethalin 750 g/ ha PE *fb* IC and HW at 40 days after sowing (DAS), imazethapyr + pendimethalin 750 g/ha PE, imazethapyr + pendimethalin 750 g/ha PE *fb*mechanical weeding at 40 DAS, Imazethapyr 60 g/ha post-emergence (POE)*fb*mechanical weeding at 40 DAS, imazethapyr + imazamox60 g/ha POE *fb*mechanical weeding at 40 DAS, acifluorfen + clodinofoppropargyl245 g/ha POE, imazethapyr 60 g/ha + quizalofop-ethyl 60 g/ha POE,imazethapyr 60 g/ha + propaquizafop75 g/ha POE,oxyfluorfen 150 g/ha PE + imazethapyr 75 g/ha POE, pendimethalin 750g/ha PE + imazethapyr 75 g/ha POE, IC at 20 DAS *fb* hand weeding 40 DAS and weedy check, replicated thrice. Black gram variety PU-31 was used as the test crop. At 60 DAS, the lowest total weed dry matter (5.76 g/m^2) was observed with imazethapyr + imazamox 60 g/ha PoEwhich was followed by IC at 20 DAS *fb* hand weeding 40 DAS(6.37g/m^2). Further, the highest WCE of total weeds was obtained in imazethapyr + imazamox60 g/ha PoE (90.91%). Among herbicidal treatments, the highest seed yield (750 kg/ ha) was recorded with the application of imazethapyr+ quizalofop-ethyl 60 g/ha PoE. The maximum net return ([1] 36420/ha) and BC ratio (1.85) were realized with the application ofimazethapyr + quizalofop-ethyl 60 g /ha PoE.

S3.28: Response of foliar nutrition on the productivity enhancement of blackgram *cv.* Vamban 6

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A field experiment was conducted at Keezhmanakudi village, Bhuvanagiri taluk of Cuddalore district,TN to study the effect of foliar application of nutrients on growth and yield of blackgram*cv.*VBN 6, during (Feb-Apr) 2017.The experiment was laid out in Randomized Block Design replicated thrice with eleven treatments *viz*.,T_1-Without foliar application(control),T_2- Foliar application of 1% pulse wonder spray on 25 and 45 DAS,T_3-Foliar application of 2% DAP on 25 and 45 DAS, T_4-Foliar application of 3% *panchakavya* on 25 and 45 DAS,T_5- Foliar application of 0.5% 19:19:19 on 25 and 45 DAS,T_6-Foliar application of 1% pulse wonder spray on 25 DAS followed by 2% DAP on 45 DAS,T_7-Foliar application of 1% pulse wonder spray on 25 DAS followed by 3% *panchakavya*on 45 DAS,T_8-Foliar application of 1% pulse wonder spray on 25 DAS followed by 0.5% 19:19:19 on 45 DAS,T_9-Foliar application of 2% DAP on 25 DAS followed by 3% *panchakavya* on 45 DAS,T_{10}-Foliar application of 2% DAP on 25 DAS followed by 0.5% 19:19:19 on 45 DAS,T_{11}-Foliar application of 3% *panchakavya* on 25 DAS followed by 0.5% 19:19:19 on 45 DAS. The result revealed that treatment T_8 recorded higher grain yieldof 1178 kg ha^{-1} and haulm yield of 2763kgha^{-1} when compared to the control.

S3.29: Use of consortium of rhizobium, phosphate solublizing bacteria and potash mobilizing bacteria in chickpea crop

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The application of chemical fertilizers distresses soil fertility and also human health. Inappropriate use of chemical fertilizer leads to the rapid decline in production levels. Moreover, the expenditure incurred on chemical fertilizers reflects an increase in the cost of production. Microbial inoculants or biofertilizers contain living microorganisms that colonize the rhizosphere and helps in the promotion of plant growth, improve microflora and soil health. A lignitebased consortium of rhizobium, phosphate solublizing bacteria and Potash mobilizing bacteria developed by Biological Nitrogen Fixation Scheme, College of Agriculture, Pune was evaluated under field condition as seed treatment in chickpea crop (variety Digvijay). Observations on various growth parameters and grain yield were recorded. The results indicated that the growth parameters and yield of chickpea crop were significantly enhanced by all the treatments over the absolute control. Maximum plant height (33.80 cm), number of pods/ plant (72) root nodules (62) and grain yield (21.23 q/ha) was recorded in the treatment of consortium @ 25g/ kg seed + application of 100 % recommended dose of fertilizers (RDF; 25:50: 30 NPK/ha). This treatment was however at par with treatment of consortium @ 25g/kg seed + application of 75% RDF which recorded plant height (31.00 cm), number of pods/ plant (67) root nodules (57) and grain yield (20.43 q/ha). Thus, seed treatment of chickpea with microbial consortium consisting of rhizobium, phosphate solublizing bacteria and potash mobilizing bacteria @ 25g / kg seed along with 75 recommended doses of chemical fertilizers was found to best for obtaining higher yield and saving of 25% nitrogen, phosphate and potash fertilizers in chickpea crop.

S3.30: Sustainable system intensification of green gram in summer fallows

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An experiment entitled "Productivity enhancement of green gram (*Vigna radiata* (L.) Wilczek) under system of crop intensification (SCI)"was conducted in farmer's field at Southern Coastal Plain (AEU 1), Varkala, Thiruvananthapuram, Kerala during February 2022 to May 2022.The objectives were to standardize the plant population and to assess the effect of foliar nutrition in enhancing the productivity of green gram in summer fallows through a system of crop intensification. The experiment was laid out in split plot design with 16 treatment combinations and four replications. The main plot treatment was spacing (S_1-spacing of 25 cm x 15 cm with single seedling per hill, S_2 -spacing of 25 cm x 15 cm with double seedling per hill, S_3 -spacing of 25 cm x 25 cm with single seedling per hill, S_4- spacing of 25 cm x 25 cm with double seedling per hill) and sub plot treatment was foliar application(F_1 - Urea at 2%, F_2 - DAP at 2%, F_3 - KNO_3 at 0.5%, F_4 - DAP at 2% + KNO_3 at 0.5% at 15 and 30 DAS). The green gram variety, CO-8 was used for the experiment. The results revealed that, planting green gram at a spacing of 25 cm x 25 cm with single seedling per hill with recommended dose of fertilizers, supplemented with foliar application of KNO_3 at 0.5% at 15 and 30 DAS could be recommended for higher productivity and profitability of the crop in summer rice fallows under the system of crop intensification.

S3.31: Growth and productivity responses of various lentil genotypes under normal and late seeded condition in new alluvial zone of West Bengal

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Being a cool season crop, lentil is very sensitive to temperature during its growth stages. It is found that delayed harvest of the preceeding crop which is most frequently rice, causes the majority of the lentil sowings to be postponed in eastern part of India. As a result, the late-sown crop suffers during the seed-filling stage due to the rising high temperatures in most of its cultivated areas and results in lower yield. With these concerns in mind, a field experiment was carried out in the new alluvial zone of West Bengal at the District Seed Farm of BCKV, Kalyani during the two subsequent rabi seasons (November-March) of 2019-2020 and 2020-2021 to examine the difference in yield between normal and late seeding conditions for various lentil cultivars. A total of ten genotypes were studied, with two planting windows for each (15th nov and 30th nov). Among 10 lentil varieties/ genotypes, genotype $C_{23}E_{21}$recorded the highest plant height (55.53 cm), higher number of nodules per plant (39.25), highest dry matter yield (64.43 g m-2) during 30 to 60 DAS, highest no of pods per plant (236.25/ plant) as well as highest seed yield (2250 kg. ha-1) while sown on normally recommended sowing date on 15 November. New genotype like ILL 10802 and conventional variety Moitree have also shown desirable result after $C_{23}W_{21}$. From this experiment, we have found that delaying the sowing window from the middle to the end of November can reduce yields by as much as 27.77 percent. Thus, farmers in that area are advised to plant their crops no later than the 15th of November, with varieties that can thrive in both early and late seeded conditions.

S3.32: Productivity and land use efficiency of different barley based intercropping systems

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The field experiment was conducted at Agronomy Farm, CCS Haryana Agricultural University, Hisar, in 2021-22 toworkout the most productive and profitable intercropping systemamong different barley based intercropping systems. Hisar exhibits the semi-arid condition with the annual average rainfall of 440 mm and situated at 29°10' N latitudeand 75°46' E longitude at an elevation of 215.2 m above mean sea level. The experiment was laid out in a randomized block design in three replicates. The treatments were i) sole barley ii) sole field pea iii) sole linseed iv) barley + field pea (3:3) v) barley + field pea (4:4) vi) barley + field pea (5:5) vii) barley + field pea (6:6) viii) barley + linseed (3:3) ix) barley + linseed (4:4) x) barley + linseed (5:5) xi) barley + linseed (6:6). The soil texture of the experimental field was sandy loam. The soil was low in available N (180 kg ha^{-1}), medium in available P (14 kg ha^{-1}) & high in available K (375 kg ha^{-1}). Sole cropping of barley recorded significantly highest grain yield of 49.63 q ha^{-1}. Among the various barley based intercropping systems, maximum grain yield (32.96 q ha^{-1}) was found in barley + Field pea (6:6), which was at par with barley + field pea (5:5). Maximum LER (1.26) and B:C (2.21) was recorded with barley + Field pea (6:6) treatment.

S3.33: Yield maximization of fieldpea through surface seeding, seed rate and seed priming under rice-based utera cropping system

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In order to find suitable seed rate and seed priming technique for getting optimum growth and yield of fieldpea as *utera* crop an experiment was carried out during *rabi* 2020-21and 2021-22 at IGKV, Raipur. The experiment consisting of three replications was laid out in Randomized Block Design (RBD) having nine treatments *viz.* T_1:Dry surface seeding 80 kg ha^{-1}, T_2:Dry surface seeding 100 kg ha^{-1}, T_3:Dry surface seeding 120 kg ha^{-1}, T_4: Soaked seed surface seeding 80 kg ha^{-1}, T_5:Soaked seed surface seeding 100 kg ha^{-1}, T_6:Soaked seed surface seeding 120 kg ha^{-1}, T_7:Seed priming (1% KNO_3) 80 kg ha^{-1}, T_8:Seed priming (1% KNO_3) 100 kg ha^{-1} and T_9:Seed priming (1% KNO_3) 120 kg ha^{-1}. Among different treatments, significantly maximum plant population was recorded with the treatment T_9: Seed priming (1% KNO_3) 120 kg ha^{-1}. This treatment also gave significantly highest seed yield (1043 kg ha^{-1}), but it remained at par with T_8: seed priming (1% KNO_3) 100 kg $ha^{-1}$and T_6: soaked seed surface seeding 120 kg ha^{-1}over other treatments. It was registered that the percent increment in the seed yield was to the tune of 83.0, 81.4 and 76.8 over T_3: dry surface seeding 80 kg ha^{-1}. The highest net realization (48031 ^{1} ha^{-1}) and benefit to cost ratio (3.25)was recorded under treatmentT_8: Seed priming (1% KNO_3) 100 kg ha^{-1} followed by T_9 : Seed priming (1% KNO_3) 120 kg ha^{-1}. In case of rice – fieldpea relay cropping system, maximum total system productivity (8494 kg/ha), net return of the system (Rs. 106902/ha) with maximum B:C ratio (2.85) were calculated with seed priming (1 % KNO3) 120 kg/ha to utera crop fieldpea during *rabi* season which was closely followed by Seed priming (1 % KNO_3) 100 kg/ha and Soaked seed surface seeding 120 kg/ha over rest of the treatments. At initial stages, moisture content in different depth remains almost similar in the experimental plot. With further increase in time, the moisture content was lost from upper layer (0-15 cm) followed by medium layer (15-30 cm) and deeper layer (30-45 cm) depth. This was true at all the stages of crop growth. Moreover, after 75 DAS almost all the moisture has been depleted from all depths.

S3.34: Phosphorus and zinc economy with phosphate and zinc solubilizing microbes in Lentil

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Methods: An experiment was conducted during Rabi 2019-20 and 2020-21 to study the effect of phosphate and zinc solubilizing microbes on growth, yield and economy of lentil at research farm of pulses section Dept.of CCS HAU, Hisar. The experiment was laid out in randomized block design with the eleven treatments *viz.* T_1 (absolute Control (Without P)}, T_2 (recommended phosphorus dose application (Control)}, T_3 (soil application of 25 kg $ZnSO_4$ per ha), T_4 (application of biophos) , T_5 (application of biozinc) , T_6 (application of biophos + biozinc) , T_7 (50 % recommended phosphorus dose application + biophos) , T_{8} (12.5 kg Zn SO_4+ biozinc) , T_9 (50 % recommended phosphorus dose application + biophos + biozinc), T_{10} (50 % recommended phosphorus dose application + 12.5 kg Zn SO_4 + biophos + biozinc) and T_{11} (recommended phosphorus dose application + nutrient mobilizer {LNm 43a}). Results: Growth as well as yield parameters were significantly affected by different treatments and were significantly higher with application of 50% recommended phosphorus dose application + 12.5 kg $ZnSO_4$ + biophos + biozinc. The soil pH did not differ significantly under different treatment. The Soil EC under different treatment differed significantly with control. The soil organic carbon was found maximum in T_{10} and it was closely followed by T_{11}. Similarly, maximum net return and BC ratio was obtained in T_{10} treatment followed by T_9.

S3.35: Green gram intercropping in jute: A sustainable way to improve jute production economy

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Currently jute is a distress sale crop and its area is declining fast due to low remuneration and labour intensiveness. To make the system sustainable green gram intercropping was tested in jute at ICAR-CRIJAF during 2021-22. During 12-19 days after jute sowing, green gram live mulch (as intercrop) and soil mulch by CRIJAF Nail Weeder jointly maintained more soil moisture at 5 cm to 10 cm depth of soil, i.e., 13.2 to 15.2 % and 19.0 to 21 %, respectively, over 7.4 to 11.7 % and 11.6 to 17.3% on respective depths under monocrop jute. This also reduced the soil temperature by 4°C and 2°C, respectively at 5 cm and 10 cm depth at 2 PM. It bettered jute equivalent yield (43.44 q/ha) over sole jute (41.26 q/ha). It also added 2.5-3.5 t/ha nitrogen rich (2.35% N) green gram waste to the soil. The cost-benefit ratio of jute-green gram intercropping system was 1:2.17 over 1:1.75 under sole jute. The intercropping yielded 5.72 q/ha green gram grain compared to grain yield potential of 14.5 q/ha in sole crop.Apart from these advantages, green gram in intercropping smothered weeds, *Cyperus rotundus* in particular, reduced weed biomass up to 76%, saved 30 mandays as second weeding became redundant. The weed control efficiency is up to 86% under this dual culture.Thus cropping intensification with green gram intercropping in jute betters soil hydrothermal regimes, smothers weeds,sustainably improves economy of jute cultivation and ensure nutrition security.

S3.36: Evaluation of different doses of foliar application of Quikon- a new generation of biostimulant on the growth, yield, and phytotoxicity in greengramcrop

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In India, biostimulants regulation was introduced in Feb 2021 as Fertilizer (Inorganic, Organic or Mixed) (Control) Amendment Order, 2021. With regulation in place, this advanced agriculture technology has opened a new window for the growers to solve their plant growth and crop production problems thereby ensuring sustainable agriculture. Mungbean is grown in a 4.07 M ha area with a production of 2.02 MMT in India. Research is limited on the impact of biostimulants on growth, and the source-to-sink relationship to enhance crop yield on mungbean. Hence, experiments were carried out to evaluate the effect of foliar application of different doses of Quikon an ultra-efficient new-generation Biostimulant obtained from an exclusive plant fermentation process from different SAUs present in different agroclimatic zones of India on the growth and yield of mungbean. The experiments were conducted at ANGRAU, Andhra Pradesh, JNKVV, Jabalpur, IIPR, Kanpur, and UAS, Raichur during the summer season of 2022. The experiments were laid out in a complete randomized block design with five replications. Recommended packages and practices were followed. Foliar application was done at the first flower appearance and grain-filling stage. Among the different doses tested, application of Quikon @ 50 ml/ha was found significantly superior followed by Quikon @ 37.5 ml/ha in increasing plant height, no. of flowers, leaf chlorophyll, protein content, the number of seeds/pods, number of pods/plants, 1000 grain weight, grain yield, and net return. No phytotoxicity symptoms were observed in any of the doses including the highest dose of Quikon @ 100 ml/ha.

S3.37: Effect of conservation tillage practices on plant height at different stages and yield in Soybean (*Glycine max* L.)

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A field experiment was conducted during *kharif 2021* and *2022* at the Holta Farm, Department of Agronomy, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H.P.) to study the effect of tillage and NPK levels on plant height at different stages and yield in soybean. The experiment comprised of twelve treatment combinations which included three tillage practices (minimum tillage, minimum tillage + crop residue and conventional tillage) and four NPK levels (50, 75, 100 and 125 % recommended dose of nutrients) which were tested in split plot design with tillage practices in main plots and different NPK levels in sub plots. Data revealed that minimum tillage + crop residue significantly performed well and ensured best growth. Results showed that minimum tillage + crop residue recorded superior effects ahead of minimum tillage and conventional tillage. Highest plant height at 30 DAS, 60 DAS, 90 DAS, harvest and grain yield in soybean was recorded under minimum tillage + crop residue. Tillage practices did not affect the initial plant stand and test weight. Highest plant height at 30 DAS, 60 DAS, 90 DAS, harvest, grain weight in soybean under 125 per cent recommended dose of nutrient. Different NPK levels did not affect the initial plant stand and test weight.Interaction effect of tillage practices and NPK levels on plant height and yield was found non - significant during both the years.

S3.38: Phosphorus and Potassium fertilization with different levels on the growth and yield of summer green gram (*Vigna radiata* L.) Varieties

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Green gram (*Vigna radiata* L.) is the third most important pulse crop in India which is mostly grown during the *kharif* and summer seasons. Every crop requires adequate fertilization to achieve maximum potential growth and yield. This research attempts to find out the optimum doses of phosphorus and potassium for green gram under Nagaland soil conditions, along with the suitable variety.The field was laid out in factorial randomized block design with total of 36 plots with plot size 4×3mwith 12 numbers of treatments replicated thrice. The treatments consist of combination of variety *viz.,* V_1: IPM 02-3, V_2: SGC-20, V_{3-}: SGC-16 and doses of phosphorus and potassium;$N_{0:}$ control, N_1: 40 kg ha^{-1} P_2O_5 + 40 kg ha^{-1} K_2O, N_2: 50 kg ha^{-1} P_2O_5 + 50 kg ha^{-1} K_2O and N_3: 60 kg ha^{-1} P_2O_5 + 60 kg ha^{-1} K_2O. The research was carried out during April-July 2021.The soil was acidic with pH 4.6, organic carbon (1.05%) and medium availability of N (250.88 kg ha^{-1}), P_2O_5 (32.81 kg ha^{-1}) and K_2O (144.64 kg ha^{-1}). A linear increase in growth attributes, yield, and stover yield was observed up to the application of 60 kg ha^{-1} P_2O_5 + 60 kg ha^{-1} K_2O. However, the result was at par with the application of 50 kg ha^{-1} P_2O_5 + 50 kg ha^{-1} K_2O which gave 48.7% higher yield (574.29 kg ha^{-1}) over control (386.02 kg ha^{-1}). Among the varieties, the performance of IPM 02-3 was superior to the other varieties in test.

S3.39: Productivity of bed planted chickpea (Cicer arietinum L.) as influenced by different intercropping systems

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A field experiment was carried out during the rabi season of 2017 and 2018 to evaluate the productivity and economic viability of bed planted chickpea based intercropping systems. The experiment was laid out in a randomized block design consisting of four replications with thirteen treatments. Results showed that sole chickpea recorded highest seed yield and it was statistically at par with seed yield of obtained under chickpea + oats fodder (2:1), chickpea + oats fodder (4:1) and chickpea + linseed (4:1) intercropping systems. However, oilseed rape and barley as intercrops showed adverse effect on yield and yield attributes of chickpea. Chickpea + oats fodder in 2:1 row ratio recorded highest chickpea equivalent yield of 24.07 and 24.77 q/ha and system productivity of 15.96 and 15.60 kg/ha/day during 2017 and 2018, respectively. Higher net returns (Rs. 63098 and 70924/ha), benefit cost ratio (1.47 and 1.63) and production efficiency (417.9 and 446.1 Rs/ha/day) were also recorded in chickpea + oats fodder (2:1) intercropping system over sole chickpea (Rs. 44862 and 53769/ha and 1.21 and 1.41) during both the years. Chickpea + oats fodder (4:1), chickpea + linseed (2:1) and chickpea + linseed (4:1) also recorded significantly higher chickpea equivalent yield, net returns and benefit cost ratio as compared to sole chickpea.

S3.40: Impact of foliar application of nano nitrogen and nano zinc on soil biological properties of mustard (*Brassica juncea* l.)

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The aim of this present investigation is to study the effect of foliar application of nano nitrogen and nano zinc on yield attributes and yield of mustard (*Brassica juncea* L.) crop. The field experiment was carried out during October to March 2022 season at Instructional Farm, Rajasthan College of Agriculture, MPUAT, Udaipur which lies in agro-climatic zone IV-A of Rajasthan, India. The field was designed in a randomized block design having 10 treatments which were replicated thrice. The treatments include the various combination RDF and nano fertilizers of N and Zn. The application treatment T6 (100% NPK Zn +1st spray of Nano Nitrogen and Zinc at 30 DAS +2nd spray of Nano Nitrogen and Zinc at 45 DAS) has significantly increased biological population (bacteria, fungi and actinomycetes) in soil after the harvest of mustard crop.

S3.41: Effect of nipping and spacing on growth and yield of pigeonpea

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A field experiment was conducted at ARS, Badnapur on medium black soil with slightly alkaline in reaction during kharif 2017-18 and 2018-19. Pigeonpea variety BDN-716 was sown on July 19, 2017 and July 9, 2018. Recommended dose of fertilizer was applied at the time of sowing. The experiment was conducted in factorial randomized block design with two factors viz., nipping's (three stages: Nipping at 45 DAS (N1), Nipping at 60 DAS (N2) and no nipping (N3) and spacing (five spacing's: 90 x 30 cm (S1), 120 x 30 cm (S2), 150 x 30 cm (S3), 180 x 30 cm (S4) and 90 x 20 cm (S5) with 15 treatments combinations. Each experimental unit was repeated five times with 7.2 x 5.4 m size in gross plot for 90 x 30 cm, 120 x 30 cm, 180 x 30 cm, 90 x 20 cm and 7.5x 5.4 m size in gross for 150 x 30 cm. Net plot 5.4 x 4.8 m for 90 x 30 cm, 4.8 x 4.8 cm for 120 x 30 cm, 4.5 x 4.8 m for 150 x 30 cm, 3.6 x 4.8 m for 180 x 30 cm and 5.4 x 5.0 m for 90 x 20 cm respectively. During two years of experimentation, significant differences in seed yield of pigeonpea as influenced by different nipping practices and spacings treatments were observed. Amongst nipping, nipping at 45 DAS (N1) recorded maximum seed yield (2013 kg ha^{-1} and 1176 kg ha^{-1}), net monitory returns (60789 Rs ha^{-1} and 29120 Rs ha^{-1}) and B:C ratio (2.8 and 2.2) than nipping at 60 DAS (N2) and no nipping (N3) respectively. Amongst spacings, spacing 90 x 20 cm2 recorded maximum seed yield (2394.78 kg ha^{-1} and 1339 kg ha^{-1}), NMR (76363 Rs $ha^{-1}$and 29120 Rs ha^{-1}) and B:C ratio (3.3 and 2.5) followed by spacings 90 x 30 cm, 120 x 30 cm,150 x 30 cm and 180 x 30 cm respectively.

S3.42: Response of mung bean crop to different levels of applied zinc, boron & molybdenum

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Fertilization of Mung bean (*Vigna radiata* L.) is one of the most crucial management techniques which effects crop growth and yield. Therefore, the present study was carried out at New Dairy Farm, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *kharif* 2019 and 2020 to assess the response of mung bean (*Vigna radiate* L.) to three levels of zinc (0, 10 and 25 kg ha^{-1}) and three levels of boron (0, 5 and 10 kg ha-1) as soil application and three levels of molybdenum (0, 5.0 and 10.0 g/kg) as seed treatment. The experiment was laid out in randomized block design with replicated three times. The results revealed that the application of 10 kg Zn ha^{-1},5 kg B ha^{-1} as soil application and 5g Mo kg^{-1} as seed treatment recorded significantly increased the plant height (58.63, 60.15 & 57.86 cm), number of branches (3.25, 3.34 & 3.15), number of cluster $plant^{-1}$(5.20, 5.41 & 5.13), pod $plant^{-1}$(33.58, 34.89 & 32.61) and seed yield ha^{-1} (761.65, 774.54 & 747.85 kg ha^{-1})whereas the interaction was found non-significant. The germination per cent was also significantly increased by 3.24% and 0.91% respectively with application of 5 kg B $ha^{-1}$and 5g Mo kg^{-1}, however their interaction was also found significant increased germination per cent of 6.75%. Similarly, the seedling length was also significantly increased by 10 kg Zn ha^{-1}&5 kg B ha^{-1} and 5g Mo kg^{-1}. It was concluded that zinc, boron and molybdenum enhanced mung bean productivity.

S3.43: Enhancing chickpea productivity under tillage practices with supplementary sprinkler irrigation

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A field experiment was conducted at Regional Agricultural Research Station, Nandyal during the rabi season of 2021-22 with an objective to study the comparison between the zero tillage, conventional tillage practices and irrigation management through sprinklers or flood irrigation at different stages of crop growth in chickpea (*Cicer arietinum* L.). The experiment was laidout in split plot design with three replications. The treatments consisted of two tillage practices viz., conventional and zero tillage/reduced tillage as main plots and seven subplots as sprinkler based supplementary irrigation viz., rainfed (control), irrigation during branching, irrigation during branching and pod development, irrigation during pod development. Irrigation during branching, irrigation during branching and pod development, irrigation during pod development through flooding. Among the tillage practices conventional tillage recorded higher grain yield (1917 kg/ha) which is superior to zero tillage (1725kg/ha). Among the different irrigation treatments significantly higher grain yield was observed with irrigation during branching and pod development through sprinklers (2042kg/ha) compared to flooding. So, the present study suggests that conventional tillage with supplement irrigation through sprinklers at branching and pod development recorded higher grain yield compared to zero tillage with flooding at branching and pod development.

S3.44: Soil phosphorus dynamics and crop productivity under pulse-based cropping system for sustainable P management in an Inceptisol

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India relies heavily on foreign import for di-ammonium phosphate (DAP) to meet the farmer's demand. Therefore, environment friendly alternatives such as crop residue (CR), animal wastes like poultry manure (PM) and farm yard manure (FYM) must be utilized as a source of P to curtail the dependency on DAP and utilize the native soil P. A field experiment the impact of integrated nutrient management (INM) on soil P fractionations and crop productivity are studied under pigeonpea-wheat system comprised of: T_1(control): No-P in any crop; T_2 (RDF): 60 Kg P_2O_5per ha in both crop; T_3: P_{36} + FYM (5 t ha^{-1}) – W_{36}; T_4: P_{36} + PM (1 t ha^{-1}) – W_{36}; T_5: P_{36} +CR (50%) – W_{36}; T_6: P_{36} + CR (50%) +PSB – $W_{36.}$ After two years of study, results showed in case of pigeonpea, labile P pools (soluble and Ca_2-P) was highest in T_4 by 18% and 4% as compared to T_1 and T_2 respectively. Similarly, soluble and insoluble P ratio was 0.47: 0.40: 0.38: 0.33:: T_4: T_3: T_5: T_1 in pigeonpea. Whereas, in case of wheat soluble and insoluble P ratio was 0.32: 0.30:0.19:: T_4: T_3: $T_{1.}$ In both the crops Ca_8-Pand Ca_{10}-P was found higher in control plots and occluded-P content was lowest among all seven fractions. In both the crops highest yield in T_6 which was 25% higher in pigeonpea. Hence, it can be concluded that organic sources are excellent in in mobilizing native soil P and improving crop productivity.

S3.45: Evaluation of different rabi genotypes of pulses under varied management practices for higher productivity and profitability under rainfed condition of Eastern India

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A field experiment was conducted at IARI Regional Station Pusa, Samastipur, Bihar during 2017-2022 to study the performance of different rabi pulses and their genotypes under varied management practices for higher productivity and profitability. The treatment consists of two tillage methods i.e. conventional tillage, ZT with residue mulch @ 3 ton/ha, three pulse crops (chickpea, lentil and grasspea) having two varieties of each pulses (local and high yielding varieties) conducted in Factorial RBD with three replications. The results revealed that higher chickpea grain equivalent yield was recorded due to ZT+RM as compared to CT. The results revealed that growing of chickpea after rice recorded maximum chickpea grain equivalent yield, which was significantly higher over the yield obtained in lentil and grasspea. However, lowest chickpea grain equivalent yield was recorded with grasspea. Growing of high yielding varieties such as Ujjwala of chickpea, Rajendra Khesari 1 of grasspea and Pusa Shivalik of lentil recorded significantly higher chickpea grain equivalent yield, which was higher than local variety. The highest net returns and net B: C ratio was recorded with zero tillage along with residue mulch (ZT+RM) applied @ 3 ton/ha. Among the crops, chickpea resulted in maximum net returns and B: C ratio followed by lentil. However, the net returns and B: C ratio was obtained lowest with grasspea. Varieties showed variations on net returns and B: C ratio. Growing of high yielding varieties fetched higher net returns and B: C ratio than local variety.

S3.46: Effect of plant geometry and fertility levels on growth and yield of mungbean

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The field experiment was conducted on deep black soil of Agricultural Research station, Badnapur District Jalna during *Kharif,* 2019-20. The experiment was laid out in Split Plot Design with three replications. The gross plot size was 5.0 x 4.5 m^2 and net plot size was 4.6 x 3.6 m^2 for each treatment. The treatments comprised with three spacing's (S_1: 30 x 10 cm^2, S_2: 45 x 07 cm^2 and S_3: 45 x 10 cm^2) in main plot and three fertilizer levels with one absolute control (F_1: Absolute control F_2: RDF 75 % (18.75:37.50:00 NPK kg/ha), F_3: RDF 100 % (25:50:00 NPK kg/ha) and F_4: RDF 125 % (31.25:62.50:00 NPK kg/ha)) as sub plots comprising twelve treatment combinations. The sowing was done on 03/07/2019 by using BM 2003-2 variety of mungbean. The crop protection measures were adopted as per the recommendations. The crop was harvested on 11/09/2019. The data on seed yield was analyzed statistically.The results from experimental findings revealed that grain yield of mungbean was significantly influenced by various treatments. The spacing of 30 x 10 cm^2 recorded significantly higher grain yield (708 kg ha^{-1}) which was found at par with spacing of 45 x 07 cm^2 (656 kg ha^{-1}). In case of fertilizer levels, grain yield of mungbean was significantly influenced with different fertilizer levels. An application of 125 % RDF produced significantly higher grain yield (785 kg ha^{-1}) and second-best treatment was found with an application of 100 % RDF (680 kg ha^{-1}). The interaction effects of spacing treatments and fertilizer levels were non-significant.

S3.47: Weed smothering effect of legumes under maize-based intercropping under Hilly terrane of Mizoram

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Mizoram comprises 96.9% area under hills and their agriculture is mainly concentrated on the hilly slopes with jhum as a major way of farming. However, the area under jhum has decreased by 72.3% since the 1990s. Agriculture is the major occupation for Mizo people, in this maize among cereals, and cowpea, french bean, rice bean and groundnut among the legumes share a major area of Mizoram foodgrains and are responsible for the livelihood and food security of Mizo people. Moreover, its productivity is very low compared to other states, possibly due to severe weed infestation and poor agronomic management. To solve this issue, an experiment was conducted from *Kharif* 2020 to 2022 at ICAR Farm, Kolasib, under RBD having ten treatments. Treatments consisting of maize as an intercrop with simultaneous sown legumes and 20 daysafter relayed sown legumes *viz*., cowpea, groundnut, french bean and rice bean under 2:2 paired row cropping 45/75 and one hand weeding (HW) at 20 DAS, sole maize with HW at 20, 40 and 75 DAS, and maize without weeding. The finding suggested that legumes with maize under 2:2 paired row cropping resulted in 44.8-70.2% and 35.4-87.9% weed smothering efficiency at 60 and 90 DAS, respectively. However, simultaneously shown maize + groundnut (2:2 paired row cropping 45/75) with HW at 20 DAS shows higher WSE, higher grain yield (276% higher than weedy check and 7.8% lower than sole maize with HW at 20, 40 and 75 DAS) and system productivity as compared to other treatments.

S3.48: Pulses–millets crop diversification by smallholders and their potential for sustainable food and nutrition security

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World's population is growing exponentially and agriculture has to fulfil their food requirements. Intensifying land usage is a key approach for raising productivity and labourutilisation per area of accessible land.Shifting to diverse farming systems may be required in the future as they promote sustainable intensification and provide numerous services and advantages from the use of thesamepiece of land. The services include providing a variety of food supplies for human nutrition, agro-biodiversity conservation, enhancing soil fertilityand raising smallholder income. Inadequate legislative assistance,scarcity of quality seedsand lack of awareness are some of the key barriers that prevent smallholder farmers from cultivating pulses and millets. Given the rising global population and rising food demand on the one handand the impacts of climate change on diminishing water supplies and soil resources on the other, millets and pulses might be significant crops for future food and nutrition security and human well-being.Crop diversification by growing millets and pulses through crop rotations or intercroppingcan provide these services and benefits on a truly sustainable footing.

S3.49: Conservation tillage integrated with sprinkler-based irrigation scheduling could enhance productivity and farm income in fieldpea under resource constraints

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Pulses requires less water (compared to other field crops of same duration) and are constrained to produce/perform optimally especially in presence of excessive soil moisture customarily retained in the soil through surface-flood irrigation. This could happen both in rainy months (June-Sept) and rain-scarce winter/fall months (Nov-Feb) supplemented with flood irrigation. Therefore, appropriate precision irrigation scheduling decision through micro irrigation (sprinkler/trickle drip) is the key for optimal crop productivity. Fieldpea, being a winter pulses/vegetables, is not the exception. When soil fertility and crop productivity are the issues, amalgamating suitable tillage (Zero or reduced tillage under conservation agriculture) decisions with appropriate irrigation scheduling could reinforce our efforts in enhancing the higher (water/nutrient) use-efficiency in the crop in question besides conserving natural resources. Therefore, precision irrigation scheduling especially through sprinkler irrigation reinforced with conservation tillage (zero/reduced ones) could be immensely helpful for enhancing the productivity (of both water and input) and use efficiency in fieldpea, an important winter pulse. In addition, conservation agriculture has also put forth management decision appropriately on the use of precious resources especially that of water strategically so as to conserve and preserve natural resources against soil deterioration and its environmental implications. Keeping this in view a permanent field experiment was undertaken at ICAR-IIPR, Kanpur during 2021-22 (initiated in 2015-16) to find the effect of conservation tillage and sprinkler irrigation for higher productivity and resource use efficiency of fieldpea.

S3.50: Conservation agriculture and efficient weed management in rice-chickpea cropping system for intensification of rice fallows

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A field experiment was initiated in 2016-17 on a split plot design comprising: four tillage methods in main-plots viz., (i) puddled transplanted rice – conventional till chickpea (PTR-CTC), (ii) puddled transplanted rice - zero till chickpea (PTR-ZTC) (30 cm rice residue retention in chickpea), (iii) zero till direct seeded rice –zero till chickpea (ZTDSR-ZTC) (residue retention in both crops), (iv) conventional till direct seeded rice - conventional till chickpea (CTDSR-CTC) and three weed control modules as sub-plots: (i) butachlor 1.25 kg a.i./ha or pendimethalin 1 kg a.i./ha followed by (fb) bispyribac sodium 20 g a.i./ha in rice and pendimethalin 1 kg a.i./ha fb quizalofop ethyl 100 g a.i./ha in chickpea (W1), (ii) butachlor 1.25 kg a.i./ha or pendimethalin 1 kg a.i./ha fb almix 4 g a.i./ha in rice and oxyfluorfen 150 g a.i./ha fb propaquizafop 100 g a.i./ha in chickpea (W2), (iii) butachlor 1.25 kg a.i./ha or pendimethalin 1 kg a.i./ha fb 1 hand weeding (W3) in rice and pendimethalin 1 kg a.i./ha fb 1 hand weeding in chickpea (W3). The results after three years (2018-19) revealed that PTR had lower weed density at 45 and 90 DAS in rice, while, ZTDSR-ZT had significantly lower weed density and dry weight over PTR-CTC at 90 DAS in chickpea. The ZTDSR-ZT and CTDSR-CT had higher rice root length and higher nodule number in chickpea over PTR-CTC. The system productivity in terms of chickpea equivalent yield in 2018-19 followed the sequence of ZTDSR-ZTC (4.69 t ha^{-1}) > CTDSR-CTC (4.60 t ha^{-1}) = PTR-ZTC (4.60 t ha^{-1}) > PTR-CTC (4.48 t ha^{-1}). Also, ZTDSR-ZT and CTDSR-CT systems fetched significantly higher net returns and B:C ratio in system. Herbicidal treatments had an edge over hand weeding in both crops. Soil moisture content in ZTDSR-ZTC with residue retention was always higher than CT without crop residue (PTR-CTC and CTDSR-CTC) across all the crop growth stages at surface soil (0-20 cm). Hence, CA practice (CTDSR-CTC and ZTDSR-ZT) with sequential application of herbicides is recommended for higher resource-use efficiency and sustainability of rice-chickpea rotation in the north-western IGP of India.

S3.51: Biofertilizer: A sustainable approach for plant and soil health

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Eco-friendly practises are one of the current issues in agriculture. Though we have reaped the benefits of the green revolution in terms of production and other side the overuse of chemical fertilisers resulting deterioration of soil health, chemical fertilisers are toxic, pollute the water and disrupt the ecological balance. This is combined with small and marginal farmer limited purchasing power, remains a key worry in our agricultural production process and we are unable to offer them with a nutritional diet. Excessive use of chemical fertilisers on the other hand, has resulted in substantial soil deterioration, nitrogen leaching, soil compaction, soil organic matter loss and soil carbon loss. Biofertilizers are gaining popularity as a viable alternative to toxic chemical fertilisers for attaining sustainable agriculture. It is vital for addressing global food demand by improving crop output and maintaining long-term soil fertility. Crop plants can interact with microbes to improve their immunity, growth, and development.The essential elements for crop growth include nitrogen, phosphorous, potassium, zinc and silica although these nutrients are normally present in insoluble or complex forms. They are made soluble and accessible to plants by certain bacteria. It is a good option for expensive and damaging chemical fertilisers since they are inexpensive, non-toxic, and environmentally benign. This can assist us in comprehending the significance of microorganisms in agriculture for long-term crop productivity.

S3.52: Effect of different bacterial and fungal microbial formulation on symbiotic traits, yield attributes, n, p uptake and yield of chickpea in vertisol

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Field experiment conducted at the research farm of R.A.K. College of Agriculture Sehore,M.P.,India during rabi season 2021-22 with ten treatments consisting of different microbes (9) and one absolute control in three replications in a randomized block design under medium black soil, low in available nitrogen (238 kg ha^{-1}), medium in phosphorus (P_2O_5-15.8 kg ha^{-1}), high in potassium (K_2O-515.2 kg ha^{-1}) and sufficient in sulphur (10.75 ppm) with normal with pH 7.4 and Ec 0.36 dSm^{1} to evaluate efficacy of various inoculants in enhancing PGP traits and controlling chickpea diseases.Findings indicate that *Trichoderma asperellum*strain NBAIR-TATP (T_9) and *Trichoderma* Bioformulation NBAIM USBSTH-501(T_{10}) recorded least number of dead plant and mortality percentage. Maximum Number of root nodules and nodule dry weight per plant observed in the treatment *Trichoderma asperellum*(T_9) followed by in the treatments *Trichoderma* Bioformulation (T_{10}) and *Pseuduomonas fluorescens* (NBAIR-PFDWD) (T_8). Growth attributing characters viz. plant height, number of branches, dry weight of plant and yield attributing characters viz. number of pods $plant^{-1}$, number of seeds $pod^{1,}$ grain yield, ,N & P uptake and protein content in seed and Dehydrogenase activity in the rhizoshere of chickpea were significantly higher in the treatment *Trichoderma asperellum*strain NBAIR-TATP(T_9) followed by in *Trichoderma* Bioformulation NBAIM USBSTH-501 (T_{10}) as against absolute control.

S3.53: Post-emergent herbicide tolerance in pulse crops: A new dimension in weed management

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The post-emergent (POST) herbicides were tested in chickpea, fieldpea, lentil in winter season and mungbean, urdbean, pigeonpea in rainy seasons using genotypes tolerance and crop selectivity. The POST herbicides such as imazethapyr 75 g a.i./ha, carfentrazone-ethyl 20 g a.i./ha, halosulfuron-methyl 70 g a.i./ha, sulfosulfuron 25 g a.i./ha (acetolactate synthase/acetohydroxy acid synthase inhibitor), oxyfluorfen 150 g a.i./ha, topramezone 20.6 g a.i./ha, tembotrione 100 g a.i./ha (pigment synthesis inhibitor), clodinafop-propargyl + Na-acifluorfen 183.5 g a.i./ha (lipid synthesis and pigment synthesis inhibitor) and metribuzin 500 g a.i./ha (inhibiting photosystem II of photosynthesis) were assessed. Fifteen genotypes of mungbean, twenty genotypes of pigeonpea, 150 genotypes of urdbean, 360 genotypes of chickpea, 330 genotypes of fieldpea and 30 lines of lentil were screened. Three lines of each genotype of mungbean, urdbean, pigeonpea in rainy season and chickpea, lentil, fieldpea in winter season were grown with treated and non-treated condition in 3 m bed (treated 1.5 m length & non-treated 1.5 m length). Crop phytotoxicity score (0-10 scale: 0= complete tolerance; 10 = susceptible), crop phenological shift (delay in maturity) and yield difference were recorded for each herbicide. Results reveled that herbicide tolerance varied among crops and genotypes. Mungbean cultivars/lines did not show any phytotoxicity against clodinafop-propargyl + Na- acifluorfen upto 245 g a.i./ha. Urdbean was found selective against clodinafop-propargyl + Na-acifluorfen upto 183.5 g a.i./ha; however, pigeonpea had phytotoxicity (scale >5) for this herbicide. Topramezone 20.6 g a.i./ha upto 21 days after sowing (DAS) was effective in broad-spectrum weed control in chickpea. Clodinafop-propargyl + sodium-acifluorfen 183.5 g a.i. ha^{-1} at 15 DAS significantly reduced the weed density and dry weight without any phytotoxicity on mungbean with higher grain yield. A metribuzin tolerant fieldpea genotype ('P 637') was registered in fieldpea at 500 g a.i./ha dose.

S3.54: Pulses for crop intensification and sustainable livelihood

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Twin strategies of productivity enhancement and sustainable intensification have led India's pulses productionto an adequate/ stable and self–sustainable level, especially during the last half–a–decade. Tactical crop improvement programme resulting in development of short–duration and high–yielding varieties with efficient plant types,cultivation of suitable pulses in greening rice-fallows, changing diverse and unique cropping systems through cropping system intensification and diversification, reducing yield gaps through technological interventions, clusterfront–line demonstrations and above all, synergy in policy support have led to tremendous impact in pulses' scenewhich resulted in a record production of ~26 million tonnes (mt) of pulses in India including a record of 11.99 mt ofchickpea (*Cicer arietinum* L.) and 4.28 mt of pigeonpea [*Cajanus cajan* L.] during 2020–21. Amalgamatedwith available resources/inputs, need–based reinforced/supplemented infrastructures, policy and technologicalbackups have further provided the required impetus to achieving near self–sufficiency in pulses. And further, with 23–25 mt of pulses production during the last 5 years in the country (25.72 m t of pulses during 2020–21), higherdegree of stability in pulses scenario is indicated now than ever before. In the changing scenario of dwindling natural resources, climate change, quest for sustainable agriculture and nutritional security, pulses will continue to occupy a prime place in cropping systems in time to come.

S3.55: Effect of gibberellic acid on yield and economics of chickpea (*cicer arietinum* l.)

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A field experiment was conducted during *rabi* season of 2020-21 and 2021-22 to study the effect of gibberellic acid on yield and economics of chickpea (*Cicer arietinum* L.). Result revealed that branches *viz*. primary (3.87), secondary (3.27) and tertiary (3.27) and no of nodules/plant (4.10) and dry weight of nodules/plant (110 mg) were recorded marginally higher in foliar application of GA_3 @ 60 ppm at pre-flowering (PF) and pod initiation (PI) during 2020-21. While in 2021-22, primary (3.93/plant), secondary (4.00/plant) and tertiary branches (2.80/plant) and no. of nodule/ plant (4.27) and dry weight of nodule/plant (90 mg) were observed higher in GA_3 @ 30 ppm at pre-flowering and pod initiation. Yield attributes *viz.* seeds/pod (1.70), grain weight/plant (31.20g) and 1000 seed weight (210 g) were obtained significantly higher in GA_3 @ 60 ppm at PF & PI stages in 2020-21 while in 2021-22, pods/plant (27.47), seed weight/plant (20.80 g) and 1000 seed weight (246.63 g) were observed significantly greater in GA_3 @ 30 ppm at PF & PI followed by GA_3 @ 45 ppm at PF & PI stages. Grain and straw yield was recorded significantly superior in GA_3 @ 60 ppm at PF & PI (1970 and 3052 kg/ha) followed by GA_3 @30 ppm at PF (1844 and 2867 kg/ha), respectively during first year experiment while, in second year, grain and stover yield was obtained significantly greater in GA_3 @ 30 ppm at PF & PI stage (2091 and 4061 kg/ha) followed by GA_3 @ 45 ppm at PF & PI (2000 and 3948 kg/ha), respectively. Gross returns (₹ 104623/ha) and net returns (₹ 84686/ha) was assessed significantly maximum in GA_3 @ 60 ppm at PF & PI during 2020-21 while in 2021-22, gross and net returns was found significantly more in GA_3 @ 30 ppm at PF & PI (₹ 112648/ha and ₹ 86459/ha) followed by GA_3 @ 45 ppm at PF & PI (₹ 107897 and ₹ 83597/ha), respectively.

S3.56: Agronomic evaluation of chickpea (*cicer arietinum* l.) genotypes for suitability to mechanical harvesting and energy efficiency

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Mechanization of pulses is vital for improving production efficiency, energy efficiency and reducing cost of production, eases in intercultural operations and in foliar application of nutrients and agro-chemicals. Moreover, manual harvesting is time consuming and expensive. Due to involvement of drudgery and scarce availability of labour, especially at the peak season of agricultural operations, mechanical harvesting of pulses especially chickpea and mungbean is being explored. In majority of pulse growing regions (Middle-East, North Africa, South Asia and West Asia) including India pulses are harvested manually. However, pulses are successfully harvested mechanically in the USA and elsewhere. Introduction of mechanical harvesting in developing countries is little unattractive by the farmers' because of spreading habit of cultivars, land holding size, prevailing environmental factors and agronomic practices practiced by the farmers'. The agronomic evaluation reveals that chickpea 'HC 5' at the crop geometry of 22.5×10cm is suitable for combine harvesting. Significantly higher productivity and energy efficiency were also realized under 'HC 5' at higher density (22.5×10cm) over 'GNG 1581' and 'JAKI 9218'. Kabuli genotypes *viz*., 'IPCK 2012-07', 'IPCK 2011-226' and 'IPCK 2011-37' and desi genotypes viz; 'IPC 2011-28', 'IPC 2012-49', 'IPC 2011-85', 'IPC 2012-31' and 'IPC 2010-142' are suitable for mechanical harvesting. Under arid region of Jodhpur, chickpea genotype, 'HC 5' recorded substantially taller plants (66.3 cm), podding height (28.2), branching angle (78.8) and plant height at maturity (68.8). Thus, agronomic evaluation finds amenability to mechanical harvesting and energy efficient cultivars of chickpea.

S3.57: Effect of soil amendments and irrigation schedules on soil carbon pools, water use efficiency and productivity of soybean under vertisol

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A field experiment was carried out at ARS, Kota, Rajasthan (Agriculture University, Kota) during *Kharif* season of 2020 and 2021 to investigate the impact of soil amendments and irrigation schedules on soil carbon pools, water use efficiency and yield of soybean under Vertisol. The experiment consisting of three levels of irrigation schedules (I_1-0.6, I_2-0.8 and I_3-1.0 IW/CPE ratios) in main plots and four soil amendments (No amendments, mustard straw, wheat straw and compost @ 5 t ha^{-1}) in sub plots were laid out in strip plot design with three replications. The data clearly indicate that maximum MWD and GWD (1.832 mm and 1.0026 mm) was found in I_3 but water stability aggregate was found maximum (0.726 %) in I_1. In case of soil amendments, highest MWD and GWD (1.954 mm and 1.0031 mm) was observed in S_3 but water stability aggregate was found highest (0.615 %) in S_1.Result showed that increasing levels of irrigation schedule significantly increased productivity with application of irrigation based on 1.0 IW/CPE ratio could not influence as compared to 0.6 and 0.8 IW/CPE. In case of application of soil amendment compost @ 5 t ha^{-1} increased significantly productivity with as compared to rest of treatments.Based on the findings, it can be concluded that application of irrigation at 1.0 IW/CPE and compost @ 5 t ha^{-1} resulted for enhancing physical stability of SOC and yield in soybean which might reduce the dependency on costly chemical fertilizer for enhancing sustainable productivity in vertisol of India.

S3.58: Additive series- a dryland technologies for improving productivity of pulse-based cropping system

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The pulse crops are grown in rainfed lands with hardly any proper management practice in terms of water, nutrient, pest and disease management. It is important to strengthen their efforts with better crop production and management strategies. Towards this, it is necessary to form a new paradigm by coupling the indigenous experience and traditional practices of dry pulse farming systems. Arid and semi-arid climate which is characterized with predominant drought is conjugated with reduced rainfall intensity and intermittent dry spells, to overcome these large scale demonstrations at farmer's field under National Innovations on Climate Resilient Agriculture (NICRA) is beingcarried out at Chikkamaranahalli cluster comprising of 6 villages of Nelamangala Taluk, Bengaluru Rural district. Simultaneous sowing of pigeonpea and field bean/cowpea in 1:1 row ratio at 90 cm × 22.5 cm and a short duration photo-insensitive field bean/cowpea in 1:1 row proportion (additive series) without losing the main crop. Pigeonpea is a long duration crop and slow growing in early stages, growing of field bean/cowpea as additive series increases the land use productivity. Pigeonpea + field bean (1:1) intercropping resulted in higher pigeonpeagrain equivalent yield (1047 kg/ha), returns (Rs. 40733 /ha) and B: C ratio (2.3268) compared to sole crop of pigeonpea (608 kg/ha, Rs.13711 /ha and 1.47, respectively. Higher sustainability yield index (0.81) was recorded for pigeonpea + field bean compared to farmer's practice of growing pigeonpea as sole crop (0.39). Thus additive series of growing short duration pulses with pigeonpea showed capability to enhance pulse production and fetch additional remuneration that improvedthe livelihood of dryland farmers.

S3.59: Effect of long duration pigeonpea (*Cajanus Cajan*) based intercropping system on system productivity and profitability under rainfed condition

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A field experiment was laid out at research farm of Tirhut College of Agriculture, Dholi (25^0 982 N $85^0$762 E and an altitude of 51.3 m above mean sea-level) a campus of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during Kharif season of 2021–22.The soil of the experimental plot was sandy loam in texture, low in organic carbon (0.34%), available nitrogen (168.8 kg/ha^{-1}), phosphorus (12.66 kg/ha^{-}) and medium in potassium (154.2 kg/ha) with pH 8.1. The treatment comprised, sole pigeonpea, sole sweet corn, sole baby corn, sole parching sorghum, pigeonpea (60 cm) + urdbean (1:1), pigeonpea (90 cm) + sweet corn (1:2), pigeonpea (90 cm) + baby corn (1:2) and pigeonpea (90 cm) + parching sorghum (1:2). The experiment was laid out in randomized block design and replicated thrice. The main as well as inter crops were sown in third week of July and pigeonpea was harvested in third week of April. However, urdbean, baby corn, sweet corn and parching sorghum were harvested in second week of October, fourth week of September, second week of October and first week of November respectively. The crop was fertilized with recommended dose of fertilizers and crop received one interculture operation 25 DAS. The plant-to-plant distance in sole as well as in intercrops was maintained by thinning third week after sowing. Pigeonpea yield reduced drastically in all the intercropping systems, except pigeonpea + urdbean in 1:1 row ratio. However, pigeonpea equivalent yield increased significantly in all the intercropping systems except pigeonpea + sweet corn (1:2) and sole parching sorghum than sole pigeonpea. Among the intercropping systems, pigeonpea + parching sorghum in 1:2 row ratio recorded significantly higher pigeonpea equivalent yield than pigeonpea + urdbean in 1:1 row ratio, pigeonpea + sweet corn (1:2) and pigeonpea + baby corn in 1:2 row ratio. Pigeonpea + parching sorghum in (1:2) row ratio also recorded higher production efficiency and economic return than rest of the intercropping systems and sole pigeonpea.

S3.60: Effect of biofertilizer inoculated mungbeanon soil mineral N dynamics in succeeding wheat

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Soil microorganisms are an integral component of nutrient cycling and are crucial determinants of soil fertility. Microbial inoculation in pulse crops is advocated for improving productivity and soil health. The present study communicates the effect of microbial inoculation in mungbean on mineral N release behavior in succeeding wheatin a field study conducted for 2 years in Sandy loam soil. Microbial inoculation treatments in munbeanconsisted of individual and conjoint inoculation of *Rhizobium* and PGPR and an uninoculated control. The succeeding wheat crop was raised with 3 N levels of 50, 75 and 100% RDF. Results revealed that total mineral nitrogen (NH_4^+-N + NO_3^--N) and NH_4^+-N in the soil decreased with increasing crop age under different treatments. However, NO_3^--N in soil increased with crop age.The increases in total soil mineral N due to the applied treatments ranged from 8.8 to 40.8% at 0 DAS and 10.8 to 76.2% at 148 DAS over the uninoculated control during 2017-18. Respective increases rangedfrom 6.6 to 38.7% at 0 DAS and 12.4 to 76.5% at 148 DAS during 2018-19.Irrespective of nitrogen levels in wheat, the highest mean total mineral Nand NH_4^+-N in soil was observed with *Rhizobium* + PGPR at all the intervals in both the years. However, the highest mean NO_3^--N in soilfluctuated among *Rhizobium* alone and *Rhizobium* + PGPR inoculation treatment up to 58 DAS, but at later intervals of 88 to 148 DAS, dual inoculation resulted in the highest NO_3^--N in soil.

S3.61: Effect of land configuration and weed management on mungbean productivity

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A field experiment was conducted at CPR, Berhampur,Odisha in silty loam soil where PH is 6.2 (Acidic), low (1.95 g/kg of soil) in organic carbon, high in P (77.8 kg/ha) and medium in available K(156 kg/ha), low in Boron (0.32 ppm) and sulphur 3.4 kg/ha in strip plot design with four replications during kharif (rainfall – 1200 mm) for consecutive three years (2015-2017) the treatment details are : A.Land configuration-L_1- Flat bed method (FB), L_2 - Broad bed furrow (BBF), B. Weed management-W_1 -Weedy check ,W_2 - Pendimethalin 30 EC @ 1.0 kg/ha-PE , W_3 -Imazethapyr 10 % SL @ 55 g/ha at 15-20 DASW_4- Pendimethalin 30 EC @ 1.0 kg/ha-PE fb Imazethapyr 10 % SL @ 55 g/ha at 15-20 DASBroad bed furrow method of planting recorded significantly and maximum grain yield (688 Kg/ha), net return Rs.13134/ha and B:c ratio 1.54 over flatbed method. It was registered higher to the tune of 12% over flatbed method of sowing. Pendimethalin 30 EC @ 1.0 kg/haPE fb imazethapyr 55 g/ha at 15-20 DAS was recorded significantly higher grain yield (730.Kg/ha), net return (Rs.18250/ha), B:C ratio 2.16. In interaction, Broad bed furrow(105 cm) with Pendimethalin 30 EC @ 1.0 kg/ha-PE fb imazethapyr 10% SL @55 g/ha at 15-20 DAS recorded highest mung bean grain yield (768 kg/ha). In interaction, broad bed furrow (105 cm) with pendimethalin 30 EC @ 1.0 kg/ha-PE fb imazethapyr !0% SL @55 g/ha at 15-20 DAS recorded highest mung bean grain yield (768 kg/ha).

S3.62: Mitigation of moisture stress through growth regulator for enhancing mungbean productivity

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The field experiment was conducted on deep black soil of Agricultural Research Station, Badnapur, District Jalna during *Kharif* 2019-20. The experiment was laid out in Randomized Block Design with three replications. The gross plot size was 5.0 x 4.5 m^2 and net plot size was 4.6 x 3.6 m^2 for each treatment. The total treatments with different foliar nutrition including control were eight and replicated thrice *viz.,* T_1: Absolute control, T_2: Water spray at flowering and pod initiation, T_3: GA_3 @ 30 ppm spray at flowering initiation, T_4: GA_3 @ 30 ppm spray at pod initiation, T_5: GA_3 @ 45 ppm spray at flowering initiation, T_6: GA_3 @ 45 ppm spray at pod initiation, T_7: GA_3 @ 30 ppm spray at flowering and pod initiation and T_8: GA_3 @ 45 ppm spray at flowering and pod initiation. The sowing was done on 04/07/2019 with variety BM 2003-2 of mungbean at 30 x 10 cm^2 spacing. The recommended doses of fertilizers were applied as a basal dose. Similarly, the crop protection measures were adopted as per the recommendations. All the PGR treatments were applied as per the technical programme. The trial was harvested on 13/09/2019. The data on seed yield was analyzed statistically.The data revealed that the different levels of PGR in mungbean influenced seed yield significantly. An application of GA_3 @ 45 ppm spray at flowering and pod initiation produced significantly higher seed yield (790 kg ha^{-1}) which was found at par with an application of GA_3 @ 30 ppm spray at flowering and pod initiation (726 kg ha^{-1}) among rest of the treatments.

S3.63: Evaluation of post emergence herbicides in pigeonpea

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *Kharif,* 2021-22 in Randomized Block Design with three replications. The experiment consisted of 13 treatments, *viz.,* T_1: Weed free, T_2: Weedy check, T_3: Two Hand Weedings at 20 and 40DAS/ Inter cultivation, T_4: Pendimethalin 30 EC @ 0.75 kg ai/ha (PE) followed by Imazethapyr 10 SL @ 100 g ai/ha at 20-25 DAS fb + One Inter cultivation at 50 DAS, T_5: Chlorimuron ethyl 25 WP @ 9 g ai/ha at 20-25 DAS, T_6: Fenoxaprop ethyl 9.3 EC @ 70 g ai/ha at 20-25 DAS, T_7: Propaquizalop 2.5 % + Imazethapyr 3.7 % w/w @ 50+75 = 125 g ai/ha at 20-25 DAS, T_8: Sodium Acifluorfen 16.5 % + Clodinafop propargyl 8 % @ 245 g ai/ha at 20-25 DAS, T_9: Chlorimuron ethyl 9 g + quizalofop ethyl 50 g ai/ha at 20-25 DAS, T_{10}: Chlorimuron ethyl 6 g + quizalofop ethyl 37.5 g ai/ha at 20-25 DAS, T_{11}: Chlorimuron ethyl 9 g + Fenoxaprop ethyl 70 g ai/ha at 20-25 DAS, T_{12}: Chlorimuron ethyl 6 g + Fenoxaprop ethyl 50 g ai/ha at 20-25 DAS and T_{13}: Imazethapyr + Imazamox @ 100 g ai/ ha at 20-25 DAS The gross and net plot sizes were 5.4 x 5.0 m^2 and 3.6 x 4.6 m^2 respectively. The sowing was done on 30-06-2021 with pigeonpea variety BDN- 711. The recommended fertilizers were applied. Similarly, the crop protection measures were adopted as per recommendations. The crop was harvested on 27 & 28-12-2021. The results revealed that weed free treatment produced significantly higher seed yield of pigeonpea, however, it was on par with treatments receiving two hand weedings at 20 and 40 DAS/ Inter cultivation; Pendimethalin 30 EC @ 0.75 kg ai/ha (PE) followed by Imazethapyr 10 SL @ 100 g ai/ha at 20-25 DAS fb + one Inter cultivation at 50 DAS and Imazethapyr + Imazamox @ 100 g ai/ ha at 20-25 DAS. GMR, NMR and B:C ratio followed the similar trend. Lower values for weed dry matter per square meter, whereas, higher values for weed control efficiency and weed index were also recorded by these treatments.

S3.64: Effect of tillage and herbicides on growth, yield, weed control and energetics of chickpea (*Cicer arietinum*)

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An experiment was conducted during 2019–20 on sandy clay-loam soil at the Rani Lakshmi Bai Central Agricultural University, Jhansi, Uttar Pradesh, to evaluate the effect of tillage and herbicides on growth, weed control, economics and energetics of chickpea (*Cicer arietinum* L.). Treatments included 3 tillage, viz. zero-tillage (ZT), ZT along with sorghum [*Sorghum bicolor* (L.) Moench] residue (ZT + R) and conventional tillage (CT), in main plot; and 4 weed-management practices, viz. pendimethalin alone, pendimethalin followed by (*fb*) clodinafop-propargyl + Na-acifluorfen, pendimethalin *fb* hand-weeding and unweeded check, in subplots. Chickpea growth and development was higher under ZT + R, which led to higher grain yield, economics, and energetics. Net returns under ZT + R were 13.5% more than ZT but 36.7% more than CT. Chickpea grown under ZT and ZT + R with pendimethalin *fb* clodinafop + Na-acifluorfen was 32.7–43.5% more energy-efficient than the same treatment under CT. This study indicated that chickpea grown under ZT + R with pendimethalin *fb* clodinafop + Na-acifluorfen was economical and energy-efficient apart from providing higher grain yield in Bundelkhand region.

S3.65: Application of growth supplements improved productivity of cluster bean and moth bean

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Exogenous application of growth supplements is known to improve plant resistance against abiotic stresses A field experiment was conducted for two years with 7 growth supplements i.e. thiourea (1000 ppm), K_2SO_4 (0.2%), salicylic acid (100 ppm), urea (2%), NPK solution (0.5%), acetic acid (20mM), $MgSO_4$ (0.5%), and water spray as control. For better comparison, cultivars of different nature of cluster bean (RGC-936 and RGC-1066) and moth bean (CAZRI moth 2 and RMO-2251) were kept. Growth supplements were applied as foliar spray at vegetative and pre-flowering stage. The experiment was laid out in factorial randomized block design and replicated thrice. Application of growth supplements-maintained water relations, enhanced membrane stability, content of photosynthetic pigment, activity of antioxidant enzymes and declined lipid peroxidation which reflected in higher yield in treated plots. Among growth supplements, K_2SO_4 showed its superiority in enhancing drought tolerance in both the crops which was at par with thiourea. In cluster bean, RGC-936 and in moth bean, CAZRI moth-2 responded better to growth supplements and reported higher yield as compare to other cultivars. Application of potassium sulphate, acetic acid and thiourea resulted in 7.5-15.6% higher seed yield over water spray. Application of growth supplements significantly improved the growth, plant water status and seed yield of cluster bean and moth bean under rainfed situation and this could be also attributed to some extent in improving leaf area, photosynthesis and harvest index probably due to more partitioning of photosynthates to the seed.

S3.66: Effect of integrated nutrient management on quality and yield of black gram (*vigna mungo* l.)

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Blackgram (*Vigna mungo* L.) is an important legume crop grown in tropical and sub-tropical regions of the world It is highly nutritious containing higher amount of 22-24% protein, 1.3% fat and 60% carbohydrates on dry weight basis and it is rich source of calcium and iron. It is the most popular pulse and can be most appropriately referred to as the king of the pulses. A field experiment was conducted during kharif season of 2019-20 at Research Station, Agriculture University, Kota. In these region soils, N, P, S and Zn deficiencies are principal yield-limiting factors for crop production. Besides some reasons were found for low production of black gram *viz*., lack of improved cultural practices, imbalanced use of fertilizers dependent only on chemical fertilizers are the major bottle necks responsible for poor yield of *Kharif* pulses. These problems can be overcome to some extent by adopting the integrated nutrient management approach which helps to sustain the soil fertility as well as productivity. Among the treatment application of higher fertility level like 125% RDF significantly increased the number and weight of nodules/plant (24.1 and 44.4 mg), grain yield (900 kg/ha), straw yield (3741 kg/ha) and biological yield (4640 kg/ha). Further data revealed that application of FYM @ 5 t/ha significantly similar increased the growth parameters and yield of blackgram. Inoculation of *Rhizobium* + *LMn*16 also resulted in significant increases growth parameters, grain and biological yield (862 and 4432 kg/ha) over other treatment.

S3.67: Effect of various *Rhizobium* strains on the growth and yield of urdbean

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To assess the effect of multifunctional rhizobacteria on yield of Urdbean, a trial was laid out using different multifunctional rhizobacteriareceived from various AICRP centres. Totally five multifunctional rhizobacteria were obtained from three different AICRP centres*viz.,* Pantnagar, Coimbatore and Ludhiana. Urdbean seeds were treated with all the multifunctional rhizobacteria along with the local best *Rhizobium* BMBS 47. Among the multifunctional rhizobacteria *Rhizobium* +PUK-171 (Pantnagar) (*Stenophomonasrhizophila*)recorded more number of nodules/plant (35/ plant) and nodule dry weight (0.045 g/plant) which is higher than other rhizobacteria. This was followed by *Rhizobium +Pseudomonas* spp. (Coimbatore) which was recorded 21.60 nodules/ plant. Uninoculated control was recorded the least nodulation as 12.3/ plant which is significantly lesser than all the other treatments. Crop was harvested at 65 DAS and the inoculated treatments were recorded higher values for number of pods/plant and plant dry weight when compared to the uninoculated control. Among the different rhizobacteria PUK-171 (*Stenophomonasrhizophila*) (Pantnagar) inoculated treatment were recorded the highest yield of 1115 kg/ha followed by NE 10 (*Bacillus cereus*) (Pantnagar Ch.) (1026 kg/ha).

S3.68: Effect of various *Rhizobium* strains on the growth and yield of mungbean

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A trial was laid out to identify the performance of different *Rhizobium* isolates received from various AICRP centres in order to screen the best *Rhizobium* isolate suitable for Mungbean. Totally seven *Rhizobium* cultures *viz.,* AKMR 12-01; AKMR 19 (Akola), LSMR 32 (Ludhiana), KGR 19-6; KGR 19-13 (Kalabugari), VMC and VMF (Vamban) obtained from various AICRP centres were used for seed treatment of mungbean seeds. Observations on plant growth parameters were recorded at 45th days after sowing to assess the effect of *Rhizobium* strains *viz.,* number of nodules/plant, root length, shoot length and yield parameters were recorded during harvest.Among the different *Rhizobium* strains, highest number of nodules and nodule dry weight was registered by VMF (Vamban) (56 nodules/plant & 0.069 g/plant respectively) followed by VMC which recorded 47 nodules/plant. Control recorded the least number of 18 nodules / plant.The results revealed that, of the seven different mungbean*Rhizobium* strains, the highest yield of 1038.6 kg/ha was recorded by VMF followed by VMC as 916 kg/ha.

S3.69: Evaluation of post emergence herbicides in urdbean

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A study on evaluation of post emergence herbicides in urdbean genotype DBGV-5, was conducted at AICRP on MULLaRP, main Agricultural Research Station, University of Agricultural, Sciences, Dharwad (Karnataka) under rainfed conditions during *kharif* 2021 in medium black soil.The Experiment was conducted in randomized block designwith10 treatments; T_1- unweeded control; T_2- weed free; T_3- hand weeding at 20 and 40 DAS; T_4- imazethapyr 10% SL @ 55 g/ha 20 DAS as post emergence surfactant 200 ml /acre; T_5- fluzifop p butyl 13.4 % W/w @ 250 g/ha20 DAS as post emergence; T_6- propaquizafop @33.3 g + imazethapyr @50 g/ha at 20 DAS (ready mix) as post emergence 750ml / acre; T_7- aciflourfen sodium @ 140 g + clodinafop propargyl @ 70 g/ha at 20 DAS (ready mix) as post emergence 350 ml /acre; T_8- fomesafen + fluzifop p butyl @ 220 g/ha at 20 DAS (ready mix) as post emergence 400 ml/acreT_9- quizalfopethyl 5 EC 50g ha^{-1} (400 ml/acre); T_{10}- propiquizafop 10EC 50g ha^{-1} (200 ml/acre) in three replications. Among the treatments, hand weeding at 20 and 40 DAS recorded significantly higher number of pods (30.2), 100 seed weight (5.28g), grain yield (914 kg ha^{-1}), higher weed control efficiency (87.8%) and lower weed dry weight (2.8g/ 0.5 m^2) than other treatments. However, among the herbicidespropaquizafop @ 33.3 g + Imazethapyr @ 50 g/ha^{-1}(29.6, 5.38g, 958 kg ha^{-1}, 81.4% and 3.40 g/0.5 m^2, respectively)recorded significantly higher growth and yield parameters with higher weed controlefficiency.

S3.70: Identification of extra early chickpea genotypes suitable for late shown condition

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Chickpea is an important Rabi pulse crop of Karnataka and being grown in an area of 713thousand ha with a production & productivity of 445.63thousand tonnes and 625 kg/ha during 2020-21, respectively. Majority of chickpea crop grown under rainfed situation in Karnataka, therefore drought and heat are major abiotic constraints for chickpea production in Karnataka. Further, climate change is expected to increase uncertainty in yields. Aim of the breeder is to identify early genotypes, these early genotypes complete their life cycle before on set of abiotic stress. Investigations were carried out at Zonal Agricultural Research Station (ZARS), Kalaburagi, UAS, Raichur during rabi 2021-22. 37 Bengal gram genotypes were evaluated in advanced yield trail along with eightnational checks (NBeG 47, RVG 204, JG 11, JG 14, NBeG 3,ICCV 96029,ICCV 96030andNBeG 857) under rainfed condition by adopting randomized block design (RCBD) with two replications. The results revealed thatfour genotypes *viz.,* KCD37EE-32(1550 kg/ha), KCD37EE-07(1537 kg/ha), KCD37EE-16 (1537 kg/ha) and KCD37EE-27 (1533 kg/ha) recorded higher yield as well as other desirable character like days to 50% flowering, days to maturity,plant height and hundred seed weight compare with eightnational checks (NBeG 47 (933 kg/ha), RVG 204 (1475 kg/ha), JG 11(1358 kg/ha), JG 14 (1125 kg/ha), NBeG 3 (1096 kg/ha),ICCV 96029 (967 kg/ha),ICCV 96030 (796 kg/ha) andNBeG 857 (783 kg/ha).

S3.71: Nutrient content and uptake by soybean under different weed management measures

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A field experiment was conducted during *kharif*2021 at ARS, Kota. The N content in seed and straw were observed significantly maximum under 2HW at 20 &40 DAS than all other treatments and weedy-check. Amongst herbicides, maximum N content in seed and straw was recorded in fomesafen+fluazifop-p-butyl220g*a.i.*/ha followed by sodium-acifluorfen+clodinafop-propargyl 245g*a.i.*/ha and propaquizafop 50g*a.i.*/ha+imazethapyr 125g*a.i.*/ha. These were associated with 7.3 to8.5 and 11.1 to12.2% higher N content in seed and straw over weedy-check,respectively. P&K content in seed and straw wasn't affected significantly by weed control practices. Results revealed that compared to weedy-check all weed control practices significantly increased N uptake by soybean seed and straw as well as total N uptake. 2HW recorded maximum and significantly higher N uptake by seed(132.8kg/ha), straw(56.9kg/ha) and total(189.7kg/ha). Application of fomesafen+fluazifop-p-butyl220g*a.i.*/ha recorded significantly higher N uptake by seed, straw and total(114.850.2 and165.0kg/ha). Weed control measures significantly increased P &K uptake by soybean over weedy-check. Application of fomesafen+fluazifop-p-butyl220g*a.i.*/ha, propaquizafop+imazethapyr 125g*a.i.*/ha and sodium-acifluorfen+clodinafop-propargyl245g*a.i.*/ha were found significantly superior in uptake of P by seed, straw and total to the extent of 184.6,171.4 &194.1; 184.5,172.1 &202.4,149.2 &164.9%, respectively over weedy-check. Fomesafen+fluazifop-p-butyl220g*a.i.*/ha, propaquizafop 50g*a.i.*/ha+imazethapyr 125g*a.i.*/ha and sodium-acifluorfen+clodinafop-propargyl245 g*a.i.*/ha were found at par with each other and statistically superior over rest of treatments in augmenting K uptake. These herbicides exhibited 202.4,188.8 &179.1% by seed; 149.2,145.0 &132.6% by straw and 164.9, 157.9 &146.4% total K uptake over weedy-check,respectively.

S3.72: Enhancing nutrient use efficiency in chickpea (*Cicer arientinum* L.) through hydrogel under protective irrigation

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A field experiment was conducted at Agril. Research Station, Badnapur during *Rabi 2021-22*. The treatments comprised of three levels of hydrogel application (0 Kg ha^{-1}; 2.5 Kg ha^{-1} hydrogel and 5 Kg ha^{-1} hydrogel) and five levels of foliar nutrients spray (F_1- water spray, F_2- urea 2%, F_{3-} thiourea 500 ppm, F_4- salicylic acid 100 ppm and F_5- NPK (19:19:19:). The experiment was laid out in split plot design with three replications having hydrogel application as main plot and foliar nutrients spray as sub plot treatment. The soil was clayey, neutral in reaction (pH 7.10) having an organic carbon content of 0.57 % and low amount of available nitrogen (167.50 $kgha^{-1}$), medium phosphorus (18.12 kg ha^{-1}) and high potassium (312.31kg ha^{-1}) content. The chickpea crop sown on October 19th, 2021 with variety Akash (BDNG 797) and harvested on March 10th, 2022.The 2.5 kg ha^{-1} hydrogel and 5 kg ha^{-1} hydrogel as per treatment was drill in line before seeding of chickpea seeds. The foliar nutrient as per treatment was sprayed at flower initiation stage (50 DAS) and pod development stage (72 DAS). Among hydrogel application treatments, application of 5 kg ha^{-1} hydrogel produced the highest seed (1936 kg ha^{-1}) and stover yield (2931 kg ha-1) and followed by 2.5 kg ha^{-1} hydrogel produced the seed yield (1869 kg ha^{-1}) and stover yield (2882 kg ha^{-1}). The increase in yield is mainly attributed to higher plant height, number of branches and nodules, weight of dried nodules, dry matter accumulation $plant^{-1}$, pods $plant^{-1,}$ seeds pod^{-1} and 100 seed weight. Application of 5 kg ha^{-1} hydrogel gave higher crop growth rate (CGR) and relative crop growth rate (RGR) and followed by Application of 2.5 kg ha^{-1} hydrogel at all the stages as compared to without application of hydrogel. The highest gross returns and net returns was also obtained under the treatment of application of hydrogel 5 kg ha^{-1} and followed application of hydrogel 2.5 Kg ha^{-1} while highest B:C ratio was received under the treatment of without hydrogel application. Foliar nutrients spray gave considerable effect on growth attributes, yield components and yields of seed and stover.

S3.73: Bioefficacy of different POE herbicides for broad spectrum weed management in chickpea

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *Rabi* 2021-22. The experiment was laid out in Randomized block design with three replications. The experiment was comprised of ten treatments. The sowing was done on 30-10-2021 by using variety BDNG-797. The crop was harvested on 25-02-2022. Significantly lower plant height was recorded by unweeded plot than herbicide treated and weed free plots. Significantly highest plant height of chickpea was observed by weed free plot and it was found at par with T_8 (Oxyfluorfen 150 g ai. ha - topramezone 20.6 g ai/ha at 14-21 DAS Pre+Post), T_7 (Oxyfluorfen 150 g ai. ha - propaquizafop 100 g ai/ha at 15-20 DAS (Pre+Post), T_6 (Oxyfluorfen 150 g ai. ha - quizalofop-p-ethyl 100 g ai/ha at 15-20 DAS (Pre+Post) and T_5 (Topramezone 20.6 g ai/ha at 14-21 DAS (Post-emergence). Weed free plot recorded significantly higher number of branches and number of pods per plant, however, it was on par with T_8 (Oxyfluorfen 150 g ai. ha - topramezone 20.6 g ai/ha at 14-21 DAS (Pre+Post), T_7 (Oxyfluorfen 150 g ai. ha - propaquizafop 100 g ai/ha at 15-20 DAS (Pre+Post), T_6 (Oxyfluorfen 150 g ai. ha - quizalofop-p-ethyl 100 g ai/ha at 15-20 DAS (Pre+Post) and T_5 (Topramezone 20.6 g ai/ha at 14-21 DAS (Post-emergence Similar trend was observed in respect of seed index. that significant differences in seed yield of Chickpea influenced by different pre + post herbicides. Weed free treatment recorded significantly higher seed yield of chickpea than the rest of the treatments during *rabi* 2021-22 however it was found at par with T_8 (Oxyfluorfen 150 g ai. ha - topramezone 20.6 g ai/ha at 14-21 DAS Pre+Post), T_7 (Oxyfluorfen 150 g ai. ha - propaquizafop 100 g ai/ha at 15-20 DAS Pre+Post), T_6 (Oxyfluorfen 150 g ai. ha - quizalofop-p-ethyl 100 g ai/ha at 15-20 DAS Pre+Post) and T_5 (Topramezone 20.6 g ai/ha at 14-21 DAS (Post-emergence. The lowest seed yield was recorded by the weedy check treatment. Similar trend was observed in case of gross monetary returns, net monetary returns and B: C ratio.

S3.74: Impact of integrated crop management practices on mung crop productivity under rice-wheat cropping system

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Mung (*Vigna radiata)* cropproved to be an ideal crop for cultivation in spring and summer season with the development of early maturing varieties. Rice -wheat cropping system is a major cropping system of Delhi region and now days, there has been stagnation or declinein the yield of rice and wheat even with balanced or integrated nutrient managementpractices. Short-duration and uniformly maturing varieties of summer mung like MH 421 has enhanced the feasibility of inclusion summer mung in rice–wheat cropping system. Keeping this in view, Krishi Vigyan Kendra Delhi carried out Cluster frontline demonstrations (CFLD) on summer mung in 30 ha area under National food security mission allotted by ATARI Jodhpur Zone II, Rajasthanin 2021.Improved and latest technology *viz*. variety MH 421, seed treatment with fungicide and bio-fertilizer, recommended seed rate, balanced use of fertilizers, weeds management and plant protection measures were demonstrated in 75 demonstrations at farmer's fields. The highest yield (12q/ha) of summer mung crop was obtained with improved production technology as compared to farmer's practice (7.5 q/ ha). In term of average mean yield (9.90 q/ha) of total demonstrations which was found 22.6 per cent higher over the farmer's practice (7.0 q/ha). Improved technology also gave higher net return of Rs. 35000/ha with a benefit- cost ratio of 2.4 as compared to farmer's practice (Rs.19800/ha, B:C ratio 1.89). Now Farmers have considered summer mung as a crop it gives the additional income with improving soil health in rice-wheat cropping.

S3.75: Response of foliar nutrition for growth and yield in chickpea

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *Rabi* 2017-18. The experiment was laid out in Randomized block design with three replications. The experiment was comprised of seven treatments.The sowing was done on 9-11-2017 by using variety BDNG-797. The crop was harvested on 5-03-2018. Results revealed that the different foliar nutrition management treatments of chickpea influenced seed yield significantly. The treatment T_3 i.e.RDF+ 1 % 19:19:19 spray at flowering and pod development stage produced significantly higher seed yield (1993 kg ha^{-1}) found at par with the treatment T_4i.eRDF+ 2% DAP spray (1914 kg ha^{-1}) at flowering and pod development stage and The treatment T_7 i.eRDF+ 2% Potassium sylvanite spray (1801 kg $ha^{-1)}$ at flowering and pod development stage while the lowest seed yield was recorded by control (1597 kg ha^{-1}). The highest gross monetary returns as well as net monetary returns was recorded by the treatment T_3 i.e.RDF+ 1 % 19:19:19 spray (Rs.75734 ha^{-1}) at flowering and pod development stage followed by treatment T_4i.eRDF+ 2% DAP spray (Rs 72745 ha^{-1}) at flowering and pod development stage. The highest B:C ratio was recorded by T_3 i.e.RDF + 1 % 19:19:19 spray (2.6) at flowering and pod development stage followed by treatment T_4 i.e.RDF+ 2% DAP spray (2.5) at flowering and pod development stage. while the lowest B:C ratio was recorded by control (2.1).

S3.76: Effect of integrated nutrient management practices on productivity and profitability of pulse-based cropping systems in arid-ecosystems

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A field experiment was carried out during 2020-21 to study the effect of various integrated nutrient management options viz. recommended fertilizers (100% recommended dose of fertilizer), 75% recommended dose of fertilizer + 5 ton FYM , 75% recommended dose of fertilizer + 5 ton FYM + Biofertilizers and 50% recommended dose of fertilizer + 5 t FYM + biofertlizers + crop residue) on the productivity and profitability of the different pulse-based cropping systems viz. (pearl millet – mustard, moth bean – custard, pearl millet – chickpea, clusterbean + sesamum (6:2) – chickpea) under hot arid environments in split plot design with three replications.The result of the study revealed that clusterbean+sesamum (6:2)-chickpea cropping system gave the higher chickpea eq. yield (23.04 q ha^{-1}), net return (Rs 81554) and B:C ratio (2.02) as compared to rest of the cropping systems. Nutrient management practices significantly improve the crop yield. Application of 5-ton FYM with 75% recommended dose of fertilizer and biofertilizers gave the higher chickpea eq. yield (5.92%), net return and B:C ratio as compared to 100% recommended dose of fertilizer.

S3.77: Growth and productivity of rajmash (*Phaseolus vulgaris* L.) as influenced by graded levels of gypsum application

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A field experiment was conducted at the Agronomic Research Farm, Faculty of Agriculture, Wadura during *kharif* 2021 with the objective to study growth and productivity of rajmash at different levels of gypsum (control, 50, 100, 150, 200, 250, 300 and 350 kg ha^{-1}. The soil was well drained, silty clay-loam with normal reaction and electrical conductivity. The soil was medium in soil organic carbon, available phosphorus, potassium and calcium and low in available nitrogen and sulphur. The experiment was laid out in Randomized Complete Block Design, each treatment was replicated thrice. The results indicated that the growth parameters (plant height, leaf area index and dry matter accumulation) were found significantly higher with 250 and 300 kg gypsum ha^{-1} and didn't increase beyond the level of 300 kg gypsum ha^{-1}. A significantly higher value of growth analysis indices was also obtained with 300 kg gypsum ha^{-1}. Seed index, seed yield, stover yield and biological yield were significantly higher with 250 and 300 kg gypsum ha^{-1}. However, with respect to harvest index, all the levels of gypsum were found at par except control and 50 kg gypsum ha^{-1}.Further increase in gypsum level significantly decreases these parameters. Benefit-cost ratio was found significantly higher with 300 kg gypsum ha^{-1} which was found at par with 250 and 200 kg gypsum ha^{-1}. Above results indicated that 250 kg gypsum ha^{-1} with recommended dose of NPK was found optimum for better plant growth and productivity and maximum economic return under temperate conditions of Kashmir.

S3.78: Topramezone (HPPD-inhibiting herbicide) for effective broad-leaved weed control and higher productivity in chickpea

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Weeds are major yield reducers among biotic constraints. The poor competition ability of chickpea (*Cicer arietinum* L.) opens the door for weeds to cause yield loss of up to 94%. Among weeds, broad-leaved weeds (BLWs) offer a major threat to chickpea production. The main objective of the study was to evaluate the pre- (PE) and post-emergence (PoE) herbicides, the dose-response of effective herbicides, application timing of herbicides and varietal evaluation against promising herbicides. The series of field experiments were conducted at ICAR- Directorate of Weed Research, Jabalpur, Madhya Pradesh, India during 2017-2021. To screen the promising PE and PoE herbicides in chickpea. The dose-response of effective herbicide to optimize the economic dose. Likewise, the application timing of promising herbicides and varietal selectivity was studied to obtain effective weed control, higher seed yield and profitable chickpea production. Results revealed that among PE herbicides pendimethalin+imazethapyr 1.0 kg/ha was effective, whereas among PoE herbicides topramezone inhibitor of a p-hydroxyphenylpyruvate dioxygenase (HPPD) enzyme at 20 and 30 g/ha were equally effective as compared to others, though it has mild and recoverable phytotoxicity. Similarly, a dose-response study was conducted to optimize the dose of topramezone and found at 20.16 g/ha provided effective weed control, higher seed yield and was economically viable. Also, the application of topramezone at 20.16 g/ha at 20 days after sowing was more effective than the later applications. Among tested chickpea cultivars, JG 14, 16 and 36 were less phytotoxic. Therefore, topramezone can be a potential option for weed control in chickpea.

S3.79: Effect of phosphorus and zinc fertilizers levels and their solubilizers on nutrient content and uptake by Fieldpea[*Pisum sativum var. arvense* (L.)]

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A field experiment was conducted during *rabi* 2021-22 at research farm, ARS, Kota. The soil of the experimental field was slightly alkaline in reaction (pH7.45), low in available nitrogen (241Kg/ha) and phosphorus (21.10kg/ha) and high in available potassium (328.4kg/ha) and low in DTPA extractable micronutrient available Zn (0.60mg/kg). Results revealed that application of different P & Zn levels significantly increased N, P, K, Zn content and uptake by fieldpea. Maximum N,P,K and Zn content in seed (3.53%, 0.235%, 0.93% and 35.11 ppm respectively) and in straw (0.89%, 0.23%, 1.22% & 11.89 ppm respectively) was obtained with 40 kg P_2O_5 + 25 kg $ZnSO_4$/ha. Similarly, highest N,P,K and Zn uptake by seed (79.91 kg/ha, 8.62 kg/ha, 21.09 kg/ha, 79.57g/kg respectively) and by straw (39.48 kg/ha, 10.42 kg/ha, 54.23 kg/ha, 52.23g/kg respectively) was obtained with 40 kg P_2O_5+25 kg $ZnSO_4$/ha. Application of 40 kg P_2O_5+25 kg $ZnSO_4$/ha gave highest net returns (₹ 55864/ha) and BC ratio (1.63) over other treatments. Among different solubilizers biophos @ 5ml/kg + biozinc @ 5ml/kg resulted in maximum N,P,K,Zn content & uptake, net returns and BC ratio. Maximum N, P, K and Zn content in seed (3.60%, 0.23%, 0.88% & 32.07ppm respectively) and in straw (0.86%, 0.22%, 1.13% & 11.89 ppm respectively) with the application of biophos@5ml/kg + biozinc@5ml/kg. Similarly, highest N, P, K and Zn uptake by seed (77.16 kg/ha, 7.77 kg/ha, 19.23 kg/ha & 70.50g/kg respectively) and by straw was obtained with biophos@5ml/kg + biozinc@5ml/kg. Application of biophos@5ml/kg + biozinc@5ml/kg gave highest net returns (₹ 52059/ha) and BC ratio (1.56).

S3.80: Effect of tillage, residue and nutrient management in different cropping systems under arid ecosystem

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A field experiment was started during kharif 2020 to study the different cropping systems under conservation agricultural practices in arid ecosystem. The experiment was conducted under split plot design with three replications. Main plot consists of three tillage management practices vis., i) conventinal tillage in both kharif and rabi crops (CT-CT), ii) Conventional tillage for kharif crops and zero tillage for rabi crops with residue retention of previous crop (CT-ZT), iii) zero tillage for both kharif and rabi crops with residue retention of previous crop (ZT-ZT), and two cropping system in sub plot viz. Pearlmillet-chickpea and clusterbean - mustrad and two level of nutrient management in sub-sub plot viz. 100% recommended dose of fertilizer (RDF) for both kharif and rabi crops and 75% recommended dose of fertilizer (RDF) for both kharif and rabi crops. The result reveals that grain yield of component crops were not significantly influenced under tillage management options and recorded maximum under CT-CT followed by CT-ZT and ZT-ZT, respectively. However, the increase in grain yield was significant under cropping systems and recorded significantly higher in clusterbean- mustard system as compared to pearlmillet-chickpea system. Among nutrient management options, 100% RDF recorded significantly higher yield of the component crops over 75% RDF in the first year. However, next year, it was not showed any significant difference with 75% RDF in terms of the yields of both season crops. System productivity in terms of chickpea equivalent yield (CEY) was not significantly affected under all the tillage management options. While in cropping systems, clusterbean- mustard cropping system was recorded significantly higher CEY (2575 kg/ha) over pearl millet –chickpea system. Further, the 100% RDF gave significantly higher CEY (2531 kg/ha) over 75% RDF (2306 kg/ha).

S3.81: Effect of seed priming on growth, yield attributes and yield of chickpea

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The synthesis and application of inoculants containing microorganisms in crops is gaining more attention worldwide. Among inoculants, mostly different crop-specific strains of rhizobia are used for legume crops to enhance their production potential. There is, however, little research on the utilization of endomycorrhizae and signal molecules like lipo-chitooligosachharide to increase yield potential in legumes, notably in chickpea. Thus, this experiment was attempted at the Agricultural Research Farm of the Institute of Agricultural Sciences, Banaras Hindu University, during the winter season of 2019-2020 with the objective of enhancing the production potential of chickpea through seed priming with microbial inoculants. The experiment consisted of eight treatments viz., T_1 (control), T_2 (Rhizobium 20g + Phosphate solubilizing bacteria 20g), T_3 (endomycorrhizae 1g), T_4 (endomycorrhizae 2g), T_5 (endomycorrhizae 4g), T_6 (endomycorrhizae 1g + lipo-chitooligosaccharide 0.33ml), T_7 (endomycorrhizae 2g + lipo-chitooligosaccharide 0.33ml) and T_8 (endomycorrhizae 4g + lipo-chitooligosaccharide 0.33ml). The experiment was laid out in a randomized block design and replicated four times. Seed priming significantly influenced plant height, dry weight, leaf area, root length, nodule number, pods per plant, grain and straw yield. Among treatments, seed priming with endomycorrhizae 4g + lipo-chitooligosaccharide 0.33 ml (T_8) proved better, recorded maximum plant height, dry matter, leaf area, nodule number, and root length. Furthermore, the endomycorrhizae (4g) + lipo-chitooligosaccharide (0.33 ml) combination resulted in higher grain (2.60-48.34%) and straw (1.05-59.16%) yields than the other treatments. Based on the obtained results, seed priming of chickpea with endomycorrhizae + lipo-chitooligosaccharide is suggested for better performance and enhanced production potential.

S3.82: Characterization of chickpea cultivar(s) for chickpea + mustard intercropping system: Cultivar performance, intercropping indices and yield advantage

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Selecting the best intercrop cultivar is crucial to realize higher yield advantage from intercropping system. A two-year field experiment was conducted to identify and characterize the best chickpea cultivar for chickpea+mustard intercropping systems for maximizing system productivity. For this, twelve chickpea cultivars were grown with mustard cultivar Varuna (5:2). The highest chickpea yield (intercrop) was observed for the *cv.*IPC 2004-134 (1106 kg ha^{-1}) followed by IPC 2010-72 (1068 kg ha^{-1}), where sole crop yield was highest with *cv.*JG 16 (1898 kg ha^{-1}). IPC 2011-112 and DCP 92-3 were the poor performers under intercropping system. Chickpea yield attributes were estimated in different rows of chickpea and the results revealed that shading effect of mustard on chickpea was more intense in the chickpea rows adjacent to the mustard rows. For instance, yield reduction in the side rows (adjacent to the mustard rows) from that of the middle rows were calculated the reductions ranged from 20.4% (IPC 2010-134) to 49.7% (JG 16). The results of the intercropping indices (completion ration and relative crowding coefficients) indicated that there was a marked variations among the chickpea cultivars for these indices, highest for *cvs.* IPC 2010-72, HC 5, IPC 2010-62, IPC 2010-142. Biplot analysis results explained the yield stability of different chickpea cultivars based on crop yield performance under sole and intercropping production systems and the cultivar IPC 2010-72 had higher yield stability over others. Hence, the results suggested that IPC 2010-134, IPC 2010-72 could be the potential chickpea cultivars for chickpea+mustard intercropping systems.

S3.83: Effect of zinc and iron on yield and economics of mung bean

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A field experiment was conducted on deep black soil of Agricultural Research Station, Badnapur during kharif 2021-22 with an objective to assess fortification of Zn and Fe in mung bean. The experiment was laid out in Factorial Randomized Block Design with three replications. The treatments comprised of T1- 0.5% $ZnSO_4$ spray at flower initiation; T2 -0.5% $ZnSO_4$ spray at flower & pod initiation; T3 - 0.5% $FeSO_4$ spray at flower initiation; T4 - 0.5 % $FeSO_4$ spray at flower & pod initiation; T5 - 0.5 % $ZnSO_4$& 0.5 % $FeSO_4$ spray at flower initiation; T 6 - 0.5 % $ZnSO_4$ and 0.5 % $FeSO_4$ spray at flower & pod initiation; T7- 25kg $ZnSO_4$ through soil application and T8- 5-10 kg $FeSO_4$ through soil application. The sowing was completed on 5 / 07 / 2021 by using BM 2003-2 variety. The fertilizer doses were applied as per treatments. Similarly, crop protection measures were adopted as per the recommendations. Results reveled that the different treatments influenced seed yield of mung bean statistically significant. Application of 0.5% $ZnSO_4$ and 0.5 % $FeSO_4$ spray at flower & pod initiation produced significantly higher seed yield of mung bean which was found on par with application of 0.5 % $ZnSO_4$& 0.5 % $FeSO_4$ spray at flower initiation. The gross as well as net monetary returns and B:C ratio followed the similar trend.

S3.84: Evaluation of pigeonpea based intercropping systems on vertisols

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A field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during kharif 2021 on pigeonpea variety BDN-711, in Randomized Block Design with three replications. The experiment was sown on 14th June 2021 using spacing as per treatments. The fertilizers and agronomic practices were adopted as per recommendation. Pigeonpea crop was intercropped with sweet corn, baby corn and parched sorghum in 1: 2 row proportions. Pigeonpea based intercropping systems were compared with the sole crops of component crops and existing pigeonpea based intercropping system of the region i.e. pigeonpea + soybean intercropping system (2:4 row proportion). Results revealed that pigeonpea +baby corn (1:2) intercropping system recorded significantly higher pigeonpea equivalent yield(PEY), however, it was on par with sole baby corn. The gross and net monetary returns followed the similar trend. Significantly higher B:C ratio was recorded by pigeonpea + baby corn (1:2) intercropping system followed by sole pigeonpea and pigeonpea + soybean (2:4) intercropping system. pigeonpea + baby corn (1:2) intercropping system recorded higher LER(1.12), competition ratio (1.25) and aggressivity (0.085) than other pigeonpea based intercropping systems.

S3.85: Sustainable intensification through pulses for improving productivity, profitability and resource use efficiency under conservation agriculture in rainfed semi-arid environments

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Field study on different cropping systems under conservation agriculture were undertaken since 2018 to 2022 at Indian Agricultural Research Institute, New Delhi. Results indicated that conventional tillage without residue recorded soil moisture depletion by 21and 13% over zero tillage with anchored residue (3 t/ha) and as mulch, respectively. Significantly higher values of soil available N, P, K and organic carbon content and moisture use efficiency were noted in zero tillage with anchored residue and as mulch compared to conventional tillage with no residue. Zero tillage with residue mulch @3 ton/ha caused significantly higher increase in chickpea equivalent seed yield and net returns over zero tillage with anchored residue and conventional tillage with no residue, which might be attributed to the higher growth and yield attributed due to availability of favourable soil environmental conditions. The inclusion of chickpea in cropping systems significantly improved soil moisture content, soil temperature, soil micro-organism populations, and N, P, K, and organic matter content compared to lentil and barley crops leading significantly improvement in growth and yield attributes and yield. The increase in system productivity in terms of chickpea equivalent grain yield was recorded by 19 and 9% over pearlmillet-lentil and pearlmillet-barley cropping systems, respectively. Maximum net returns were also obtained in pearlmillet-chickpea cropping systems. The results of the study showed that the intensification of cropping systems through pulse crops like chickpea in pearlmillet based cropping systems can provide higher yield and monetary gain under rainfed conditions of semi-arid region.

S3.86: Assessment of maize and pearl-millet intercropped cowpea followed by chickpea and mustard under conservation agriculture-based tillage in rainfed situations

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Experiment was conducted since 2018 to 2022 at Indian Agricultural Research Institute Research Farmto assess rainfed maize and pearl-millet intercropped cowpea followed by chickpea and mustard under conservation agriculture (CA)-based tillage. The 15-treatments viz., 3 CA-based establishment viz., T1 = Ridge planting+3 t/ha residue mulch; T2 = Furrow planting+3 t/ha residue mulch and T3 = flatbed planting in horizontal strips and 5 cropping systems i.e., C1 = maize-chickpea; C2 = maize+cowpea-mustard; C3 = pearlmillet-chickpea; C4 = pearlmillet + cowpea-mustard; C5 = cowpea-barley in vertical strips. Experiment was layout in strip plot design and replicated thrice. Crops were raised with recommended package of practices for Delhi region. Results indicated that both ridge and furrow planting with residue mulch provided the highest system productivity in terms of maize equivalent yield (MEY) (6.85 and 6.96 t/ha) and system water use productivity (9.67 and 10.20 kg/ha/mm) over flatbed, respectively. However, ridge planting+residuemulch during kharif and furrow planting+residuemulch during rabi season found the highest system productivity in terms of MEY and water productivity. Among the cropping systems, maize + cowpea-mustard system resulted the highest system productivity in terms of MEY and water productivity (9.44 t/ha and 13.57 kg/ha/mm) followed by maize-mustard system (7.20 t/ha and 10.67 kg/ha/mm) and pearlmillet-chickpea (6.33 t/ha and 7.07 kg/ha/mm), respectively. However, the lowest MEY was recorded with cowpea-barley system. Thus, ridge or furrow planting with crop residue mulch in maize+cowpea-mustard/chickpea and pearlmillet-chickpea cropping system are the most productive options under rainfed conditions.

S3.87: Effect of different phosphorus sources and P solubilizers on growth, yield and nutrient uptake of soybean (*Glycine max* L. Merrill)

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A field experiment was conducted at Agricultural Research Station Farm, Bagalkot during *kharif* (2019). The experiment consisted of 12 treatments with different phosphorus sources and P solubilizers. The experiment was laid out in a randomized block design with three replications. Among treatments tested soil application of 100 per cent RDP through DAP and seeds inoculated with liquid formulation of *Pseudomonas striata* recorded significantly higher leaf chlorophyll content(46.23), seed yield (2385 kg ha^{-1}) and haulm yield (2615 kg ha^{-1}) and was on par with treating the soil with 100 per cent RDP through SSP and seeds inoculated with liquid formulation of *Pseudomonas striata* with leaf chlorophyll of 46.02 seed yield of 2278 kg ha^{-1} and haulm yield of 2554 kg ha^{-1}. Soil application of 100 per cent RDP through DAP and seeds inoculated with liquid formulation of *Pseudomonas striata* recorded significantly higher uptake of Nitrogen (30.81, 141.8 and 232.49 kg ha^{-1}), Phosphorus (5.26, 23.83 and 37.20 kg ha^{-1}) and Potassium (20.18, 93.26 and 151.68 kg ha^{-1}) at flower initiationstage, pod initiation stage and at harvest respectively.

S3.88: Influence of post-emergence herbicides on weeds, growth and yield of chickpea (*Cicer arietinum* L.) during r*abi* season in irrigated condition of Rajasthan

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The field experiment was carried out during three consecutive Rabi seasons (2019-20 to 2021-22) at Agricultural Research station, Kota to find out the suitable post emergence herbicide for control of weeds at broad spectrum for enhancing the productivity of chickpea. The experiment was laid out in Randomized Block Design comprising eight treatments with three replications. Results showed that significantly minimum number of weeds [3/m^2 (1.85)], weed dry weight [8 g/ m^2] and maximum WCE (96.32%) at harvest was recorded under weed free check. Among the herbicide treatments, application of pendimethalin 30% EC + imazethapyr 2% (1.0 kg/ha) as pre emergence along with one hand weeding recorded significantly lower number of weeds [20/m^2 (4.56)], weed dry weight [39 g/m^2] and WCE (82.93%) which was significantly higher over application of topramezone @ 20.6 & 25.7 g ai/ha at 14 and 21 DAS and quizalofop-p-ethyl 100 g a.i./ha. Weed free check recorded significantly highest seed yield (2470 kg/ha). Among the herbicidal treatments, application of pendimethalin 30% EC + imazethapyr 2% (1.0 kg/ha) PE + 1 HWrecorded significantly highest seed yield (2282 kg/ha) which was found significantly superior over the rest of the treatments. Similarly, the highest net returns (Rs. 95003/ha) was obtained under weed free check treatment followed by application of pendimethalin 30% EC + imazethapyr 2% (1.0 kg/ha) PE +1HW (Rs. 88225/ha). However, the highest B:C ratio was fetched under topramezone 20.6 g a.i./ha at 21 DAS followed by application of pendimethalin 30% EC + imazethapyr 2% (1.0 kg/ha) PE +1HW treatment.

S3.89: Effect of customized fertilizers grade (cfg) on yield and economics of chickpea under South-Eastern Rajasthan

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A field experiment was carried out during *Rabi* season (2019-20, 2020-21 and 2021-22) at Agricultural Research Station, Kota (Agriculture University, Kota) Rajasthan to obtain higher yield of chickpea through customized fertilizer (based on nutrient uptake of NPK, S, Zn and Mo). The experiment was laid out in Randomized Block Design comprising five treatments *i.e.*, RDF (recommended level of $N:P_2O:K_2O$ @ 20:40:20 kg ha^{-1}); RDF1 (Recommended level of $N:P_2O:K_2O$:S:ZnSO4:Na_2MoO_4 @ 20:40:20:20:25:1 kg ha^{-1}); CFG1 (5.5:4.6:4.5:8.3:1.4:0.8:0.08:0.034 percent ratio of N:P:K:S:Zn:Fe:B:Mo) based on recommendation (100%) @ 100 kg ha^{-1}, CFG2 based on recommendation (75%) @ 75 kg ha^{-1} and CFG3 based on recommendation (125%) @ 125 kg ha^{-1} with four replication. On the basis of three-year pooled analysis of data, it could be concluded that among the different customized fertilizer grades (CFG) significantly higher pods per plant (70.8), seed yield (2512 kg/ha), net return (Rs. 101565/ha) and BC ratio (2.90) of chickpea was obtained with application of CFG3 (NPKSZnMo) based on recommendation (125 %) over the RDF (Recommended level of NPK) and CFG2 (NPKSZnFeBMo) based on recommendation (75 %) which was found statistically at par with CFG1 (NPKSZnMo) based on recommendation (100%) and RDF1 (recommended level of NPKSZnMo). Further data, revealed that CFG1 (NPKSZnMo) based on recommendation (100%) and RDF1 (recommended level of NPKSZnMo) was recorded significantly higher growth and yield attributes, yield and economics of chickpea over RDF (Recommended level of NPK) and CFG2 (NPKSZnFeBMo) based on recommendation (75%).

S3.90: Bio-efficacy of different herbicides for broad spectrum weed management in Chickpea

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during Rabi, 2017-18. The experiment was laid out in randomized block design with three replications. The gross plot size was 3.60 x 6.20 m2 and net plot size was 3.00 x 6.00 m2. The experiment was comprised of ten treatments, viz., T1: Pendimethalin 30EC (0.75-1.0 kg/ha) PE + one hoe at 25-30 DAS, T2: Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE, T3: Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE + one hoe at 30-35 DAS, T4: fenoxyprop-ethyl 9.3% w/w (60g/ha) POE at 25-30 DAS, T5: pendimethalin 30EC + omaze 2% (RM 1.0 kg/ha) PE, T6: Pendimethalin 30EC + Imaze 2% (RM 1.0 kg/ha) PE + one hoe at 30-35 DAS, T7: Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE + Imaze 2% (Tank mix 1.0 kg/ha), T8: One hoe at 25-30 DAS, T9: Weed Free (two HW at 20-25 DAS and 30-35 DAS) and T10: weed check The sowing was done on 04-11-2017 by using BDNG-797. The recommended doses of fertilizers were applied as basal dose. Similarly crop protection measures were adopted as per the recommendations. The crop was harvested on 28-02-2018. The data on seed yield was analyzed statistically. The data showed significant differences in seed yield of chickpea as influenced by different weed management practices. Weed free treatment recorded significantly higher seed yield (2009 Kg ha-1) of Chickpea than rest of the treatments. Next best treatment was T3 i.e. Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE + one hoe at 30-35 DAS (1928 kg ha^{-1}). However, it was at par with treatment T2 i.e. Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE (1824 kg ha^{-1}), T1 i.e. application of Pendimethalin 30 EC (0.75-1.0 kg/ha) PE + one HW at 25- 30 DAS (1706 Kg ha^{-1}). The lowest seed yield (997 Kg ha^{-1}) was recorded by the weedy check treatments i.e. T10.The lowest weed dry matter at both stages (35 DAS and 75 DAS) as well as weed index and maximum weed control efficiency was recorded by the treatment T3 i.e. Pendimethalin 38.7 CS (0.75-1.0 kg/ha) PE + one Hoe at 30-35 DAS (1928 kg ha^{-1}).

S3.91: Evaluation of pigeonpea + speciality corn and pigeonpea + parching sorghum intercropping systems

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The experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *kharif*, 2021 on pigeonpea variety BDN-711, in Randomized Block Design with three replications. It comprised of 8 treatments such as T_1: Sole Pigeonpea variety BDN 711, T_2: Sole Sweet corn variety Sugar 75, T_3: Sole Baby corn variety HM 4, T_4: Sole Parching sorghum variety PDKV HurdaKartiki, T_5: pigeonpea + soybean (2:4 row proportion), t_6: pigeonpea + sweet corn (1:2 row proportion), t_7: pigeonpea + baby corn (1:2 row proportion) and t_8: pigeonpea + parching sorghum (1:2 row proportion). The experiment was sown on 14 June 2021 using spacing as per treatments. The gross and net plot sizes were 7.2 x 6.0 m^2 and 5.4 x 5.8 m^2 respectively. The fertilizers and agronomic practices were adopted as per recommendation. The pigeonpea and intercrops were harvested up to 8-9 th Jan. 2022. The data obtained on growth and yield of component crops was analyzed.Results revealed that during the year 2021-22, pigeonpea + baby corn (1:2) intercropping system recorded significantly higher pigeonpea equivalent yield (PEY), however, it was on par with sole baby corn. The gross and net monetary returns followed the similar trend. Significantly higher B:C ratio was recorded by pigeonpea + baby corn (1:2) intercropping system followed by sole pigeonpea and pigeonpea + soybean (2:4) intercropping system. Pigeonpea + baby corn (1:2) intercropping system recorded higher ler (1.12), competition ratio (1.25) and aggressivity (0.085) than other pigeonpea based intercropping systems.

S3.92: Effect of foliar spray of nutrients for yield maximization of mungbean

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The field experiment was conducted on deep black soil of Agricultural Research Station, Badnapur during *Kharif,* 2021-22. The experiment was laid out in Randomized Block Design with three replications. It consists of 8 treatments namely, T_1: Water spray, T_2: 2 % Urea, T_3: 2% DAP, T_4: NPK (18:18:18) @ 2%, T_5: 0.5 % $ZnSO_4$, T_6: 2% Urea+ 0.5 % $ZnSO_4$, T_7: 2% DAP + 0.5 % ZnSO4 and T_8: NPK (18:18:18) @ 2% + 0.5 % $ZnSO_4$. The gross plot size was 5.4 x 5.0 m^2 and net plot size was 4.8 x 4.8 m^2. The sowing was done on 05/07/2021 by using BM 2003-2 variety. The fertilizers doses were applied as per treatments. Similarly, crop protection measures were adopted as per the recommendations. The crop was harvested on 20/09/2021. The data on seed yield and economics was analyzed statistically.Seed yield of mungbean was statistically influenced by various treatments. Application of NPK (18:18:18) @ 2% + 0.5 % $ZnSO_4$ recorded significantly higher seed yield of mungbean, however, it was on par with application of 2 % DAP + 0.5 % $ZnSO_4$ and treatment receiving 2% Urea+ 0.5 % $ZnSO_4$. The gross as well as net monetary returns and B:C ratio followed the similar trend.

S3.93: Effect of fertilizer doses, organic manure and biofertilizer for yield maximization of mungbean and their effect on succeeding rabi safflower crop

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The field experiment was conducted on deep black soil of Agricultural Research Station, Badnapur during *Kharif,* 2019-20. The experiment was laid out in Factorial Randomized Block Design with three replications. The treatments comprised of three fertilizer levels (A_1: RDF 75 % (18.75:37.50:00 NPK kg/ha), A_2: RDF 100 % (25:50:00 NPK kg/ha) and A_3: RDF 125 % (31.25:62.50:00 NPK kg/ha)), two FYM levels (B_1: Control and B_2: 5 t/ha) and three biofertilizer levels (C_1: *Rhizobium* (Local based), C_2:*LNm 16** (Ludhiana Nutrient mobilizer 16) and C_3: *Rhizobium* + *LNm16**). The gross plot size was 5.0 x 4.5 m^2 and net plot size was 4.6 x 3.6 m^2. The sowing was done on 06/07/2019 by using BM 2003-2 variety. The fertilizers doses were applied as per treatments. Similarly, crop protection measures were adopted as per the recommendations. The crop was harvested on 16/09/2019. The data on seed yield was statistically analyzed.The results revealed thatthegrain yield of mungbean was significantly influenced by different fertilizer levels. An application of 125 % RDF produced significantly higher grain yield (732 kg ha^{-1}) among treatments while an application of 100 % RDF (662 kg ha^{-1}) found second best treatment. The grain yield of mungbean was significantly influenced by application of FYM. An application of 5 tonnes FYM per ha produced significantly higher grain yield (773 kg ha^{-1}) over control. Application of different biofertilizer levels significantly influenced the grain yield of mungbean. An application of *Rhizobium* + *LNm16** produced significantly higher grain yield (741 kg ha^{-1}) as compared to other treatments.

S3.94: Biofortification of Zn and Fe in chickpea through agronomic intervention

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *Rabi* 2017-18. The experiment was laid out in Spilt Plot Design with four replications.The treatments comprised of two varieties in main plots and six nutrient levels as sub plots comprising twelve treatment combination. The sowing was done on 02-11-2017 by using Chickpea variety BDNG-797 and Digvijay and six nutrient levels, N_1-Recommended Dose of NP (Control), N_2-RDF+ o.5% Zn foliar application (two times), N_{3-} RDF+ o.1% Fe foliar application (two times), N_{4-} RDF+ Zn and Fe through foliar application (two times), N_{5-} RDF + seed treatment -2 gm Zn/kg of seed and N_{6-} RDF+ soil application of $ZnSo_4$@25 kg/ha (recommended practice). The crop was harvested on 22-02-2018.Chickpea genotype Digvijay recorded significantly superior higher seed yield (1949 Kg ha^{-1}) than other BDNG-797 genotype. (1736 Kg ha^{-1}). Among the Six nutrients levels treatment N_{4-} RDF+ Zn and Fe through foliar application (two times) recorded significantly higher seed yield (1989 Kg ha^{-1}) which was found at par with treatment N_2-RDF+ o.5% Zn foliar application (two times), N_{3-} RDF+ o.1% Fe foliar application (two times) and N_{6-} RDF+ soil application of $Znso_4$@25kg/ha (recommended practice). While the lowest seed yield was recorded by control (RDF). While the interaction between varieties and nutrients levels were found to be non-significant. While the highest GMR, NMR and B; C ratio was observed when variety Digvijay was given RDF and foliar application of 0.5% Zn and 0.1% Fe sprayed two times before flowering and pod initiation stage.

S3.95: Effect of stress mitigating chemicals and sulphur on plant population and grain yield of mungbean

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The field experiment was conducted during the *kharif* season 2019 to investigate the effect of stress mitigating chemicals and sulphur on plant population and grain yield of mungbean [*Vigna radiata* (L.) Wilczek]. The experiment laid out in Factorial Randomized Block Design with sixteen treatment combinations comprised of four stress mitigating chemicals and four sulphur levels with three replications. The result shows that initial plant population of mungbean was found unaffected by all the treatments. Application of thiourea @ 500 ppm (FI) enhanced significantly final plant population and grain yield of mungbean and significant increment in both traits were also observed in the treatment of sulphur @ 40 kg/ha. The interaction effect of stress mitigating chemicals and sulphur levels had a significant effect on grain yield of mungbean.

S3.96:Effective weed management for higher productivity in urdbean [*Vigna radiata* (L.) Hepper] under rainfed conditions

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Urdbean [*Vigna mungo* (L.) Hepper] is one of the important pulse crops cultivated worldwide in tropical and subtropical regions of the world. It is mainly cultivated in marginal and rainfed areas generally during *kharif*where inadequate weed management is a major constraint in harnessing its production potential and it may up to 40%. The experiment was conducted to develop cheaper methods of weed control with effective herbicidesduring *kharif* 2019 at ARS, Kota with ten treatments viz., T_1=weedy check, T_2=two hand weeding at 20 and 40 DAS, T_3=pendimethalin 30% EC @ 1.0 kg *a.i.*/ha PE, T_4=propaquizafop 2.5% @ 33.3 g/ha + imazethapyr 3.75% ME @ 50 g/ha PoE, T_5=acifluorfen-sodium 16.5% EC @ 140 g/ha + clodinafop-propargyl 8% EC @ 70 g/ha PoE, T_6=fomesafen 11.1% @ 220 g/ha + Fluazifop-p-butyl 11.1% @ 220 g/ha PoE, T_7=T_3fb T_4, T_8=T_3fb T_5, T_9=T_3fb $T_6$and T_{10}=fluazifop-p-butyl 13.4% @ 250 g/ha PoEin RBD and replicated thrice. The post emergence (PoE) application was done at 20 DAS.Among herbicides maximum grain yield (827 kg/ha) and net returns (Rs 21171/ha) was recorded in treatment T_7being at par withT_9 with 109.37 and 96.20; 596.50 and 567.64 per cent higher over weedy check, respectively.No phytotoxicity effect on the crop was observed by application of herbicides. Similarly, minimum and significantly lower weed count and weed dry matter and maximum weed control efficiency was recorded withT_7however, it recorded at par results with T_9.

S3.97: Bio-efficacy of post-emergent herbicide imazethapyr in common bean (*Phaseolus vulgaris* L.) under temperate rainfed condition of Kashmir

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A field experiment was conducted for two years during kharif season of 2021 and 2022 at the Agronomic Research Farm of the Faculty of Agriculture, Wadura to study the bio-efficacy of post-emergent herbicide imazethapyr in common bean at different doses of 0.025, 0.050, 0.075, 0.100 and 0.125 kg ha^{-1} applied at 25 days after sowing (DAS). Herbicides pendimethalin (1.0 kg ha^{-1}) and oxyflourfen (0.150 kg ha^{-1}) were applied as pre-emergence. Doses of imazethapyr was also compared with hand hoeing at 25 DAS. Total fourteen treatments including weed free and weedy checkwere compared under randomized completely block design. Oxyflourfen caused phytotoxicity (necrosis of leaves) after emergence, with more intensity after rains. However, symptoms of the phytotoxicity was started to disappear at 20 DAS. All the growth and yield parameters were found significantly higher in pendimethalin treated plots over oxyflourfen treated plots, irrespective of post-emergent treatments. Pendimethalin 1.0 kg ha^{-1} followed by imazethapyr 0.075 kg ha^{-1} was found optimum with respect to plant height, leaf area index and dry matter accumulation at 40 and 60 DAS. Seed yield observed withimazethapyr 0.075kg ha^{-1} was also found at par to 0.100, 0.125kg ha^{-1} and hand hoeing, but all these treatments were not significantly superior to weed free plots. Weed control efficiency and weed index of 72.2% and 14.9% were calculated with pendimethalin 1.0kg ha^{-1} followed by imazethapyr0.075 kg ha^{-1} , showing effective weed control measure in common bean in Kashmir valley.

S3.98: Genotypic differences in response to heat stress in mungbean and phosphorus placement in chickpea

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Grain legumes such as mungbean and chickpea provide high quality protein and nutrition for human and livestock consumptions and maintain soil fertility. Insufficient resilience to environmental stresses such as heat stress, drought and phosphorus acquisition could have a negative impact on yields. Knowledge about genetic variability is needed to improve the crop resilience to environmental stresses and boost grain yield. Studies on various crops have shown that high temperature stress around reproductive stage could adversely affect the grain yield via effects on pollen viability. In this study, pollen viability reduced from around 70% to 30% across fourteen mungbean genotypes. However, the total seed yield per plant increased significantly for five genotypes, resulting from increased number of total pods with the heat stress. Mungbean genotypes with relatively more indeterminate growth habit mitigated the impact of heat stress on pollen viability by increasing the post stressed vegetative and reproductive growth. In another study, deep placement of phosphorus (P) increased the pod yields for more responsive early maturing chickpea varieties. This study, however, finds significant variability in P uptake and P utilisation efficiency among chickpea varieties. Data suggests that the root surface area may not be necessarily important for total P uptake, rather ability of varieties to utilise P within the plant is more important. The observed genetic variation in tolerance to heat stress in mungbean and response to P placement strategies in chickpea could be exploited through the breeding programs to develop more resilient varieties to environmental stressed for future climates.

S3.99: Study on seed quality enhancement, storability and field performance of kabuli chickpea varieties

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The field and laboratory experiments were conducted at Regional Agricultural Research Station, Vijayapur during 2018-19. The experimental design was Factorial Randomised Block design with two *kabuli* varieties (KAK 2 and MNK 1) and seven treatments involving polymer (10 and 20 ml/ kg), vitavax (3 g/kg) and their combinations along with castor oil (10 ml/kg). Among the treatments, combination of vitavax powder (3 g/kg) + polymer coat (20 ml/kg) has recorded significantly higher seed quality parameters, protein content, dehydrogenase activity, reducing and non-reducing sugar content followed by vitavax powder (3 g/kg) + polymer coat (10 ml/kg) combination throughout the storage. MNK 1 *kabuli* variety has better storability due to its bold seed nature providing more food reserves.Further, the stored seeds were treated with bioagent *Pseudomonas flurescence*(30 g/kg) to study the field performance. The treatment combination of vitavax powder (3 g/kg) + polymer coat (3 ml/kg) + *Pseudomonas flurescence* (30 g/kg) has recorded higher seed yield (21.95 q/ha) compared to control. Among the varieties, MNK 1 has responded better compared to KAK 2 (28.26 q/ha) for the best treatment combination with 34% and 24% increase in seed yield over their control (13.04 and 22.70 q/ha, respectively) due to the inherent difference in their yield potential.

S3.100: Evaluation of post emergence herbicides in pigeonpea

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *Kharif* 2021-22. The experiment was laid out in Randomized Block Design with three replications with thirteen treatments.The sowing was done on 30-06-2021 with pigeonpea variety BDN- 711. The results revealed that weed free treatment produced significantly higher seed yield of pigeonpea, however, it was on par with treatments receiving two hand weedings at 20 and 40 DAS/ Inter cultivation; Pendimethalin 30 EC @ 0.75 kg ai/ha (PE) followed by Imazethapyr 10 SL @ 100 g ai/ha at 20-25 DAS fb + one Inter cultivation at 50 DAS; and Imazethapyr + Imazamox @ 100 g ai/ ha at 20-25 DAS. GMR, NMR and B: C ratio followed the similar trend. Lower values for weed dry matter per square meter, whereas, higher values for weed control efficiency and weed index were also recorded by these treatments.

S3.101: Strengthening existing pulse-based rainfed integrated farming systems in Northern Karnataka for stabilizing the farm income

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The study area is fraught with low productivity of pulses, poor integration of farming systems and low income and employment. As a result, farmers' income from agriculture has not improved substantially. Thus, crop diversification and intensification with integrated farming systems harness the potential to raise pulse production and income in rainfed areas. The study attempts to identify the existing farming systems and develop an efficient farming system for increasing and stabilizing farm income and employment and managing weather aberrations in the dry areas of Vijayapura district through the rainfed integrated farming systems (RIFS) approach. A multi-stage survey method using a random sampling procedure was followed for selecting blocks, villages and farmers. The survey results indicated that crop (C) and crop + large ruminants (CLR) were the existing traditional RIFS in rainfed (RF) and partially irrigated (PIR) situations. Further, crops and horticulture with large ruminants' systems (CHLR) was practiced in PIR. Overall, pulses like pigeonpea and chickpea were the major crops and buffaloes, cattle and goats were major animal components irrespective of farming category and situation. Based on these results, the on-farm interventions were implemented in different RIFS modules like natural resource management, crop, livestock, perennial tree, fodder and optional module under both RF and PIR situations in farmers' fields under CLR and CHLR farming systems. It was observed that the higher system productivity (an increase of 26.60 – 36.80%), profitability (an increase of 34.12 – 42.66%) and employment generation in the pulse-based RIFS with interventions of different modules over without interventions.

S3.102: Use of PGR & nutrients for enhancing the productivity of chickpea

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The role of different PGR's and nutrients in plant tolerance to drought stress is a significant because they regulate multitude of metabolic process. the present study was conducted at Agricultural Research Station Dharwad Farm during the year 2019-20, 2020-21 to investigate the influence of PGR's and nutrients as morph physiological biophysical, biochemical & yield parameters for enhancing the productivity chickpea under rainfed condition the experiments consist of eight treatments applied which were chickpea magic 0.6%, 0.8%, 1%, NAA 30PPM urea 2% & control. among all the treatment foliar application of chickpea magic 0.8% at flowering and pod formation stage recoded higher yield (1757.50 kg/ha) compare to control (1300.50 kg/ha) and also recoded higher synthetic rate (28.35 µ mol CO_2 m^2 S^{-1}) compare to control 24.25 µ mol CO_2 m^2 S^{-1}, proline content 3.01 µ mol g compared to other treatment and also recorded relative water content was more in 0.8% chickpea magic (77.55%) compare to control 69.80%.

S3.103: Enhancing productivity of common bean (*Phaseolus vulgaris* L.) through organic sources of nutrients and non-chemical weed management practices in Kashmir Valley

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A field experiment was conducted at Faculty of Agriculture, SKUAST-Kashmir, Wadura during 2021 and 2022 on clay loam soil. The soil of the experimental field was low in available nitrogen, medium in available phosphorus and high in available potassium with high organic carbon content. Four organic nutrient sources vermicompost (1 t ha^{-1}), farm yard manure (6 t ha^{-1}), vermin-compost + vermin-compost (3 + 0.5 t ha^{-1}), and control treatment were in main plots and six non-chemical weed management practices namely brown sarson mulching, black poyhtene sheet, manual weeding, weed mulching, weed free and weedy cheek were supplemented in sub-plots. The experiment was laid out in split plot design. The data during both years revealed that the growth parameters and yield attributes were significantly higher with vermin-compost. The data on weed management practices indicated that all the weed management practices enhanced the grain yield compared to control weedy check. Among the mulching applied black polythene sheet provided excellent control of weeds enhancing yield of crops as well as weed control performance. Thus, vermi-compost (1 t ha-1) and application of black polythene sheet can be applied to common bean as non-chemical approach for enhancing productivity.

S3.104 Evaluation of Phosphorus use efficiency in Urdbean genotypes on Vertisol of Dharwad, Karnataka, India

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Urdbean is an important pulse crop of Karnataka, which is cultivated in an area of 1.38 Lakh ha with a production of 0.47 Lakh tones and a low productivity of 1.36 q $acre^{-1}$. Low productivity is attributed to various management practices. Among the different urdbean management practices, nutrient management especially Phosphorus plays an important role in limiting urdbean yields that needs immediate attention. Keeping this in view, a pot experiment was conducted at ICAR-IIPR, Regional Centre, in Vertisols of Dharwad, Karnataka, India during *kharif* season of 2021 to evaluate the efficiency of phosphorus in prominent 15 genotypes of urdbean. The genotypes used include UH82-41, IPU96-1, IPU2K99-1, IC-274045, Pratap Urd-1, SYNP-2, Sarda Mash, IC-261179, IC-323943, Barabanki Local, PLU-59, KC-153, STY-2289, DBGV-5 and DU-1. There were two Levels of Phosphorus i.e. 0 and 50 kg P_2O_5 ha^{-1} with two replications and the crop was sown in cemented pots. The crop was harvested at maturity and grain and straw yield, P content and uptake and its use efficiency was worked out. The results revealed that PUE of various genotypes of urdbean ranged from 6.2% to 42.5% with STY2289 genotype recorded higher PUE of 42.5%. Among 15 genotypes of urdbean higher PUE of >25% was observed in STY2289 (42.5%), DBGV5 (38.5%) and SYNP2 (27.1%). These genotypes with higher P Use efficiency could be utilized with improved crop management practices to increase the overall urdbean productivity in the region.

Nutri-Smart Pulses and Data-driven Decision Making

S8.1: Quantification of 2-acetyl-1-pyrroline in sonamung (*Vigna radiata* L. Wilczek) through gas chromatography-mass spectrometry method

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Mungbean or greengram (*Vigna radiata* L. Wilczek), is a high-value food and cash crop in the rice-based farming systems of Bangladesh and also South and Southeast Asia. Aromatic Mung (Sonamung) has an aromatic compound that plays an important role in its consumer preference and attracts high prices to the local and global market. In this study, 55 aromatic genotypes of mungbean were examined for their volatile profiles using headspace solid-phase microextraction (HS-SPME) with a gas chromatography-mass spectrometer (GC-MS) and to investigate the relationships between 2-acetyl-1-pyrroline (2AP) content and proline and methylglyoxal (MG), which are important factors for the biosynthesis of aroma. The aromatic character was characterized by two methods, 1.7% KOH sensory test and GC-MS analysis. Both methods produced the same results. Twenty-eight volatile compounds were detected in mungbean germplasm, in which Butanenitrile, 5-Hexen-2-one, 5-methyl-3-methylene, 4,4,4-Trifluoro-2-butanone, 1,7-Nonadien-4-ol, 1-Methyl-3-(2-methylpropyl) cyclopentane, 1-Oxa-2-azacyclopentadiene had not been reported earlier in mungbean. In seeds, 2AP content was varied from 0.067 to 0.437 ppm using HS-SPME, coupled with GC-MS. The highest amount of 2AP was documented in E54 (0.437 ppm), followed by E33 (0.379 ppm) and E55 (0.350 ppm). Proline and MG contents were found to be higher in E33 than in E54. In PCA biplot and correlation analysis, 2AP, proline, and MG were shown to be the key contributors to the scent of mungbean. Thus, the result revealed that volatile profiling information of potential parents, can be used in the aromatic breeding program, and also the higher levels of proline and MG might contribute, to the higher 2AP biosynthesis in fragrant in sonamung.

S8.2: Evaluation of vegetable soybean genotypes for yield traits and lipoxygeanse activity

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Vegetable soybean [Glycine max (L.) Merrill] is an important leguminous vegetable whose pods are harvested when they are still green and the seeds have expanded to fill 80–90% of the pod width. Lipoxygenase enzyme is responsible for off-flavor in soy based foods. Therefore, with the objective of identifying high yielding genotypes having minimum Lipoxygenase activity, 34 diverse vegetable soybean genotypes were evaluated in randomized block design with three replications under Indian Eastern Plateau and Hill Region. The genotypes AGS-458 (0.399 kg/plant; 13.34 t/ha) and AGS-404 (0.379 kg/plant; 12.65 t/ha) were found to be promising for graded green pod yield. Additionally, AGS-404 also exhibited the lowest lipoxygenase enzyme activity (6.33 ÄA/min/mg soluble protein X 10^{-3}). AGS-336 was the earliest (62.33 days) to reach 1st green pod harvest stage (R6 stage). High heritability coupled with high genetic advance as per cent of mean was observed in most of the traits like plant height, days to 50% flowering, 100-green seed weight of 2-seeded pods, 100-green seed weight of 3-seeded pods, graded green pod yield/plant, green seed yield/plant, and lipoxygenase enzyme activity of edible shelled unripe green seeds of vegetable soybean. Correlation study revealed that the traits viz., number of days to first harvest, leaf length, plant height, 100-green seed weight of 3-seeded pods and 100-green seed weight of 2-seeded pods were positively and highly significantly correlated with graded green pod yield per plant. Genetic divergence analysis of 34 vegetable soybean genotypes for 14 green pod yield characters grouped them into 4 clusters and the genotypes AGS-402 (Cluster III) and AGS-332 (Cluster IV) were found to be the divergent genotypes, which could be used as parents in hybridization programme to produce high yielding vegetable soybean lines/varieties.

S8.3: Effect of processing on proximate composition of biofortified varieties of lentils

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Biofortification is the process of improving the nutritional quality of food crops. In this research, the lentil biofortified varieties L4717 and IPL-220 were processed. The processing included soaking, boiling and pressure cooking and proximate composition was estimated by methods as described in AACC (2000). The soaked lentils in both varieties showed highest values of crude protein (L4717-26.15% & IPL-25.60%) while the crude protein in boiled lentils was least. Moisture was higher in the boiled and pressure-cooked samples than control and soaked lentils which indicated higher level of water activity in boiled and pressure-cooked samples which plays a vital role in food storage. Soaked grains retained higher crude fat and crude fibre content than other two processing methods which shows that heat treatment affects crude fat and crude fibre significantly. Crude fat and fibre both were highest in control and reduced after processing and lowest loss was seen in soaking in both of the varieties (L4717-1.61% & 3.43% and IPL-220-1.85%& 4.23% respectively). This research showed that there is significant effect of processing on proximate composition of both varieties of lentils.

S8.4: Utilization of pulse-milling by-products: Effect of protein on the bio-accessibility of calcium

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India, the major producer of pulses, generates ~2.5 million tonnes of by-product waste from milling industry, mainly contributed by green gram, black gram, pigeon pea and bengal gram. Recent studies showed that the pulse-milling by-products are rich source of protein and minerals, however, their bio-accessibility is limited. Although some studies proved the efficacy of protein to improve the bio-accessibility of minerals such as iron and zinc, however, no study evaluated the protein-ligand interaction and phytic acid on calcium bio-accessibility. The milling by-product from green gram (GG), black gram (BG), pigeon pea (PP) and bengal gram (CD) were fractionated sequentially through 850, 710, 355, and 250µm sieves. The aspirated fraction of 850 and 710µm sieves were combined to obtain husk fraction. The total protein, calcium, bio-accessible calcium, and phytic acid contents were estimated in all the fractions using standard methods. Calcium-chelating activity of protein extract from each fraction was also determined.

The results showed that the fraction B of GG had highest protein content (32.89%) along with highest in-vitro calcium bio-accessibility (21.97%), which was independent of total calcium content of the fraction. Furthermore, the study suggested that the protein might reduce the calcium-chelating action of the phytic acid as the phytic acid content (1.18g/100g) was the highest in this fraction. Variations in the functional properties of by-products protein extracts suggest their potential utility in development of desired food products. Further, characteristics of the protein extract from different fractions and their chelating activity shows their promising role as food ingredient.

S8.5: Towards Mitigating Malnutrition in Pulses through Biofortification

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Global human population is suffering with the problem of malnutrition specifically children and women. The growing malnutrition results in weaken the human health and their functioning system which becomes more sensitive to attack of several diseases or may lead to death in many cases. To eliminate these nutritional deficiencies pulse grains are considered as an imperative source as these contains an ample amount of proteins, carbohydrates, fat, vitamins and various micronutrients like Zn, Fe, Se etc. Pulses are also effective towards reducing the risks of coronary heart disease. Pulses are rich in bioactive compounds such as phytochemicals and antioxidants that may contain anti-cancer properties. Phytoestrogens may also prevent cognitive decline and reduce menopausal symptoms. Public health authorities recommend pulses as part of healthy diets and a key food group for preventing non-communicable diseases and optimizing health. It is important that pulses are consumed by all categories of population: low-income and wealthy groups and in all countries – developing, with transition economies and developed. Pulses may be stored in dry places for long periods. Moreover, the proportion of food waste at the consumption stage due to spoilage is very low therefore pulses are a very good option for household food security. Even though, there is urgent need to enhance the concentration of these micronutrients in pulse grain to ensure the intake of a consistent and sufficient amount of all essential elements in food on regular basis. Malnutrition is a result of eating too little, too much or eating an unbalanced diet that does not contain the right quantity and quality of nutrients to be healthy. For human being 18 nutrients are identified as essential. Although, more than 22 mineral nutrients are required by the human body for its normal function. Zinc and iron deficiencies are a growing public health and socio-economic issue, particularly in the developing world. Biofortification have a key role towards enriching pulse grain in essential nutrients during the crop growth period. Biofortification of grain pulses is a new public health approach to control vitamin A, iron, and zinc deficiencies more specifically in poor countries. It is a sustainable way, and it can reach undernourished populations in remote areas. In all the pulse crops, it is possible to combine the high micronutrient density trait with high yield, economically.

S8.6: Biofortification of Zn and Fe in lentil through agronomic intervention

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Micronutrients are important growth promoting elements not only for crops but also for human being. For developing countries like India, micronutrient malnutrition among the people of every age is very common. The impact is highly seen in poor and landless rural people who can't afford diverse foods or supplements in their diets with needed nutrients. To alleviate this micronutrient deficiency, biofortification has come to the surface as a potent option. Biofortification of crops can increase the level of micronutrients in final food products. Pulses are the cheapest sources of proteins, vitamins and micronutrients especially Zn and Fe and can be supplied to the people through daily diet. Agronomic biofortification is the effective way to reach the poorest of the poor rural masses to enhance the composition of desired nutrient in their diet. Hence the role of agronomic biofortification in solving hidden hunger or micronutrient malnutrition is tremendous. Biofortification of pulses through inventive agronomic interventions, viz. seed priming, foliar fertilization and soil application could be a faster, easy and attractive measure to add micronutrient concentration in the human diet. Among ferti-fortification strategies, soil and foliar methods are established practices, but cost cutting and procuring high-quality micronutrient fertilizers are a major concern in developing nations. However, micronutrient application through seed priming not only improves germination, stand establishment, plant vigour, and yield but also micronutrient concentration in the grain. The effectiveness of ferti-fortification largely depends on crop genotype, soil type, soil fertility, cropping system, environmental factors etc.

S8.7: Vegetable Soybean: A crop with enormous potential

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Vegetable soybean (edamame) [*Glycine max* (L.) Merrill] is an excellent source of plant-based protein (38-42%) containing all the essential amino acids, phosphorus, iron, zinc, thiamine, riboflavin, vitamin-E, dietary fiber, higher isoflavones and sucrose content (8-12%). Vegetable soybean offers numerous health benefits like strengthening bones, improving lung function, maintaining healthy skin, reducing the risk of cardiovascular diseases and breast cancer. The lower trypsin inhibitor levels and lower cell density makes it more digestible than grain type soybean with only a shorter cooking time. Vegetable soybean is a short duration crop as it is harvested at an immature stage, i.e., R6 (full seed stage) when the pod cavity is completely filled but the pod shell is still green. As a legume crop, vegetable soybean is a low input, soil- enriching crop that can help farmers to minimise insect-pest and disease attack in the farm and will have long-term effect for agricultural sustainability. Despite of its nutritional and medicinal values, the crop is less preferred by consumers due to its 'beany flavor' which is majorly due to the enzymatic oxidation of linoleic acid and linolenic acid by lipoxygenase genes (Lox). It also contains several anti-nutritional factors like trypsin inhibitors, saponins, lectins, phytases and lipoxygenases which are biologically active and need to be eliminated prior to human consumption. It is also not much popular due to lack of awareness, lack of industries and less availability of commercial seeds. Therefore, the development of bio fortified varieties with less anti-nutritional factors and cultivars resistant to diseases and pests will certainly help to stimulate edamame production and its utilization in domestic as well as international market. Widespread introduction of vegetable soybean in India would be ideal to help combat malnutrition, particularly of protein and iron deficiencies.

S8.8: Genotype × environment interactions effect on grain iron (Fe) and zinc (Zn) concentration in pigeonpea [*Cajanus cajan* (l.) millsp.] using AMMI model

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Billions of peoples are directly affected from the micronutrient malnutrition called hidden hunger affecting one in three people. Micronutrient Iron (Fe) and zinc (Zn) deficiencies affect large numbers of people worldwide. Iron (Fe) deficiency leads to maternal mortality, mental damage and lower disease resistance of children. Likely Zinc (Zn) deficiency is responsible for stunting, lower respiratory tract infections and malaria and diarrhea disease in human beings. Keeping the biofortification in sight, the twenty pigeonpea genotypes were evaluated to analyze genotype × environment interaction for iron and zinc concentration in the seeds across three locations *i.e.* Vijayapur, ICRISAT (Patancheru) and Kalaburagi. Pooled analysis of variance over locations displayed highly significant (P=<0.001) differences between genotypes, environment and genotype × environment interaction for Zn and Fe micronutrient. Among 20 genotypes, the ranges for seed Fe concentration across location was 32.19 mg/kg (ICPL 161) to 34.63 mg/kg (ICPH 2447) and for seed Zn concentration it was 31.02 mg/kg (ICPL 161) to 35.93 mg/kg (ICPH 2441). AMMI stability model was used for G × E interaction study, AMMI 1 and 2 biplots revealed that genotypes ICPH 2429 and ICPH 4686 were stable for the Fe concentration in seeds and genotypes ICPH 2438 and ICPH 2447 were stable for the Zn concentration in seeds. Based on AMMI stability value, genotypes namely ICPH 2429, ICPH 2441 and ICPH 3314 for Fe concentration in seeds and ICPH 2438, ICPH 3314 and ICPH 4689 for Zn concentration in seeds ranks top three for their stability across the locations.

S8.9: Insights into the biochemical basis of pod shattering in common bean (*Phaseolus vulgaris* L.) from Western Himalayas

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Pod shattering is the one of the important domestication syndromes. From an agricultural perspective it is generally an undesirable process, and in common bean, pre-harvest shattering loss is the major form of yield loss by shattering. Thus, deciphering the physical, biochemical and genetic basis of pod shattering is important to unravel the mechanisms of parallel evolution and also because this will provide breeders with key information to manipulate this trait to reduce yield loss. There are only few published records are available in common bean. In the present study a core set of 254 lines were evaluated for shattering response using Random Impact Apparatus. Based on the shattering response using a random impact assessment 40 contrasting lines were selected for biochemical analysis. Pod lignin content range from of 3.83 to 17. 08 mg/g, pectin content ranged from 5.17 to 29.44 per cent. Cellulose ranged from 11.51 to 39.08 per cent, whereas electrical conductivity ranged from 296.33 to 1012.15 ds/cm. Among trait associations, shattering score was negatively correlated with various pod biochemical traits including cellulose (-0.453), followed by starch (-0.424), lignin (-0.323) and pectin (-0.187) with no substantial relationship with EC. Lignin, pectin, cellulose and starch content in bean pod were significantly higher in the resistant genotypes compared to susceptible genotypes, whereas reverse relationship was observed in case of EC content. The results in this study suggested that the chemical analysis of dry pod shell may provide useful information on breeding and selection of the shattering resistant cultivars in common beans.

S8.10: Genetic variability for seed morphology and protein content in field pea (*Pisum sativum* (L.) germplasm

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Field pea (*Pisum sativum* L.) often known as dry pea is one of the important pulse crops grown in India, famous for its protein-rich diet. Seed traits are important components which play an important role both in varietal identification and in deciphering trait association. One hundred sixty genotypes were examined for five seed morphological traits *viz*., seed surface, seed cotyledon colour, testa mottling, seed shape and hilum colour along with seed size and protein content. Among the test genotypes 145 had smooth while 15 showed wrinkle seed surface. Based on seed cotyledon colour, the genotypes were divided into four classes *viz*., brown (03), cream (125, green (24) and yellow (08). Majority of the genotypes did not show testa mottling (132) and hilum colour (151). There was only one genotype (EC598649) showing cylindrical shape while 9 had dimple and remaining had spherical shaped seeds. Based on 100 seed weight, twelve genotypes were classified as large seeded (>20g), fifty-four as medium (15-20g) and remaining eighty-five as small (<15g) seeded genotypes. The seed protein content among the 160 field genotypes varied significantly. The range of seed protein was between 15.23 per cent and 39.44 per cent with a mean of 20.55 per cent. The highest seed protein content was recorded in the genotype IC398023 (39.44 %), followed by IC279142 (37.85 %) whereas, lowest was found in EC598609 (15.23 %). The superior genotypes may be utilised in field pea improvement programme based on their association with other desirable traits.

S8.11: Assessment of biofortified dry bean lines for agronomic performance and seed micronutrient attributes in India

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The common bean (*Phaseolus vulgaris* L.) is a vital source of protein and minerals (iron and zinc) for millions of people in developing nations including India. In this study, a panel of diversity encompassing 101 biofortified lines collected from CIAT gene bank, Colombia, and five Indian elite cultivars was evaluated for agronomic performance and seed micronutrients (iron, & zinc) concentration in augmented block design by utilizing three check varieties, Arun, Uday and Amber. Results indicate a wide range variation of agronomic traits and allowed the identification of accessions reasonably carrying favourable trait combinations. The analysis of seed micronutrient (Fe & Zn) indicated substantial variation for these minerals in biofortified bean lines. It was found that the iron concentration of seed ranges from 62.10 to 185.10 mg/kg, with a mean value of 94.25 mg/kg and zinc concentration of seed having mean value of 38.24 mg/kg, with a range of 24.08 to 84.35 mg/kg. Furthermore, promising 30 genotypes were streamlined out of 109 bean lines were evaluated for seed micronutrients. Many of the improved lines assessed in this study had higher nutritional contents than existing cultivars, indicating the possibility of producing new biofortified cultivars.

S8.12: Interrelationship study among pod yield and nutritional quality traits in lablab bean [*Lablab purpureus* (L.) Sweet]

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Lablab bean [*Lablab purpureus* (L.) Sweet],an important legume of eastern India, has remained less focused for research purposes. Keeping in view of its enormous potential as a nutrient-rich crop, a research was conducted at ICAR-Research Complex for Eastern Region, Patna to assess the variability and correlations among pod yield and nutritional quality traits in lablab bean. Twenty five genotypes (collected from diverse geographical area) were evaluated in augmented block design during *Rabi*2020-2021. Data were recorded on twenty-two horticultural and nutritional quality traits. A wide range of variation was observed for the traits under study. Based on *per se* performance, four promising genotypes were identified. The genotype RCPD-1 was identified as high yielder (105-110 pods/plant) with bushy plant type, pods of which contained high protein (23.74g/100g), iron (5.97mg/100g), zinc (2.59mg/100) and phosphorous (460mg/ 100g).RCPD-2 was identified asa good source of iron (10.5mg/100g) and calcium (408mg/100g). RCPD-3 was prolific bearer with highest vitamin A content (30.85mcg/100g). The genotype RCPD-24 was identified as a good source of antioxidant (87.7% and 86.74% for DPPH and ABTS, respectively). We also performed amino acid profiling of RCPD-1. Among essential amino acids, threonine wasthe most abundant (4.53±0.39g/100g) followed by isoleucine (2.44 ±0.17g/100g). Significant positive correlations of number of pod per plant were observed with phosphorous content and antioxidants (DPPH and ABTS content) and of protein with zinc and phosphorous content. This indicated the potential of multiple trait selection. The information generated on interrelationship of pod yield and nutritional traits is unique in lablab bean.The outcomes of this study maybe applied tofurther improvement of yield and nutritional quality traits of lablab bean.

S8.13: Insights into phenolic composition and antioxidant potential of common bean (Phaseolus vulgaris)

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The seed coat of pulses is rich in phenolic compounds and manifests potent antioxidant activity. The immense genotypic variability for seed coat colour in common beans (*Phaseolus vulgaris*) presents an exciting research area which can be harnessed to identify genotypes with unique phenolic profiles and superior antioxidant potential. Fifty common bean genotypes of different seed coat colours were investigated for their total phenolic content (TPC), total flavonoid content (TFC) and condensed tannin content (CTC).Antioxidant activities were assessed usingdifferent antioxidant assays i.e., FRAP, CUPRAC and DPPH and phenolic compounds were quantified using HPLC. The TPC, TFC and CTC varied significantly among genotypes and ranged from 0.4 to 3.27 mg GAE/g seed, 0.1 to 1.8 mg CE/g seed and 0.57 to 2.99 mg TAE/g seed respectively.The antioxidant activity of these genotypes varied from 0.39 to 5.12 mg TROLOX Eq/g seed and the bluish-black cultivar EC 932147 was found to have the highest antioxidant activity. Free and bound phenolics from each common bean cultivar were extracted and the phenolic profilewas explored. Gallic acid, proto-catechuic acid, p-coumaric acid, ferulic acid, sinapic acid, ellagic acid, catechin hydrate, myricetin, quercetin and kaempferol were detected in common bean cultivars. The polyphenol ellagic acid, and the flavonolsmyricetin, quercetin and kaempferol were detected in only a few cultivars. Among all genotypes, the black-seeded cultivar EC 931743 showed the most diverse phenolic profile. The findings of this research can be utilized in plant breeding and also for the development of antioxidant-enriched pulse-based functional foods.

S8.14: Physiological upscaling of crop response of Chickpea (*Cicer arietinum* L.) with hormonal and nutritional interventions

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Chickpea (*Cicer arietinum L.*), known as the 'King of Pulses', is the third most important protein-rich pulse crop. Regulation of plant growth is largely mediated by plant growth regulators which play a key role in metabolism. Paclobutrazol is a growth retardant and its use in appropriate time and concentration can improve yield by favourably partitioning the assimilates. The micronutrient like boron (B) plays an important role in photo assimilate translocation and improves flower retention, pollen fertility, germination, pod setting and development. Ethylene (C_2H_4) has an influential role in initiating senescence of the vegetative organs and remobilization of assimilates therefrom to the sink organs like developing seeds. The present investigation was done to study the effect of paclobutrazol, boron and ethylene on different phenological, biochemical, yield and yield attributing traits in chickpea (variety JG-14). The treatment method considered varied concentrations of paclobutrazol, boron, ethylene and their combinations applied as foliar. Analysis of data revealed significant difference between the treatments. It was found that pod weight per plant was recorded highest in the treatment having paclobutazol@ 90ml/ha + boron@ 0.5%. Seed yield showed highly significant correlation with seed protein content, seed soluble sugar and seed starch.Highest seed weight and yield was recorded for the treatment containing paclobutrazol@ 90ml/ha + boron@ 0.5% + ethylene @500gm/ha.A combination treatment of boron @0.5%/ha. + paclobutrazol @ 90 ml/ ha can be used for higher seed/pod of this chickpea variety (JG-14).

S8.15: Insight into the biochemical basis of delayed cooking trait in Western Himalayan common beans (*Phaseolus vulgaris* L.)

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Cooking quality is an important determinant of bean cultivar acceptability by farmers and consumers and has assumed greater importance in view of energy costs of cooking process. In the present study 40 contrasting bean genotypes based on cooking time score were analyzed for biochemical parameters viz., amylose-amylopectin ratio, lignin, pectin, cellulose, crude fiber. Wide range was recorded for the biochemical parameters viz., amylose/amylopectin ratio (0.50 to 0.96 mg/g), lignin (7.22 to 35.76 mg/g), pectin (27.63 to 39.12 mg/g), cellulose (10.02 to 46.67 %), crude fiber (3.33 to 13.33 %). Cooking time score was positively correlated with cellulose (0.688), followed by crude fiber (0.655) and negatively correlated with pectin (-0.59), followed by lignin (-0.51). Among other traits lignin was positively correlated with pectin, crude fiber was positively correlated with cellulose and negatively correlated with lignin. PCA concentrated 57.8 % variability in the first two principal components with eigen value greater than unity. The biplot constructed based on first two PCs revealed the trait relationship of biochemical parameters with the cooking time score. In terms of biplot cooking time score was significantly correlated with crude fiber, cellulose while negatively correlated with lignin, pectin. Comparative analysis revealed that genotypes with longer cooking time has higher pectin and lignin than easy to cook beans, whereas, reverse was the case in case of cellulose and fibers. The present study established the biochemical basis of delayed cooking trait in common bean and can be used for high throughput screening for large germplasm sets.

S8.16: Bioactive compounds in fractions of milling byproduct from urdbean

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Urdbean is consumed as whole, split with husk or in form of dehusked splits, i.e., dal. Due to strong bond between seed coat and cotyledons, milling of urdbean is done with abrasive dehusking rollers. In multiple passes for maximum dehusking, cotyledon powder gets mixed with outer husk, and milling byproduct is generated. In the study bioactive compounds, viz., protein, phenol, antioxidant and fibre, of milling byproduct and its fractions, were determined for two urdbean cultivars, namely, IPU-11-02 and IPU-94-1, to explore potential for edible usage. Calorific value was also determined. In this study, water treated urdbean varieties were milled in abrasive emery roller. Milling byproduct obtained was fractionated into three particle sizes, i) >1.0 mm, ii) >0. 25 mm and iii) <0.25 mm. Protein, phenol, antioxidant and fibre for each fraction were determined using Lowry, CUPRAC, Folin-Ciocalteu Assay and IS-11062 methods, respectively, for whole grain, dehusked dal and byproduct fractions. From the milling byproduct cotyledon powder (<0.25mm) can be extracted. The cotyledon powder obtained from milling byproduct has higher protein content than dehusked dal. The faction >1.00 is rich in phenol, antioxidant and fibre. Difference in calorific value of each fraction was not significant. The results indicate that milling byproduct from urdbean can be utilized for edible purposes.

S8.17: Genetic enhancement for nutritional qualities in grain legumes

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Grain legumes are 2nd most consumed food crop after cereals. It is also known as "Poor man's meat". Legumes are an integral component of the human food because they provide low-cost, nutrient-rich proteins, vitamins, and minerals, and aid in preventing chronic diseases. Among the legume crops, grain legumes contribute nearly 27 per cent of the world food production and act as the single largest source of vegetable protein (~33%) in the human diet. Due to issues like malnutrition and hunger, which is more prevalent in current world, discussion on enhancing the nutritional qualities gains more importance at their juncture. Main nutritional qualities in grain legumes are rich in carbohydrate, high source of protein, dietary fiber, low glycemic index and storage of micronutrient but anti-nutritional factors also present in grain legumes like enzyme inhibitor, lectins, phenolic compounds and phytic acid. Approaches for improvement of nutritional profile through dietary diversification, food fortification, food supplements and food biofortification. Conventional breeding approaches like introduction, pure line selection, recombinant breeding, mutation breeding, ideotype breeding and modern breeding approaches like QTL mapping and introgression, marker assisted selection, genome editing, transgenic breeding are tactics used for nutritional qualities improvements in grain legumes. Considerable work has been done in this direction like chickpea line IPC-2005-62 with 26.7% protein content released for commercial cultivation, Ipa-280-10 pea mutatnt show 90% reduction in phytic acid content, Pusa Vaibhav, Pusa Ageti masoor & IPL 220 varieties are biofortified lentil for Fe and Zn micro-nutrient trait.

S8.18: Biofortified Pulses: An Option to Alleviate Dual Problem of *Hidden Hunger* and Nutritional Insecurity

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Hidden Hunger is posturing threat to more than half of the world's population. In reality, the diets of a large part of the world's population are deficient in Fe, Zn, Ca, Mg, Cu, Se or I, which affects human health and nutritional security. Since, biofortified plants have the greater potential to nourish nutrient-depleted soils; help increase crop quality, productivity; and provide nutritional benefits. Biofortification of pulses through inventive agronomic interventions viz; seed treatment (seed priming and seed coating); foliar fertilization and soil application could be a faster, easy and attractive measure to add micronutrient concentration in the human diet. Research efforts made at Jodhpur also confirmed the genotypic variation in the mungbean, wherein, genotype 'GM 4' substantially fetched higher Zn concentration in grain (46.6 mg/kg) and stover (36.0 mg/kg). Application of Zn at 6 kg/ha to mungbean added significantly higher Zn concentration in grain (39.6 mg/kg) and stover (29.2 mg/kg). Among breeding approaches of biofortification, use of high zinc and iron containing pulse genotypes under breeding programme for developing biofortified pulses is proved an effective measure. Some pulses genotypes rich in Zn and Fe viz; lentil 'IPL 220' (62-63 mg Zn and 87-112 mg Fe/kg seed), mungbean 'ML 803' (38 mg Zn/kg seed), mungbean 'HUM 1' (89 mg Fe/kg seed) and cowpea 'Pant Lobia 1' (40 mg Zn and 82 mg Fe/kg seed) will be marvellous in developing biofortified pulses. Therefore, breeding and agronomic approaches of biofortification are the solution to alleviate hidden hunger and ensuring nutritional security.

S8.19: Evaluation of advanced breeding lines of chickpea for parching quality in various soaking media

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Chickpea is a *Rabi* season annual legume crop with 738 Mbp genome size. Malnutrition is affecting the young children causing stunting and lower BMI in developing countries like India. Under such circumstances, chickpea can serve as a rich source of protein to fulfill their dietary needs. Therefore, the present investigation has been undertaken to evaluate the performance of advanced breeding lines of chickpea for parching quality. In order to assess the safe method for parching in chickpea different soaking medias were used such as NaCl, NaOH, Na_2CO_3, without soaking and $Ca(OH)_2$ at 2.5%. The soaking of chickpea seeds were carried out for 15 minutes at room temperature. The drained seeds were air dried and parched at 240p C for 1 minute. Among all the soaking media $Ca(OH)_2$ performed best with golden yellow color and pleasant taste for parching quality while the other treatments NaOH and Na_2CO_3 showed poor result with dark yellow color appearance and less puffing size for the advanced breeding lines of chickpea. The results showed that parching helped in significant reduction of seed mass and increase of the seed volume. The parched chickpea will somehow reduce the protein malnutrition in children in the developing countries in the upcoming future.

S8.20: Processing Interventions for the Reduction of Anti-Nutrients Factors in Pulses

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Pulses are important source of protein in our daily diet. However, the nutritional value of legumes and pulses may be adversely affected by the presence of several anti-nutritional factors (ANFs) such as phytic acid, saponin, tannin, flavonoids, trypsin and chymotrypsin inhibitors and oxalates etc. These toxic substances reduce their nutritive value by chelating minerals, proteins and other nutrients and inhibiting their digestibility and utilization. These compounds acted as inhibitors to block the function of digestive enzymes (proteases) in animals, as bind to receptors in the intestinal tract and related organs or inhibit protein biosynthesis, as bind to micronutrients (Mg, Ca and Fe) lowering its bioavailability leading to foetal malformations, neurotoxic disturbances, and cardio-vascular diseases etc. There are various traditional methods and technologies, which can be used to reduce the levels of these anti-nutrient factors. Several processing techniques and methods such as fermentation, germination, debranning, autoclaving, cooking, roasting, ultrafiltration and high pressure processing soaking etc. are used to reduce them. Soaking the seeds in plain water and mineral salt solution for 12 h decreased phytic acid to the maximum (46–50%). Cooking results in increase of protein and starch. It also inactivate trypsin inhibitor activity, reduce phytic acid, tannin and oligosaccharide content. In Extrusion cooking, the process can easily deformed proteins as high temperature and shear force is applied. The combination of soaking, sprouting, cooking and fermentation appeared to have beneficial effects which improve the nutrient quality and reduce ANFs to safe levels.

S8.21: Effect of microwave heating as pre-treatment for milling of pigeonpea

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Pigeonpea is mostly consumed in the form of dehusked splits, i.e., dal. Due to gum content and strong adhesion between seed coat and cotyledons, milling of pigeonpea is considered as difficult-to-mill kind of pulse. Dehusking operation is performed with the help of emery coated abrasive rollers. Different pre-milling treatments are employed to loosen the husk of pigeonpea. In the present study, microwave heating was explored as pre-treatment of pigeonpea. Pigeonpea grains were heated using microwave oven at the exposure time of 30, 60, 90 seconds at 300, 600 and 900 wattage levels to know the effect of microwave on the milling recoveries of pigeonpea. Cleaned and graded pigeonpea were treated with microwave and milled in a lab scale universal grain testing mill in single pass. Milling was performed with emery disks of different grit sizes, coarse, medium and fine, for the experimentation. The Box-Behnken experimental design (Response Surface Methodology) was used experimentation and data analysis. The results indicated that coarse emery though gives better dehusking efficiency but result into powdering losses, whereas low dehusking was observed with the fine emery grits. Medium grit size gives the higher dal recovery in comparison to coarse and fine emery grits.

S8.22: Genetic studies on seed size and protein content in chickpea [*Cicer arietinum* (L.)]

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Pulse crops are a valuable source of dietary protein, especially in developing countries. Appearance of seed is a key market factor in chickpea and acceptability varies with cultural preference. Seed size, having a direct relationship with seed weight in chickpea, is one of the important growth parameters to consider for enhancing yield. Eighty nine genotypes were evaluated for seed size, based on hundred seed weight (g) and seed protein. There was a wide variability for seed size among the genotypes under study having hundred seed weight range between 4.2 g (ICC 11551) and 42.1 g (ICCV 0510) with an average seed size of 22.1 g. Both GCV (36.91%) and PCV (37.19%) estimates were high with high heritability of 98.54 per cent, moderate GA (16.60) and high GAM (75.49%) for the trait. The seed protein content among the test genotypes varied significantly and it ranged from 12.88 per cent (AKG 58) to 23.10 (SA-1) per cent with a mean of 20.46 per cent. The trait exhibited low GCV (2.23%) and PCV (2.97%) and showed moderate heritability (56.35) with low GAM (3.45%). The four genotypes, ICCV 05107, BGD 223-1, S3-3 and PUSA 244, promising for productivity, seed size and protein content were identified. The genotypes contrasting for seed traits may serve as parents in development of mapping population in *desi* chickpea and the genotypes with high seed protein coupled with bold seeds can be utilized in breeding for quality traits.

S8.23: Progress in Urdbean Biofortification Research for Iron and Zinc concentration

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Urdbean is a profoundly growing pulse crop in India and can be a global food legume due to its rich nutrient profile. Enhancing the nutrient status of this crop species for the high concentration of iron and zinc is required to combat micronutrient malnutrition. In a recent study, 83 urdbean genotypes of diverse origins were evaluated for iron and zinc concentrations. Analysis of variance found that genotype effects were significant for both traits over both locations. Iron concentration ranged from 19"235 mg/kg (mean 117 mg/kg) and 16"255 mg/kg (mean 91 mg/kg) among evaluated genotypes at the first and second locations, respectively. For zinc concentration, it ranged from 5"134 mg/kg (mean 44 mg/kg) at the first location, while at the second location it was between 12"59 mg/kg (mean 29 mg/kg). For high iron concentration, the most stable urdbean genotypes (PU 31 and IPU 99"43) were identified. Similarly, highly stable genotypes for the high concentration of zinc were BGP 28 and HPU 120. Similarly, in another study, a set of urdbean genotypes of diverse origins were validated as high sources for iron and zinc concentrations based on replicated field trials. The mean value of Fe and Zn concentrations were 97.1 mg/kg and 14 mg/kg, respectively, over the locations. Fe and Zn concentration ranged between 86.7 (LBG-787) to 116 (WBU-108) mg/kg and 11.2 (VBN-7) to 18.2 (IPU99–79) mg/kg, respectively. Proximate parameters like moisture, protein, fat, ash, total fiber, and total carbohydrate contents were 11.5, 25.3, 1.1, 2.95, 13.9, and 57.5%, respectively. The phytic acid content was stable over the locations, ranging from 13.7 mg/g to 14 mg/g for the tested urdbean genotypes. In this study, genotype, PLU 429, which had Fe concentration ranging between 81.6 and 93.5 mg/kg, is a superior genotype with the lowest PA content (10 mg/g) over the three test locations. Fourier Transformed Infrared Spectroscopy profiling detected three urdbean- specific sharp peaks. In GGEBiplot analysis, the most stable urdbean genotypes with high Fe concentration were PU-30 (102 mg/kg) and Shekhar 2 (105 mg/kg), and Zn concentration WBU137–2 (15.2 mg/kg) and UH85–5 (15.4 mg/kg) were having high concentration as well as comparatively higher stability. Now, these high Fe and Zn lines are used in hybridizations.

S8.24: Strategies for Identifying Stable Lentil Cultivars (*Lens culinaris* Medik) for Combating Hidden Hunger, Malnourishment, and Climate Variability

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Micronutrient deficiencies (Fe and Zn) remain common between many children under the age of five in developing and under developed nations, irrespective of the fact that many important preventative approaches are now available. This type of malnutrition can have a number of urgent and long-term repercussions, such as stunted growth, an increased risk of infectious disease, and poor development consequences, all of which might ultimately led to a child not reaching his or her complete potential. The stable cultivars of lentils, which are rich in micronutrients, may address the problem. Understanding the genotype and environmental parameters that affect G E interactions is essential for plant breeding. We used GGE and AMMI (additive main effects and multiplicative interaction) models to study genetic stability and GE for grain Fe, Zn, Al, and anti-nutritional factors like phytic acid content in sixteen commercially produced lentil cultivars over several different six geographical locations across India. Significant genetic variability was evident in the Fe and Zn levels of different genotypes of lentils. The amounts of grain iron, zinc, and phytic acid varied from 0.76 to 2.84 g/100g (dw), 114.10 to 49.90 mg/kg, and 74.62 to 21.90 mg/kg, respectively. The environment and GE had an impact on the concentration of grain Fe, Zn, and phytic acid (PA). Heritability estimations ranged from low to high (53.18% to 99.48%). The study indicated strong correlation between the contents of Fe and Zn, a strategy for simultaneously increasing Fe and Zn in lentils may be recommended. Our investigation also revealed the stable and ideal genotype L4076 (Pusa Shivalik) for Fe concentration and L 4717 for Zn content (Pusa Ageti), these will play vital role as stable donors in the lentil bio-fortification.

S8.25: Agronomic fortification of pigeonpea with Zinc and Iron

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The field experiment was conducted on deep black soil of Agril. Research Station, Badnapur during *kharif,* 2021 with variety BDN-711 in Randomized Block Design in three replications. It consisted total 8 treatments *viz.,* T_1: RDF (Absolute control), T_2: soil application of 25 kg $ZnSO_4$, T_3: soil application of 5 kg $FeSO_4$, T_4: soil application of 25 kg $ZnSO_4$ + 5 kg FeSO4,T_5: foliar application of 0.50% $ZnSO_4$ at flower and pod initiation, T_6: foliar application of 0.50% $FeSO_4$ at flower and pod initiation, T_7: foliar application of 0.50% $ZnSO_4$ + 0.50% $FeSO_4$ at flower and pod initiation and T_8: Water spray (control). The experiment was sown on 01st July 2021, using 90 x 20 cm^2 spacing. The gross and net plot sizes were 5.4 x 5.0 m^2 and 3.6 x 4.6 m^2 respectively. The fertilizers were applied as per recommendation. Similarly crop protection measures were adopted as per necessity. The trial was harvested on 23/12/2021 and threshed on 24/12/2021. The data on seed yield was statistically analyzed. Results revealed that foliar application of 0.50% $ZnSO_4$ + 0.50% $FeSO_4$ at flower and pod initiation along with recommended NPK recorded significantly higher seed yield of pigeonpea than rest of the treatments, however, it was on par with soil application of 25 kg $ZnSO_4$ + 5 kg $FeSO_4$. Gross returns and net returns followed the same trend. Significantly highest B:C ratio was recorded by treatment receiving foliar application of 0.50% $ZnSO_4$ + 0.50% $FeSO_4$ at flower and pod initiation.

S8.26: Fortification of Zinc and Iron through foliar spray in mungbean

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The field experiment was conducted on deep black soil of Agricultural Research Station, Badnapur during *Kharif,* 2021-22. The experiment was laid out in Randomized Block Design with three replications. The treatments comprised of T_1: 0.5% $ZnSO_4$ spray at flower initiation, T_2: 0.5% $ZnSO_4$ spray at flower & pod initiation, T_3: 0.5% $FeSO_4$ spray at flower initiation, T_4: 0.5 % $FeSO_4$ spray at flower & pod initiation, T_5: 0.5 % $ZnSO_4$ & 0.5 % $FeSO_4$ spray at flower initiation, T_6: 0.5 % $ZnSO_4$ and 0.5 % $FeSO_4$ spray at flower & pod initiation, T_7: 25 kg $ZnSO_4$ through soil application and T_8: 5-10 kg $FeSO_4$ through soil application. The gross plot size was 5.4 x 5.0 m^2 and net plot size was 4.8 x 4.8 m^2. The sowing was done on 05/07/2021 by using BM 2003-2 variety. The fertilizer doses were applied as per treatments. Similarly, crop protection measures were adopted as per the recommendations. The crop was harvested on 22/09/2021. The various treatments statistically influenced seed yield of mungbean. Application of 0.5 % $ZnSO_4$ and 0.5 % $FeSO_4$ spray at flower & pod initiation produced significantly higher seed yield of mungbean which was found on par with an application of 0.5 % $ZnSO_4$ & 0.5 % $FeSO_4$ spray at flower initiation. Similar trend was observed in respect of gross monetary returns, net monetary returns and B:C ratio.

S8.27: Genotypic response of chickpea cultivars to different zinc management regimes

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A field experiment was conducted during *rabi* season of 2021-22 at new research farm ICAR-IIPR, aiming to identify best genotypes in chickpea for higher internal zinc (Zn) use efficiency. For this, 25 chickpea genotypes were grown in three levels of zinc gradients/management *i.e.* (i) control, (ii) soil application of $ZnSO_4$ at 25 kg/ha and (iii) foliar spray of 0.5% $ZnSO_4$ at the pre-flowering and pod formation stages. There is large genotypic variation in plant Zn uptake and seed Zn concentration in the collection of chickpeas. The internal Zn use efficiency index ($IUEI_{Zn}$) of the selected genotypes varied between 0.4 to 1.7. The genotypes JG 16, GNG 2171, and IPC 10-62 were found to have increased response to soil application of Zn (38.2 % IUE_{Zn} higher over average value); while the genotypes, GNG469, Vijay, and GNG 2171 exhibited higher IUE_{Zn} (32.9 %) over the mean value of all genotypes in response to foliar application. Vijay, GNG 469, JAKI 9218, GNG 2171, RSG 888 were categorized under both Soil and Foliar Zinc Responsive Genotypes based on IUE_{Zn} of soil and foliar application. Overall zinc uptake data of all the chickpea genotypes tested in these experiments shows an average zinc uptake of 14.6% and 43% higher in soil and foliar applications respectively, in comparison to no application of zinc (Control). Breeding initiatives for chickpeas with high zinc input efficiency can employ this germplasm. This helps to execute environmentally responsible farming methods while maximizing the potential of marginal soils.

S8.28: Development and evaluation of ready to use therapeutic foods from pulses for severely malnourished children

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The Ready to Use chewy bar was prepared by the addition of selected pulses cowpea/ green gram/ soy bean / horsegram (15%). The sugar syrup was prepared and boiled till it reaches 115°C. To the sugar syrup pulse mixture, milk powder and butter, dried amla (5%) and moringa powder (5%) was added and mixed well so that no lumps were formed and then transferred to grease plate and cut into desired shapes and allowed to cool. The products were then sealed and stored for further studies. The product obtained highly acceptable sensory scores for color, texture, flavor, Taste and over all acceptability. The nutrient quality of the product was on par with the emergency ration. The minerals and vitamin requirement were partially met by the amla and moringa powder added.

S8.29: Biofortified pulses: A solution to malnutrition by enhancing the nutritional value

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Pulses and legumes belong to family *Fabaceae* which are chickpeas, mung beans, soybeans, peas etc. Pulses are rich source of plant protein in many diets. They are also rich in dietary fibres and complex carbohydrates resulting in low glycemic index. The high lysine and folate content makes pulses perfect for making composite flours with cereals. Fortification is addition of essential micronutrients including minerals to improve its nutritional quality. With the help of biofortification, the nutritional value of pulses and legumes can be increased by using different breeding techniques, agronomic approaches and transgenic methods. Biofortification with genetic engineering approach is an alternative when variation in desired traits are not available in natural germplasm. Along with increasing the concentration of micronutrients, this approach can also be used for removal of antinutrients that can enhance bioavailability of micronutrients. Like with the help of genetic engineering approach, the concentration of essential amino acid methionine was significantly increased in transgenic common bean plants. Recently CRISPR technologies has also been used to generate mutant lines in *Glycine max.* Thus, biofortified pulses help in reducing malnutrition among the population. The Food and Agriculture Organization of the United Nations designated 2016 as "International Year of Pulses" with an aim to enhance public awareness of the nutritional value of pulses and the global food security.

S8.30: Identification and characterization of the amino acid transporter gene family in chickpea (*Cicer arietinum*) and their involvement in seed storage protein accumulation

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Amino acid transporters (AATs) are crucial for the growth and development of plants because they are involved in transport of amino acids across the cellular membranes. The genome wide distribution of AAT gene family is not studied so far in chickpea (Cicer arietinum L.). We identified 109 AAT genes belonging to 10 subfamilies based on their phylogenetic locations and sequence composition. To delineate the roles of these genes, we studied the chromosomal distributions, cellular localization, gene structures, duplication patterns, conserved promoter motifs phylogenetic analysis and tissue expression patterns of the 109 AAT genes in chickpea. Comprehensive investigation of the CaAAT genes expression profiles in various vegetative and reproductive development phases revealed that chickpea AAT genes display preferential expression patterns in diverse tissues. Analysis of mature seed transcriptome data of two chickpea genotypes having significant differences in their total protein content lead to identification of 12 members of this family. Using qRT-PCR, 7 of these AATs members were validate showed similar kind of expression pattern as predicted by in-silico analysis, in Low Protein Content (LPC) as compare to High Protein Content (HPC). Using different bioinformatic tools we predicted the location of these AATs and found that most of the AATs are present on the plasma membrane. Our study provides insights on the putative biological role of AAT genes in chickpea, which will facilitate their functional characterization and role in various developmental stages, stress responses and involvement in nutritional quality enhancement.

S8.31 Effect of stages of harvesting and threshing methods on seed quality and storability of soybean [*Glycine max* (L.) Merrill] cv.Dsb-21

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Investigations were carried out to determine the most appropriate stage of harvesting and threshing method with minimal impact on seed quality characteristics of soybean seeds. The field experiment was conducted in 'H' Block of seed unit in two factorial randomised complete block design (RCBD) in three replications with the different treatments of harvesting soybean pods at 90, 100 and 110 days after sowing (DAS) and the threshing of seed crop was done by three methods viz., Stick beating, Tractor trampling and Mechanical thresher and storage experiment was conducted for a period of 180 days under the ambient condition in laboratory of the Department of Seed Science and Technology, University of Agricultural Sciences, Dharwad.

The results revealed that among harvesting stages, soybean harvested at 90 DAS recorded the highest germination (90.71%), seedling dry weight (1.30 g), vigour (2768), oil content (20.68%) and lower mechanical damage (11.16%), electrical conductivity (0.34 dS/m) and protein content (39.11%), Delayed harvest viz., 100 DAS and 110 DAS resulted in increased protein and seed leachates, mechanical damage and decreased oil content. Among threshing methods, beating with sticks proved superior for germination (92.70%), seedling dry weight (1.35 g), vigour (2850) and oil (20.10%), protein content (39.60%) and lower mechanical damage (10.16%). While, tractor trampling shown higher mechanical damage (15.71%), EC (0.38 dS/m) and minimum germination (85.65%), seedling dry weight (1.21 g), vigour (2508). During storage there was no significant difference in protein, oil and moisture content of seeds but EC increased and germination percentage, vigour were reduced in all the treatments. Results obtained indicated that for good seed quality, soybean pods should be harvested at 90 DAS and threshed by beating with sticks.

Key words: Minimal impact, Seed leachates, Vigour, Protein content

S9.1: Development of seed and product sale portal for digital marketing

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A Web-based seed and product sale portal for soybean has been developed to promote online marketing using the potential of information technology. The system is developed using ASP.NET at front end and SQL Server at back end. The system has provision for selling Breeder Seed, Foundation Seed, Truthfully Labeled (TL) Seed and Certified Seed. It also has a separate facility for selling different Soya based food products viz Tofu, Milk, Upma mix, Cookies, Sev, Laddu etc. The user can initially book the items to purchase. The booking is then confirmed by the authorized official and after this he can complete the payment process with the generation of payment receipt. The system is linked to E-payment gateway implemented at the institute to ease the financial transaction. It has a separate module to enter different products, its packaging size, cost, availability status etc. Thus, it can be easily customized for any crop. The system is functional and is available at institute website https://iisrindore.icar.gov.in. The user needs to complete the registration process to get login details for using the system. Farmers and different clienteles are using the system across the country and they are satisfied with the easy-to-use system interface. The development of the system has promoted the soya food uses among different clientele across India which was a bigger challenge earlier. Moreover, the seed sale platform has opened a single window for farmers to get a good quality seed of different popular varieties and thus led to a transparent seed distribution system.

S9.2: Digitalization in Chickpea Breeding Management in India

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Chickpea breeding efforts, dating back to more than a century, have significantly contributed to realization of record production of 13.75 MT in 2021-22 in India through development of high yielding, stress resistant varieties having desirable seed quality and market preference traits. To accelerate the rate of genetic gain, there is utmost need to increase the efficiency of breeding by utilizing modern genomics and breeding tools, reduced breeding cycle and better breeding data management system for pedigree, breeding nursery and trial data. Chickpea researchers in India including NARS partners and ICRISAT, BMGF and EiB have collaborated for modernizing the databases including electronic data capture, storing and sharing; deployment of breeding management system (BMS) in breeding activities, statistical analysis and decision making and historical data migration. To formally align the national breeding programmes together, the blueprint for varietal development i.e., *Product Profile* of *desi* and *kabuli* varieties for different zones have been developed by prioritising the essential and desirable traits, benchmarks and timeline of product development. Integration of BMS has standardized breeding activities in terms of common nomenclature for crosses, nurseries and trials; pedigree management, planning for crossing, nursery, generation advancement; creation of experimental design and analysis, standard ontology and real time data recording through data loggers. Chickpea researchers have finalized the crop code (CHP), institute code (IIPR: IIPKP, IIPBP), trials naming (T CHP R22 IIPLP STL GY), nurseries naming (N CHP R22 IIPKP F6) and cross code naming (CHP IIPKP x 22 0001). Besides, zone-wise data of IVT (Desi - Irrigated; timely sown) trial of AICRP on Chickpea for the period 2006-07 to 2019-20 has been migrated in the BMS on ICAR server (https://bms.icar.gov.in/ibpworkbench/controller/auth/login). This has led to centralized availability of breeding data in a standardized format, aiding breeding decisions, facilitating teamwork and securing data availability from one generation to the next.

S9.3: Digitalization of breeding pipeline of desi chickpea trials of ICAR-IIPR, Kanpur in the Breeding Management System (BMS) platform

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To have a deep insight into the desi chickpea breeding program of ICAR-IIPR, Kanpur, digitalization of advanced breeding lines in station trials was done in Breeding Management System (BMS) platform. Advanced breeding lines (ABLs) which were subjected to Station trials for rainfed, timely sown and late sown conditions for the seasons 2019-20, 2020-21 and 2021-22 at ICAR-IIPR were digitalized. Advanced breeding lines developed for Station trials with genotypes amenable to mechanical harvesting were also digitalized for the above three seasons. Relevant crosses of the ABLs were generated in the BMS since 2005 and by generation advancement through pedigree breeding scheme, nurseries (segregating population) and germplasm lists (harvested/ selected entries) were duly documented portraying the breeding history of the ABLs evaluated. Crosses were designated with unique cross IDs, selected lines over the generation were designated with unique GIDs and reference following the selection method with due documentation of selection intensity. By 2021 Dec., IIPR chickpea program had 201 germplasm lists (2005-2021) and 188 nurseries (2005-2021) duly documented in the BMS platform which can be retrieved from the BMS server housed at IASRI. During the process, standard file nomenclature protocol was designed which was followed in the documentation process and product profiles for desi chickpea breeding pipelines were meticulously designed for the north eastern plain zone and central zone of chickpea production belts of India. On the basis of those breeding objectives, donors and recipient genotypes to be involved in crossing program were imported in BMS platform with proper passport information.

S9.4: Database and Information System for Coordinated Research Trials of Pulse Crops

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Data Collection, submission, analysis and retrieval in smoother and easier way are the major aspects of All India Coordinated Research Project of Pulse Crops. In the manual system of data collection, compilation, analysis and report generation of the coordinated trials data, the problems *viz.*, lack of complete information, accurate, correct and uniform data analysis, delay in preparation of report etc. were observed. To address these issues, a database and information system has been developed to submit, analyze and retrieve the AICRP plant breeding trials data for pulse crops. This system has three basic components *viz.,* Administrator end, User end and Database. It has developed using Client-server Architecture comprising Client-side interface layer, Server application layer and Database layer. All the layers are independently developed using WAMP (Windows, Apache, Mysql and PHP) technology. The system has three online functional modules *viz.*, Data submission & retrieval, Data analysis and Report generation. Various data entry forms have been designed and developed for entering the basic information about the plant breeding trials of a particular centre related to data booklet details, general notes on growing conditions and yield data. The system is designed to be user-friendly and is completely menu-driven.

S9.5: Development of Digital Platform for Retrieval of Quality Seed Production data for Pulses

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Contents on detail of Seed hub centres, Seed target, Seed production, Seed lifting, expenditure incurred, Seed balance etc. have been collected, analysed and stored in digital format. A user-friendly interface has been designed for data entry and updation. Different links have been customized for development of digital platform. A prototype software has been developed for retrieval of seed hub information system using WAMP (Windows, Apache, Mysql and PHP) technology. System architecture contains three-tier architecture *viz.*, client-side interface layer, server-side application layer and database layer. System has 3 basic functional modules *viz.*, Database Design Module, Data Management Module and Report Generation Module. Total 9 database tables (*viz.*, User Master Table, Crop Master Table, Centre Master Table, Seed Category Table, Seed Target Table, Seed Production Table, Seed Distribution Table, Revolving Fund table and Infrastructure Development table) have been designed under Database Design Module. Database Management Module is used for data entry, updation, submission and analysis. Total 10 reports *viz.,* Target-wise report, Production-wise report, Target/Production summary report, Variety-wise seed production report, Year-wise target/production report, Seed distribution report, State-wise seed production report, Revolving fund report, Seed summary report and Infrastructure development report were also generated in Report Generation Module. System provides the information needs of farmers, researchers, exporters and policy makers and also serve as an information highway for sharing seed information through digital platform.

S9.6: Accelerating data-driven breeding in pigeonpea using breeding management system (BMS)

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Pigeonpea is the most popular food legumes in semi-arid regions of the world. Breeding with latest genomic interventions have led the development of high yielding resilient varieties, with that we have achieved a modest success in India. It has been concluded that, difficulties in handling the written experimental data, long generation turnover, complexity of biological traits and low selection response are the key bottlenecks which prevents delivery of higher genetic gains. To improve the genetic gain, breeding programs will require decisions that are informed by the breeder's experience and modern datasets. Consciously, the digitalization of the pigeonpea breeding in India was started in 2017 by using the BMS software through ICAR-ICRISAT project. In 2019, ICAR and BMGF have collaborated for data-driven breeding in pigeonpea. This has brought significant digitalization in pigeonpea breeding activities. Under this project, 146 germplasm lists were uploaded on the BMS portal to create studies like nurseries and trials. A total of 64 nurseries from 2008 to 2020 and 29 trials from 2013 to 2020 were made available. The hybrid station trials of pigeonpea from 2013-2020 has also migrated to the BMS. Currently, the field layout, experimental design, and data sheets of pigeonpea breeding trials are being generated through BMS. For more efficient data observation, the correct time, date, and weather analysis can be quickly recorded by using the Palmtop device. Now we can sort, store, and retrieve data accordingly and this will help breeders make data-driven selections of advanced lines for next generation breeding programs.

S9.7: Exploration of data-driven approaches for improving sustainable pulses production

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Pulses play a pivotal role in a country like India for all categories of people due to its rich protein content. As a result, the production of pulses was not commensurate with the demand. the dependency on imported pulses continues to grow in the country. Crop breeders make probabilistic decisions in the context of environmental and genetic uncertainties and under constraints imposed by time and cost. Crop breeding involves direct selection-based phenotypic observation, followed by predictive breeding using statistical models for quantitative traits constructed based on genetic experimental design and, more recently, by incorporation of molecular marker genotypes. Decisions regarding the advancement of a specific plant genotype is challenging due to a very limited number of observations. But identifying subsets of varieties that are performing similarly to the current commercial seeds in a variety of environments can help to identify potential commercial cultivars. Predictive models built using various computational methodologies have been employed to facilitate data-driven decision-making in terms of selecting breeding materials and designing hybridization schemes. To aid the decision making, machine learning can be used to predict the yield of a genotype based on past observations of multiple genotypes. Machine learning is an important decision support tool for crop yield prediction, including supporting decisions on what crops to grow and what to do during the growing season of the crops. Several machine learning algorithms have been applied to support crop yield prediction research.

Modern Tools for Crop Improvment

S4.1: KCD-11: Coalesce approach to improve wilt resistance in JG-11 variety of chickpea (*Cicer arietinum* L.)

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JG-11 is an elite high yielding mega *desi* variety of chickpea with medium seed size, medium maturity duration and extensively cultivated across India. The variety in recent years, have become susceptible to Fusarium wilt (FW) caused by *Fusarium oxysporum ciceris*. To improve JG-11, we used WR 315 as the donor parent and followed the pedigree breeding method to generate breeding material. From true F1 selection to F6 generation, the material was planted in wilt sick plot at Zonal Agricultural Research Station Kalaburagi (Latitude: 17.36 and Longitude: 76.82). Four high yielding lines were selected based on primary yield trial and percent disease index. In addition, SNP markers associated with FW resistance were also used to validate the presence of resistance alleles for race foc 4 in these lines. Based on two years yield and enhanced disease resistance over JG-11, two lines [JG11 x WR315, JG11-1 and JG11 x WR315-2] were selected for MLT at UAS, Raichur and Initial Varietal Trial (IVT) under All India Coordinated Research Project (AICRP) on Chickpea. The lines were promoted to second year MLT at UAS, Raichur based on yield stability across five locations and One line (JG 11 x WR315-2) promoted to AVT under Advance Varietal Trial of AICRP on Chickpea during 2021-22. Based on two years evaluation of JG 11 x WR315-2 in MLT and station trials, an increase in 9 % and 11 % yield advantage over recurrent parent (JG 11) and 15 % and 12 % yield advantage over regional check (SA-1) respectively were recorded further based on the yield stability across nine locations in two years and enhanced disease resistance over JG-11, the line (JG11 x WR315-2) being proposed under the name of KCD-11 (Kalaburagi Chickpea Desi-11) for farm trials, LSDs and same has been accepted during ZREAC & ZREFC meeting on 26th to 28th May 2022 held at UAS, Raichur for the zones 1, 2 and 3 of Karnataka. The selected line is anticipated to cater the needs of chickpea growers with dual advantage of yield increment and disease resistance.

S4.2: Cross species amplification and molecular diversity analysis in ricebean

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Molecular diversity among 45 ricebean genotypes and a greengram cultivar, CO 7 was assessed using 25 adzukibean derived microsatellite markers. All the markers exhibited amplification, implying the transferability of the markers to ricebean. Number of alleles varied from one to three with an average of 1.76 alleles per marker. The allele size ranged from 110 to 250 bp among ricebean genotypes, whereas it ranged from 110 to 250 bp in greengram cultivar. PIC value ranged from 0.198 to 0.689 with 0.488 as an average value. Out of 25 markers, 13 markers were found to be polymorphic among ricebean genotypes. Apart from this, 13 markers differentiated the ricebean genotypes from the greengram cultivar, CO 7 and these polymorphic markers could be used for molecular confirmation of inter specific hybrids. Dissimilarity values between the ricebean genotypes and the greengram cultivar, CO 7 were greater when compared to the dissimilarity values within the ricebean genotypes. Dendrogram and the tree generated based on Ward's and neighbour joining methods classified the genotypes into five clusters and three groups, respectively. The markers identified to detect the DNA polymorphism in the present study could be used to improve ricebean as well as greengram at intra and inter specific level, respectively.

S4.3: Stability analyses of seed size in greengram [*Vigna radiata* (L.) Wilczek]

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Seven greengram entries with three check varieties viz., CO 7, CO 8 and VBN 4 were evaluated under multi-location trial to identify a large seeded genotype suitable for Tamil Nadu. All these genotypes were evaluated for 100-seed weight at five locations during *kharif* 2019 and *rabi/ summer* 2019-20 seasons in Tamil Nadu. Data from 9 environments (*kharif* season of one location was excluded) were analyzed for stability analyses *viz*., AMMI (Gauch, 1988) and GGE Bi-plot (Yan and Kang, 2002). Genotype VGG18002 (G10) (5.8 g), VGG16058 (G7) (5.4 g) and VGG17109 (G9) (5.7 g) recorded significantly higher mean performance than the best check variety CO 7 (4.7 g). As per AMMI bi-plot 1, the genotypes VGG18002 (G10), VGG16058 (G7), COGG1702 (G3), COGG980 (G4), VBN4 (G5) and CO8 (G2) recorded less interaction with environments. Genotype VGG17076 (G8), VGG16047 (G6) and VGG17109 (G9) recorded high interaction with environments. As per AMMI bi-plot 2, genotypes COGG980 (G4), COGG1702 (G3) and VGG16058 (G7) recorded lesser interaction with environments. In GGE bi-plot analysis, two mega environments were identified viz., Killikulam *kharif* 2019 (E4) and Madurai *rabi/summer* 2019-20 (E7) in one mega environment and all other environments together as another mega environment. Genotypes VGG18002 (G10) and VGG17109 (G9) were the winners in mega environment 1 and 2 respectively. Based on overall performance, genotypes VGG18002 (G10) and VGG16058 (G7) were identified as superior genotypes with stable performance for large seed size.

S4.4: Transcriptomics of *Vigna aconitifolia* for developing a gene expression atlas

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Demand for food legumes as one of the basic nutritional requirements is inflating globally. Due to supply-demand imbalance, conventional pulses are becoming unreachable for a sizable population due to their rising prices, thereby suffering acute malnutrition debilities. The underutilized species *Vigna aconitifolia* (Moth Bean) is an important legume crop and is valued for its seeds for their high protein content that can be recommended for human wellness. Despite its economic potential, genomic resources for this crop are scarce and there is limited knowledge of the developmental process of this plant at a molecular level. Therefore, we have chosen to study the molecular mechanisms that regulate plant development in *V. aconitifolia*, with a special focus on flower and seed development. We have performed a comprehensive *de novo* transcriptome assembly using six types of tissues of *V. aconitifolia* (var. RMO-435), namely, leaves, roots, flowers, pods, and seed tissue in the early and late stages of development, using the Illumina nextseq platform. We obtained 150938 unigenes with an average length of 937.78 bp. Real-time PCR analysis further validated that the unigenes displayed significant differential expression in the late stages of seed development. The *Vigna aconitifolia* transcriptomic resources generated in this study will provide foundational resources for gene discovery with respect to various developmental stages under stress conditions. Using the data from this analysis, we will develop a stress-resistant (abiotic/ biotic) and high-yielding varieties with enhanced yield as well as nutritional quality employing plant biology based approaches.

S4.5: Identification of major locus conferring resistance to urdbean leaf crinkle virus disease in blackgram [*Vigna mungo* (L.) Hepper]

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Urdbean Leaf Crinkle Disease (ULCD) is a major factor causing severe yield loss in black gram production. The symptom of the disease appeared as extreme crinkling, curling, puckering, and rigidity on the leaf. Yield loss was observed 62-100%. The disease causing virus was not yet identified. Identification of quantitative trait loci linked with ULCV is highly helpful in the breeding program. Hence, in this study, major locus conferring resistance to ULCD in black gram was identified using QTL analysis with a population of 94 $F_{2:3}$ recombinant inbred lines. The population was derived from the cross between resistant parent CO 5 and susceptible parent TU 68. Artificial epidemic conditions for ULCD were created by the mechanical sap inoculation method. The phenotypic observation of ULCD of the $F_{2:3}$ population was taken on 60 days after inoculation. Disease score was given based on percent disease incidence on 60 days after infection (DAI). A total of 575 SSR markers were screened between parents and 31 markers were identified as polymorphic. Ten linkage groups were established with 31 SSR markers with a total genetic distance of 396 cM. Using these markers, a single locus was identified on linkage group 3, which explains up to 17.98 percent of the variation for the ULCD resistance. This new QTL will be thoughtful in the breeding program for the development of ULCD resistance.

S4.6: Characterization and evaluation of mung bean genetic resources

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Mung bean (*Vigna radiata,* family Fabaceae) is an important leguminous crop cultivated in tropical and subtropical regions of Asia. India contributes about 50% of annual world production of mung bean. Easy digestibility, low flatulence potential compared to other legumes and presence of higher folate, iron, amino acids, proteins, dietary fibre, unsaturated fatty acids, vitamin, calcium and phosphorus makes mung bean a preferred nutritive food. Characterization and evaluation of 4100 germplasm accessions (including both indigenous and exotic) of mung bean available at ICAR-NBPGR Genebank was conducted in augmented block design with 5 checks (IPM-2-14, SML 668, MH 421, PDM 139 and IPM-2-3) during *kharif* 2019 and 2020 at ICAR-CAZRI, Jodhpur under a DBT funded program on minor legumes. Data analysis of 23 agro-morphological traits demonstrated existence of wide variation in morphological and yield attributing traits. Variability was recorded in days to 50% flowering (31-89), number of pods (2.0-173.3 plant^{-1}), seed yield (0.1-46.4 g plant^{-1}), 100 seed weight (1.25-8.0 g) and dry biomass (8.0-194.0 g plant^{-1}) with CV of 17.8, 52.6, 58.2, 30.0 and 45.4% respectively. Variability was also recorded in morphological traits like growth habit, raceme position, pod attachment to peduncle and pod pubescence. Based on this agro-morphological data and biochemical data, a core set of 400 accessions representing complete genetic diversity has been developed. This core set will be evaluated for biotic and abiotic stresses and nutritional factors. Further this phenotypic data and genotypic data will be used for Genome Wide Association Studies (GWAS) in mung bean.

S4.7: Genomic resources in *Vigna radiata*: An important legume of India

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Mungbean (*Vigna radiata*) is amongst the most popular legume crops of India. Seeds and sprouts of this plant are great source of carbohydrates and proteins. In addition to these macro-elements, mungbeans are also good source of flavonoids such as vitexin and polyphenols that protect the plant against stress. However, these measures still fall short of protecting the plant against some major abiotic and biotic stresses, which lead to considerable loss in crop yield. Stress response in plants is a highly regulated process with much yet to be discovered regarding the molecular mechanisms involved. We believe that much of this information is embedded in the genome and many such regulatory mechanisms could be deciphered by understanding the genome. Therefore, we have assembled a high-quality chromosome-level assembly of the mungbean genome for *V. radiata* cv. IPM02-3. We have annotated the genome to identify ~27,000 protein coding genes. Long-reads based sequencing of transcripts has helped generate full-length transcripts which were analysed to identify long non-coding RNA sequences. Besides, we have also identified molecular markers like simple sequence repeats in the genic and genomic regions of the mungbean genome. This data also helped us develop a differential gene expression profile for drought response based on the publicly available short read data for mungbean in well-watered and drought conditions. The high-quality genome assembly will also act as a reference to identify other structural variants. Therefore, this study will prove to be a credible addition to the repertoire of genomic resources for important pulses of India.

S4.8: Designing, validating and expression analysis of different R Genes in compatible and incompatible *Vigna* - MYMIV interactions

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Interspecific hybridization of mungbean with other *Vigna* species can provide stable and high level of resistance to Yellow Mosaic Disease. Understanding genetic control of YMD resistance in *Vigna* has revealed both dominant and recessive nature of resistance controlled by one or two genes with different gene action. Obstruction of viral invasion in plant cell wall, restriction in viral DNA replication, and early onset of antioxidant defense responses have been identified as key defense mechanisms against YMD resistance in *Vigna mungo*. However, the nature, actions and class of R genes imparting YMD resistance in other *Vigna* species also need to be investigated. The present study was designed based on differential expression of different classes of R genes in compatible and incompatible *Vigna* - MYMIV interactions. The primers were designed for amplifying plant resistant protein (R protein) domain specific regions (NB-ARC; SgS3; RdRp3) from genome of different *Vigna* species. R protein domain specific sequences were shortlisted (with candidate genes, type species) and retrieved from NCBI database, followed by multiple sequence alignment through ClustalW online software on different *Vigna* sp. genome. A total of 29 primers with 3 domain specific regions were designed using Primer3 online software, were amplifying with specific amplicon size (90 – 195bp) and moreover without primer dimer formation. Most of the primers were amplified on genomic DNA of four resistant and two susceptible genotypes of different *Vigna* sp. genome. Total RNA was isolated and cDNA was prepared from mock and MYMIV inoculated leaf tissues of both resistant and susceptible genotypes of different *Vigna* species at 1, 5, 10, 15-, 20-, 25- and 30-days post inoculations. SYBR green assay was performed in qRT-PCR to study differential gene expression in both compatible and incompatible interactions.

S4.9: Marker assisted analysis for seed longevity in six soybean [*Glycine max* L. (Merrill)] crosses

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Soybean seeds are prone to mechanical damage and field weathering which affects their viability, rendering the seeds useless after a few months of storage. To study the inheritance of seed longevity in Indian genotypes, six crosses *viz.* DT-21 × PS-24, PS-1347 × PS- 124, DT-21 × BHATT, AGS-25 × JS-335, PS-1556× EC-389148 and PS-1592× PS-1241 were made based on seed size. The characterization of seed longevity in different genotypes, their F_1 and F_2 generations was done based on morphological data, methanol stress test, biochemical and molecular marker data analysis after harvesting and eleven months of storage. The germination test data for F_2 population fitted in 3:1 ratio in crosses DT-21 × BHATT and PS-1556× EC-389148 while rest of the crosses fitted in the ratio 15:1, which revealed the involvement of one or two genes in the inheritance of seed longevity. A sharp increase in superoxide dismutase and catalase activity was observed in good storer genotypes after storage. The marker polymorphism survey was carried out using 15 SSR markers, of which seven were polymorphic with a PIC value ranging from 0.11 (Satt169) to 0.753 (Satt453). Un-weighted pair group method arithmetic average (UPGMA) analysis revealed 5 clusters in the cross DT-21 × PS-24, 6 in PS-1347 × PS- 124, 7 in DT-21 × BHATT, 9 in AGS-25 × JS-335, 6 in PS-1556× EC-389148 and 5 in PS-1592× PS-124. Based on similarity coefficient ranges F_2 generation plants showing good seed longevity were identified. Among the parents, BHATT, PS-1241, AGS-25, JS-335, PS-1556 and EC-389148 showed good seed longevity based on all the parameters. In the F_2 population of the six crosses 34 plants were found to be good storers.

S4.10: Molecular diversity and dynamics of root architecture in chickpea (*Cicer arietinum* L.) under two moisture regimes

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Twenty chickpea genotypes were studied to decipher the root dynamics under well watered (WW) and low moisture stress (LMS) conditions at flowering along with molecular diversity analysis. Root study was carried out in poly bags and the traits were measured using WinRHIZO root image analyser. ANOVA indicated significant difference among the test genotypes for most of the traits under consideration. Root length varied between 18 to 32 cm under WW, while it ranged between 15 and 36 cm under LMS condition. The range of root volume was 0.064 to 0.374 cm^3 and 0.064 to 0.284 cm^3 under WW and LMS conditions, respectively. The diversity based on Mahalonobis D^2 statistics grouped the genotypes into 5 and 4 clusters with largest cluster having 12 and 16 genotypes, respectively under WW and LMS conditions. The clustering showed that the pipeline variety, DIBG205 being clustered with ICC4958, drought tolerance donor, under both the conditions. Molecular diversity using 18 SSR markers on QIAxcel advanced system revealed high polymorphism with 16 markers being polymorphic with 8.722 alleles per marker and an average PIC value of 0.798. The marker associated with drought QTL hotspot, TAA170, exhibited highest number of marker alleles (15) with PIC of 0.851. There were six clusters, with Cluster-I being largest (13 genotypes) and it was interesting to note DIBG205 and ICC4958 grouping together in Cluster-IV. The genotypes superior for root traits and information on genetic diversity will be extremely useful in choosing appropriate parents and for précised selection in breeding for climate resilience focussing on drought tolerance.

S4.11: Inheritance studies and molecular mapping of the genomic region governs the seed viability in soybean (*Glycine max*.)

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The "Golden bean" or soybean has 18-20% healthy oil and 40–45% high-quality protein along with countless other vital nutrients. However, it consistently endures loss of seed viability during ambient storage from harvest to the next planting season, which is a significant barrier for the production of high-quality seeds. In this study genetics and mapping of the loci linked to seed viability were undertaken. Five highly viable genotype (>90% germination) viz. EC-1023, EC-105790, G2651, UPSL34, UPSL736 and three poorly viable genotype (<70% germination) viz. MACS-565, PK1243, VLS61 were hybridized. Three crosses yielded F_1 hybrids that each were promoted to the next generation. Cross EC1023 x VLS61 and their derived $F_{2:3}$ seeds, were exposed to 72 hours of accelerated ageing (AA) at 41°C and 100% RH, followed by a germination. After AA test, germination % of EC1023 and VL5-61 were 40 and 14, respectively, whereas range of $F_{2:3}$ seeds were 4.16 to 71.42 %. The seed viability is governed by polygenes, as evidenced by the continuous distribution of germination % of $F_{2:3}$ seeds. Parental polymorphism was studied with 506 SSR markers indicated it to 20.35% which was not uniform across the chromosomes; Chr. 15 had 46.15% polymorphism as against 15.78% on Chr. 3 and 4. Through ICIM mapping 8 QTL for seed viability on Chr. 6, 7, 8, 10, 13 and 17, respectively, were mapped. Two of the eight QTLs appear to be major QTLs, and other seems as minor ones. Previously reported markers linked to seed viability were also validated in the parental genotypes. The genetics of seed viability, the QTLs and markers found in this study, will pave the way for molecular breeding to generate genotypes with improved seed viability.

S4.12: Rapid detection of *Fusarium oxysporum* f. sp. *ciceris* in chickpea using xylanase transcriptional activator (xlnR) gene based LAMP technique

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Among the pulse crops, chickpea has a major contribution of ~ 49% towards total pulses produced in India. There are several biotic stresses that affect chickpea production, of which Fusarium wilt caused by *Fusarium oxysporum* f. sp. *ciceris* (Foc) is the major yield limiting factor. During chickpea season several soil-borne pathogens produce similar symptoms that create confusion in detection, to overcome these hurdle accurate and rapid with less instrument-centric technique is required to improve the diagnosis of the pathogen. Loop-mediated isothermal amplification (LAMP) is an alternative amplification technology, which is highly sensitive, quicker, and less susceptible to inhibition from DNA preparations than other PCR-based methods. LAMP technique includes, use of six primers (two internal, two external and two loop primers) and depends upon auto-cycling DNA synthesis by a DNA polymerase with high strand displacement activity. In the present study, xylanase transcriptional activator (xlnR) gene-based LAMP primers were used for standardization. The LAMP reaction was optimized at 65°C for 30 min with slight modifications in manufacturer protocol. A LAMP gave clear-cut differences based on colorimetric methods. In LAMP reaction, observed the expected results where pink colour represented the negative control, while yellow colour indicated as positive which contains DNA template of FOC. The results of same reaction mixture run on the 2% agarose gel, observed multiple bands in presence of Foc while no bands in negative control. This LAMP-assay is highly sensitive and rapid diagnostic tool for the detection of Foc. Further, this technique eliminates the confusion of field symptoms induced by the Foc and other soil-borne pathogens which intern helps in implementation of better management practices for Fusarium wilt of chickpea.

S4.13: Marker- assisted backcross breeding to introgress bruchine pest and MYMV disease resistance in blackgram [*Vigna mungo* (L.) Hepper *cv* MDU 1]

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Marker assisted backcross (MABC) breeding technique was employed to introgress the Quantitative Trait Loci (QTL) regions for the bruchine resistance and Mungbean yellow mosaic virus (MYMV) disease resistance from resistant donor TU 68 into the popular blackgram variety MDU 1. Bruchine pest and MYMV disease is the major pest and disease of blackgram that renders the crop growth and yield under severe epiphytotic conditions. Foreground selection was performed using six markers namely, CEDG 020, CEDG 067 in LG 5, CEDG 302, GMES 1248 in LG 8 and CEDG 180, CEDG 116 in LG 10 linked with bruchine pest and MYMV disease resistance. In addition, 40 SSR markers that found polymorphic among the MDU 1 x TU 68 population were used in background selection. Among the background introgressed lines (BILs), recurrent parent genome recovery ranged from 64.8 % to 72.4 %. Among these introgressed lines viz., BIL-95-5, BIL-95-3, BIL-95-1, BIL-135-5, BIL-33-2, BIL-20-3, BIL-20-1, BIL-135-2 and BIL-95-2 showed superior yield performance than the recurrent parent MDU 1. All the introgression lines exhibited resistance to bruchine infestations significantly. Hence, these lines can be further advanced to row yield trial to evaluate yield parameters, bruchine resistance and MYMV disease resistance to release as variety.

S4.14: Validation of SCAR molecular markers linked with resistance to anthracnose disease in dry bean genotypes

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Common bean anthracnose caused by *Colletotrichum lindemuthianum,* is one of the major destructive diseases in the dry bean production areas of foothills of Himalayan region of India. Therefore, employing molecular tools to aid in the early selection of anthracnose-resistant source harbouring target alleles increases efficiency while saving the time and cost of breeding programs. The current study intends to identify and validate sequence-characterized amplified region (SCAR) markers targeting anthracnose disease resistance alleles for aided selection by using fifty dry bean genotypes, including parental lines, breeding lines and germplasm. Molecular analysis using 15 sequence-characterized amplified region (SCAR) markers revealed polymorphism among the genotypes. These markers exhibit the great potential to assist in the selection at different stages of the breeding program and may be readily incorporated into marker-assisted selection. The SCAR markers SAS13, SBB-14, SH-18, TGA1.1 and SAB-03 have shown to be useful for marker assisted selection (MAS) of the target resistance genes. This study has also identified local landrace/parental lines as potential donors for resistance breeding against *C. lindemuthianum* in India.

S4.15: Next generation sequencing based assessment of genome-wide mutations induced by gamma rays and electron beam in urdbean [*Vigna mungo* (L.) Hepper]

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Gamma rays (GR) and electron beams (EB) are the most widely used physical mutagens in mutation breeding. However, the nature of genome-wide mutations induced by these mutagens are lacking in important legumes like urdbean. In this respect, two urdbean mutants viz., 'TU-43' and 'PM-32' isolated earlier from 400 Gy of GR and EB, respectively, were subjected to Illumina-based whole genome sequencing. Single base substitutions (SBSs), short insertions and deletions (InDels) were identified by comparing the genomes with that of 'Pant U-31' (ASM1909614v1 in NCBI). GR (8,45,028) induced large number of variants in comparison to EB (7,28,161), with the latter evoking higher proportion of SBSs (91.6% vs 82.3%) and lower InDels (8.4% vs 17.7%). Albeit with similar transition to transversion ratio (~1.9), EB induced marginally higher G>A, C>T transitions and C>A, G>T transversions. GR and EB generated more single base deletions and insertions involving A, T than C, G bases. Deletions and insertions of up to 216 and 140 bases, respectively, emanated in GR as against 60 and 46 bases in EB. GR predominated in both shorter and longer InDels and elicited 2.4x more InDels than EB. Mutations by EB primarily targeted intergenic and stop codons, while intragenic and intronic regions, start codons and splice sites were in GR's radar. Thus, it is postulated that GR potentially produces more mutagenic effects than EB, though most of them are in the non-intended regions. Contrarily, EB produces less genome-wide mutations per se, but noticeably in the envisaged regions.

S4.16: Authentication of InDel marker specific to mitochondrial genes to differentiate A2 and A4 source of CMS line in pigeonpea

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Cytoplasmic male sterility system is emerging boon in pigeonpea hybrid breeding for enhancing the productivity and production. CMS-based hybrid technology is based on three component systems namely, sterile (A), maintainer (B), and restorer (R) lines. 'B' line majorly helps to maintain the sterility in 'A' lines and 'R' line having a nuclear *Rf* gene that restores fertility in '*A×R'* progenies. Pigeonpea has eight different cytoplasms (A1 to A8) which are potent sources of male sterility. Among all, A2 and A4 cytoplasms derived from *Cajanus scarabaeoides* and *Cajanus cajanifolius*, respectively, are been commonly used to exploit the heterosis in pigeonpea. In the present study, we used six CMS lines, in that four were previously confirmed A4 CMS lines as reference and two newly developed 'A' lines to detect the potential CMS source and validate the InDel marker. The new CMS lines namely ICP-2047A and 2043A were derived from A4 cytoplasm were compared with ICP-2089A from A4 and GT-33A, GT-290A and ICP-67A derived from A2 cytoplasms. The InDel marker used was nad7a_del marker (*F: 52 -CTGACGGATGCCTACTATR-32 and R: 52 -CATCTCCTTCGACCTTAG-32)* specific to A4 CMS mitochondrial gene with the amplicon size of 160bp. According to the study of Bohra et al. (2017) polymorphism was observed in A4 cytoplasms where in A2 there is no difference. The absence of DNA polymorphism in A2-CMS is in agreement with the results of Bohra et al. (2017) and Sinha et al. (2015) who asserted the nad7a_del marker to be unique to A4-CMS which has been confirmed by our study.

S4.17: The isolation, culture and callusogenesis of microspore of soybean (*Glycine max* L.)

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Soybean (*Glycine max* L. Merrill, 2n=2x=40) is a widely utilised crop for protein and oil content. Soybean androgenesis has been a challenging process and is yet to be advanced significantly to develop haploids useful in crop improvement. The current research aims to standardise different conditions for pre-treatment, isolation and induction of microcalli in soybean. Standardisation of bud size (3.5 to 4.0mm) from donor plants and pre-treatment of bud with temperature shock (24^0C for two hours) was the best for microcalli induction. Under sterile conditions, anthers were dissected and placed in a microcentrifuge tube with 300 ìl of 2% sucrose, 2% sorbitol and 0.3 M mannitol for maceration. Macerated anthers were transferred into a 5 ml tube with 3 ml of 2% sucrose, 2% sorbitol, 0.3 M mannitol. The resulting microspore solution was centrifuged for 6 minutes at 2500 RPM. Supernatant was discarded and pelleted microspores were re-suspended in 300ìl of induction media (BNN / B5 modified media). Microspores were cultured in BNN as callus induction media supplemented with 10 mgl^{-1} 2, 4- dichlorophenoxyacetic acid, 0.2 mgl^{-1} N6 - benzyladenine, 2% sucrose and 2% sorbitol. The resulting auxin cytokinin ratio was found suitable for microcalli induction from soybean microspore.

S4.18: Studies on Genetic Diversity and Path analysis in Pigeon pea (*Cajanus cajan* (L.) Millsp.) under Bundelkhand region of Uttar Pradesh

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The present investigation was carried out at P.G. Research farm of College of Agriculture, Banda University of Agriculture and Technology, Banda, Uttar Pradesh, India in augmented block design-II during *kharif* 2020-21. The highest positive significant correlation was found between seed yield and the traits such as days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and shelling percent at phenotypic and genotypic level. Path coefficient analysis revealed that the highest positive direct effect on seed yield per plant exerted by harvest index, days to maturity, 100-seed weight, number of primary branches per plant, number of secondary branches per plant and pod length at Phenotypic and Genotypic level. In cluster analysis, seventy-three germplasm lines were grouped into five different non-overlapping clusters in which cluster I had the maximum number of genotypes (25) followed by cluster III (19 genotypes), cluster II (14 genotypes), cluster V (9 genotypes) and cluster IV (6 genotypes). The first five principal components showed 67.89% of the total variation among the tested genotypes. The genotypes which showed highest genetic diversity can be used as parents in hybridization program. Early flowering was found in genotype IPA-10W-8-1, IPA-12W-16, IPAM-15-2, IPAB-11-20-2, IPA-12W-46, IPA-12W-3 and IPAB-10-13 had the highest seed yield per plant.

S4.19: Identification and differential expression analysis of histone acetyltransferase gene families in chickpea and soybean genomes

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Legumes are agriculturally important crops having the unique ability to fix atmospheric nitrogen. These crops add high amount of nitrogen rich organic matter into agricultural soil and facilitates circulation of soil nutrients and water retention in soil. Legumes are an essential component of human diet because of high protein, high dietary fibre and low-fat contents. Chickpea (*Cicer arietinum*) and soybean (*Glycine max*) are two major leguminous crops grown in India. One of the most significant post-translational modifications of histone proteins found in the chromatin of eukaryotic organisms that controls the expression level of many stress- and development-responsive genes is histone acetylation. The acetylation of the N-terminal lysine residues of core histones is carried out by histone acetyltransferase (HAT) genes. Numerous crops, including *Arabidopsis*, rice, wheat, litchi, grapes, *etc*., have previously undergone HAT gene identification and differential expression study. In this current study, genome wide identification of HAT genes has been performed for chickpea and soybean and a total of 26 HAT genes (9 CaHATs and 17 GmHATs) have been identified. These genes can be categorized into six distinct classes based on phylogenetic analysis, conserved domain, motif, and gene structure analyses which reveal the class HAC being the most predominant class. Differential gene expression analysis using publicly available datasets indicated that HAT genes have significant roles in abiotic stress management and various stages of tissue development of these two legumes. This current study will be helpful for future researcher to study the roles of HAT genes in other crops.

S4.20: SSR-based genome–wide association studies for yield related agronomic and biochemical traits of grass pea germplasm collected from China and Bangladesh

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Grass pea (*Lathyrus sativus* L.) is an important food crop cultivated in dry land agricultural ecosystem. It is an important source of dietary protein to millions of people living in low-income countries in South-east Asia and Africa. This study emphasizes the development of genomic resources and their application in marker–trait association for 17 yield-related traits in 400 grass pea genotypes from China and Bangladesh. These traits were evaluated using 56 polymorphic markers using GLM (general linear model) (P+G+Q) and MLM (mixed linear model) (P+G+Q+K) in the tassel software based on the linkage disequilibrium and population structure analysis. Population structure analysis showed two major groups and one admixed group in the population. For statistically significant loci pairs of linkage disequilibrium (LD) mean value (D') was 0.479. A total of 99 and 61 marker-trait associations in GLM and MLM model linked to the 17 traits were accepted at 5% level of significance. Among these markers, 21 markers were associated with more than one trait; 12 marker-traits association passed the Bonferroni correction threshold. Both model found six markers (C41936, C39067, C34100, C47146, C47638 and C43047) significantly associated with days to maturity, flower color, plant height and seed per pod were detected in the Hebei and Liaoyang location ($P<0.01$), and the interpretation rate (R^2 value) 11.2 to 43.6%. Conferring to the consequences in this study, the association analysis methodology may operative system for quantitative, qualitative and biochemical traits related gene position mapping and support breeders to improve novel approaches for advancing the grass pea quality.

S4.21: Attempting De-novo domestication in Pulse crops using CRISPR editing technologies

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Modern agriculture is highly reliable and mostly depends upon narrow wider but superior crop varieties. Focusing on the same set of traits is ignoring the vast diverse gene pool of wild relatives that are found to be beneficial for human kind. Crop improvement using conventional and molecular breeding approaches leveraging plant genetic diversity using crop wild relatives (CWRs) has been one approach to address these issues. De-novo domestication— targeted introduction of domestication traits/loci using introgression or genome editing of CWRs—is being explored as a supplementary approach. By using CRISPR editing technology, either targeting specific loci (precision editing) or stacked up genes (multiplex editing) can help this strategy. As observed in tomato by in *S. pimpinellifolium,* targeted a total of eight gene while domestication, looking to improve architectural traits, day-length insensitivity, fruit size and shape, and vitamin A and C content has successfully doubled the yield of *S. pimpinellifolium* and increased lycopene contents to 500% (Li et al., 2018; Zs€og€on et al., 2018). This can be explored in pulse crops such as soybean, chickpea and pigeonpea whose whole genome sequencing has potentially revealed the selection sweeps that underwent selection pressure during domestication. Targetting loci such as shattering [*GmSHAT1-5; Shatterproof2; SHATTERING1* (*C.cajan_24676*)], *pod dehiscence, determinacy could the potential genes, targeted while precising the editing via CRISPR Cas system.* An attempt in *Vigna stipulacea* (Takahashi *et al.* 2019), combined ethyl methanesulfonate (EMS) mutagenesis with the forward phenotypic screening results with notable reductions in seed dormancy and pod shattering.

S4.22: Speed breeding protocol for faster delivery of climate resilience varieties and hybrids in pigeonpea

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Pigeonpea is a highly photosensitive crop. It only flowers when the photo-period is less than ten hours limiting the breeder for annual advancement of the generation, anticipating twelve years of wait for release a variety/ a hybrid. Henceforth, an experiment was taken up to check the possibility of speed breeding and standardize the protocol for the same. Accordingly, genotypes ICPL 11255, TS3-R, ICPL 87119 and ICP 7035 across, super-early, early, medium, and longer durations were tested at four different photo-periods i.e 8, 9, 10 and 13 hours in optimization chambers. Four different dark chambers were set up with heliospectra-elixia lights, temperature set at 35æ%C/ 22æ%C (D/N), humidity of >55% and need based irrigation as well as nutrient supply. The Analysis of variance explained the significant difference between the photoperiods, genotypes and photoperiod x genotype interaction for both days to flowering and plant height. The genotypes flowered earlier in 8 hours photoperiod, followed by 9 and 10 hours and no flowering at 13 hours as well as in control. Whereas, the higher plant height was noticed in 13hrs and lowest in 8 hours of photoperiod. A significant interaction between photoperiod x genotype was noticed both for days to flowering and plant height. As a result, a reduction of 22-35 days for flowering and about 54.6 cm to 118.7 cm reduction in height under speed breeding justifying its possibility. It helps in faster generation advancement as well as development of newer parents and R lines in hybrids, thus delivering climate-resilient varieties and hybrids in pigeonpea.

S4.23: Regulatory roles of long non-coding RNAs and micro-RNAs during Fusarium wilt infection in Pigeonpea

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Fusarium wilt in pigeonpea caused by *Fusarium udum* (Butler) is a crucial biotic restraint for pigeonpea production world-wide which may cause 30-100% loss in grain yield. In this present study, Transcriptome data obtained from NCBI SRA data belonging to root tissues of fusrium inoculated and non-inoculated plants from both ICP 2376 (susceptible) and ICP 8863 (resistant) cultivars at 36 hours post inoculations were utilized to mine lncRNAs and micro-RNAs. A total of 96615710 clean pair end ILLUMINA reads from 4 transcriptome libraries were used for reference-based assembly. Total 61739 transcripts belonging to 35804 genes were identified from the assembly. A total of 5829 long-noncoding RNAs were identified using tools such as CPC2, PLEK, Transdecoder, ORF-finder etc. A total of 124 conserved micro-RNAs belonging to 37 families were identified from the transcriptome data. Among the MIR-families MIR-166, MIR-167, 390 and MIR-393 are the dominant ones, total 3243 genes along with their transcript variants were targeted by the identified micro-RNAs. Total 15776 transcripts were targeted by the identified lncRNAs, among them 7528 trans-acting and 12427 cis-acting in nature. The targets include various transcription factors like ethylene-responsive transcription factor, MADS-box, Bhlh, C2H2, b-ZIP, GATA, HSFs etc. which are linked to response of plants during diseased condition. Besides that mRNAs code for ubiquitin-conjugating enzyme, pathogen related proteins, homeobox-leucine zipper protein were identified as lncRNAs and miRNAs targets. The integrated study of lncRNAs, miRNAs and their targets provide a regulatory insight for fusarium wilt disease in pigeonpea.

S4.24: Identification of long-noncoding RNAs and micro-RNAs and their regulatory actions in response to Fusarium wilt in Chickpea

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Fusarium wilt is a major problem in chickpea. Shoot transcriptome data from two contrasting genotypes (KWR108-Resistant and GL13001-Susceptible to Fusarium wilt) were utilized for this study. A total 86002683 pair-end ILLUMINA reads from 4 transcriptome libraries (Data collected from NCBI) were used for reference-based assembly. A total of 29852 genes containing 52782 transcripts with 29474 loci were identified from the assembly utilizing HISAT2 and Stringtei software. CPC2 software was used to calculate the coding potential and grouped them in coding and noncoding one. Further, the noncoding transcripts were utilized for the identification of long-noncoding RNAs and micro-RNAs; a total of 4169 long-noncoding RNAs and 195 conserved micro-RNAs belonging to 54 families were identified. Among the MIR-families MIR-156, MIR-166 and MIR-171 are the dominant ones; a total of 4063 genes along with transcript variants were targeted by the identified micro-RNAs via psRNAtarget software. A total of 13339 transcripts were targeted by the identified lncRNAs, among them 6569 trans-acting and 10881 cis-acting in nature. The targets include various transcription factors like TCP2, TCP4, MADS-box, Bhlh, C2H2, b-ZIP, GATA, HSFs, etc., which are associated with the disease. Besides that, various auxin-responsive factors, pathogen-related proteins, squamosa promoter-binding-like proteins, and homeobox-leucine zipper proteins are identified as lncRNAs and miRNAs targets. The integrative study of lncRNAs, miRNAs, and their targets render a regulatory perception for fusarium wilt disease in chickpea.

S4.25: Population structure and molecular diversity analysis in field pea (*Pisum sativum* L.)

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The population structure analysis for the 160 field pea genotypes was carried out using STRUCTURE tool. Four population structure groups *viz.,* G_1, G_2, G_3 and G_4 were identified based on the delta 'k' values obtained from model-based simulation using cluster harvester in such a way that mean likelihood was maximized (135.6) while, mean alpha was (0.0398) minimized when the number of populations was set at four. The maximum allele frequency divergence was observed between first and third group (0.0676) while, minimum was between fourth and third (0.0233). The largest group was third group with 51 genotypes, followed by second (38), first (37) and fourth (34) group. To decipher molecular diversity, 21 SSR markers were used for screening 160 genotypes, of which, 15 markers exhibited polymorphism. A total 53 marker alleles were obtained across the markers with number of alleles per marker ranging from 2 to 9 with a mean of 4.73 alleles. Maximum number of data points, in terms of marker alleles, were obtained for the marker AA446 (9) followed by AA92 (8). Polymorphic Information Content (PIC) revealing the informativeness of the markers ranged between 0.209 (AA67) and 0.832 (AA446). Nine out of fifteen polymorphic markers showed PIC value more than 0.5. The genotypes having genome amalgamation of different population structure groups, might harbour specific traits corresponding to those groups and may be useful in crop improvement programme if the desired traits without any linkage drag are harboured.

S4.26: Genetic base of lentil cultivars developed in India as revealed by pedigree analysis

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Lentil is among the oldest domesticated crops in the world. It is a cool season food legume playing a significant role in human and animal nutrition as well as soil fertility. It can be grown in rotation to cereal crops which promote sustainable cereal-based production system. It is the most important crop because of high protein content and fastcooking characteristic. To develop new varieties compatible for facing logarithmic climate change, the new gene pool of varieties must be broadened by introducing wild species, land races and exotic germplasm into breeding practices. The present study quantifies the genetic base of released varieties that provide indirect information about the relatedness of the varieties. In lentil, pedigree analysis of the varieties bred for over 70 years in India covering 81 varieties was performed. Ludhiana local, was most frequently used as a parent in more than 20% of the released cultivar followed by Bihar local (> 17%), LG171 (> 14%) and JLS1 (>12%). Ancestor Ludhiana local collected from Punjab was used in the development of L 9-12 variety in 1972. Similarly, Bihar local parent was used in the development of T 8 variety in 1967. Both these ancestors have wider adaptability. The relative genetic contribution (RGC) from ancestors was found maximum of Ludhiana local (0.087), Bihar local (0.070), LG171 (0.054) and JLS1 (0.041). However, 36 out of total 60 parents used only once in the pedigree. Extensive and repetitive use of superior genotypes in lentil improvement programme of India led to genetic erosion and narrowing of genetic base as evident from significantly low superiority of the recently released varieties of lentil. Hence, the integration of new germplasm is of paramount importance for broadening the genetic base of lentil cultivars.

S4.27: Traversing from Genomic Assisted Breeding to Genomic Selection towards Yield Resilience in Chickpea

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Development of chickpea varieties with resilience to changing climate is a challenge. QTL hotspot from ICC4958 was introgressed into Pusa 372 and JG 16 using the MABC approach leading to the development of Pusa Chickpea 10216 and Pusa JG 16 that have been identified and released for the cultivation in Central Zone. The genomic selection technologies of identifying the superior parents for increasing breeding value (GEBV) has been initiated. It predicts breeding values of lines using genome-wide marker profiling and allows selection of lines prior to field-phenotyping, thereby shortening the breeding cycle if coupled with speed breeding or off-season advancement. A collection of 320 elite breeding lines was selected and phenotyped extensively for yield and yield related traits at two different locations (Delhi and Patancheru, India) under rainfed and irrigated conditions and genotyped. Later the advanced breeding lines from All India Testing were included in this base population. Phenotyping and genotyping data were used with six statistical GS models to estimate the prediction accuracies. GS models were tested for yield related traits *viz.,* seed yield, 100 seed weight, days to 50% flowering and days to maturity. Prediction accuracy for the models tested varied from 0.138 (seed yield) to 0.912 (100 seed weight), whereas performance of models did not show any significant difference for estimating prediction accuracy within traits. Superior parents were selected on the basis of training of these models onto the test population. These were having higher GEBVs. The progeny are being genotyped for the next round of GS.

S4.28: Dynamic transcriptome profiling of mungbean genotypes pinpoints the putative genes linked with resistance to mungbean yellow mosaic virus

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Yellow mosaic disease (YMD), incited by mungbean yellow mosaic virus (MYMV), and is a primary viral disease that reduces mungbean production in South Asia, especially in India. There is no detailed knowledge regarding the genes and molecular mechanisms conferring resistance of mungbean to MYMV. Therefore, disclosing the genetic and molecular bases related to MYMV resistance helps to develop the mungbean genotypes with MYMV resistance. In this study, transcriptomes of mungbean genotypes, VGGRU-1 (resistant) and VRM (Gg) 1 (susceptible) infected with MYMV were compared to those of uninfected controls. The number of differentially expressed genes (DEGs) in the resistant and susceptible genotypes was 896 and 506, respectively. Among them, 275 DEGs were common between the resistant and susceptible genotypes. Functional annotation of DEGs revealed that the DEGs belonged to the following categories defense and pathogenesis, receptor-like kinases; serine/threonine protein kinases, hormone signaling, transcription factors, and chaperons, and secondary metabolites. Further, we have confirmed the expression pattern of several DEGs by quantitative real-time PCR (qRT-PCR) analysis. Collectively, the information obtained in this study unveils the new insights into characterizing the MYMV resistance and paved the way for breeding MYMV resistant mungbean in the future.

S4.29: CRISPR/Cas9 based gene editing of chickpea (*Cicer arietinum* L.) for yield attributing trait

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Chickpeas (*Cicer arietinum* L.) are vital to nutritional security and widely grown pulse globally. The most important agronomic trait in chickpea breeding is yield. BIG SEEDS1 (BS1) gene from the model legume *Medicago truncatula,* encoded the transcription regulator which negatively regulates primary cell proliferation and plays a key role in the control of the size of plant organs (seeds, seed pods, and leaves etc). Deletion of this gene leads to significant increase in the size of plant organs, including leaf and seed. In the present study, nucleotide sequences of BS1 gene of *desi* chickpea (ICCV 4958) and *kabuli* chickpea (CDC Frontier) were retrieved from the database and translated. Comparative studies of BS1 sequences of *desi* and *kabuli* chickpea at protein level indicated difference in protein size with conserved TIFY domain. To understand the natural variation at the BS1 locus, allele mining using primer walking concept were done in the panel of chickpea genotypes (*desi*, *kabuli* and *wild*) varying in seed size and weight. sgRNAs specific to BS1 locus was designed and tested *in vitro*. Different sgRNAs targeting different positions of TIFY and CCT-2 domain were used for editing. Embryonic axis explants were bombarded independently and regenerants were established based on kanamycin selection in Plant Biosafety Level 1 Facility. Self seeds were harvested from established plants. Putative transgenic chickpea lines indicated increased in leaf size, stem length and seed weight as compared to wild type.

S4.30: Transgenic chickpea expressing insecticidal *cmVip3Aa* for resistance to gram pod borer (*Helicoverpa armigera* H.)

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Bacillus thuringiensis derived Vip3 proteins exhibit control against wide range of Lepidopteran pests. Vip3 genes are different from Cry toxins as they do not share any sequence homology and binds to different receptor sites in the insect midgut. The gram pod borer (*Helicoverpa armigera* H.) is major pest of chickpea that infest all growth stages and preferentially feeds on the chickpea pods. In the present study, we have evaluated the effectiveness of transgenic chickpea line expressing codon modified Vip3Aa toxin against this pest. The native *Vip3Aa* sequence was derived from NCBI data base (Accession Number L48811) and was codon modified for effective expression in chickpea. The synthetic codon modified *cmVip3Aa* gene was used for direct transformation of embryonic axis explants of chickpea (*cv*. DCP 92–3), with transformation efficiency of 4.30%. The detached leaf insect bioassay result for the selected transgenic chickpea lines indicated moderate toxicity against gram pod borer, however critical deformations in the growth parameters of the tested gram pod borer larvae was observed. Larval mortality (up to 39.75%) was recorded along with reduced larval feeding (up to 82.91%) and reduced larval weight gain (up to 68.23%) as compared to control lines (non-transgenic chickpea lines). The results obtained indicated effectiveness of cmVip3Aa toxin against gram pod borer and its suitability as donor in crossing with the present *Cry1Aabc* harboring chickpea lines for enhancing the effectiveness spectrum and delaying insect resistance.

S4.31: Speed Breeding of chickpea (*Cicer arietinum* L.) for rapid generation advancement

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Chickpea is a long day (LD) annual pulse and generation time is one of the major bottlenecks in the breeding program. Shortening of generation cycle using cost-effective methodologies are pivotal for enhancing *genetic gain* in chickpea for rapid development of varieties and faster fixation of traits. We report two pronged strategies in chickpea *viz*. 1. Extending the duration of light exposure (using fluorescent and LED) and manipulating temperature regime and 2. *In vitro* regeneration of green seeds, collected from field grown plants. A panel chickpea genotypes of varying maturity durations (JG14, JG11, JAKI9218, KWR108, KPG59, GNG1581, JG16, RVG202, JGK5, GCP105, RSG888, HC5, ICC96029, BGD9971, ICC96030, SA-1, BG3043) were assessed under fluorescent and LED lights (RED, WHITE and BLUE) fitted culture room programmed to 22/2 h (Day/night) photoperiod and 22/17°C (Day/night) temperature regime. Light levels were adjusted to 400-500 µmol m^{-2} s^{-1} at adult plant height and humidity was set to 60-70%. Chickpea genotypes responded to simulated conditions, with 50% flowering within a range of 40-60 days (raised under fluorescent light) and 35-45 days (raised under LED light) after sowing, and subsequent seed set with a span of next 30 days, in thirteen responding genotypes. Besides ratio of filled/ unfilled pods were higher in plants grown in LED light compared to fluorescent lights. In another intervention, pods at different stages of development have been harvested from field-grown chickpea plants of the panel, and the developing green seeds were subjected to germination. 20-24 days old immature chickpea seeds, after anthesis, were found suitable for germination under *in vitro* conditions. Taken together, these two strategies can significantly reduce generation time and accelerate seed to seed cycle for rapid generation advancement in chickpea.

S4.32: Marker Assisted Introgression of *Fusarium* Wilt Resistance Loci in Chickpea Variety PKV Kabuli 4

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Chickpea (*Cicer arietinum* L.) is an ancient and one of the most important pulse crop grown all over the world. However, the productivity of chickpea is limited due to fungal disease wilt caused by *Fusarium oxysporium* f. sp. *ciceris*. It has a potential to cause up to 100% yield losses in congenial condition. An average loss in Vidarbha is 8-15 %. In the present investigation, PKV Kabuli 4 genotype developed at Dr. P.D.K.V. Akola is being used as recurrent parent. Similarly, WR-315 is resistant to all races of wilt, well-proven resistance source which is used as a donor parent. Parental polymorphism survey was done using different polymorphic markers and identified the true crosses of chickpea. Identified putative QTLs of *Fusarium* wilt in F_2 population. Introgressed plants were selected in BC_1F_1 generation using informative markers. Selected the introgressed plants in BC_1F_2 generation using linked foreground markers and used for the execution of BC_2F_1 crosses. Recurrent parent genome recovery was calculated using the background markers in the BC_1F_2 generation. Gene targeted markers may provide an important and focused link between DNA sequence polymorphism and traits. The different molecular markers like SSR linked with *foc* genes can also be used for introgression of resistance in chickpea cultivars by marker assisted selection program (foreground selection). Markers mapping entire chromosomes of recurrent parents will be used for marker-based genome recovery studies (background selection). Long term objective is to develop Chickpea variety having Fusarium resistance, which can be used to mitigate the losses imposed by *Fusarium* wilt.

S4.33: Analysis and expression of *VrLEA* encoding genes in *Vigna glabrescens* reveal its role in heat tolerance

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Creole-bean (*V. glabrascens*) is a tetraploid species, identified as potential source of thermo-tolerance. The genome sequence of *V. glabrascens* is not done yet. Late embryogenesis abundant (LEA) genes are known to play role in adaptation to various abiotic stresses including high temperature. The LEA proteins were identified from their closely related species such as *Vigna radiata*, *V. angularis*, and *V. unguiculata*. The 55, 64, and 82 LEA genes were identified in mungbean, adzuki bean, and cowpea genomes, respectively; which were grouped into eight different classes. Our analysis revealed that the cowpea genome comprised of all eight classes of LEA genes, mungbean genome did not consist of LEA-6. Likewise, LEA-5 and LEA-6 were absent in adzuki bean. *In-silico* expression of these candidates in cowpea genome revealed their expression in different tissues including seeds under stress conditions. Four genes such as *VrLEA-2, VrLEA-40, VrLEA-47* and *VrLEA-55* were significantly up-regulated in *V. glabrascens* under heat stress indicated the basis of heat tolerance. The results of the present study increase our understanding of LEA genes and provide robust candidate genes for future functional investigations and basis for improving heat stress tolerance in *Vigna* crops.

S4.34: Molecular Assessment of Genetic Diversity in Mungbean [*Vigna radiata* (L.) Wilczek]

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Mungbean [*Vigna radiata* (L.) Wilczek] is an important food legume in India and is often considered as a rich dietary protein source. The present study assessed genetic diversity in 50 mungbean genotypes at the molecular level using forty SSR markers. Of these 40 SSR primers, thirty SSR primers were found polymorphic with 49 amplicons. Cluster analysis was carried out using the UPGMA (Unweighted Pair Group Method Using Arithmetic Averages) method of clustering. According to the dendrogram, all 50 mungbean genotypes were grouped into five major clusters, cluster I with 36 genotypes, cluster II with 3 genotypes, cluster III with five genotypes, cluster IV with four genotypes, and cluster V with 2 genotypes. However, these major clusters were further resolved into many sub-clusters among which cluster I have most of the sub-clusters. This study revealed that the SSR markers provide an easy and simple technique for preliminary genetic diversity assessment of mungbean genotypes. Moreover, this study reported that the cultivated mungbean genotypes have a narrow genetic base and there is a need to exploit an additional source.

S4.35: Detection and classification of yellow mosaic disease in *Vigna mungo* using convolutional neural network deep learning models

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The yield of the blackgram (*Vigna mungo*) crop is negatively impacted by Yellow Mosaic Disease (YMD). Both quantity and quality of the blackgram suffer significantly from this disease. Accurate diagnosis, flawless identification, and early detection will guide the cultivators for proper and timely management of the disease. Deep learning-based pre-trained models have revolutionized the classification and identification of plant leaf diseases in recent times. It is widely being used for plant leaf disease identification and classification using different models. In the present study YMD of blackgram has been classified using four deep learning models namely; DarkNet-19, SqueezeNet, AlexNet, and GoogLeNet. During the field investigation, datasets with images of three classes; healthy, moderate, and susceptible were collected, pre-processed, and augmented to create a set of 1100 images of each healthy, moderate and susceptible plants. Seventy percent of the images were used for the training of the models and thirty percent of the images were used for its validation. The results obtained for different deep learning architectures DarkNet-19, SqueezeNet, AlexNet, and GoogLeNet showed validation accuracy and loss scores of 96.09, 60.74, 94.41, and 93.85%, and 0.2319, 0.6923, 0.2429 and 0.1399, respectively. Thus, for the YMD disease classification in blackgram, DarkNet-19 showed the highest accuracy and SqueezeNet showed the lowest accuracy among the four models used in this study. This can be further utilized to detect the disease intensity (1-9 scale) in real time, using the computer vision system.

S4.36: Genetic diversity and population structure analysis in cowpea

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Cowpea (*Vigna unguiculata* L. Walp.) is an edible grain legume which is cultivated widely in tropical and sub-tropical geographical locations. Genetic diversity and population structure of 21 cowpea popular genotypes were evaluated using simple sequence repeat (SSR) molecular markers. Initially 144 primer pairs were used, out of which 71 gave polymorphic amplicons. A total of 184 amplicons with an average of 2.562 alleles per polymorphic marker was observed. The average effective number of alleles (Ne) was 1.928 alleles per genotype. Presence of higher Shannon's information index (I) of 0.651 is an indicator of higher diversity in the given set of cowpea lines. The total accessions were stratified into 2 groups (K=2) in population structure analysis. The phylogenetic analysis was also in accordance with the structure, as only 2 major clusters were formed. Our results provide a framework for future studies aimed at the conservation and management of cultivated cowpea germplasm in India, and a good starting point for the selection of parental lines for cowpea genetic improvement programs.

S4.37: Genetic Analysis of Yield and Yield Components using North Carolina Design-III in Lentil (*Lens culinaris* Medikus)

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The present investigation was undertaken at GBPUA&T, Pantnagar during *rabi* 2018-2021 crop season to release variability in form of BIPs from inter-varietal crosses using North Carolina Design-III. BIPs were developed from three lentil crosses *viz*., PL 6 x PL 8; PL 6 x L 4147 and L 4147 x PL 7 during 2018-19. BIPs along with $F_{2:3}$ progenies were evaluated in RBD during 2019-20 and data was recorded on 13 quantitative traits *viz*., 50% flowering, maturity, plant height, primary branches/plant, secondary branches/plant, pods/plant, pods/cluster, seeds/pod, seed diameter (mm), 100-seed weight (g), seed yield/plant (g), biological yield/plant (g) and Harvest index. The mean performance of bi-parental populations generated from all three crosses was greater than corresponding F_3 generations for all characters except days to 50% flowering and maturity in cross 'PL 6 x PL 8' and 'PL 6 x L 4147'. Analysis of variance for NC-III design revealed significant means sum of squares for females in sets, males in sets and interaction in sets for all traits studied except seeds/pod in all three crosses. Results indicated sufficient genetic variability in the experimental material for most of the traits. The genetic analysis of BIPs indicated the importance of both additive and dominance variance for all traits. Estimates of dominance variance were greater than the additive variance for all the traits except 100-seed weight. Therefore, selection in early segregating generations to improve these traits may not be effective and be delayed to later generations when most of the loci become homozygous.

S4.38: Influence of mesorhizobial strains on plant growth and symbiotic performance of chickpea (*Cicer arietinum* L.)

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Inoculation effect of three mesorhizobial strains namely *Mesorhizobium ciceri*, *Mesorhizobium mediterraneum* and *Mesorhizobium* sp. were evaluated in chickpea genotypes (BG 372 and BG 3022). All strains produced IAA whereas *M. ciceri* and *Mesorhizobium* sp. showed P-solubilization potential. A pot experiment was conducted using sterilized sand and vermiculite and observations on nodulation potential and plant growth in chickpea were recorded at different growth stages namely seedling stage, early vegetative stage, late vegetative stage, flower initiation stage, 50% flowering stage and harvest stage. At early growth stages (seedling and vegetative phase), nodules were round and white colour however, cylindrical and pinkish nodules were observed at flower initiation and 50 % flowering stage. Light microscopic images of chickpea root nodules showed V shaped bacteroids. Nodule fresh weight was peak at 50% flowering with *Mesorhizobium* sp. inoculation in BG 372 whereas in BG 3022, highest nodule fresh weight was observed at flower initiation stage. *In-planta* acetylene reduction activity of chickpea root nodules showed higher activity with *Mesorhizobium* sp. with BG-372 genotype (1003.33 nmoles of C_2H_4 /mg fresh weight nodule / hr) and *M. ciceri* with BG-3022 genotype (958.47 nmoles of C_2H_4 /mg fresh weight nodule / hr) at flower initiation stage. Positive correlation among nodulation potential, N uptake and plant growth was observed. Positive correlation among nodulation potential, N uptake and plant growth was observed. Our study gave the clear evidence that different *Mesorhizobium* strains vary with their performance and inoculation effect also differ with chickpea genotypes.

S4.39: Genetic diversity study using SSR markers in early maturing pigeonpea (*Cajanus cajan* L. Millsp) genotypes

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Pigeonpea, *Cajanus cajan* (L.) Millsp. (2=22) is the second most important pulse crop in India after chickpea. With the objective to explore the genetic variability of the crop the present study focuses on evaluating ninety-three early maturing (less than 140 days) pigeonpea germplasm accessions along with seven check varieties using 50 microsatellite or simple sequence repeat (SSR) markers. Molecular analysis revealed that the population was sufficiently diverse with an average allele frequency of 81.58 per genotype. The 50 markers yielded a total of 134 alleles with an average of 2.68 alleles per locus. The number of alleles ranged from 2 to 8. Out of the 50 SSR markers, 39 were polymorphic with average polymorphic information content (PIC) of 0.43 per marker. Highest PIC value was obtained for the marker CcM 2505 (0.86). Dendrogram obtained through cluster analysis based on Unweighted Pair Group Method with Arithmetic Mean (UPGMA) differentiated the accessions significantly into two major clusters which further comprised of different sub-clusters. Cluster I had higher diversity comprising of all the 93 genotypes under the study, as compared to cluster II, which comprised of the check genotypes. Hence prospective genetic variability of the population calls for subsequent marker-trait association studies in the accessions enabling selection of superior genotypes for different breeding objective such as higher yield, earliness, dwarf and determinate plant type, disease and insect resistance. The selected genetically diverse and superior genotypes will be utilized in hybridization programs for exercising background selections during trait transfer.

S4.40: Physiological responses and insight into expression of *Stay green related (SGR)* gene modulate delayed leaf senescence in *Vigna glabrescens* reveal its role in thermo-tolerance

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The leaf senescence is a phenomenon, which activates with aging and induced by the stress. An investigation was carried out to delineate the mechanism of thermo-tolerance in *Vigna glabrascens*. The leaf function and molecular responses were studied over the three different environments as control (35-38^{o}C), cold (20-30^{o}C), and heat (45-48^{o}C) stress. The higher leaf injury was clearly visible in the mungbean leaves whereas minor injury was recorded in TCR-20 under heat and cold. The delayed chlorophyll reduction was noticed in the *V. glabrescens* leaves whereas significant reduction in *V. radiata*. TCR-20 was able to maintain the RWC and MSI in both young and old leaves whereas drastic reduction was noticed in shikha under heat stress. The expression of stress related candidate genes revealed that the higher expression of SOD, POD and GST in young leaves over control, whereas the expression of CAT was found up-regulated in old leaves during the temperature stress, indicating their differential mechanism to maintain the thermo-stability. The *VrSGR-1* was significantly up-regulated in young leaves under heat (6-fold) and cold (7-fold); whereas about 3-fold up-regulation was noticed in old leaves during the temperature stress. The *VrSGR-2* was also expressed as similar to *VrSGR-1* in young leaves but expression was lower than the *VrSGR-1*. Whereas in older leaves, it was expressed as 3-fold increase under heat stress but it was down regulated under cold stress. The results provide the novel insight into SGR modulating delayed leaf senescence of older leaves and thermo tolerance in *V. glabrescens*.

S4.41: Chickpea long non-coding RNAs (lncRNAs): genome-wide discovery and functional prediction under salt-stress

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LncRNAs, also known as long non-coding RNAs, are significant RNA molecules with a length of 200 bp that plays critical role in controlling gene expression, especially in response to abiotic stresses. In this study, we discovered lncRNAs in chickpea roots that were activated by salt stress and hypothesized the complex regulatory functions of these lncRNAs. The distribution of 3452 new lncRNAs across the 8 chickpea chromosomes was discovered. 4446 differently expressed lncRNAs were found when salt-tolerant (ICCV 10, JG 11) and salt-sensitive cultivars (DCP 92-3, Pusa 256) were compared. We hypothesized that 3373 lncRNAs, would be cis-regulating their target genes, and 80 distinct lncRNAs were shown to interact with 136 different miRNAs as eTMs (endogenous target mimic) targets, implicating them in the regulatory network of the salt stress response. These lncRNA's association in targeting salt stress response-related genes, such as potassium transporter, transporter family genes, serine/threonine-protein kinase, aquaporins like TIP1-2 and PIP2-5, and transcription factors like AP2, NAC, bZIP, ERF, MYB, and WRKY, was revealed by functional analysis of the lncRNA. Additionally, 614 lncRNA-SSRs (simple sequence repeats) were discovered in chickpea as a new generation of molecular markers with greater specificity and efficiency. The comprehension of the whole functional role of possible lncRNAs will be facilitated by the overall findings, which will provide deep insight to the molecular basis of chickpea salt tolerance.

S4.42: Harvest Index used as a Tool in segregating populations for improvement of seed yield in Chickpea (*Cicer arietinum* L.)

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Present investigation was carried out in on F_1, F_2, BC_1 and BC_2 generations to study the harvest index in chickpea (*Cicer arietinum*). Four rows of each F_1, F_2, BC_1 and BC_2 generations of 8 different crosses were sown during *Rabi* 2021-2022. The plot size was 4.0 meter row length with row to row and plant to plant spacing of 30 cm x 10 cm. respectively. The observations were taken at physiological maturity for number of pods/plant, seed index, seed yield/plant (g/plant), biological yield/plant and harvest index on three randomly selected plants from each progenies of chickpea during *Rabi* 2021-2022 at Pulses Research Farm, CCSHAU, Hisar, Haryana. It is evident that among the different 32 segregating populations, F_1 cross combination namely (H12-22 x ICC 4958) recorded the highest harvest index (68.49 %) followed by BC_1 generation of the crosses namely (H12-55 x Pusa 547) x Pusa 547 (60.0 %), (H 12-55 x H 13-36) x H 12-55 (58.62 %) and H 12-22 x H 12-17) x H12-22 (58.49 %). Segregating population in early generation selection may be considered useful because it reflects higher yield in F_1 and BC_1 progenies were selected for high pod number, seed yield/plant and high harvest index. On the basis of above studied, it was concluded that the crosses involving H 12-55 as a parent are showing maximum harvest index ranging from 58.49 % to 68.49 %. Harvest index is the best and foremost effective selection criteria for improvement in seed yield.

S4.43: Identification of sources of resistance and validation of SSR markers linked to Fusarium wilt and Pigeonpea sterility mosaic disease in Pigeonpea (*cajanus cajan* (l.) Millsp.)"

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A set of 120 pigeonpea (*Cajanus cajan* (L.) Millsp.) genotypes was evaluated at the AICRP on pigeonpea ZARS, UAS, GKVK, Bengaluru during *Kharif* 2021 to identify resistant sources to Fusarium wilt (FW) and Sterility mosaic disease (SMD), to validate the markers linked to disease resistance, and to study genetic variability for yield-related traits. Based on the *per cent* disease incidence (PDI), seven and seventeen genotypes were found resistant to FW and SMD, respectively. The six genotypes namely ICPL 15023, ICPL 15063, ICPL 19467, ICPL 19482, ICPL 19489, and ICPL 19499 were found resistant to both diseases. A total of 13 markers linked to resistance to FW and 15 markers to SMD resistance were utilized for the validation study. Out of the total markers, seven markers (ASSR 23, ASSR 229, ASSR 363, CcGM 03681, HASSR 18, HASSR 121, and HASSR 128) and four markers (AHSSR 50, AHSSR 34, AHSSR 20, and CcM 0588) linked to resistance to FW and SMD, respectively, differentiated the resistant and susceptible genotypes effectively. High variability was observed in these genotypes in two different environments. High PCV, GCV, and heritability values were observed for yield traits in both environments and also across environments. K-means clustering analysis categorized the genotypes into eight clusters indicating substantial genetic diversity among the genotypes. The cluster IV contained resistant genotypes and high-yielding genotypes in cluster VIII. The genotypes with combined resistance namely ICPL 15023, ICPL19467, and ICPL 19489 also showed yield performance *on par* with the best check BRG3.

S4.44: Marker Assisted Pyramiding of Foc genes for developing wilt (*Fusarium oxysporum f.sp. ciceri*) resistant Pusa 372 Chickpea lines

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Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceri*) (FW) is a major disease that can cause up to 90% yield loss in Chickpea (*Cicer arietinum* L.). The presence of eight physiological races of *Foc* (0, 1A, 1B/C, 2, 3, 4, 5 and 6) makes it a complex task in the development of disease-resistant cultivar. Pusa 372 is a mega variety of *desi* chickpea with medium maturity duration and it has been extensively cultivated in the Central Zone of India has become susceptible to FW and yield has reduced drastically. Subsequently, the introgression lines developed in Pusa 372 using WR 315 as donor parent and were subjected to foreground selection using three SSR markers (GA16, TA 27 and TA 96), while 48 SSR markers uniformly distributed on all chromosomes, were used for background selection to observe the recovery of recurrent parent genome (RPG). Multi-location evaluation of 17 advanced introgression lines (BC_2F_3) in four locations (Amla, Badnapur, Sehore, New Delhi) for grain yield (kg/ha), days to fifty percent flowering, days to maturity, 100 seed weight and disease incidence was done using randomised block design in two replication. Multi Trait Stability Index (MTSI) results revealed that genotype (IL.) 1, 4 and 3 were stable for the multiple characters studied. But, based on GGE (genotype × environment interaction), the lines IL.11, 12 and 3 were identified for higher yield and better stability values. Based on MTSI and GGE, IL.3 may be considered as a stable line for multiple traits including yield superiority.

S4.45: *Agrobacterium rhizogenes*-mediated Transformation and Induction of Hairy Roots in Grasspea

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Grasspea is an important protein rich crop, possess climate-smart traits such as tolerance to drought and flood, and is adaptable to grow in any kind of soil. However, the presence of the neurotoxic compound 'â-ODAP' in its seeds and other plant parts hinders in utilizing its full potential as a climate-smart crop. Genetic modification is one of the approaches for improving grasspea. Efficient and rapid transformation is a prerequisite for genetic modification. Here, we report *Agrobacterium rhizogenes*-mediated transformation and induction of hairy roots in grasspea. Cotyledon explants with hypocotyl from five-day-old seedlings were used as explants. Hypocotyl formed callus 7-8 days after co-cultivation and hairy roots 11–12 days after co-cultivation in induction medium. Hairy roots grew very quickly and spread throughout the culture medium within 19 days after co-cultivation. Using this method, over 60% of infected explants produced hairy roots within one month after infection. Based on high transformation efficiency and rapid induction of hairy roots, this method represents a rapid and efficient platform for quickly performing gene function study or genome editing construct validation in grasspea.

S4.46: Screening and development of yellow mosaic disease resistant lines in soybean (*Glycine maxx*. L. Merill)

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Soybean is a grain legume recognized for its two-fold use as vegetable and oilseed giving both quality consumable protein (38-44 %) and oil (18-22 %). However the widespread occurrence of yellow mosaic disease influences its production negatively. Therefore, the study was conducted at College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India during *kharif* 2019-20 to identify diverse YMD resistance soybean genotypes. After phenotyping under field condition, molecular screening was performed by using 25 microsetellite markers to analyse the YMD resistant lines in soybean. A set of five gene-based markers were hand-picked for screening all the 60 soybean genotypes for Yellow Vein Mosaic Virus disease. A total of 17 alleles were discovered with a mean of 3.40 alleles per locus for different markers. The gene diversity varied from (0.5044 to 0.6128) Satt305 and Satt308 with a mean value of 0.5628 and Polymorphic Information Content (PIC) values varied from (0.4279 to 0.5359) with an average value of 0.4756, respectively. The primer which showed highest gene diversity and PIC values was Satt308 while the lowest gene diversity and PIC values was observed from the primer Satt305. The major allele frequency varied from Satt305 (0.6333 to 0.4667) Satt308, respectively, with a mean value of 0.5200. The SSR molecular markers with higher PIC worth might be utilized for screening of enormous quantities of germplasm line(s), which decrease the use of resources and the time resulted in high yielding soybean varieties with a low incidence of YMD.

S4.47: Genetic diversity, population structure and association analysis for the flowering trait in a diversity panel of Indian National Genebank moth bean (*Vigna acontifolia*) collection using genotyping by sequencing

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Moth bean (*Vigna aconitifolia),* is an underutilized heat and drought-tolerant legume, mainly grown in arid regions and is highly valued for its protein-rich seeds. Despite its economic importance, the crop is not explored at the genomic level due to the non-availability of sequence-based genomic resources such as SSRs and SNPs. In this study, we are reporting genetic diversity, population structure and marker-trait associations for the flowering in a large collection of moth bean (428 accessions) using genotyping by sequencing (GBS). A total of 9078 high-quality SNPs were identified through GBS and used for estimating diversity and association analysis work. The accessions belonging to the North-western region of India showed higher genomic variability than accessions from other regions implicating this region as its center of diversity and domestication. Association analysis using phenotyping data of five environments across two locations and using seven multi-locus models revealed 28 potential genomic regions associated with days to 50% flowering trait. Further, genomic localization of moth bean SNPs on the genome of closely related *Vigna* species demonstrated that moth bean is most closely related to *Vigna mungo*. The flowering related candidate SNPs/genes identified in this study can be validated further and exploited in moth bean breeding programs to develop early-maturity varieties.

S4.48: Generation of mutant population in grasspea (*Lathyrus sativus*) using Gama rays and Electron beam radiations

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Genetic variability was created in grasspea by subjecting 8000 seeds (1600 in each category of dose) of Mahateora variety to five doses (200, 300, 400, 500 and 600 Gy) of gamma rays and electron beam at BARC, Trombay, Mumbai and evaluated in the field along with non-treated seeds (control) during *rabi* 2021-22. Observations were recorded for germination, growth and reproductive behaviour. LD_{50} was determined to be at 300 Gy for gamma and 200 Gy for electron beam. Seedling data showed only 34.75 % plants emerged in the highest dose (600 Gy) of gamma rays followed by 41.18 % plants in 500 Gy. Further, 33.93 % (600 Gy) plants produced flower followed by 40.18 % (500 Gy) plants. Only 33.75 % plants (600 Gy) produced seed followed by 39.87 % (500 Gy) whereas maximum plants (64.0 %) produced seed in 200 Gy as compared to control (100 %). Similar trend was also noticed in electron beam treated grasspea seeds where only 0.38 % plants emerged in 600 Gy dose followed by 0.75 % plants (500 Gy) and 22.62 % plants (400 Gy). Only one plant could flower in highest dose (600 Gy) followed by two plants in 500 Gy. No seed set was observed in 600 Gy electron beam followed by 0.063 %, 0.25 % and 1.81 % seeds in 500, 400 and 300 Gy. Results clearly indicate that electron beam treatment was more lethal as compared to gamma rays. Seeds were collected separately to grow M_2 populations of both the treatments.

S4.49: An efficient hairy root system for genome editing of ODAP pathway genes in *Lathyrus sativus*

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Grass pea (*Lathyrus sativus)* is an ideal legume crop for resource-poor farmers, having resistance to various biotic and abiotic stresses. The pulse is rich in proteins and is the only known dietary source of homoarginine. It thrives with minimal inputs making it a promising crop in grain legume breeding programs with immense potential for food security. Despite these advantages, the global area under its cultivation has decreased because of the presence of an anti-nutrient compound, â-N-oxalyl-L-á,â-diaminopropionic acid (â-ODAP), which results in neurolathyrism both in humans and animals. Multiple efforts in the past have resulted in the development of improved varieties with low ODAP; however, due to variations in response to the environment, stable lines have not been developed for large-scale cultivation. Research efforts are scanty, and no tools for gene functional studies are available in this crop. In this work, we investigated the biological role of one of the ODAP pathway genes, Oxalyl-CoA Synthetase (OCS), by functionally complementing the *OCS* mutant of *Arabidopsis*. Further, functional characterization in the native system has been pursued by establishing a hairy root system where we have successfully demonstrated genome editing of the *OCS* gene. This system will be helpful for functional genomic studies of other ODAP pathway genes.

S4.50: Comprehensive BURP superfamily study in Chickpea revealed RD22 genes involved in salinity stress tolerance

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BURP domain-containing proteins constitute a novel identified unique plant-specific protein that plays a crucial function in plant development and metabolism response to various stresses. Many BURP domain-containing proteins, unique to plants, have been identified through systematic categorization & reported in various species. The BURPs are still explorative and no systematic investigation, or inclusive analysis, done so far. Here a complete set of fifteen BURP genes in total were identified. These genes consist of assorted structures and were allocated on chromosomes 2, 4, 5, 6, 7, 8, and Scaffold 653. On analyzing the phylogenetic relationships, these BURPs were classiûed into four subfamilies, of which one is identified as a new subfamily, BURP18. Motif analysis, gene structure study, stress and hormone-related cis-element analysis in promoter regions, co-expression network analysis, and quantitative expression studies of CaBURPs were also performed. The results here depicted a comprehensive profile of the Cicer BURP gene family and provided the preliminary step towards the assortment of CaBURP genes for cloning and functional analysis in *Cicer arietinum*. Their expression profiles in various tissues and in different stress conditions were analyzed and validated by interacting genes using qRT-PCR. The data predicted an insight into the evolution of the BURP gene family and proposed that numerous such genes may be important for plants to combat stress conditions. The growth process in a plant involves cell wall expansion. Here, we have shown that CaRD22 interacts with CaEXPA, a beta-expansin to predictively participate in cell wall loosening preferably associated with stress tolerance.

S4.51: Biofortification in pulses with micronutrients through genomic approaches

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Micronutrient malnutrition, also called "hidden hunger," is a form of malnutrition caused by a lack of micronutrients in the diet. Agricultural production methods fuelled by green revolution efforts has replaced traditional food crops that contained higher quantities of protein and vital micronutrients. Crop productivity and yield have greatly increased as a result of the extensive use of advanced technology in agriculture nutritional quality of crops get reduced significantly. Due to this, millions of people worldwide now unable to consume the recommended daily amounts of protein and micronutrients, leaving the other half of the world's population deficient in nutrients. It affects a large proportion of the world's population, including women and pre-school children in countries with a high dependence on staple crops. For the relief of micronutrient deficiency, biofortification of pulses through wide hybridization and modern biotechnological approaches offers a cost-effective and sustainable solution. By using transgenics in the appropriate pathways or by using them during processing, it is also possible to improve the bioavailability of current or biofortified micronutrients. Transgenic breeding was less explored in pulses for biofortification and few pulses like chickpea, common bean, soybean, and lupines are modified to overcome malnutrition. The basic aim of biofortification of pulses through transgenic breeding is the enrichment of essential amino acids, iron and zinc fortification, and reduction of anti-nutrients compounds. NBTs rely on gene silencing, gene silencing, gene editing, overexpression, and gene transfer from other species for the acquisition of balanced nutritional profiles in mutant plants.

S4.52: CRISPR/cas9 based genome editing to improve yield and symbiotic nitrogen fixation in Chickpea

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Most of the cultivated chickpea genotypes produce 1-2 seeds per pod but the seed size varies from genotype to genotype. *Cicer cuneatum* produces 5-6 seeds per pod but fails to cross with cultivable genotypes of *C. arietinum*. To break the yield barrier in chickpea, we are utilizing CRISPR/ cas9 to knockout CKX gene coding for Cytokinin dehydrogenase. Cytokinin dehydrogenase plays a key role on metabolic degradation of cytokinin. Genome-wide analysis indicated the presence of 10 CKX genes in chickpea genome. Transcriptome analysis using RNA-seq data of 27 tissues (chickpea transcriptome atlas) indicated that three CKX genes are expressed profusely in flower tissues. Genetic variations (SNPs/InDels) in 10 CKX genes were surveyed using re-sequencing data of chickpea minicore and wild species. Results indicate that the casual variants are observed in *C. echinospermum* and few missense mutations were identified in functional domains (FAD and Cytokinin binding domain). Similarly, host legume-genetic factor responsible for symbiotic efficiency is a hurdle on establishment of effective symbiotic nitrogen fixation in field environment. Though large diversity of (Nodule-specific Cystiene Rich) NCR genes in model legumes *viz., Medicago truncatula* and *Aeschynomene* was revealed; only few of them were assigned with biological functions. Availability of rich genome sequences of chickpea gave an opportunity to employ reverse genetic approach to reveal the biological function of NCR genes. Two NCR genes from chickpea were selected based on high level nodule-tissue specific expression and analyzed for the presence of PAM sites and gRNA were designed using CRISPOR tool.

S4.53: Genome wide association study (GWAS): Its importance and application in crop Improvement

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To fulfil the food requirements of an expanding population of human, with its enhancing income levels and nutritional requirements, more food production is required. Plant breeders efficiently detect and incorporate desirable character into crop plants to meet demand. Whole genome sequencing has been widely accessible in a vast range of species exhibiting phenotypic variances as a consequence of the gradually declining cost of DNA sequencing, encouraging the use of genome-wide association studies (GWAS), in the area of plant breeding. Almost all commercially significant crops, including mung bean, corn, sorghum, millet, and rice, have undergone GWAS for the selection and enhancement of beneficial features. A technique known as a genome-wide association study (GWAS) is used to investigate relationships between a group of single-nucleotide polymorphisms (SNPs) and desired phenotypic attributes. On the basis of linkage disequilibrium (LD) through genotyping and phenotyping of different individuals, quantitative evaluation is perform. Early in the twenty-first century, new high-throughput DNA sequencing technology and associated "-omics" methods underwent a fast development that is now transforming several fields of biology. Due to these advancements, it is now possible to conduct previously unachievable investigations on the genetic basis of abiotic stress tolerance in crop plants. Many of these legume crops, a number of which have a long history of supplying nutritional and food security to people living in semiarid locations with poor soil fertility, are "orphan" or understudied or "orphan" crops. In this abstract, we summarise the basics of GWAS, their applications and underlying statistical models.

S4.54: Next generation breeding for climate-smart pulses: current status and future opportunities

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The notions of food production, food security and climate change are intrinsically linked. The rapidly escalating world population in conjunction with changing habits of global food consumption under the climate crises on the rage poses daunting challenges for acclaiming sustainability and security in global food sector. Pulses are multipurpose crops, inherently perceptive to climate struggles due to their adaptive calibration of nitrogen fixation abilities and can contribute to mitigating their effects, besides being economically viable sources of plant proteins. Given their pivotal role in agricultural ecosystems, substantial research has been invested to boost the productivity of pulse crops. Futuristic goals aimed at further improvement of pulses has become imperative in the vigorously transitional global scenario where formidable anthropogenic activities are triggering irreplaceable depletion of natural resources. Lately, next generation sequencing has been viewed as the valve of becoming in the molecular breeding arena, for enhancing the genomic resources in pulse crops with the deployment of high-throughput DNA markers, candidate genes and QTLs for predicting plant phenotypes and whole genome sequences. Application of NGS to generate *de novo* transcriptome and whole genome assemblies, refinements in DNA sequencing technologies and computational analytical tools, along with the varied array of sequenced pulse genomes available now, offer novel insights on crop evolution and breeding history. Integration of new generation omics-facilitated crop improvement programmes for climate resilience with generation acceleration procedures like genomic selection and speed breeding could greatly accelerate progress in the genetic upgradation of pulses to emerge as climate smart crops.

S4.55: Development of robust and effective *Agrobacterium*-mediated genetic transformation system for CRISPR/Cas9-based genome editing in pea (*Pisum sativum* L.)

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Pea (*Pisum sativum* L., 2n = 14), belongs to the family Fabaceae (Leguminosae), is one of the most important legume crops having a narrow genetic base owing to self-pollination, making it difficult to develop novel cultivars. Conventional breeding techniques for crop improvement are inefficient, time-consuming, and complicated in pea. To overcome this challenge, CRISPR/Cas9 genome editing technology is gaining more importance. Many researchers have tried to develop an efficient genetic transformation system for pea, but these attempts have been characterized by low transformation efficiency and reproducibility. This study aims to optimize *Agrobacterium*-mediated transformation by refining several parameters like explants selection and *in-vitro* regeneration. In this study, three explants were used for *in-vitro* regeneration: cotyledonary nodes (CN), embryonic axis, and nodal segment, with CN being the best with the highest regeneration efficiency (30 shoot buds/explant). Therefore, CN was used for *Agrobacterium*-mediated transformation. Following that, the GUS Histochemical assay and PCR analysis were used to validate the identification of positive transgenic plants. The *phytoene desaturase* (*PDS*) gene mutation or knockout impairs photosynthesis and carotenoid biosynthesis, resulting in albinism and plant growth retardation, and is used as a marker gene for the CRISPR/Cas9 platform. Following that, an *Agrobacterium*-mediated plant expression vector for Cas9 nuclease and multiple gRNAs targeting the *phytoene desaturase* (*PsPDS*) gene were used to validate the CRISPR/Cas9 system's efficiency. The shoots of putative transformants were analysed by vector-specific primers and tested positive by sequencing. The optimized parameters for genome editing will be further utilized for the genetic improvement of various pea traits.

S4.56: CRISPR/Cas9 technology in genetic improvement of legume crops for quality food and nutritional security

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Targeted genome editing using CRISPR/Cas9 technology can provide novel avenues for functional genomics and a solution to certain constraints of different food legume crops. This technology has broadened the options to modify, delete or correct specific regions of DNA in plant cells efficiently with high precision. The ICRISAT utilizes this technology in chickpeas to improve yield, seed size, and quality. Recently, the CRISPR/Cas9-mediated gene editing technology has been successfully used in cowpea (*Vigna unguiculata*) for the disruption of symbiotic nitrogen fixation by targeting a symbiosis receptor-like kinase gene. The success of CRISPR/Cas9 in the genus *Vigna* suggests that gene editing can be applied to other *Vigna* species such as greengram, blackgram, ricebean. Abiotic stress tolerance, disease resistance, and quality traits would be some of the early targets for gene editing in these crops. This technology combined with traditional breeding techniques could significantly improve the food quality in addition to higher yield. Development of high yielding varieties with different desirable characteristics such as herbicide resistance and higher carotenoids content in chickpea, removal of the allergens in pea, removal of the major anti-nutritional factors (tannins, vicine, convicine, etc) in fababean, removal of the unpleasant beany flavor of soybean seed products and resistance to soybean mosaic virus can be early possible by CRISPR/Cas9 technology. However, the successful application of this technology for food legumes improvement will depend on the availability of efficient protocols for plant transformation and regeneration of whole plants, along with a favorable regulatory framework and public acceptance of gene-edited crops.

S4.57: Identification of novel genes associated with herbicide tolerance in Lentil (*Lens culinaris* ssp. *Culinaris* Medik.)

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Weeds are a major constraint in lentils, causing significant yield losses. Manual weed management is laborious and expensive. Therefore, the development of herbicide tolerant lentil cultivars is essential to improve lentil productivity. Sources of tolerance to herbicides were identified in lentil; however, field selection is slow and requires validation. Marker assisted selection (MAS) is effective to increase selection accuracy at early generation. This study was aimed to identify SNP markers associated with herbicide tolerance. We phenotyped 292 lentil accessions against different dosages of metribuzin and imazethapyr at Marchouch and Terbol from 2013/2014 to 2019/2020. The best linear unbiased phenotypic estimates (BLUPs) were obtained using REML model for all accessions. Highly significant differences among accessions were observed for herbicide damage score (HDS), herbicide reduction (RI) for days to flowering (DF) and maturity (DM), yield (SY), pods numbers (NPP), and seeds numbers (NSP). A total of 10271SNPs markers uniformly distributed across lentil genome were assayed using Multispecies Pulse SNP chip developed at Agriculture Victoria, Melbourne. The identification of associated markers was attempted using meta-GWAS. Only 125 SNPs markers were highly associated with measured traits. Among them, a single SNP marker was highly associated with HDS ($\log_{10}(p)$= 6.3), four SNPs with RI_{DF}($\log_{10}(p)$= 5.6 to 9.3), three SNPs with RI_{DM} ($\log_{10}(p)$=5.4 to 9.1), and finally 14 SNPs with RI_{NPP} ($\log_{10}(p)$=5.2 to 8.1). These highly significant markers were dispersed in chromosomes 1, 2, 4, 5, 6 and 7. These results would be useful to initiate MAS for herbicide tolerance in lentils.

S4.59 Identification, Characterization and gene expression of *ZIP* gene family in Pulses

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Zinc deficiency afflicts up to 40% of the world's human population, mainly in developing countries where people depend on cereal-rich diets for sustenance, metals are transported from the soil into the root and then must cross both cellular and organelle membranes as they are distributed throughout the plant. Specific metal transporters are required. Such understanding will require knowledge of how metal levels are sensed by plants and how metals control gene expression. In the present study primers for metal transporter gene *ZIP* was designed by IDT tool. Basic nutrient was provided to pulses including *Lens culinaris* and *Glycine max* using Hoagland solution, cDNA libraries were prepared which resulted in *ZIP* gene characterized by its protein sequences, amino acid composition and also analyzed through phylogenetic tree and multiple sequence alignment. The expression analysis was performed by Q-PCR using cox gene as an control. Gene expression was seen by using cDNA from all treated and *untreated L. culinaris* and *G. max* seedlings when subjected to different concentrations i.e., 100mM, 150Mm and 200 mM for 6hr, 12hr and 24 hrs respectively. The expression of zip gene of zinc treated versus control (untreated) of seedlings was calculated using BioRad IQ-5 software. In *L. culinaris* level of zip gene expression was highest at 100 mM for 24 hr (10.06 fold) followed by zinc treatment at 150 mM for 24 hr (8.93 fold) and 200 mM 6 hr (7.06 fold) and lowest at 150 mM for 12hr (3.06 fold) and in *G. max* the highest level of gene expression was obtained at 6 hr whereas, lowest expression level was obtained for 24hrs of zinc treatment, For 150 mM of zinc treatment the transcription level of *ZIP* gene was highest at 12hr whereas, lowest expression level was obtained for 24hrs. For 200 mM of zinc treatment, the highest level of gene expression was attained for 6hr while expression gradually declined for 12hr and 24hr Overall ZIP gene expression were highest at 100 mM for 6hr (2 fold) and lowest zinc treatment at 150mM for 24hr (0.65 fold). From such type of studies, it can be concluded that identifying and characterizing such genes will be helpful in biofortification studies.

Revisiting the Roots

S5.1: Organic blackgram productivity as influenced by the application of organic and liquid manures

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Good management practices increase the yields of the pulses and economic value especially, under the fully organic conditions. The integration of liquid and solid fertilizers and enrichment of the available sources ensures improved nutrient availability throughout the crop growth period. Field experiments have been conducted to evaluate the nutrient management techniques in organic blackgram during winter and *kharif*, 2022 in Wetlands, Tamil Nadu Agricultural University, Coimbatore. The experiments were laid out in split plot design replicated thrice which comprised of organic manures in the main plot: M_1- Farm Yard Manure @ 12.5 t ha^{-1}, M_2- vermicompost @ 2.5 t ha^{-1}, M_3- enriched FYM @ 750 kg ha^{-1} and M_4- enriched vermicompost @ 1 t ha^{-1} and foliar sprays of liquid manures at first flowering and 10 days after 1st spray: S_1- Panchagavya @ 3%, S_2- fermented egg extract @ 5%, S_3- fermented fish extract @ 5%, S_4- farmers effective microorganisms @ 5% and S_5- Jeevamruth @ 5%. Grain yield was sizeable during Experiment-I (829 kg ha^{-1}) and II (873 kg ha^{-1}) with the application of vermicompost @ 2.5 t ha^{-1} + Panchagavya @ 3% spray twice while it recorded lower value with the application of FYM @ 12.5 t ha^{-1} + Fermented egg extract @ 5% spray. Yield parameters like the number of clusters $plant^{-1}$, number of seeds pod^{-1}, pod length (cm) and haulm yield (kg ha^{-1}) recorded similar trend. Non significant response was found in test weight (g) and harvest index during both the experiments.

S5.2: Soil fertility and horse gram (*Macrotyloma uniflorum*) productivity as affected by different methods of jeevamrit application under mid hills of Himachal Pradesh

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A field experiment was conducted during *kharif* 2019 at experimental farm of Himachal Pradesh Krishi Vishvavidyalaya, Hill Agricultural Research and Extension Centre, Bajaura, Kullu, India to study the effect of methods of jeevamrit application on soil fertility and productivity of horse gram. The experiment comprised of nine treatments with three levels of jeevamrit as soil application (0, 500 and 1000 l/ha) and three levels as foliar application (0, 5 and 10 %), evaluated in Factorial Randomized Block Design. Results revealed that the soil application of jeevamrit exhibited significant effect on soil fertility whereas on contrary its foliar application did not manifest any significant effect. With increase in levels of soil applied jeevamrit, available N, P and K significantly improved and their maximum (260.4, 66.8 and 192.4 kg/ha, respectively) build up was observed with soil application of jeevamrit @ 1000 l/ha and minimum in control. Besides productivity of horse gram was found to be significantly influenced by different levels of soil and foliar applied jeevamrit. Highest grain and straw yield (12.8 and 14.9 q/ha, respectively) was recorded with 1000 l/ha of soil applied and 10 percent foliar applied jeevamrit whereas the lowest was recorded in control. Furthermore, the yield attributes were also significantly influenced by soil and foliar applied jeevamrit wherein the highest plant height, number of pods/plants, number of grains/pod and 100 grain weight were reported in the treatment corresponding to 1000 l/ha of soil applied jeevamrit with 10 percent of its foliar spray.

S5.3: Effect of organic sources of nutrients in Blackgram (*Vigna Mungo* L.) under mid-hill conditions of Himachal Pradesh

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Pulses are an important group of crops in India. In India, pulses are generally cultivated as rainfed crops. Among all the pulses, blackgram (*Vigna Mungo* L.), is one of the important pulse crops, grown across the country. In order to evaluate the effect of organic sources of nutrient on growth and yield of blackgram a field experiment was conducted at Research Farm, Department of Organic Agriculture and Natural Farming, CSKHPKV Palampur during the *Kharif* season 2021, The experiment was laid out in RBD comprising of eight treatments with different combinations [T_1 - *Bijamrita* + *Jiwamrita* (5%, 10%, 10%, and 10%, respectively at time of sowing, 21, 42 & 63 DAS) + Mulching (10 t/ha), T_2 – *Bijamrita* + *Ghanajiwamrita* (250 kg/ha) + Mulching (10 t/ha), T_3 - *Bijamrita* + *Jiwamrita* (5%, 10%, 10%, and 10%, respectively at time of sowing, 21, 42 & 63 DAS) + *Ghanajiwamrita* (250 kg/ha) + Mulching (10 t/ha), T_4 - Farm yard manure (10 t/ha), T_5 - Farm yard manure (10 t/ha) + *Ghanajiwamrita* (250 kg/ha), T_6 - Biofertilizers (*Rhizobium* + PSB) + Farm yard manure (10 t/ha) + Vermiwash at 15, 30 & 45 DAS (1:10), T_7 - Biofertilizers (*Rhizobium* + PSB) + Vermicompost (7.5 t/ha) + Vermiwash at 15, 30 & 45 DAS (1:10), T_8 - Absolute control]. The highest values of plant height, dry matter accumulation, absolute growth rate, yield attributes, grain yield, gross and net returns were recorded in T_7 whereas the highest benefit cost ratio was recorded in T_6 treatment.

S5.4: Growth and yield of urdbean [*Vigna mungo* (L.) Hepper] influenced by vermicompost and vermiwash

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At Agronomy farm, S.K.N. College of Agriculture, Jobner (Rajasthan) a field experiment was carried out during *Kharif*, 2020 on loamy sand soil. The experiment comprising 20 treatment combinations with different doses of vermicompost and vermiwash was carried out in a 3 times replicated factorial randomised block design. Results revealed that application of vermicompost 4.5 t/ha significantly enhanced the growth attributes of urdbean *viz.*, plant height, number of branches/ plant, dry matter accumulation at 50 DAS and at harvest and LAI (leaf area index) also yield attributes *viz.* number of pods/plant, seed/pod and test weight were recorded superior with this treatment over preceding levels. It also recorded significantly higher seed, stover and biological yields (940, 1920 and 2860 kg/ha) over lower levels. Results further showed that application of vermiwash 10 % foliar spray at the time of flower initiation stage also resulted in significant increase in the above mentioned parameters. It was further concluded with the experiment that application of vermicompost 4.5 t/ha and foliar spray of vermiwash 10 % were found at par with the following levels of vermicompost 6.0 t/ha and foliar spray of vermiwash 15 % regarding growth parameters and yield of urdbean.

S5.5: Effect of organic practices on productivity and profitability of pulse-based system in comparison to the inorganic management

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A fixed plot field experiment on pulse-based cropping system was taken up to develop the package of practices for improved cultivation following organic cultivation since 2017. Two cultivation practices were followed involving organic and inorganic/recommended practice with the main crop of pearl millet during *kharif* and two packages (normal and maximum yield research involving foliar supplement for sub factor, only during *rabi*) with chickpea and wheat were selected in order to optimize yield under the existing agro-ecosystem defined by existing soil and climatic condition. Under organic packages, nutrients were supplemented with farmyard manure (FYM) and FYM+biophos+biozinc+vermiwash along with need based organic plant protection measures against pests and diseases. Results indicated that significantly higher yield in wheat (5.73 t/ha) can be realized through organic practice only (FYM+biophos+biozinc+vermiwash). The higher economic gain in terms of gross returns and B:C ratio (1.83) was recorded under organic cultivation compared to the conventional in green manure-wheat-mungbean cropping system. Organic with foliar application of biophos and biozinc significantly increased *Cyperus rotundus*, *Chenopodium album*, *Coronopus didymus*, *Medicago denticulata* than inorganic fertilization in wheat. Organic practice (FYM) had higher total narrow-leaved, broad-leaved and total weed density than inorganic fertilization in chickpea. The organic practices had higher productivity and profitability in chickpea over the inorganic practices under pearlmillet-chickpea system.

S5.6: Comparative economic analysis of organic and inorganic farming using Levene's test approach: a case of low hills of Himachal Pradesh

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The present study was conducted to examine the comparative economics of organic and inorganic vegetable farming in low hill zone of Himachal Pradesh. The simple random sampling technique was used to select a sample of 100 farmers. The Levene's F test was used in SPSS software to analyse the comparative economics of organic and inorganic cultivation of vegetable crops. The results of the study showed that the returns per hectare from organic vegetable farming are higher in cauliflower (Rs. 283588.43/ha), potato (Rs. 412750.00/ha) and tomato (Rs. 338541.66/ha) as compared to inorganic farming, whereas, in case of peas, inorganic cultivation gave higher returns (Rs. 230167.36/ha). It was observed that there exist significant differences in the returns obtained from organic and inorganic cultivation of the vegetables. The findings suggest that in order to achieve sustainability, we should switch to organic crop agriculture especially in vegetables. To implement organic farming with all of its benefits, the government should offer a number of programmes and other services.

Innovative Extension Approaches

S7.1: Development of seed entrepreneurs skill to the resource poor farmer under seed hub-pulses

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Pulses are mainly cultivated by the resource poor farmers in Tamil Nadu. Their standard of life is very low due to poor farm income. The seed hub project was introduced from 2016-17 onwards among the farmers to produce the quality seeds to enhance the pulses production through National Pulses Research Centre, Vamban, Pudukkottai, Tamil Nadu. The farmers are actively involved in contract seed production programme and increased farm income. Smt. Selvi, 52 years old woman actively involved in farming from Kurunthadimanai village of Alangudi (Tk), Pudukkottai (Dt) in an area of about 6.0 acres of land. She cultivated cereals and pulses for commercial purpose which was not remunerative. After, introducing seed hub scheme at National Pulses Research Centre (NPRC), Vambanwhich undergone skill development training programmes which created the awareness and practical know how on pulses seed production. She has taken up seed production of new pulses varieties and realized the seed yield of 750 kg/acre and obtained Rs. 75000/- per acre which is double fold increase in income than commercialproduction. Similarly, Thiru. Piramayan, aged 62, Nemmeli village of Pattukkottai Taluk, Thanjavur Dist., Tamil Nadu, basically a rice grower and Sri. Viswanathan, aged 56, Tindivanam, Villupuram Dist., Tamil Nadu, a foreign business man are actively involved in the pulses seed production and developed as successful seed entrepreneurs.

S7.2: Influence of rapid roving survey on pesticide usage pattern by farmers of pigeonpea bowl of Karnataka

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Kalaburagi is well known for cultivation of pigeonpea and is called as "Tur Bowl". However this crop in ravaged by many insect pests, among them pod borers are major threat. Farmers who have made effort to manage the pests using insecticides will get better yield. The chemistry of pesticides during last 25 years is very dynamic, availability of all groups of pesticides in the market and many times farmers were totally confusion to select right pesticides for management of major pests of pigeonpea. Therefore to guide and give precise advisory service at real time in the farmers field of kalaburagi district entire scientific team of Kalaburagi campus of UAS, Raichur is conducted rapid roving survey during flower initiation to pod maturity stage of pigeonpea at weekly interval since from 1998 to 2021 (24 years). In this survey scientist interact with the farmers on the field spot and educate the farmers regarding pest incidence level, their damage and management if necessary. More emphasizing on green chemistry molecules and safe handling of pesticides in the field itself. In this survey collected the data through interviewing the farmers of each taluk representing from varied villages in a defined schedule. The total 17068 farmers were interviewed and required information gathered during survey were compiled and analysed during the survey conducted from 1998 to 2021. Initially (1998 to 2002) the farmers used highest OP compounds (24.1%) insecticide group was followed by pyrithroids (15.68%) and Carbamates (14.34%) most of them have red symbol. In the next five years (2003-2007) the insecticides usage pattern was more inclined towards new insecticides particularly Indoxacarb (yellow) and Spinosad (blue) contributed 53.7%. The use of organochlorins, carbamates and OP compounds was declined. From 2008 to 2012 the real era of new insecticides usage was started with more safer insecticides 83.12%. In the next 9 years (2013-2021) use of Emamectin benzoate was increased to the extent of 70% and next wereChlorantraniliprole (9.7%) and flubendiamide (10.25%). On the other hand average pest damage was brought down from 35-45% (1998) to 5-8% (2020). At the same time average number sprays were also reduced from 9.35 (1998) to 1.90 (2020). Scientist efforts are played important role in bringing this radical change.

S7.3: Impact on yield and economics of fieldpea (*Pisumsativum L.*) through cluster frontline demonstrations in North East India, India

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Krishi Vigyan Kendra plays an important role in bringing the research scientists face to face with farmers. The main aim of KrishiVigyan Kendra is to reduce the time lag between technology generation at the research institution and its transfer to the farmers for increasing productivity and income from the agriculture and allied sectors on sustained basis.The study was carried out to assess the performance of cluster frontline demonstrations (CFLDs) in terms of grain yield, extension gap, technological gap and economic gains in field pea variety Prakash, Aman and Rachna in three states of North East i.e. Assam, Arunachal Pradeshand Sikkim during 2016-2020 in *rabi* season. KrishiVigyan Kendra of Assam, Arunachal Pradesh and Sikkim conducted 1901 demonstrations in 650 ha area, 710 demonstrations in 310 ha area and 70 demonstrations in 30 ha area during 2016-2020 respectively through improved production technology. The results reveal that the average yield of demonstration plots was highest in Arunachal Pradesh i.e 1488 kg/ha as compared to farmers' practices 839 kg/ha with 77.35 per cent increase in yield followed by Assam 1055 kg/ha and Sikkim 955 Kg/ha compared to farmers' practices. When economics viability was taken into consideration it was found that in Assam net return was Rs. 28539/- per ha, Arunachal Pradesh net return was Rs. 24928/- per ha and Sikkim 32155/- per ha was recorded under demonstration plot over farmer practices which is highly encouraging and it is suggested to adopt these technologies for sustainable production of field pea in North East India.

S7.4: Impact of seed hub on quality pulse seed production and productivity in Solapur district of Maharashtra

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To ensure the availability of location specific high yielding verities and quality seed, the Ministry of Agriculture and Farmers welfare, Government of India implemented the project entitled "creation of Seed Hubs for increasing indigenous production of pulses in India" during 2016-17 and provided funds for seed multiplication and infrastructure facilities across the country. Under this project seed hub pulses has been sanctioned to Krishi Vigyan Kendra Mohol, Dist. Solapur, working under Mahatma Phule Krishi Vidyapeeth Rahuri (MS). The objective of this programme was to increase indigenous production of pulses and make available quality improved, high yielding, climate resilient varieties to farmers, to achieve self sufficiency in respect of seeds at village level itself. Farmers of selected village for seed hub are working under the technical support and guidance of KVK scientists. They were trained technically and made more sound by adopting good agronomic practices to fulfill the objective. ICAR given target of 200qt for Kharif season and 800 qt for Rabi season every year to Krishi Vigyan Kendra Mohol (Solapur II). With respect to the target received, KVK Mohol produced 355.34, 567.59, 784.88, 528.50, 752.00 quintal seed production during the year 2016-17, 2017-18, 2018-19, 2019-20, 2021-22 respectively. Pigeonpea varieties BDN -711 and Phule Rajeshwari performed well and gave higher seed yield as compared to local and old varieties. Machine Harvesting of Chickpea can reduce cost of production, prevent risk of harvest losses, improve resource use efficiency and reduce drudgery for women who carry out the manual harvesting. Machine-harvestable chickpea varieties have the potential to enhance chickpea area and production, and can help reach the country's goal of self-sufficiency in pulse production as well as doubling farmers income. Due to wide acceptance by farmer there is huge horizontal expansion of chickpea variety Phule Vikram in the district. All procured seed of pulses (Pigeonpea and Chickpea) sold to the farmers through state Agriculture Department, Sale counter of MPKV Rahuri and KVK, Mohol.

S7.5: Impact of cluster front line demonstrations (CFLDs) on the productivity and profitability in summer green gram

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Front line demonstration is an appropriate means for demonstration of improved technology and innovations in agriculture for large scale popularization among the farming community. A three years study was carried out by conducting cluster front line demonstrations (CFLDs) at farmers' fields duringsummer seasons in various villages of Faridabad district of Haryana from 2019 to 2021. A total of 250 demonstrations were laid out in three years in an area of 100 ha by the active participation of farmers with the objective to demonstrate the improved technologies of pulses production potential. The improved technologies consisted of use of modern variety, seed treatment with biofertilizrs viz., *rhizobium* and PSB culture, chemical weed control, balanced fertilizer application and integrated pest management. Results showed that a very positive impact of CFLDs was on the yield and other aspects. Yield was recorded higher under demonstrated trials as compared to farmer's local practices. The average yield of 5620 kg/ha under improved technology was recorded in summer green gram for the years 2019 to 2021 than 4230 kg/ha under farmers practice. In spite of increase in yield of pulses, technological gap, extension gap and technology index was also existed. The improved technology gave higher gross return, net return with higher benefit cost ratio over farmer's practices. The result indicated that the cluster front line demonstrations (CFLDs) have given a good impact on summer green gram production in district Faridabad.

S7.6: Enhancing farmer's income through cluster front line demonstration of mungbean in transitional plain of inland drainage zone of Rajasthan

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The mungbean (*Vignaradiata)* is a superb source of high-quality protein (25%), which significantly contributes to boosting the income of small and marginal farmers in Rajasthan's transitional plain inland drainage zone. Due to the non-adoption of the recommended package of methods, low yield and profitability are two key obstacles to traditional Mung bean growing. One of the most effective methods for transferring technology is cluster front line demonstration (CFLD). In order to popularise better mungbean production technique, CFLDs were held at farmer's fields by KrishiVigyan Kendra, Nagaur-I under the Agriculture University, Jodhpur (Rajasthan).With a coverage area of 10 hectares, a total of 25 Cluster Front Line Demonstrations (CFLDs) were held in the Nagaur district's Roon village. Use of the improved variety (IPM 2-14), line sowing, balanced fertilizer application, efficient weed management, and integrated pest management are among the cultivation techniques covered by the CFLD. The local soil was a sandy loam with a pH of 8.5, limited organic matter, low phosphorus, and moderate potassium. The mungbean field demonstrations were conducted during Kharif-2021 on farmers' fields and the results showed that the average yield of the demonstrations was 1013 kg/ha, an increase of 22 % over the average farmer practices (831 kg/ha). The demonstrations reported average cultivation costs of Rs. 21365/ha, gross returns of Rs. 79369/ha, net returns of Rs. 58004/ha, and benefit cost ratio of 3.71:1, which were, respectively, 6.75, 31.29, 43.43, and 22.85% greater than farmers' practices.

S7.7: Development and validation of "Farmwomen Led Integrated Local Seed Network" model for improving availability of quality pulse seeds

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Traditional pulse growing areas are suffering from setback due to non availability of quality seeds at appropriate time and desired quantity. For meeting the seed demand, farmers have an unorganized seed network for sell and exchange of seeds informally with doubtful genetic purity. However the farmer seed network only provides local land races and some improved varieties in public domain. Hence, for improving the quality seed availability, development and validation of a viable local seed network is imperative. So, a pulse seed network model was developed and validated with small and marginal holder farm women of 6 villages of Nayagarh District of Odisha through suitable interventions in their seed networks operating at community level. The model was validated and obtained 73.0 % score. Farmwomen Led Integrated Local Seed Network Model being an inclusive model studies the viability and sustainability of the seed activities and ensures empowerment to farmwomen. The first stage of model deals with determining the value for cultivation and use by estimating yield stability, climate resilience and product quality of the potential local cultivar. Second stage of the model focuses on strengthening of local institutional mechanism through mobilization of village clusters for input internalization, quality control and marketing. Third stage of model necessitates institutional mobilization towards formation of business group, targeted aggregation and centralized processing, packaging, quality control, labelling and linkage with distribution network, branding, promotion and market access. However, the model needs to be tested in multiple locations and necessary location specific modifications will increase its usefulness.

S7.8: Enhancing production potential of pigeon pea through front line demonstrations in south eastern Rajasthan

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The pigeon pea [*Cajanuscajan* (L.) Millsp.] is the most important pulse crop in India and grown in Kharif season. Economically it is the second most important pulse crop after chickpea in India accounting for about 20 % of total pulse production. Low productivity of pigeon pea in India as well as Rajasthan is mainly due to non-adoption of improved technology. Looking to the above facts, ten demonstrations each year were conducted (Kharif, 2020 and 2021) to evaluate the impact of improved technology on productivity and profitability of pigeon pea in south eastern Rajasthan at farmer's fields. The soils of the region are poor in organic carbon (0.45±0.07) and available nitrogen (268 ± 6 kg/ha) but are low to medium in available P_2O_5 (24.2 ± 1.0 kg/ha) and medium to high in available K_2O (300 ± 6 kg/ha). Improved technology of pigeon pea includes full package of practices of the zone V (Humid south eastern plain of Rajasthan). PA-291 variety of pigeon pea was used for demonstrations. Each demonstration was taken in 1.0 ha area at different location of Hadoti region of south eastern Rajasthan.For assessing impact of improved technology (IT), the adjoining field with similar area cultivated to pigeon pea crop by the farmer himself was considered as control plot (Farmers practice). Mean data of two year revealed that pigeon pea yield (1380 kg/ha) increased by 26.37 % as compared to farmers practices.

S7.9: Quality seed production of pulses through seed hub project at KVK, Dewas

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To make India self-sufficient in pulses production through productivity enhancement, availability of quality seed needs special attention. Non availability of quality seed especially in pulses is a major constraint in enhancing production and productivity of these crops. This is primarily due to lack of organized seed production programme for pulses and poor seed multiplication rate. There is a need of about 25- 30 lakh quintals of quality seed every year to achieve 30% seed replacement rate to enhance production and productivity of pulse crops. To increase indigenous production of pulses and make available location specific improved / high yielding /climate resilient varieties to farmers, government, non-government organizations, Ministry of Agriculture and Farmers Welfare, Government of India implemented the project entitled "Creation of Seed Hubs for increasing indigenous production of pulses in India" during 2016-17 for ensuring timely availability of sufficient quantity of quality seed of pulses and provided funds for seed multiplication facilities across the country. Under this project, seed hub centre were also sanctioned to Krishi Vigyan Kendra, Dewas, Madhya Pradesh. Accordingly seed production of newly released and high yielding / farmer's preferred varieties were taken up as per the targets fixed in the farmers field through participatory mode by regular monitoring for ensuring genetic purity of seed. During the first two years of the project (2016-17 & 2017-18), seed production programme was taken up through the registered seed society of the district and hence no seed was procured from them. From 2018-19 onwards KVK itself was registered as a seed society and from there the seed was procured from farmers by the KVK and processing, packaging, tagging and marketing was done by KVK, Dewas. During 2018-19 to 2021-22, total 1885.58 q foundation (F1) and certified seed of different pulses like Urd bean (110.08 q), pigeon pea (2.64 q), chick pea (1734.30 q) and moon bean (38.56 q) was produced by KVK Dewas at farmer's field. From the economic point of view, it was also observed that farmers earned Rs 1,58,18,356 as additional income from seed production.KVK got total gross amount of Rs. 1,44,09,375 from pulses seed production programme during four years (2018-19 to 2021-22) while the net profit was Rs. 45,07,641. The profit generated out of seed sale has been utilized by Seed-Hub for development of additional facilities/workforce as needed for scaling quality seed production of pulses.

S7.10: Impact of improved mungbean variety on farmer's income and nutritional security

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During 2016-2021, frontline demonstrations on improved variety of mungbean i.e. IPM-2-14 were conducted in selected farmers' fields of Dharwad district, Karnataka State, India. During early summer most of farmers used to cultivate local cultivar of mungbean known as *"Kari-hesaru"* characterized by small seed size with black seed coat color, highly susceptible to yellow-mosaic virus disease and low in seed yields. Lower mungbean yields with non-availability of improved mungbean varieties in the region have led to reduction in area of mungbean cultivation in paddy fallows during early summer season by the farmers in the region. Transfer of technology of improved mungbean cultivars through front line demonstrations were conducted by ICAR-IIPR Regional Research Station along with University of Agricultural Sciences, Dharwad in farmers' fields with supply of improved variety seeds of mungbean i.e. IPM-2-14. Due to the introduction of improved mungbean variety, the area under cultivation of late rabior early summer mungbean in Dharwad district has increased substantially. Farmers were able to harvest mungbean yield of 8-10 q ha^{-1} with the cultivation of IPM-2-14 variety in 65-70 days. The local cultivar "*Kari-hesaru*" produced meagre yield of 2-3 q ha^{-1} in around 85-90 days duration. The cultivation of improved mungbean variety i.e. IPM-2-14 produced higher yields with greater net returns for the farmers and also served as food and nutritional security. The frontline demonstrations conducted on mungbean variety i.e. IPM-2-14 at the farmers' fields revealed that the adoption of this improved variety coupled with improved production technologies significantly increased the crop yields and produced higher net returns to the farmers. The improved mungbean variety i.e. IPM-2-14 was short duration, resistant to yellow mosaic virus (MYMV) and high yielding and this has led to its greater adoption in the farmers' fields during late rabior early summer in the region.

S7.11: Impact of cluster frontline demonstrations on yield and economics of redgram

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Redgram is commonly known as Tur or Arhar in India and is the second important pulse crop in the country after gram (chana). The ability of redgram to produce high economic yields under soil moisture deficit makes it an important crop in rainfed and dry land agriculture. ICAR-Agricultural Technology Application Research Institute (ATARI), Zone-X conducted 3318 cluster frontline demonstrations on redgram in an area of 1371 ha through the KVKs of the zone during 2019-22 under National Food Security Mission (NFSM) with the objective of increasing the productivity and profitability of redgram and to reduce the yield gap. Results revealed that the average redgram yield registered under the demonstration was 10.76 q/ha with improved technologies in comparison to 8.6 q/ha under farmer's practice with an increase of 25.11%. The average gross returns (76025 Rs/ha), net returns (50411 Rs/ha) and B: C ratio (2.87:1.0) recorded were more under demonstration when compared to farmers practice (48180 Rs/ha gross returns, 22751 Rs/ha net returns and 1.86:1.0 B: C ratio). The average increase in net income was 27660 Rs/ha with the demonstrated technologies. Regarding the yield gap analysis, average extension gap of 2.16 q/ha, technology gap of 14.23 q/ha and technology index of 56.93% was recorded. The extension and technology gap could be reduced further by conducting large scale demonstrations paving the way for horizontal spread through location specific research strategies for different farming systems thereby increasing farmers' income and attain self-sufficiency in pulses production in our country.

S7.12: Impact of cluster frontline demonstrations on yield of greengram during 2021 and 2022 in Bhiwani (Haryana)

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Krishi Vigyan Kendra Bhiwani conducted cluster frontline demonstrations (CFLDs) on Green gram during the year 2021 and 2022 in and 3 and 5 villages, respectively. The study reveals that the variety MH-421 recorded average grain yield (9.11q/ha) which was (22.17%) higher over the farmers' practice (7.09q/ha). The average grain yield in demonstration during 2021 and 2022 recorded was 10.47q/ha and 7.75q/ha, respectively. Average grain yield in the check during 2021 and 2022 recorded was 8.02q/ha and 6.17q/ha, respectively. There was 60% gap in adoption of improved variety MH-421, 85% in seed treatment, 95% in fertilizer application and 65% in proper and timely weed management.

S7.13: Impact of cluster frontline demonstrations on yield of chickpea during 2019-20 and 2020-21 in Bhiwani (Haryana)

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Krishi Vigyan Kendra Bhiwani conducted cluster frontline demonstrations (CFLDs) on chickpea during the year 2019-20 and 2020-21 in 5 and 4 villages, respectively. The study reveals that variety CSJ-515 recorded the average grain yield (18.12q/ha). It was 29.88% higher over the farmer's practice (12.71q/ha). Average grain yield in demonstration recorded was 21.25and 15.0q/ha during 2019-20 and 2020-21, respectively. Average grain yield in farmers' practice recorded was 14.75 and 10.67q/ha during 2019-20 and 2020-21, respectively. There was 90% gap in seed treatment between recommended and farmers' practice, 90% in fertilizer application, 95% in biofertilizer (Rhizo+PSB) application, 98% in proper and timely weed management, 95% gap in *Helicoverpaarmigera* management.

S7.14: Performance of chickpea (*CicerArietinum* Linn) as influenced by cluster front line demonstration in Alwar district of Rajasthan

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For promoting and encouraging farmers for pulse production in the country the Ministry of Agriculture and Farmers Welfare, Govt. of India had initiated a nation-wide Cluster Frontline Demonstration (CFLD) program under National Food Security Mission-Pulses (NFSM-Pulses) since 2015-16. The scheme is implemented in a mission mode through a farmer centric approach. The scheme aims to target the selected village by making available the improved technologies in integrated crop management mode. Average productivity of Chickpea in Alwar district have very less than the potential yield (2500 kg/ha). The present investigation was carried out to evaluate the performance of improved variety with the scientific package of practices (POP) on production, productivity and profitability adoption and horizontal spread of chickpea. The KVK, Navgaon (Alwar-I) was conducted CFLDs on Chickpea variety CSJ 515 at farmer field in adopted villages during Rabi season 2016-17 to 2019-20. Three hundred CFLDs were conducted in 120 ha area with active participation of farmers and scientific staff of KVK. According to data analysis, the highest grain yield (2093 kg/ha), seed index (26.85 gm), net return (Rs 66263.1 /ha) and benefit cost ratio (3.36) were obtained in demonstrated practices (DP) as compared to farmer practice (FP) in which average grain yield (1769 kg/ha), seed index (17.88 gm), net return (Rs 52894.1 /ha) and benefit cost ratio (3.08) were recorded, respectively. Thus, the result undoubtedly indicates that the use of improved variety and POP with scientific interventions under CFLDs program contribute to increase the production, productivity and profitability of chickpea.

S7.15: Technological interventions to bridge the yield gaps in chickpea (*Cicerarietinum*L.)

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Chickpea (*Cicerarietinum* L.) is largely produced pulse crop in India accounting for a share of 40% of the total pulse production. ICAR-Agricultural Technology Application Research Institute (ATARI), Zone-X carried out a study to assess the yield gaps between improved package of practices under cluster front line demonstrations (CFLDs) and farmer's practice (FP) in Chickpea (*Cicerarietinum* L.) variety JG-11 under rainfed conditions. CFLDs on Chickpea were conducted in farmer's fields during *Rabi* season of 2019-20, 2020-21 and 2021-22 at select villages spread across 689.8 ha covering 1638 demonstrations. Results revealed that the average chickpea yield under the demonstration was 1750 kg/ha with improved technology and was 1443 kg/ha under farmer's practice with a difference of 21.27%. The average gross returns (Rs.95190 /ha), net returns (Rs.53856.21 /ha) and B:C ratio (2.34:1.0) recorded were more in demonstration compared to farmers practice (Rs.75744.55/ha, Rs.36217.10 /ha and 1.88:1.0, respectively). The average increase in income in the demonstrations were Rs.13850 /ha, Rs.22898 /ha and Rs.21591 /ha during 2019-20, 2020-21 and 2021-22, respectively. Results of yield gap analysis showed an average extension gap of 306 kg/ha, technology gap of 750 kg/ha and technology index of 30%. The yield gaps can be minimized with the successful adoption of the technologies demonstrated in the CFLDs. Further dissemination of the improved technologies among farmers require effective extension methods like seed production and distribution, training programmes, field days and exposure visits to the farmers' fields.

S.16: Farmers participatory large scale seed production in blackgram for higher income and seeds exchange among farmersthrough FPO under World Bank funded TNIAM project

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In Pudukkottai district, the pulses are cultivated in an area of 4751 ha during 2020-21 with productivity of 552 kg/ha. The low yield is mainly attributed to non-adoption of improved practices like use of quality seeds, seed treatment, proper spacing, spraying of micro nutrient and plant protection methods. A large-scale demonstration was conducted for seed production in blackgram through farmers participatory mode in 75 ha area covering 118 farmers during 2020-21 and 50 ha in 87 farmers field during 2021-22 under World Bank funded Tamil Nadu Irrigated Agriculture Modernization Project (TNIAMP) by adopting YMV resistant variety, seed treatment with bio-fertilizers, spraying of pulse wonder @ 5 kg /ha and need based application of azadirachtin 0.03% for getting higher yield and income. In experimental plot, the maximum yield obtained was 1050 kg/ha and minimum of 887.5 kg/ha with an average yield of 962.5 kg/ha, where as in farmers practices, it was 612.5 and512.5 kg/ harespectively and theaverage yield was 562.5kg/ha during 2020-21. During 2021-22, demo plot has recorded maximum yield of 1063 kg/ha and minimum of 913 kg/ha with an average yield of 987.5 kg/ha, where as in farmers practices, it was 637.5 and 490 kg/ harespectively and theaverage yield was 587.5 kg/ha. In demo plot the yield was 28.16 per cent higher than control plot with higher BCR of 2.96 and it was 1.71 in farmers practice. Moreover, the seeds produced were exchanged among farmers through FPO and thus increased the area under pulses cultivation.

S7.17: Role of cluster frontline demonstration (CFLD) technology on enhancement of green gram yield in Sirsa, Haryana, India

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Pulses are popularly known as "Poor man's meat" and "rich man's vegetable" which contributes a significant nutritional security due to high enrichment of protein. Green gram is an important legume crop that plays an important role in the food and nutritional security of people in the developing countries like India. It is a soil building crop, it fixes atmospheric nitrogen through symbiotic fixation, there by helps in N cycling within the ecosystem. Cluster front line demonstrations of green gram were conducted by Krishi Vigyan Kendra, Sirsa (Haryana) during three summer seasons from 2019-20, 2020-21 and 2021-22. A total 175 front line demonstrations were conducted on green gram in 70 ha area by the active participation of the farmers with the objective of improved technologies of green gram production potentials. The yield levels were considerably lower under local practices because of considerable variation in the extent of adoption of recommended technology. Highest grain yield was obtained in demonstrated plots with an average yield of green gram under improved technology 8.5 q/ha, whereas average yield obtained with farmers practice was 7 q/ha. Demonstration plots yield was 21.43 per cent more as compared to farmer'sfields (7 q/ha) practices. Average net return of Rs. 23146/ha with mean B: C of 2.23 was obtained with improved technologies. The present study is convincing the farming community for higher productivity and net returns with the adoption of recommended improved package of practices.

S7.18: Inclusion of pulses provides sustainable livelihood to small farmers

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Ambala district geographical area is 154000 ha, of which 132000 ha is the net sown area with 156% cropping intensity. Soils of the district are sandy loam (78%) and loam (22%). Major cropping system prevail in the district is rice-wheat. Inclusion of pulses was done and the based on the performance, one successful case is established. Mr. Sandeep Saini is a progressive farmer from village Akbarpur of Ambala. He has 1.30 ha land which is sandy loam with good quality of ground water for irrigation and source of irrigation is tube well. Most of the farmers of the village cultivate Rice-Wheat cropping system. KVK, Ambala adopted Akbarpur village under Doubling Farmers Income and Mr. Sandeep Saini as a leader farmer. He has been associated with KVK from last 5-6 years and implements high cropping intensity. He has been sowing Lentil crops under Cluster Front Line Demonstration of NFSM programme last 3 years. As a progressive farmer he started to cultivate short duration varieties with high cropping intensity i.e. Rice- Potato- Lentil- Moong (RPLM) for increasing his income. Sowing of all these crops *i.e.* Rice-Potato-Lentil-Moong through new technology. Recommended dose and time of application of seed and fertilizer as per KVK intervention is being applied. Increasing cropping intensity minimizes risk and increase income through different crop in a year. During the crop growing period of 2020-21 farmer income was Rs. 417000/ha through high cropping intensity which was 400%. There is the horizontal spread of the technology among the farmers.

S7.19: Economic assessment of fieldpea variety IPFD 1-10 (Prakash) in Jalaun district of Uttar Pradesh

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Fieldpea is the third most popular rabi pulse in India after chickpea and lentil. In India, eight states viz; Uttar Pradesh, Madhya Pradesh, Jharkhand, Assam, Odisha, Manipur, West Bengal, and Bihar produce nearly 92% of the country's fieldpeas. Uttar Pradesh in India and Jalaun district in Uttar Pradesh ranks first in the area and production of fieldpea. The present study was conducted to examine the adoption pattern and economic assessment of fieldpea variety IPFD 1-10 (Prakash) developed by ICAR-Indian Institute of Pulses Research (IIPR), Kanpur in Jalaun district of Uttar Pradesh. The primary data was collected from the Maheva block of the Jalaun district for the year 2021-22 with the help of a structured survey schedule and focus group discussion. A total of 80 farmers cultivating fieldpeas were interviewed. The results revealed that 83.33 % of the sampled farmers cultivated a single variety, while 16.66 % adopted multiple varieties of either fieldpea or vegetable pea, or both. Fieldpea varieties viz; IPFD 1-10 (Prakash), IPFD 10-12, IPFD 99-13 (Vikas), and IPFD 12-2, developed by ICAR-IIPR, Kanpur were together adopted by almost 50 % of the sampled farmers. IPFD 1-10 (Prakash) was the leading variety adopted by the sampled farmers in the study area. The yield of IPFD 1-10 (Prakash) was found to be greater by 20.12 % than the local check variety. The yield advantage resulted in an increase in the net return of the IPFD 1-10 (Prakash) by 26.96 % as compared to the local check variety. The study further revealed that IPFD 1-10 (Prakash) was liked by the farmers for its yield potential, optimum plant height, seed size, shape, texture, and cooking taste. The unavailability of the seeds and unawareness about the variety were found to be major constraints in the adoption of the IPFD 1-10 (Prakash) in the sampled area.

S7.20: Farmers' constraints to using recommended mungbean production technology in Rajasthan's Jaipur district

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Pulses are the main source of quality protein and a rich source of energy, minerals and certain vitamins. The study was conducted in Jaipur district of Rajasthan. Jaipur district comprises of sixteen tehsils, out of which 3 tehsils viz., Dudu, Phulera and Phagi were selected purposely. Two gram panchayats were selected randomly from each tehsils. Two revenue villages were selected from each selected gram panchayat on the basis of random sampling method. Thus the total 12 villages were selected. Total 120 mungbean growing farmers (respondents) were selected randomly through proportional allocation to the size of sample. Among all the five categories of constraints the "marketing constraints" (66.20 MPS) with highest intensity were found most important while "financial constraints" (57.36 MPS) were found at last rank perceived by farmers or by the overall respondents in adoption of recommended cultivation practices of Mungbean. The constraints like "lack of knowledge about plant protection measures" (technical constraints), "high cost of insecticides and pesticides" (financial constraints), "lower minimum support prices (MSP) of produce fixed by the government" (marketing constraints), "High losses during storage due to stored grain pests" (storage constraints) and "natural calamities" (general constraints) were perceived as major constraints by overall respondents in the adoption of recommended production technology of Mungbean.

S7.21: Impact of cluster front line demonstration on yield and economics of pigeonpea under NFSM in Beed district of Maharashtra, India

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The cluster frontline demonstrations on BDN 711 variety of pigeonpea were conducted by Krishi Vigyan Kendra, Khamgaon of Beed District, Maharashtra State. Demonstration were conducted during 2019-20, 2020-21 and 2021-22 on 20 ha area in 50 number of demonstration each year. Pigeonpea variety BDN 711 which is released by Vasantarao Naik Marathada Krishi Vidyapeeth is resistant to wilt, terminal drought and suitable for medium type of soil. Improved cultivation practices were demonstrated in farmers' field for three consecutive years. The result of the demonstrations showed higher yields compared to farmers' practices followed for pigeonpea cultivation. The average increased per cent seed yield is 31.11 over the years from cluster frontline demonstrations compared to check plots. However, during the year 2021-22, the per cent increase in seed yield was 44.00. The huge variation in farmers practices adopted in the cluster villages. The other parameters like extension gap, technological gap and technology index were derived for assessment of technology adoption rate. The average technology gap and technology index were 540 kg/ha and 25.74 per cent, respectively. The improved technology recorded higher average seed yield 1660 kg/ha. over farmers practice 1267 kg/ha. The improved technology gave higher average gross return (97967 Rs./ha.), average net return (70633 Rs./ha.) with higher benefit cost ratio (2.43) as compared to farmers practices. The results clearly indicated that the beneficial impact of cluster front line demonstrations over the farmers practices towards enhancing the productivity of pigeonpea cultivation in Beed district of Maharashtra state, India.

S7.22: Pulses seed production: A profitable venture for resource poor farmers of Virudhunagar district

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Pulses (food legumes) occupy an important place in Indian agriculture. It provides food, nutrition and environmental security in bringing income and employment opportunity through various improved technological interventions. India has to import 3-4 mt of pulses every year to meet its domestic demand. There is an urgent need to increase both productivity and production of pulses to bridge the gap between demand and supply. In this regard, NFSM sponsored seed hub programme is in implementation at KVK, Virudhunagar with the objective of to increase indigenous quality seeds which are high yielding and climate resilient for distribution to the farmers, government, non-government organizations on time as per indent or demand to achieve self sufficiency in respect of seeds at village level itself. The seeds are procured from the farmer by KVK with 20 to 40 rupees extra than the market price. Farmers of selected villages take up seed production under the technical support and guidance of KVK scientists. They are trained technically to adopt good agronomic practices to fulfil the objective. About 90 farmers from 20 villages participated actively in this participatory seed production programme. Under this seed hub programme 94,320 kg of pulses seeds were produced in an area of 150 ha from 2017 to 2022 and 4716 ha area is brought under pulses cultivation. The seed hub farmers gained more gross income (Rs.36018 /ac) and net income (Rs.16560 /ac) and BC ratio (2.17) compared to the grain production. This holistic approach boosted pulse production towards self sufficiency decides providing income to the farmers and ensuring nutrition and livelihood improvement to the resource poor farmers of Virudhunagar district.

S7.23: Enhancement of pulses cultivation under seed hub project in Sirsa district of Haryana

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The primary source of protein and nutrient are the major pulses like green gram and chickpea which are not able to meet the demand due to low availability. Pulses seeds are the major contributor to economic growth of developing countries like India and also promise the soil health management by nitrogen fixation and its ability. Good quality of seeds is the major step for enhancing the pulses yield and replacing the old varieties from the cultivation chain followed by the farmers. Seed hub project promises the timely and sufficient availability of pulses seeds for farmers and other organization. Seed hub is a special project which was implemented in 2016 by GOI this involves 8 ICAR Institutes, 47 centres of All India Coordinated Research Projects (AICRPs) located in State Agricultural Universities (SAUs) and 95 Krishi Vigyan Kendras (KVKs). Seed hub was incorporated in Krishi Vigyan Kendra Sirsa in 2018-19 with the procurement of 94.44 quintals of green gram seed from 5 farmers and distributed to 29 farmers. In 2019-20, 2020-21 and 2021-22 procurement of green gram seed was 88.90, 57.83 and 159.84 quintals, respectively. Similarly, in 2019-20, 2020-21 and 2021-22 procurement of chickpea seed was 189.10, 68.82 and 46 quintals, respectively. In the seed hub project, seed was collected from few farmers and distributed to needy farmers to increase the area of pulses cultivation. Seed hub provides good opportunities to KVKs for the extension of pulses cultivation among the local farmers.

S7.24: Evaluation of front line demonstration on chickpea in Buldhana district of Maharashtra, India

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The study was carried out Krishi Vigyan Kendra, Buldhana in Buldhanadistrict during 2018-19 and 2019-20. Total 100 front line demonstrations were conducted on chickpea in 40 ha by the active participation of the farmers with the objective of improved technologies of chickpea production potentials. The improved technologies consist improved variety (Raj Vijay -203), balanced fertilizers (soil test based) application and integrated disease and pest management, etc. The demonstrations recorded an average yield ranging from 1823-1960 kg/ha with a mean of 1891 kg/ha. The per cent increased yield in demonstration was 18.53% during 2018-19 and 20.02% during 2019-20 respectively, over the local check. The average extension gap, technology gap and technology index were 285-327 kg/ha during the period under study. The demonstrated field gave higher gross return (Rs. 75975/ha) and mean net returns (Rs. 50167/ha) with average benefit: cost ratio (2.94) compared to the local checks. Present results clearly show that the yield and economics of chickpea can be boost up by adoption of recommended technology.

S7.25: Constraint analysis and upscaling strategies to increase arid pulse production in western Rajasthan

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The diverse agro-climatic situation in India supports the cultivation of different pulse crops across the country, including arid regions. From a consumption point of view, pulses are important crops because they are rich sources of proteins and constitute a significant part of animal feed in arid regions. During 2021-22, India exported 410,375.89 MT of pulses to the world for the worth of Rs. A total of 2,834.23 crores and pulses are grown on an area of 30.37 million hectares with an annual production of 26.96 million MT. This paper discussed the constraints faced by farmers for the adoption of pulse production technologies and upscaling strategies to increase arid pulse production in the region. The study is based on secondary data collected from the internet and published sources. The major constraints perceived by the farmers were lack of awareness about improved pulse technologies and poor adoption of improved varieties and production technologies by farmers. In addition, lack of knowledge and skills on pulse processing and value addition, attitude of farmers toward improved pulse technologies, hesitation to change the existing cropping pattern, i.e., behavioural change, poor marketing infrastructure and insufficient and untimely availability of high-yielding varieties seeds of pulse crops were other major constraints. To overcome these constraints, governments may focus on providing technological, economical, institutional and capacity building for interested farmers and build societal institutions for faster diffusion of pulse technologies in the arid region of the country. These strategies may help enhance farmer income, minimize risk and increase the standard of living in arid regions.

S7.26: Pulse crops for sustainable cropping intensification and doubling farmer's income: evidences from Farmer FIRST programme

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Farmer FIRST programme was implemented in Fatehpur district of Uttar Pradesh during 2016 to 2020 for enhancing farmers' income through adoption of scientific farming practices. this program has been implemented in three villages namely Kharauli, Mirai, and Karchalpur from Devmai block of Fatehpur district in Uttar Pradesh since 2016-17. Based on the participatory rural appraisal and rank based quotient (RBQ), the prioritized problems in the villages were: low crop productivity of traditional varieties, low income, mono-cropping, seasonal unemployment, pests & diseases in crops. Hence, interventions were designed and implemented to tackle these pervasive problems through integrated approaches for food, nutrition and livelihood security. Since 2016-17, interventions comprising crop based (cereal, pulse, oilseed and vegetables), livestock based (poultry and goat) and pisci culture were adopted in the villages. After four years, a significant increase in cropping intensity from 210% to 290% has been recorded. In the year 2017-18, 90 farmers cultivated the mungbean crop and the average yield of mungbean recorded 9.30 q/ha. Income gained Rs. 18590/ha and B: C ratio 2.25 in compared to local variety (7.50 q/ha). The local variety recorded income of Rs. 14330/ha and B:C ratio of 2.13.Similarly, the average yield of chickpea ('JG 16') of 27.8 q/ha with an income of Rs 77970/ha was recorded as compared to local variety (yield 23.5 q/ha and income Rs 67450/ha). Similarly demonstrations were also conducted in the year 2018-19 by covering 90 farmers. The summer mungbean resulted in higher system productivity and profitability as compared to farmers practice such as monocropping of rice and continuous rice-wheat rotation. Also, improved varieties of crop increased the yield and income of farmers than that of local varieties. Thus, inclusion of in fallow period increased the cropping intensity and income.

S7.27: Role of KVK in enhancing area under blackgram cultivation in Kancheepuram district

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Pulse production after Paddy cultivation is one the major practices followed in Kancheepuram district. Area under coverage is 924 ha (2021-22). Blackgram cultivation contributes a larger area in this regard. Farmers are harvesting on an average of 6.25 q/ha whereas the potential yield of latest varieties are 9.88 q/ha (Vamban 8). The yield gap is mainly due to lack of awareness on latest varieties, non-adoption of integrated crop management practices and incidence pest and diseases. In order to enhance area under blackgram and increase production and productivity in the district, KVK conducted programmes on adoption of new varieties and seed production techniques through NFSM sanctioned cluster frontline demonstrations and seed hub project. It was observed that in terms of yield there was steady increase in yield (9.50 q/ha) compared to farmer's practice (6.50 q/ha). It also indicated that in terms of economics, blackgram production recorded higher net returns (Rs. 28855.00/ha) compared to farmer's practice (Rs. 17,250.00) during these years. The Benefit Cost Ratio was 1.75 and 1.39 for demonstration and farmer's practice respectively. This indicates the farmers to go in for adopting recent technologies for increasing production and productivity of blackgram thereby profitability is achieved.

S7.28: Value transformation along lentil value chain in Uttar Pradesh state of India

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India is the second highest lentil producing country globally with 18.05 percent of the world's lentil production (FAO, 2020). Lentil is cultivated on 1.47 million ha across wide range of agri production situations in India. Uttar Pradesh state is a major lentil producing state of India, accounting for 33and 34 percent of total area and production of lentil in the country. Value chain of lentils of Uttar Pradesh state were analysed during 2019-21 using descriptive research design. Four marketing channels were documented with presence of series of actors for furthering lentil from producers to consumers. Producers had limited direct access to dealers or processors for sale of produce, while commission agents served as the main connection between each pair of marketing nodes. Total value added along lentil value chains varied from Rs.31623 to 3337.80/t for split lentils and Rs 19335.7 to Rs 21591.90/t for whole lentils. Estimation of progressive value build up in lentil value chain reflected that producer added about 58.71 to 60.39 percent of total value of split lentil, while they added 68.73 to 71.37 percent of the value in case lentil whole grain.Across all value chain actors, market margins were observed to be highest for processors (41.18 to 57.19%) in case of split lentil, while wholesalers received maximum marketing margins in furthering whole grains (19.13 to 20.49%). Marketing cost was highest (37.14 to 67.09 %) for processors. Producer share in consumer rupee was highest for lentil wholegrain (70.25 to 72.83 %) across all the channels.

New Vistas in Stress Resilience-Biotic Stresses

S6.3: Identification and evaluation of stable chickpea germplasm and advance breeding lines for biotic and abiotic stresses to enhance productivity in Kalyan Karnataka region

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Pulses stand next to cereals in terms of their importance in human diet and for vegetarians in particular as they are the main source of proteins in comparison with cereals. Chickpea is an important Rabi pulse crop of Karnataka grown on an area of 0.71 lakh ha with production & productivity of 4.45 lakh tonnes and 625 kg/ha during 2020-21, respectively. However, the productivity of the state was less than 50 *per cent* of the national average (1192 Kg/ha) (Project Coordinator's Report 2021-22, AICRP on Chickpea). There is huge gap between demand and supply due to various bottlenecks in chickpea production. The biotic stress like fusarium wilt and dry root rot (DRR), and abiotic stress like drought and heat are the major production constraints in chickpea production. Aiming to breed more resilient and resistant varieties of chickpea, adapted the path of phenotypic evaluation for wilt, DRR, drought and heat to breed for these traits of interest. From 2019-20 to 2021-22 for three crop season an intensive study was conducted with a 148 chickpea germplasm lines (selected from 578 core germplasm screening during 2018-19 for morphological and physiological traits) in an augmented design and screened for biotic and abiotic traits under field conditions (Wilt and dry root rot under sick plots, drought and heat under late sown conditions). From this study, promising and stable genotypes were identified for biotic stresses like Fusarium wilt (21 R) dry root rot (15 MR) and abiotic stress like drought (20 T) and heat (12 T). Lot of advances have taken place in chickpea for combating problems like resistance wilt, DRR, drought and heat, where none or only moderate levels of resistance/tolerance have been identified, it is recommended that aggressive efforts be made to transfer resistance/tolerance genes from identified germplasm.

S6.4: Genetic diversity studies and fusarium wilt screening in chickpea (*Cicer arietinum* L.) germplasm

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Two hundred and eighty chickpea germplasm including two checks (JG-11 and SA-1) were tested with an objective to explore the genetic divergence by using Mahalanobis D^2 statistics. The field experiment was carried out during *Rabi* 2021-22 at Zonal Agricultural Research Station (ZARS), Kalaburagi. The magnitude of genetic divergence was studied using data obtained from five quantitative traits. The 280 genotypes including checks were divided into seventeen clusters based on their D^2 values. Out of seventeen clusters, cluster II (89 genotypes) was the largest followed by cluster I (83 genotypes), cluster III (31 genotypes), cluster VIII (29 genotypes), cluster VII (24 genotypes), cluster VII (15 genotypes). The remaining clusters IV, V, IX, X, XI, XII, XIII, XI, XV, XVI, XVII are solitary with one genotype per cluster. Cluster VII displayed maximal intra-cluster distance (425.66), followed by cluster VIII (401.40). Inter-cluster distance was recorded maximum between cluster XIV and cluster XVI (4352.70), followed by cluster X and cluster XIV (3578.44), cluster XVI and cluster XVII (3383.30), cluster XIV and cluster XV (3063.34), cluster VI and cluster XVI (3050.80). Same set of germplasm were also screened for fusarium wilt in wilt sick plot, 30 germplasm lines showed resistant (10.71%), 83 moderately resistant (29.64%), 44 moderately susceptible (15.71%), 31 susceptible (11.07%) and 92 highly susceptible reaction to fusarium wilt. The per cent disease incidence (PDI) ranged from 0.44 (ICCV 16116) to 49.49 (ICCV-171101) among germplasm with resistance check WR-315 was 4.25% and for the susceptible check JG-62 is 86.42%. Clusters XIV and XVI had extreme genetic distance and the germplasm lines in these cluster also showed moderate resistance to fusarium wilt.

S6.5: Diversity and distribution of bruchid species infesting edible stored pulses in India

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A survey was carried out across 74 locations covering 24 states in India to investigate the distribution and diversity indices of bruchids infesting edible stored pulses. A total of 81 stored grains representing 14 pulse crops were sampled. Five bruchid species were identified infesting samples, three of which were *Callosobruchus* species. *C. analis* was distributed on 50% of the samples and locations, followed by *C. maculatus* and *C. chinensis*. Despite *C. analis* being present in the majority of samples, *C. maculatus* was the most abundant and dominant species. Six of the twenty-four states recorded all three *Callosobruchus* species, eight states recorded any two of the three, and the remaining ten states recorded any one of the three. *C. analis* and *C. chinensis* were abundant in four of the six regions, with *C. chinensis* being most abundant in the northeast region. The overall index of species diversity was 1.1, while Effective Number of Species was 3. Madhya Pradesh, Andhra Pradesh, and Uttar Pradesh had higher diversity indices, while West Bengal and Tamil Nadu had lower. Crops with the highest diversity indices included chickpea *desi*, *Kabuli* and field pea. Small-scale storage conditions had higher infestation parameters than large-scale. The highest infestations were found in fieldpea, cowpea, chickpea, horsegram, and mungbean, while urdbean had the lowest. *C. chinensis*>*C. analis*>*C. maculatus* was the order of species for grain infestation and damage, whereas it was opposite for grain weight loss. Infestation and damage were positively correlated with grain moisture and storage duration. The study provides critical information on the diversity of bruchid species infesting edible stored pulses across the country. It will aid in the effective management of bruchids under storage conditions by designing appropriate future studies based on the species prevailing *vis-a-vis* storage conditions, crops stored, and area of occurrence.

S6.7: Unravelling the seed borne nature, systemic localization and symptoms-based inoculum advancement of *Fusarium oxysporum* f. sp. *ciceri* incited wilt in chickpea

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Wilt disease of chickpea caused by *Fusarium oxysporum* f. sp. *ciceri* is one of the uniformly distributed across the globe. This disease has a unique property of perpetuation as seed and soil borne. Mostly the pathogen form chlamydospores for their survival in the soil but mycelia and resting spore also survived in the seed and lead to primary infection and produce disease. In the present investigation seed borne nature, systemic movement of infection, relationship with types of symptoms and time of infection investigated. Systemic progression of pathogen in different genotypes was evaluated based on the occurrence of infection at 5 different stages of pod formation such as infection at <10% pod formation stage; infection at 25% pod formation; infection at 50% pod formation; infection at 75% pod formation; infection at 100% pod formation. Systemic infection or progression of pathogen to different parts of plants was highest in plants showing chlorosis symptoms when compared to plants showing drooping symptoms. Higher infection was found in the seeds of chlorosis plants (32.5%) compared to drooping plants (7.5%). Different late wilter lines were collected for studies of progressive systemic infection in parts like root, stem, stalk and seed. Mean systemic Infection in the root (93.5), stem (74), stalk (44) and seeds (32.5) of plant showing chlorosis symptoms was highest as compared to the root (91.5), stem (69), stalk (26.5) and seeds (7.5) of plants showing drooping symptoms. Infection in the roots is more than 90% irrespective of infection at any stage of pod formation. Infection in the stem was highest when the plants were infected at <10% pod formation (73.75) and was lowest when the plants were infected at 100% pod formation (66.25). Infection in the stalk was highest when the plants were infected at <10% pod formation (56.25) and was lowest when the plants were infected at 100% pod formation (12.5). Infection in the seed was highest when the plants were infected at <10% pod formation (36.25) and was lowest when the plants were infected at 100% pod formation (2.5).

S6.8: Influence of powdery mildew and anthracnose disease severities on yield and growth parameters of greengram

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Greengram [*Vigna radiata* (L.) Wilczek] suffers from many foliar diseases among them powdery mildew (PM), anthracnose (AN), are the major constraints in production of greengram, which causes both qualitative and quantitative losses. The yield and growth parameters of greengram showed significant differences with range of PM disease severity, maximum 65.72 % yield losses recorded in > 40 % PM severity and disease severity of 1- 20 % revealed yield losses up to 31.80%, however 21-40 % disease severity reduced the yield up to 39.93 %. Similarly, incresing range of Anthracnose disease severity significantly reduced the yield and growth attributed characters. The disease severity >40% alone reduced the yield losses up to 42.81% as compared to 18.35 % yield reduction was recorded in disease severity ranged from 1-20%. Perhaps, 18.35% reduction of yield over control was computed in disease severity ranged from 1-20%. Same set of experiment were carried out to assess the effect of range of dual infection of PM and AN disease on reduction of yield. Progressive development of dual infection drastically reduced the yield and growth attributed parameters of greengram. The per cent reduction of yield 74.89, 41.41 and 36.30 were recorded in disease severity ranged from >40%, 20-40% and 1-20 %, respectively. Time of PM and AN disease emergence on crop growth period significantly contributed the yield losses and growth attributed characters.

S6.9: Induction in pigeonpea defense enzymes of upon exogenous application of signalling compounds against *Maruca vitrata* (F.) herbivory

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Pod borer resistant (AL 1747) and susceptible (MN 1) pigeonpea genotypes were treated with signalling compounds [Jasmonic acid (JA) @ 100 µM and salicylic acid (SA) @ 5 mM] at 50 per cent flowering under net house conditions to ascertain the effect of the exogenous application on *Maruca vitrata* herbivory through the induction of defense related enzymes. The specific activity of superoxide dismutase (SOD), catalase (CAT), lipoxygenase II and III (LOX II and III) was measured from the flowers at 1, 4 and 7 days after treatment (DAT). In all the treatments, SOD, CAT and LOX activities were significantly higher in AL 1747 as compared to MN 1. In AL 1747, the pre-treatment with JA followed by infestation by *M. vitrata* (PJA+MV) resulted in significantly highest induction of aforementioned enzyme activities in the flowers, followed by JA+MV at 1 DAT. Application of SA also resulted in the induction of enzyme activities; however, the effect was not as pronounced as JA at 1 DAT. After 4 DAT, a general decline in the enzyme activities was observed in all the treatments in both the genotypes. It can be concluded that exogenous application of both JA and SA triggered the induction of antioxidative response, the first line of defense, in pigeonpea against *M. vitrata*. Signalling compounds, at their respective promising concentrations, hold immense potential for inducing resistance in pigeonpea against *M. vitrata* by modulating the plant biochemistry by elevating the levels of defensive compounds in the crop and ultimately reduce the performance of pest.

S6.10: Sustainable approaches for management of *Heterodera cajani* Koshi in Urdbean

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The cyst nematode, *Heterodera cajani* is economically important nematode pest of pigeonpea, urdbean, mungbean, cowpea and causing serious yield reduction in pulse crops. The protective cyst stage of this nematode enables them to withstand desiccation and greatly enhances their dispersal and survival. The management of *H. cajani* is difficult because of less availability of nematicides and highly costly along with hazardous to animals and environment. Hence, we evaluated the organic amendments (neem seed cake, and neem seed powder); bio agent, *Trichoderma harzianum,* FYM enrichment with *T. harzianum* and chemical nematicides (Carbofuran 3G and Carbosulfan 25DS) for management of *H. cajani* in urdbean under pot condition. The treatment effects were found most effective in reducing significantly the nematode infection and increasing the yield attributes as compared to control. The cyst population per cc soil was significantly reduced in neem cake (5.8), neem seed powder (5.6), *T. harzianum* (6.0), *T. harzianum* + FYM (5.0) Carbofuran (5.0), and Carbosulfan (8.0) as compared to control (35.3). An average of 48.00 cysts per plant root was observed in control treatment which is significantly reduced in neem cake (7.6), neem seed powder (5.6), *T. harzianum* (6.2), *T. harzianum* + FYM (7.0) Carbosulfan (8.3) and Carbofuran (7.6). The plant growth characters and yield attributes were significantly increased ($P<0.05$) in treated pots as compared to control. Hence, organic amendments and bio agent can be applied to suppress the *H. cajani* infection in urdbean and enhance the yield attributes.

S6.11: Antifungal efficacy of green synthesized zinc oxide nanoparticles against the stem rot of legumes

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The present research work reports the green route mediated zinc oxide nanoparticles (ZnONPs) using the Indian beech plant that completely inhibits the phytopathogenic fungus, *Sclerotinia sclerotiorum. S. sclerotiorum* causes stem rot in the family of Fabaceae or Leguminosae and severely affects lentils, chickpeas, soybeans, faba beans, green peas, peanuts, lupin, alfalfa, etc. It also affects mustard, canola, sunflower, etc. resulting in a major loss to the yield and quality of agriculturally important crops. The synthesized ZnONPs were non-toxic, environmentally benign, cost-effective, stable for more than a year, completely solubilized, and easy to handle. The characterization of the synthesized ZnONPs was done through UV-Vis spectroscopy, scanning electron microscopy, energy dispersive X-ray analysis, X-ray diffraction and fourier transform infrared spectroscopy. The *in vitro* antifungal assay of the synthesized ZnONPs was performed using the poison food technique against *S. sclerotiorum*. The zone of inhibition was observed at concentrations of 10, 25, 50, 100, 250, 500, 1000 and 2000 ppm. The percentage of the growth inhibition of the mycelium was calculated for 3, 5 and 7 days of interval. It has been observed that with the increasing concentrations, the percentage of inhibition was also increased with 100% inhibition at 2000 ppm. Hence, the obtained result concludes that the synthesized ZnONPs possess the potential and efficacy of the chemical fungicide and functionalization of the green domain. Therefore, the green synthesized ZnONPs could efficiently control stem rot and can be established as a next-generation fungicide for biological control in crop improvement and plant disease management.

S6.13: Bio-efficacy of newer insecticides against tur pod fly, *Melanagromyza obtusa* (Malloch) (Diptera: Agromyzidae) on pigeonpea

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The studies on bio-efficacy of newer insecticides against pod borer complex of pigeonpea wAS conducted during the *Kharif* season 2019-20 at Research cum Instructional Farm, IGKV, Raipur, (C.G.). The experiment comprised of eight treatments, out of which seven were insecticides *viz.,* Buprofezine 25 SC, Diafentiuron 50 WP, Dinetofuron 20 SG, Flubendiamide 480 SC, Deltamethrin 2.8 EC, Thiamethoxam 25 WG and Quinalphos 25 EC including untreated control. The bio-efficacy of different treatments against tur pod fly was ordered as Flubendiamide 480 SC > Dinetofuron 20 SG > Thiamethoxam 25 WG > Diafenthiuron 50 WP > Bufrofezine 25 SC > Quinalphos 25 EC > Deltamethrin 2.8 EC in consideration of effectiveness.

S6.14: Development of cost effective media for VIP3 production from indigenous *Bacillus thuringiensis* strain - F8.IIPR and its bio-efficacy against pod borer

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Bacillus thuringiensis Berliner produces many insecticidal proteins among them Vegetative Insecticidal Protein-3 (VIP3) is known for its insecticidal activity against wide array of lepidopteran pest like *Helicoverpa armigera* Hubner, *Spodoptera litura* Fabricius, *S. frugiperda*, *S. exigua* etc. The production of VIP3 protein is routinely done in terrific broth (TB). The present experiment was executed for finding a cost effective media for VIP3 production. The pure culture of indigenous *B. thuringiensis* strain F8.IIPR (NAIMCC-SB-0065) was inoculated in TB along with 2 agro based media *viz*., Groundnut seed meal broth (GSM) and Sesame seed meal broth (SSM) for VIP3 production. The *Bt* growth in 3 media was spectrophotometrically measured [ë=600nm] at different time intervals. Even though the OD values of GSM (0.907) and SSM (0.897) were lower than TB (1.704) at 25 h post inoculation, they had recorded higher percent insect mortality (GSM: 100 & SSM: 86.67) in pod borer larva (*H. armigera*) than TB (73.33); Whereas the uninoculated GSM and SSM had recorded only 20% mortality. The VIP3 protein were isolated and purified by ultrasonication followed by $(NH_4)_2SO_4$ precipitation followed by dialysis in 20mM TRIS HCl (pH 7.4) and concentrated. The purified VIP3 from 3 media were tested against 4 days old pod borer larvae by artificial diet contamination method. The results revealed that GSM VIP3 has recorded lowest LT_{50} (3.43 days) followed by SSM (4.22 days) and TB (4.42 days); Further, the LC_{50} and LC_{90} for the GSM VIP3 is found to be 5.1485µg/µl and 8.12184 µg/µl. The results show identification of promising indigenous media for VIP3 mass production and it can be formulated as liquid biopesticide.

S6.15: Distribution pattern, genetic variability, phylogeny and recombination of begomoviruses causing yellow mosaic diseases in pulse crops in India

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A survey of pulse crops showing yellow mosaic was carried out in different zones of India. Total 214 samples of mungbean, urdbean, cowpea, horsegrame and mothbean were processed to amplify full-length DNA molecules of the 3 begomoviruses, *Mungbean yellow mosaic virus* (MYMV), *Mungbean yellow mosaic India virus* (MYMIV) and *Horsegram yellow mosaic virus* (HgYMV) using species specific primers in PCR. The PCR products were sequenced directly. A total of 156 full-length DNA-A and DNA-B molecules were assembled and analyzed. PCR results and sequence data analysis revealed involvement of single and mixed infection in pulse crops. Among the three begomoviruses, MYMIV is widely prevalent in all the zones but its prevalence is more in North. Infection of all the three viruses was recorded in samples from South. Mixed infection of two or three viruses was more in South than in North. Phylogentic analysis of DNA-A sequences revealed that the zone and crop-wise grouping is not present; whereas, DNA-B sequence analysis indicated zone-wise grouping in MYMIV population. MYMIV population is subdivided into number of sub-clades indicating the high level of genomic diversity in both DNA-A and DNA-B. MYMV and HgYMV were mostly present in south zone with a few exceptions. The recombination analysis revealed the presence of significant number of putative recombination events in all the three viruses under study. The presence of mixed infection provides opportunities for the exchange of genetic materials between the species which may lead to the development of new strain/virus species.

S6.16: New convenient disease rating scale for the resistant screening against Begomoviruses causing yellow mosaic disease in different crops

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The utmost care is required for the measurement of disease in resistance screening as a minor error may lead to the inappropriate selection and collapse of the entire breeding program. Resistance screening aims to select the highly resistant or resistant germplasm. For this, we should pay more attention to the germplasm showing no disease symptoms or very mild symptoms. Severely symptomatic plants efficiently represent crop loss; therefore, they cannot be ignored in the disease appraisal. However, it does not have any significance in the resistance screening. Accordingly, modifying a disease rating scale by focusing more on plants with mild symptoms can enhance precision. The proposed disease rating scale has been prepared on this principle. Proposed rating scale, a score of 0 indicates no visible symptoms, 1 indicates small yellow specks covering 0.1 to 5%, 2 indicates the yellow mottling of leaves covering 6 to 10%, 3 indicates yellow mottling of leaves covering 11 to 30%, and 4 indicates yellow mottling and discoloration of 31 to 100% leaf area of the plant. The scale uses absolute values as it is estimated by the observer based on visual observation. However, the categorization of the disease reaction of various genotypes is based on PDIx which is a calculated value; it has been represented as more than an absolute value. The line having a disease rating of 0 is considered disease free, >0 to <13 is highly resistant, >13 to <26 is resistant, >26 to <50 is susceptible, and >50 to 100 is highly susceptible.

S6.18: Yellow mosaic disease resistance in wild *Vigna* sp. and potential green bridges for Begomoviruses in Punjab

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Deployment of novel resistance genes from wild and cultivated *Vigna* sp. is the most economic approach for managing Yellow Mosaic disease in mungbean. Further, it is also critical to identify green bridge species for the pathogen serving as source of primary inoculum for disease development. In present study, a set of 12 *Vigna* accessions were evaluated for YMD resistance by infector row method. Resistance was confirmed by whitefly mediated artificial inoculation and by detection of virus at different days post inoculations (DPI). Under infector row method, the lowest disease severity was observed in accession *V. umbellata* whereas the highest disease severity was observed in *V. trilobata*. In case of artificial inoculation technique, *V. umbellata*, *V. sublobata*, and *V. radiata* var. *satulosa* showed no symptoms where as other accessions showed resistant to moderately susceptible disease reaction categories. Further, at 25 DPI, the total DNA from highly resistant *Vigna* species was subjected to PCR with MYMV and MYMIV specific primers and no virus was detected in all the accessions whereas susceptible mungbean variety SML 1082 was showing presence of both the viruses, indicating the mixed infection. Genomic DNA of thirty-six weed samples was subjected to rolling circle amplification (RCA), out of which, nine weeds showed expected amplificon of ~2.8bp. Enriched DNA of these nine weed species was amplified with the degenerate primers PALIc1960 and PARIv72. The nucleotide-BLAST results of sequences revealed the co-occurrence of MYMIV virus with Tomato leaf curl Palampur virus, Ageratum enation virus and Papaya leaf curl virus.

S6.19: Early generation selection for Fusarium wilt resistance in chickpea

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Breeding for Fusarium wilt resistance has been integral to chickpea varietal development in the country. Two pathotypes and six races of *F. oxysporum* f.sp. *ciceri* have been reported in different parts of the country. Resistance to wilt has been reported to be governed by mono or oligogenes showing recessive inheritance. Early generation screening for wilt resistance will save resources and streamline the breeding program. In the current study, the effect of early generation screening on population structure has been studied using F3 and F4 generation of the several crosses. The material for the present study consisted of 100 single plant progeny rows from 31 crosses in F3 (20 crosses) and F4 (11 crosses) and their parents (29) which were screened in the Fusarium wilt field sick plot at ICAR-IIIPR Kanpur during 2021-22 having predominantly race 2 of the pathogen. The F4 crosses were also screened for resistance during previous year. Based on the disease reaction, the parents and the progeny lines were classified as Resistant (<10% severity), Moderately resistant (11-20% severity) or Moderately Susceptible (21-50% severity) and Susceptible (>50% severity). Among 20 crosses in F3, six were resistant and three were moderately resistant. Among the 11 F4 crosses, 4 crosses each showed resistant and moderately resistant reaction. In general, presence of even single resistant or moderately resistant parent increased the chance of having resistant progenies in both F3 and F4 generation. Besides, the F4 generation crosses, having already undergone one cycle of selection in the sick plot exhibited more resistant progenies than the F3 generation crosses. The present study clearly demonstrated the effectiveness of early generation screening for fusarium wilt resistance. Both resistant and moderately resistant parents can be utilized for breeding for wilt resistance.

S6.20: Management of wilt disease of lentil through application of talc-based *Trichoderma* bio-formulation in Bundelkhand districts of Uttar Pradesh

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Lentil (*Lens culinaris* M.), an important dietary source of protein and other essential nutrients and grown in many parts of the world including India is susceptible to a number of diseases. Among them, wilt caused by soil borne fungus *Fusarium oxysporum* f.sp. *lentis* is known to cause substantial yield losses particularly in areas where lentil is grown under rainfed conditions. The present work was aimed at the evaluation of the talc-based formulation of *Trichoderma* as seed treatment against lentil wilt in farmers' fields. Field trials were carried out consecutively during Rabi 2020-21 and 2021-22 crop seasons at Hamirpur and Banda district using IPL-220 a popular cultivar. Crop raised from untreated seeds served as control. It was observed that bio formulation treated seeds results in significant increase in plant population (80-90 plant/m^2 area), germination percentage 85-88%, fresh weight (7.40-10 g) dry weight (0.30-0.37g), plant height (32-38cm), root length (12-14 cm) roots nodulation (15-22), number of pods/plant (30-40) and 1000-grain weight (38-40g) of lentil. Significant reduction in *Fusarium* wilt disease incidence 17.55-32.00 % (2020-21) to 13.83-35.50 % (2021-22) and increase in grain yield percent over check 19.14-27.05 % to 15.66-19.76 % were observed respectively during both years of crop seasons. Therefore, utilising this *Trichoderma* bio-formulation has important roles in mitigating the huge production losses due to devastating *Fusarium* wilt disease of lentil in Bundelkhand districts of UP, India, where the crop is often grown under rainfed conditions.

S6.21: Ecofriendly management of biotic stress through development of stress resistant, high yielding varieties

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Chickpea (*Cicer arietinum* L.) is a major pulse crop of global importance, owing to its immense role in human nutrition, soil fertility and agricultural sustainability. India is the largest producer cultivating chickpea in 9.99 m. ha. and producing 11.91 m. tons (2020-21). Wilt caused by *Fusarium oxysporum* is a serious disease of chickpea causing yield losses upto 10-60 percent as per severity. Use of fungicides is a costly input adding to the cost of cultivation besides leaving the harmful residues in the seed and soil as well. The best eco-friendly approach to meet the global demand of pulses at a cheaper rate affordable to the masses is through development of disease resistant, high yielding, nutrient rich varieties and genotypes. On the basis of testing in AICRP coordinated trials (2019-2021), the chickpea genotype RKG 19-1 (JAKI 9218 x ICCV 00108) has been identified as a high yielding genotype showing resistance against wilt consistently for three years. The mean days to flowering and maturity of RKG 19-1 is 59 and 111 days and 100 seed weight of 25gm. Owing to its high yield potential and resistance to biotic stress (wilt); it has also been designated as donor (male parent) for attempting hybridization in chickpea. A few crosses involving RKG 19-1 have been attempted to generate breeding material combining high yield with stress resistance. It can be hoped that these crosses will be useful for development of high yielding, biotic stress resistant chickpea varieties for sustainability and nutritional security.

S6.22: Exploring the biochemical paradigm of powdery mildew resistance in blackgram genotypes (*Vigna mungo* (L.) Hepper)

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Powdery mildew (*Erysiphe polygoni* DC.) is one of the major diseases in blackgram during cold weather season which reduces up to 50 per cent of the yield. The present study deals with exploring the biochemical characteristics such as protein content, total phenol, total sugars, reducing sugars, non-reducing sugars and the enzyme activity of peroxidase, catalase, phenylalanine ammonia lyase, superoxide dismutase, malondialdehyde and ascorbate peroxidase in relation to powdery mildew resistance in four blackgram genotypes *viz.,* VBN(Bg) 4, Mash 1008, Mash 114 and LBG 17. The protein content, total sugars and reducing sugars were lower in case of resistant genotype, LBG 17 whereas contrarily it was higher in the susceptible genotypes, *viz.,* VBN(Bg) 4, Mash 1008 and Mash 114. The resistant genotype, LBG 17 exhibited 11% decrease in protein content under disease incidence, while also displayed 32% increase in phenolic content. The enzymatic activity of LBG 17 was comparatively higher than the other genotypes under study. This clearly depicts the protein content, phenols and other components like reducing sugar also influence the resistant mechanism of powdery mildew in blackgram and hence selection of resistant genotypes can be made based on the above aspects besides selection through phenotype, gene action and molecular marker study.

S6.23: Diversity, identification and characterization of *Trichoderma* isolates and their effectiveness against *Fusarium* wilt of lentil

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Productivity of lentil, an important pulse crop world-wide is severely affected by wilt disease caused by *Fusarium oxysporum* f.sp. *lentis*. Antagonistic properties of *Trichoderma* spp. have been exploited for the eco-friendly management of *Fusarium* wilt of lentil. The current work focused on identification, characterization and diversity of *Trichoderma* isolates with potential to suppress wilt incidence and exploit them for better production of lentil crop. Fifteen *Trichoderma* isolates were isolated from rhizospheric soil collected from different locations of Bundelkhand area of U.P. Cultural and morphological characters such as colony colour (white to green), growth rate, shape of conidia (globose, sub-globose and ellipsoid) and pattern of conidiation (either formation of ring or no ring formation) and microscopic features such as branching patterns of conidiophores, the arrangement of phialospores and their shape, size and colour were recorded. BLAST analysis of ITS sequences obtained in PCR using ITS 1 and ITS 4 primers revealed that *Trichoderma* isolates under study belonged to two different *Trichoderma* species of which fourteen were *Trichoderma harzianum* and one was *Trichoderma asperellum*. These ITS sequences were submitted to NCBI data base under accession numbers-OP783872, OP783874, OP783876, OP783884, OP783875, OP783882, OP783870, OP783878, OP783880, OP783879, OP783869, OP783866, OP783862, OP783881 and OP783885. The antagonistic activity of *Trichoderma* isolates against *F. oxysporum* f. sp. *lentis* evaluated *in vitro* indicated that the *Trichoderma harzianum* isolate IIPRJ-1 showed maximum (65.75%) inhibition percentage against *F.oxysporum* f.sp. *lentis*. This study also revealed that morphological and genetic diversity among different isolates of *Trichoderma* may not be dependent on geographical locations.

S6.24: Laboratory investigation on management of *Macrophomina phaseolina*

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Mungbean is an important *Kharif* pulse crop widely grown in various regions of Maharashtra. Among different biotic constraints *Macrophomina phaseolina* (Tassi.) Goid is one of the major limiting factor in mungbean cultivation. The isolated pathogen from the mungbean leaf blight disease was studied for the in vitro efficacy of different fungicides against *Macrophomina phaseolina* and it was revealed that, all the systemic fungicides significantly inhibited the growth of test fungus. Fungicides propiconazole and tricyclazole showed complete inhibition (100 %) of *M. phaseolina* at all three concentrations (0.05, 0.10 and 0.15 %). Carbendazim also completely restricted the growth at 0.15 %. Among the non-systemic and combi. fungicides tested, 100 % growth inhibition was recorded in fungicide carbendazim 12 % + mancozeb 63 % at all concentrations (0.15, 0.2 and 0.25 %), whereas least mycelial inhibition was observed with copper oxychloride. Other fungicides *viz*, mancozeb, thiram, captan and propineb also found effective against *Macrophomina phaseolina*.

S6.25: Identification of resistant source against Sterility mosaic disease of Pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Pigeonpea [*Cajanus cajan* (L.) Millsp.], also referred to as red gram or arhar, is an important grain legume crop predominantly grown in the Indian subcontinent as an important source of dietary protein. Sterility mosaic disease (SMD), also known as "green plague of pigeonpea" as the infected plants are pale green with excessive vegetative growth and no - poor flowering and it is posses severe threats in pigeonpea production. The estimated an annual yield loss of over US$300 million in India alone. To overcome this issue, breeding for resistant varieties is considered to be one of the most effective and economic methods of reducing the crop losses and has received the top priority. Forty nine genotypes including checks were screened for SMD resistance by adopting leaf stapling technique at field condition during *Kharif* 2021-22 at RARS, Warangal. Based on the percent disease incidence (PDI), the genotypes could be classified as Resistant (0-10%), Moderately resistant (11-35%) and susceptible (35-100%). out of forty nine genotypes screened , six genotypes *i.e.,* WRG-441, WRG-443, WRG-468, WRGE-160, WRGE-165 and WRGE-159 showed resistant reaction (0-10%) to SMD infection while twenty genotypes (WRGE-138, WRGE-137, WRGE-155, WRGE-162, WRGE-133, WRG-429, WRG-432, WRG-447, WRG-463, ERG-485, WRG-488, WRG-489, WRG-496, WRG-486, WRG-390, WRG-391, WRG-446, ICPIL-17101, ICPIL-17103 and ICPIL-17114) were moderately resistant to disease and remaining 23 genotypes are recorded as susceptible to SMD. Therefore, these six resistant genotypes may be utilized for SMD resistance breeding programme.

S6.26: Deciphering resistance to frogeye leaf spot in soybean germplasm under Mid-Himalayan region

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Soybean [*Glycine max* (L.) Merr.] is the unique grain legume globally known for its dual purpose use as pulse and oilseed containing 38–44% protein and 18–22% oil. The seed protein content of soybean is higher than non-vegetarian diet and therefore, it is also known as poor man's meat. This crop is affected by many pathogens but frogeye leaf spot caused by *Cercospora sojina* Hara is one of the major disease occurring in epidemic form in sub-humid mid hill agro-ecological zone of Himachal Pradesh causing considerable yield losses. Deployment of genetic resistance through identification of genotypes which are resistant to the prevalent races of pathogen and its incorporation in a high yielding variety is the most economically sound strategy to manage the disease. Keeping above in view, 322 germplasm lines were grown in a randomized block design with two replications at the experimental farm of Department of Genetics and Plant Breeding, CSK HPKV Palampur, during *kharif* 2022. The lines were sown in two rows per replication having length of two meter and spacing of 45cm × 10cm. These germplasm lines were screened under natural field conditions for frogeye leaf spot reaction on the basis of 0-9 scale given by Stonehouse (1994). Among all 322 genotypes, only 17 genotypes *viz*., IC 15089, EC 241756, JS 97-52, AMS-MB-5-18, BR 15, JS 20-69, AGS 205, JS 79-82, MACS 58, CAT 1149, DS 321, TGX 803-99E, TGX 573-209-23, VLS-59, EC 550828, JSM 245 and NRC 2007-1-3 showed the resistant reaction at both early and later plant stages under natural field conditions. These genotypes can be further tested for resistance by artificially inoculating with pathogen. The genotypes found as resistance at both natural and artificial conditions can be used in future soybean improvement programme to introgress the resistance in high yielding soybean varieties.

S6.27: Potential mungbean genotypes being tested for resistance to *Macrophomina* blight disease

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Mungbean (*Vigna radiata* L. Wilczek), is one of the most important pulse crops grown in India. It belongs to the family Leguminosae. Mungbean is affected by about sixty fungal, three bacterial and five viral diseases. Among that, *Macrophomina phaseolina* (Tassi) Goid is one of the most damaging seed and soil borne pathogen, infecting about 500 plant species in more than 100 families throughout the world. During the study of screening promising mungbean genotypes against *Macrophomina* blight, the result of screening revealed that, among the twenty-five genotypes two BPMR 145 and AKM 12-23 showed resistant reaction against the fungus under glasshouse condition. Nine genotypes found moderately resistant and eleven genotypes reported moderately susceptible, while only two genotypes Phule M 818-8 and BM 2019-1 gave susceptible reaction. Vaibhav genotype showed highly susceptible reaction against *Macrophomina* blight. The per cent disease intensity among the twenty-five mungbean germplasm lines screened during Kharif 2019-20 was range between 00.00 to 39.38. Data indicate that, two genotypes BPMR 145 and AKM 12-23 showed resistant reaction to *Macrophomina phaseolina*. Fourteen genotypes found moderately resistant and seven genotypes were found moderately susceptible. The genotypes Vaibhav and BM 2019-1 recorded highest disease intensity therefore are confirmed as susceptible. None of the genotypes was found highly susceptible under field condition.

S6.28: Performance of mid early and medium duration pigeonpea genotypes against pod borers

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Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the important legume crop grown in Telagana, India. Since years long, its yield potential has not been fully realized due to biotic stress noticed at the reproductive stage of the crop especially pod borer complexes. Thus, keeping this in view, present study was conducted to identify resistant cultivars from certain pigeonpea genotypes against pod borer complex at Regional Agriculture Research Station, PJTSAU, Warangal, Telangana during *Kharif*, 2021-22. The materials of the study, eleven genotypes of mid early duration and fourteen genotypes of medium duration along with check varieties were collected from breeding lines maintained at RARS, Warangal. Present investigation observed that the mean number of *Helicoverpa armigera* larvae/plant and No. of webs of *Maruca vitrata* per plant was recorded low in the entries WRGE-141, WRGE-150, WRGE-147, WRG-459, WRG 463 and WRG-443 at 50% flowering. However, the percent pod damage due to *H. armigera*, *M. vitrata* and *M. obtuse* was low in the entries, WRGE-138, WRGE-142, WRGE-134, WRGE-150, WRGE-149, WRGE-155, WRGE-147 (with PSI rating 3 and 4) of mid early duration and WRG-437, WRG-423, WRG-426, ICPIL-17114, WRG-429, WRG-463 (with PSI rating 3 and 4) of medium duration. Further, the entries, WRGE-138, WRGE-155, WRGE-134, WRG-463 (1823 Kg/ha) and WRG-437 has recorded more yield than other entries and check varieties. Thus, the genotypes WRGE-138, WRGE-149, WRGE-142, WRG-437 and ICPIL-17114 were found promising against pod borers and can be used as resistant donor line in pigeonpea breeding program aiming at grampod borer resistance.

S6.29: Testing of different varieties of pigeonpea against major pests

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The experiment on testing of different varieties of pigeonpea was conducted during *Kharif* season 2021-22 at research farm of Pulses Improvement Project, MPKV, Rahuri for their reaction to *Helicoverpa armigera* (Gram pod borer) and *Melanogromyza obtusa* (Pod fly). This experiment was conducted in randomized block design replicated thrice with the different varieties of pigeonpea viz., 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 6124, 2165, 2166, 2167, 2168, 2169 and Rajeshwari. Out of 20 varieties of pigeonpea, varieties of 2167 and 2161 was recorded minimum per cent pod damage due to *H. armigera* infestation, which recorded 2.33 % and 2.51 % pod damage and pest susceptible rating PSR-2 and PSR-3, respectively. While varieties of 2169 and 2155 was recorded minimum per cent pod damage due to pod fly (*M. obtusa*), which recorded 3.21 % and 3.28 % pod damage and pest susceptible rating PSR-3 and PSR-4, respectively.

S6.30: Evaluation of insecticides against pod fly (*Melanagromyza obtusa* Malloch) in pigeonpea

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The experiment on evaluation of insecticides against pod fly (*Melanagromyza obtusa*) in pigeonpea was conducted during *Kharif* season 2019-20, 2020-21 and 2021-22 at research farm of Pulses Improvement Project, MPKV, Rahuri. This experiment was conducted in randomized block design replicated thrice with nine treatments *viz*., T_1- buprofezine 25 SC @ 200 g a.i./ha, T_2- diafenthiuron 20 SG @ 40 g a.i./ha, T_3- diafenthiuron 50 WP @ 350 g a.i./ha, T_4- flubendiamide 480 SC @ 30 g a.i./ha, T_5- lufenuron 5.4 EC @ 30 g a.i./ha, T_6-deltamethrin 2.8 EC @ 12.5 g a.i./ha, T_7- thiamethoxam 25 WG @ 50 g a.i./ha + 2.5 kg Jaggary/ha, T_8- quinalphos 25 EC @ 350 g a.i./ha and T9 untreated control. The treatment of thiamethoxam 25 WG @ 0.4 g/lit + 5 g jaggery/lit. of water proved to be most significantly superior and which was recorded 1.44 per cent pod damage and 1.30 per cent grain damage due to pod fly (*Melanagromyza obtusa*). This treatment also recorded highest grain yield i.e. 18.10 q/ha and which was at par with the treatments of flubendiamide 480 SC @ 30 gai./ha, diafenthiuron 20 SG @ 40 gai./ha and deltamethrin 2.8 EC @ 12.5 gai./ha.

S6.31: Induced post-invasive defences in the non-host plant *Parthenium hysteropohrus* L. prevent root cortical colonization by *Macrophomina phaseolina* (Tassi) Goid.

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Dry root rot (DRR) disease of chickpea is caused by the broad range necrotrophic fungus, *Macrophomina phaseolina* (Tassi) Goid. The host germplasm does not provide durable resistance to DRR which is particularly devastating under concurrent drought. Even moderately resistant chickpea varieties become susceptible under combined stress. We hypothesized that nonhost resistance (NHR) is durable even under combined stress. Among the 48 potential nonhosts of *M. phaseolina,* we identified *Parthenium hysterophorus* L., an Asterid weed as a potential nonhost using blotter paper assay and extensive stereomicroscopic observations. *P. hysterophorus* prevented epidermal necrotic lesions. Results from confocal microscopy showed that *M. phaseolina* is unable to infect the root cortex even under significantly increased inoculum load and the NHR was durable even under combined stress. Furthermore, dual RNA-sequencing to elucidate the putative molecular mechanisms involved in NHR revealed that *M. phaseolina* made an active attempt to infect the nonhost and used distinct detoxification mechanisms when infecting the nonhost. *P. hysterophorus* also showed an active defence response characterized by a differential expression of certain orthologous gene involved in the cell wall synthesis, phytohormone signalling and other defence response pathways which likely contribute to the NHR. Further, non-orthologous genes in the terpenoid and phenylpropanoid biosynthesis pathways were also upregulated possibly correlating to the distinct detoxification mechanisms used by the fungus while infecting the nonhost. We, therefore, conclude that *P. hysterophorus* exhibits post-invasive NHR to *M. phaseolina* and the general defence, phytohormone signalling, secondary metabolic pathways are likely contributors to NHR.

S6.32: Evaluation of Pigeonpea genotypes for resistance to wilt disease

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A total one hundred thirty four entries of Pigeonpea were screened in the wilt sick plot under high disease pressure in field condition to find out levels of their resistance against wilt along with one row of ICP2376 a highly susceptible entry. The plot was artificially inoculated with chopped stem pieces of wilted plants of pigeonpea at the time of final land preparation. Observation was recorded on the basis of total number of plant and number of wilted plant in each entry, per cent wilt incidence was calculated and the entries were categorised as resistant, moderately resistant and susceptible. Out of one hundred thirty four entries of pigeonpea, fifty six entries *viz*. NAM 88, TJT501, BDN2019-5, 2019-9, WRGE134, ICPIL17103, AKTE16-21, PT11-4-4-4-1, 2017-1, WRGE124, PT10-1-1-2, BDN2013-2, 716 , JKM189, NAM92, 151, BDN2019-34, AKTM1914, PT12-5-5-1,GJP2011, SKNP1715, BAUPP16-38, 18-7, WRG391, LRG471, PT11-16, GRG 622, GJP1915, AKTM1637, IPAL20-1, 20-24, IPA19-26, 19-43, 19-6, 18-8, 14-2, 15-19, 13-1, BRG4, 5, BSMR203, 736, BWR243, 853 , 253, 553, 571, 316, BSMR2, 651, 339, BWR23, 164, 153 and 133 were found resistant and forty seven entries viz. AL2324, PusaArhar21-1, 21-27, 21-29, CRG16-09, PT12-19-2, AKTE1905, LRG467, RVSA14-2, WRGE138, PT2017-2, RVKT383, BDN2013-5, RVSA2020-6, 2020-7, 2020-8, LRG224, 275, AKTM1917, GJP2008, WRG390, RKPV 821-01, NPD18-03, KA19-05, IPAL20-1, 20-11, PUSA197, MAL53, IPA15-21, 14-6, 15-1, 16-18, GTH1, SKNPCH1906, WRG65, 1, MAL13, 57, BRG1, 2, 3, BSMR175, 164, 79, 26, 254 and 134 were recorded moderately resistant and remaining entries showed susceptible reaction against the disease. Entries found resistant to moderately resistant may either be used as donor parent in breeding programme for development of resistant varieties or if yield level is comparable with existing varieties it may be released for general cultivation.

S6.35: Impact of date of sowing and weather parameters on insect pests infesting summer mungbean

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An experiment was conducted to access the effect of three dates of sowing and weather parameters on major insect pests of mungbean during summer 2021 and 2022. During both the years, in the first date of sowing, amongst the sucking pests, whitefly appeared from second and fourth week of March and remained till third week of April and first week of May. Whereas in the second date of sowing, the incidence was noticed from third week of March and continued till first week of May. In the third date of sowing, it started from third and fourth week of March, respectively and continued till first week of May during both years. Thrips were seen in the flowers from third and fourth week of March and remained till third week of April and first week of May. Whereas, in the second date of sowing the incidence of thrips was noticed from last week of March and continued till first week of May, respectively. In the third date of sowing, it started from last week of March and continued till first and second week of May. Podborer, *Heliothis armigera* was observed from fourth week of March and remained till first week of May during both years. Whereas, in the second date of sowing, the incidence was noticed from third and fourth week of March and continued till first and second week of May. In third date of sowing, it started from fourth week of March and continued till second week of May. During 2021, maximum and minimum temperatures showed a highly significant positive effect on whitefly and thrips population. During 2022, maximum relative humidity showed a highly significant positive effect on whitefly and thrips population. The *H. armigera* larval population showed a positive significant impact with minimum relative humidity during the same year. Thus, in nutshell it can be said that pod borer damage at harvest was lower (8.20% and 7.50%) in the mungbean crop sown on 26th February with highest yield (800 and 725 kg/ha) in both the years. Also, it can be concluded that with the increase of temperature and relative humidity, the insect pests population also increased which had a direct negative impact on yield parameter of summer mungbean.

S6.37: Identification of resistance sources of chickpea against dry rootrot caused by *Rhizoctonia bataticola* (Taub.) Butler

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Chickpea (*Cicer arietinum* L.) commonly called as Bengal gram is the world's third most widely grown legume after French bean (*Phaseolus vulgaris* L.) and peas (*Pisum sativum* L.). The pathogen *Rhizoctonia bataticola* (Taub.) Butler is an important soil borne fungus causing dry root rot disease in chickpea. Chickpea mini core collection composed of 211 germ plasm accessions representing the diversity of the global chickpea germ plasm collection of 16,991, maintained at the International Crops Research Institute for the Semi-Arid Tropics to identify the sources of resistance to dry rootrot were evaluated in sick pots against *R. bataticola* in artificially inoculated soil at RARS, Vijayapur, Karnataka. Among the 211 germplasm accessions evaluated against Dry root rot, only eight germplasm (ICC 12947, ICC 13077, ICC 14778, ICC 14799, ICC 13628, ICC 15264, ICC 12328 and ICC 11764) were found to be moderately resistant, 49 accessions were moderately susceptible, 55 accessions were susceptible and 82 were highly susceptible. The remaining 17 accessions were not germinated due to external environmental conditions which are not suitable for the germination of some germplasm which are collected from various regions of world.

S6.38: Insecticidal effects of some plant essential oils on pulse beetle, *Callosobruchus analis* (F.)

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The bruchids (Coleoptera: Chrysomelidae) are the most serious post-harvest pests of store legumes worldwide. Bruchid infestation leads to both quality and quantity deterioration of stored legumes. Over the years, synthetic insecticides and fumigants are consistently used for the disinfestation of stored grains. Besides, the residue problem in the edible stored grains, the development of resistance to synthetic insecticides have been reported in stored grain pests. Lately, plant essential oils (EOs) are recognized as safer and potential bioactive compounds against many stored grain pests. Insecticidal, sub-lethal and residual effects of *Pogostemon cablin* Benth*, Mentha arvensis* L.*, Cymbopogon martinii* (Roxb.) Wats.*, Pelargonium graveolens* L. and *Acorus calamus* L. EOs were investigated against *Callosobruchus analis* (F.). Among the EOs, *P. cablin* demonstrated highest contact toxicity (LC_{50}: 0.040 µl/cm^2) to adult beetles. All the EOs possessed concentration-dependent repellent property (41–99 % repellency), while *C. martinii* exhibited strong repellency to adult beetles. Although all the EOs significantly reduced the egg laying and adult emergence at sub-lethal exposures, *A. calamus* EO showed strong deterrence to oviposition (> 97 %) and adult emergence was completely inhibited. EOs possessed significant residual toxicity, where *M. arvensis* and *A. calamus* treated mungbean seeds were totally free from bruchid damage (0 % seed damage) for > 70 days post-treatment. These insecticidal EOs can be used for developing the eco-friendly grain protectants to manage the bruchids. However, further studies are needed to develop the improved delivery methods considering the volatile nature of EOs and to assess the insecticidal properties of chemical constituents of potential EOs.

S6.39: Escape resistance in field pea against *Phytomyza horticola* Goureau, as influenced by sowing time and its correlation with plant metabolites

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Field pea or dry pea (*Pisum sativum* L.) is one of the important, highly productive cool season food legume crops and pea leaf miner, *Phytomyza horticola* Goureauis is a pest of high economic importance, associated with the crop**.** A panel of twenty eight diverse field pea genotypes including checks was selected to screen them with respect to their susceptibility to the pest and to study the influence of sowing time on the extent of infestation of pea leaf miner. The correlation of infestation with the host primary and secondary metabolites was also examined. In late sown condition, only 8 genotypes were categorized as 'Susceptible', 2 genotypes under 'Moderately Resistant', 3 genotypes under 'Intermediate', whereas 15 genotypes were categorized as 'Moderately Susceptible'. None of the genotypes could be categorized as 'Very Highly Resistant', 'Highly Resistant', 'Resistant', 'Highly Susceptible' and 'Very Highly Susceptible' in case of late planting. In case of timely planting, only 9 genotypes were categorized under 'Moderately Susceptible', 7 genotypes each under 'Moderately Resistant' and 'Intermediate' and 5 genotypes grouped under 'Highly Resistant' category. None of the genotypes categorized as 'Susceptible' or beyond that in case of timely planting. Most of the genotypes which showed susceptibility under late sown condition had expressed more level of resistance in the timely sown crop. Although, different field pea genotypes differed significantly in terms of quantity of primary and secondary metabolites estimated, only the total phenol content was found significantly and positively correlated with the per cent infestation in the late sown genotypes.

S6.40: Evaluation of advanced breeding lines of mungbean for yield and MYMV resistance

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Mung bean [*Vigna radiate* (L.) R. Wilczek] is an important short duration pulse crop and rich in easily digestible protein. In India it is mainly grown during *kharif* season. But recently, it has been becoming more popular during summer season especially in paddy fallow areas. Success of mungbean cultivation during summer season mainly depends on the availability of high yielding, photo and thermos-insensitive, short duration (60-65 days) and MYMV resistance mungbean cultivars. In the present study, advanced genotypes of mungbean (42 advance breeding lines) were evaluated in randomised block design for various agronomic traits and MYMV reaction under natural field conditions. Wide range of variation was observed for days to flowering and days to maturity, seed yield and 100-seed weight. The genotypes such as IPM-21-23-1 found to be earliest to mature (56 days) followed by IPM-205-7 (58 days) and IPM-21-15-3 (59 days), while, the genotypes viz, IPM-21-15-2 (1530 Kg/ha), IPM-1711-1 (1494kg/ha), IPM-21-23-1 (1486kg/ha) and IPM-1620-6 (1436kg/ha) were produced higher seed yield (Kg/ha) compared to check IPM-2-14 (1295kg/ha). Out of 42 genotypes screened under field conditions for MYMV, six genotypes such as IPM-21-15-2, IPM-14-10, IPM-21-23-1, IPM-1711-1, IPM-205-7 and IPM-16-20-6 revealed highly resistance reaction to MYMV compared to highly susceptible check-DGGV-2. These identified promising MYMV resistance genotypes could be more suitable for cultivation in Karnataka during summer season.

S6.41: Evaluation of cluster bean genotypes for multiple disease resistance to strengthen genetic improvement programme

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Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] popularly known as guar, is one of the most important Kharif legume and is well adapted to arid and semi-arid regions of the world. It is a drought-resistant crop and can be grown successfully in area where average rainfall is 30-40 cm. It is cultivated mostly as rain fed and warm season crop in semi-arid zones of northern India. Rajasthan state is leading producer of cluster bean production in India. Biotic stress in plants is caused by living organisms, especially fungi, bacteria, viruses, nematodes etc. adversely affect growth, development of crop. In the Indian context, fungal and bacterial diseases are the major constraints in the production and productivity of cluster bean. The important diseases of cluster bean are Bacterial leaf blight (BLB) (*Xanthomonas axonopodis* pv. *cyamopsidis*) and dry root rot [*Macrophomina phaseolina* (Tassi) Goid] which causes major losses in yield of cluster bean crop. BLB is greatly influenced by certain environmental factors prevailing in arid environment, disease causing 47-58% yield losses at 69-72% blight intensity. The occurrence of disease is favored by spattering rains, high humidity (80-90%) and moderate temperature (27-30°C), which are usually available during rainy season (August-September) coinciding with most vulnerable stage of the crop. However, Warm growing conditions and soil moisture stress are among the important factors, which governing survival and occurrence of *M. phaseolina* induced diseases in severe form. Biotic stress in plants is caused by living organisms, especially fungi, bacteria, viruses, nematodes etc. adversely affect growth, development of crop.

S6.42: Effect of insecticide modules against pod borer complex in pigeonpea (*Cajanus cajan* (L.) Millsp.)

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An investigation was undertaken to evaluate different insecticide modules against pod borer complex of pigeonpea at Pulses Research Unit, Dr. P.D.K.V., Akola (M.S.) during 2021-22. The experiment was laid out in randomized block design with seven modules and three replications. M1 (Thiodicarb 75WP *fb* Chlorantraniliprole 18.5 SC *fb* L. cyhalothrin5 EC), M2 (Thiodicarb 75WP *fb* Flubendiamide 39.35 SC *fb* L-cyhalothrin 5 EC) M3 (Thiodicarb 75WP f*b* E. benzoate 5 SG fb Quinolphos 25 EC) M4 (Ethion 50 EC *fb* Chlorantraniliprole18.5 SC *fb* Quinalphos 25 EC) M5 (Ethion 50 EC *fb* Flubendiamide 39.35 SC *fb* L. cyhalothrin 5 EC) M6 (Ethion 50 EC *fb* E. benzoate 5 SG *fb* L. cyhalothrin5 EC) M7 (Untreated Control). Each module having three sprays one at 50% flowering, second at 15 days after first spray and third at 20 days after second application. The performance of each insecticide module was judged on the basis of larval incidence, pod damage, grain damage, yield and incremental cost benefit ratio. Considering the effectiveness of various insecticide modules in recording lowest larval population of *H. armigera* and *E. atomosa* (0.26 and 0.29 larvae/plant respectively) lowest per cent pod damage (5.07%) and grain damage (2.00%) was recorded in module M1 followed by module M2. Whereas, in the case of pod fly, module M2 recorded lowest larval population (0.35 larvae/10 pods) and lowest per cent pod (4.8%) and grain damage (4.33%) at harvest. Though, the module M1 recorded higher yield (15.69q/ha) the highest ICBR was recorded in module M2 (1:4.69).

S6.43: Seed inoculation: A quick, easy and reliable technique for rapid field screening of pigeonpea against Fusarium wilt

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Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of the most important grain-legume grown in Indian-subcontinent. India stands first in the production and acerage of pigeonpea in the world. But, the susceptibility of pigeonpea to Fusarium wilt caused by *Fusarium udum* is a main stumbling block for achieving the desirable productivity. The use of resistant cultivars is the cheapest and safest method to manage this problem. Identification of pigeonpea germplasm resistant to *Fusarium* wilt is a continuous exercise. Generally, the screening of pigeonpea genotypes is performed in wilt-infested fields/sick plot. So far, several inoculation techniques, *viz*., root-dip inoculution, soil infestation, stem inoculation, etc. have been tested/employed for resistant screening of pigeonpea against *Fusarium* wilt, but only few can be practically employed in field. Therefore a new technique was developed for easy, and precise inoculation of pigeonpea with wilt pathogen. In this technique, the seeds of pigeonpea wilt susceptible genotype ICP 2376 were treated with fungal inoculum (1×10^6 cfu) and kept overnight for incubation. The treated seed were sown directly into soil, keeping untreated seed as control. This technique was compared with direct soil infestation. After seed inoculation, 40.0% plants were showed wilting symptoms within 2 months of inoculation as compared with 10.0% infestation in case of inoculation direct soil infestation method. This technique was found to be very effective for rapid inoculation as well as disease development. Further, validation of this technique is necessary for successfully screened in the field, to confirm the rapidity and effectiveness of the technique.

S6.44: Comparative volatile profiling of chickpea genotypes under biotic stress

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Chickpea (*Cicer arietinum* L.) is the third most important legume crop of the world grown in nearly 52 countries. It is rich in minerals, dietary fibers and carotenoids, also contains high amounts of unsaturated fatty acids and serve as an inexpensive source of high quality plant protein for millions of people in developing countries. The major biotic barrier in chickpea production and productivity is gram pod borer, *Helicoverpa armigera* (Hubner), it is cosmopolitan, polyphagous pest infesting 225 plant species belonging to 46 families. The migratory nature, polyphagy, short life cycle, multivoltinism and insecticide resistance in *H. armigera* make its management a very difficult task. In this context, host plant resistance plays an important role in management of the pest with means to minimize the extent of crop losses and insecticide use. So the present investigations we carried out on screening and volatile profiling of chickpea genotypes under biotic stress. Seeds of six chickpea genotypes *viz*., GL-15026, GL-15017, RSG-956, RSG-959, ICCL-86111 (resistant check) and ICC-3137 (susceptible check) were sown in plastic pots filled with potting mixture. Pre-starved third instar larvae of *H. armigera* were released on six week old chickpea plants @ one larva per plant and were allowed to feed for 4 hours and were removed. Non-infested plants were considered as control for respective genotypes. To mimic insect infestation, leaves were wounded with a punch machine (Mechanical damage) until 15–20% of leaf area was removed in time span of 4 hours. The volatiles released by the plants were collected through dynamic headspace collection method and the extracts were analyzed through Gas chromatography-Mass Spectroscopy. The PCA analysis of GC-MS profile data for each genotype revealed differential pattern of volatile compounds released by plant under control, larval damage and mechanical damage. The volatiles such as 1-ethyl-2-methyl- Benzene, Mesitylene need to be further explored to determine their role in defense against insect pest, *H. armigera*.

S6.46: Physical mutagenesis for induction of resistance against legume pod borer (*Maruca vitrata* F.) in cowpea [*Vigna unguiculata* (L.) Walp]

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Legume pod borer, *Maruca vitrata*, has emerged as a major pantropical pest of leguminous crops. The lack of genetic resistance against this oligophagous pest makes it imperative to rely solely on chemical control as biological means are far from effecting a breakthrough. Environmental concerns and lurking resurgence of insecticide resistance associated with chemical use impels development of *Maruca* resistant varieties. A gamma-rays based mutagenesis programme to induce resistance in otherwise elite Trombay cowpea variety, 'TC-901', was conceptualized under a Coordinated Research Project of the International Atomic Energy Agency, Vienna, jointly with the FAO of the United Nations. M_1 generations (200 Gy, 250 Gy) were raised under protection, while M_2 generations comprising of ~40,000 plants were evaluated at Trombay hotspot with pigeonpea in vicinity for pest load augmentation. Three putative tolerant mutants (MR1, MR2 and MR3) were identified with pod damages in the range of 27 – 45% as against the parent (78 – 85%). Post confirmation of tolerance in subsequent generations (M_3, M_4), ten insect-resistance pathway associated genes with respect to Pyralidae/Crambidae families of lepidopteran pests were identified from literature survey for qPCR expression studies. Differential gene expression analysis of three mutants, their parent and a highly susceptible variety 'Lola' showed isoprene synthase gene to be five-fold upregulated, while isocitrate dehydrogenase, phenylalanine ammonia lyase and geranyl geranyl pyrophosphate synthase genes were 2.5-fold upregulated in tolerant mutants. Choice and no-choice assays-based confirmation of resistance under controlled conditions, development of mapping population and molecular tools and agronomic evaluation of these mutants are underway.

S6.49: *EF-1α* gene genealogy indicates that Indian isolates of *Fusarium oxysporum* f.sp. *lentis* are polyphyletic

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Lentil (*Lens culinaris* Medikus subsp. *culinaris*) is one of the major pulse crops. Lentil wilt incited by a soil borne fungus, *Fusarium oxysporum* f.sp. *lentis* (Fol) is the most destructive disease responsible for even 90% crop losses if conducive weather conditions prevail. The *F. oxysporum* population is divided into *formae specialis* and races based on their ability to infect different host genera and different varieties within the host genera, respectively. The *formae specialis* in *F. oxysporum* are assumed to be monophyletic; however few gene genealogy studies have revealed different *formae specialis* to be polyphyletic. To identify whether the Indian Fol isolates are monophyletic or polyphyletic, we have selected the *EF-1α* as it is an excellent marker for phylogenetic analysis of *F. oxysporum*. *EF-1α* gene sequences of Fol isolates and other *formae specialis* were obtained from NCBI database. The analysis using 52 sequences was performed through PAUP 4.0 software. The parsimony analysis was done with heuristic search option with TBR (tree bisection reconnection), branch swapping algorithm, and 1000 bootstrap replications. The parsimony analysis was done on 1897 total characters out of which 926 were parsimony informative. The Fol did not form a distinct grouping when compared with other *formae specialis* but were distributed in all the three clades demonstrating its polyphyletic origin. The results in current analysis indicate that the isolates of Fol have distinct genetic background therefore to develop molecular markers for specific detection of this *formae specialis* we need to explore the genetic determinants of pathogenicity to lentil.

S6.51: Molecular variability and management of *mungbean yellow mosaic virus* in greengram

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Roving survey conducted on mungbean yellow mosaic virus (MYMV) disease in four districts during *kharif* 2021 and summer 2021-22. Average maximum incidence of 16.85 percent was recorded in Gadag and the lowest incidence of 11.58 percent was noticed in Bagalakot district during *kharif,* whereas maximum incidence of 30.10 percent was recorded in Dharwad and the lowest incidence of 20.59 percent was noticed in Bagalakot district during summer. DNA fragment of ~695 bp corresponding to MYMV coat protein (CP) gene was amplified using MYMV specific coat protein gene primers. The sequence analysis revealed that, MYMV Belagavi isolate showed 99.28 per cent similarity to MYMV-Mo2-Belgaum clone (MN698295.1). MYMV Dharwad isolate showed 99.01 per cent similarity to MYMV-Mo2-Belgaum clone (MN698295.1) and variability studies of MYMV-Dharwad and MYMV-Belagavi isolate showed the variation at 11 and 10 nucleotides base pairs positions respectively. This indicated that, both the isolates are closely related to MYMV. Five genotypes viz., DGG-262(DA-16), DGG-96(TARM-128-1), DGG-218, 436714(50), IPM 2-14 showed resistance reaction. Six genotypes showed moderately resistant reaction. Seventeen genotypes were moderately susceptible and remaining fifty-five were susceptible to highly susceptible. Among different chemicals tested for the management of mungbean yellow mosaic disease, seed treatment with Imidacloprid 60 FS @ 5ml//kg of seeds followed by foliar spray of Thiamethoxam 25% WG 0.3 g/l at 25 days after sowing found effective and recorded 5.54 and 11.51 % during *kharif* and summer respectively. Maximum seed yield of 8.93 q/ha and 6.98 q/ha was recorded during *kharif* 2021 and summer 2021-22 respectively.

S6.52: Status of *Macrophomina* blight, Yellow mosaic and Powdery mildew diseases of mungbean in Marathwada region

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Survey of *Macrophomina* blight, Yellow mosaic and Powdery mildew diseases of Mungbean in Marathwada region revealed that improved varieties BPMR 145 and BM 2003-2 shown low disease incidence than Kopargaon and JL 781. Survey was conducted in Aurangabad, Jalna, Beed and Latur district of Marathwada region. The eighteen (18) field locations of total 21 ha were surveyed in *Kharif* 2021. The *Macrophomina* blight was recorded 05 to 36.29 percent. Yellow mosaic disease was in the range of 3 to 21.67 per cent. Powdery mildew disease was in the range of 1.6 to 4.3 scale.

S6.55: Compatibility among *Trichoderma* isolate and systemic fungicides for their efficacy against *Fusarium* wilt of chickpea and lentil

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Fungicides are used frequently to manage plant diseases effectively, but human health and environmental concerns often put pressure on growers to reduce the number of applications. These fungicides have inhibitory effects on the biocontrol agents. For sustainable and effective plant disease management activity of biocontrol agents should not be gets hampered by the application of fungicides. To check the compatibility of *Trichoderma* isolates with fungicides MATCO and Bavistin (Carbendazim) were evaluated with 10 Potential *Trichoderma* isolates on 5 different (100,250,500,750 & 1000PPM) fungicides concentrations. MATCO (Mancozeb and metalaxyl) was compatible with all the selected 10 Potential *Trichoderma* isolates up to 1000PPM while Bavisitn (Carbendazim) was not found to be compatible at any selected concentration with any of the selected *Trichoderma* isolate. Therefore, MATCO can be applied along with *Trichoderma* isolates up to 1000PPM concentration in integrated disease management. Bavisitn and MATCO were found to be effective against *Fusarium oxysporum* f.sp. *lentis* and *Fusarium oxysporum* f.sp. *ciceris* management. Maximum inhibition of both pathogens was achieved at 1000 PPM concentration of both the fungicides. To develop an effective disease management programme, the compatibility of potential bioagents with fungicides is essential. Combination of chemicals and compatible bioagents in an IDM strategy protects the seeds and seedlings from soil-borne and seed borne inoculums. The combination of biological control agents with fungicides would provide similar disease suppression as achieved with higher fungicide use.

S6.57: Management of chickpea rust *Uromyces ciceris-arietini* (Grogn.) Jacz. & Beyer through novel fungicides

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Chickpea rust is an important disease appears at the maturity of the crop and was not earlier considered as a major constraint in chickpea production. Of recent it is emerging as one of the major chickpea disease in the Peninsular India. The farmers cultivated chickpea cultivars in the region are low in resistance to rust and hence a field experiment was conducted during 2019-20 and 2020-21 *rabi* seasons at ICAR- IIPR RRS Dharwad to evaluate fungicides. The field experiment was laid out in RBD design with chickpea variety JG11. Chickpea was sprayed soon after the disease appearance and second spray after 15 days. The results indicated that, foliar spray of Difenconozole 25% EC at 1.0 ml L^{-1} was effective and reduced rust severity up to 73% followed by a combi product of Tebuconozole 50% + Trifloxystrobin 25% WP at 1.0 g L^{-1} and Propinonozole 25% EC at 1.0 ml L^{-1} with 70% and 46% respectively compared to control. The two-year higher average grain average yield of 1319 kg ha^{-1} and 1306 kg ha^{-1} was recorded with the treatment Tebuconozole 50% + Trifloxystrobin 25% WP and Difenconozole 25% EC, respectively and were not significant. The control recorded lower average grain yield of 852 kg ha^{-1}. Two sprays of fungicide Tebuconozole 50% + Trifloxystrobin 25% WP provided higher benefit cost ratio of 2.29 followed by Difenconozole 25% EC (2.23) and Propinonozole 25% (2.13). The Difenconozole 25% EC at 1.0 ml L^{-1} and Tebuconozole 50% + Trifloxystrobin 25% WP at 1.0 g L^{-1} are the effective fungicides for management of chickpea rust in Peninsular India.

S6.58: Exploring the virulence role of powdery mildew effectors as keys to biotic stress management in legumes

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Powdery mildew (PM) disease, caused by obligate biotrophic ascomycete fungi, is responsible for severe yield losses in economically important legumes such as pea, lentils, and mung bean. PM fungi secrete a battery of effectors through specialized infection structures termed haustoria to colonize their hosts. Exploring the role of these effectors is crucial for understanding the mechanism of pathogen virulence and for developing effective disease management solutions in legumes. Recent studies on the cereal PMs have identified a class of ribonuclease domain-containing effectors, known as RALPHs (RNase-like proteins expressed in Haustoria), that exhibit both virulence and avirulence properties. Research from our lab has shown that this class of effectors is also prevalent in the pea PM, *Erysiphe pisi*. To further explore the role of RALPH effectors, we performed a comparative genomics analysis of cereal and dicot-adapted PM pathogens. Surprisingly, sequence analysis revealed that the catalytic residues responsible for RNase activity are only conserved in a few *E. pisi* RALPHs. Spatial and temporal expression analysis revealed that the majority of the *EpRALPHs* are preferentially expressed in haustoria, particularly during the early stages of development. A preliminary investigation into the virulence function of a highly expressed *Ep*RALPH suggests that the effector promotes pathogenesis through host cell death suppression. Identification of the host protein interactors of this effector is underway to discover the host signalling pathway(s) modulated by the pathogen for successful colonization. We are also targeting these effectors through a nanotechnology-based approach for PM disease control in legumes of agronomic import.

S6.59: Efficacy of systemic, nonsystemic and combi fungicides against *Fusarium oxysporum* f. sp. *ciceri* under *in vitro* condition

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The present study was conducted under *in vitro* condition to evaluate effectiveness of eight systemic (*viz.* Carbendazim, Thiophanate methyl, Difenoconazole, Azoxystrobin, Metalaxyl, Fosetyl, Tebuconazole and Propiconazole and eight non-systemic and combo fungicides (Mancozeb, Propineb, Carbendazim+Mancozeb, Carboxin+Thiram, Tebuconazole + Trifloxystrobin, Pyraclostrobin+ Metiram, Metalaxyl + Mancozeb, Captan + Hexaconazole) on radial mycelial growth *Fusarium oxysporum* f. sp. *ciceri* at various concentration 500 to 1500 ppm in systemic and 1500 to 2500 ppm in non-systemic and combo fungicides. Among these systemic fungicides only one Carbendazim fungicide was most effective and shown there was no mycelial growth and cent per cent inhibition of mycelial growth *i.e.* 100 % percent inhibition at all the concentrations whereas, in case of non-systemic and combi fungicide Carbendazim 12% + Mancozeb 63 % WP was found most effective shown 0.00 mm mycelial growth and cent percent inhibition followed by Tebuconazole 50% + Trifloxystrobin 25% WG (2.22 mm and 97.53%).

S6.60: Efficacy of Seed treatment Insecticides against Stem fly and Sucking Pest Complex in Pulses

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Green gram and black gram are the important pulses in India and about 30 per cent yield loss are due to insect pests. Stem fly and sucking insect pests *viz*., whiteflies, aphids, leaf hoppers and thrips causes moderate to severe damage in the early stages. The management practices are initiated after infestation, which leads to poor establishment and reduced yield. Seed treatment is one of the viable option to manage stem fly and sucking insect pests in pulses. The seed treatment insecticides *viz*., thiamethoxam 30FS @ 10 ml/kg, imidacloprid 600FS @ 6ml/kg, tetraniliprole 480FS @ 7ml/kg and fipronil 250FS @ 7ml/kg were evaluated against stem fly and sucking pests in black gram and green gram. The seeds were treated with respective insecticides and shade dried one day before sowing. Each treatment was sown in 4 rows of 5m length and replicated four times along with untreated control. The infestation of stem fly and sucking insect pests were recorded at weekly intervals. In black gram and green gram thiamethoxam 30FS and fipronil 250 FS recorded the lowest stem fly population. Thiamethoxam 30FS recorded the lowest sucking pest population at 15 DAS *viz*., whitefly 3.25 nos. /plant, leaf hopper 0.5 nos./plant and aphids 0.50 nos./plant, whereas at 35 DAS imidacloprid 600 FS recorded the lowest sucking pest population. More or less similar trend was observed in green gram. The natural enemies population was on par with that of untreated control at 15 DAS. The results clearly indicated that the insecticidal seed treatment is a viable option to manage stem fly and sucking insect pest incidence in pulses. It also reduces one or two insecticide spray in black gram and green gram.

S6.61: Impact of Intercrops to manage pod borer complex in short duration pigeonpea

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The cultivation of short duration pigeonpea is becoming popular whenever the monsoon is delayed and as pure crop. To manage biotic stresses the treatments *viz*., groundnut (one row) + application of *Bacillus thuringiensis* var *kurstaki* (2.0g/l.) at 50 % flowering stage followed by second and third application of spinosad @ 0.5 ml/l. at 10 days interval (T1), sunhemp + application of *c* at 50 % flowering stage followed by second and third application of spinosad @ 0.5 ml/l. at 10 days interval (T2), sesame + application of *Btk*(2.0g/l) at 50 % flowering stage followed by second and third application of spinosad 0.5 ml/l. at 10 days interval (T3), application of *Btk*(2.0g/l) at 50 % flowering stage followed by second and third application of spinosad @0.5 ml/l. at 10 days interval (T4) and Untreated control (T5) were evaluated against pod borer complex in short duration pigeonpea Co 7. The incidence of pod borer complex didn't recorded significant difference among the intercrops but differed from untreated control. The incidence of *M. vitarata* and *H. armigera* after first spray in T1, T2, T3 and T4 was 1.50, 1.75, 1.25 and 1.50 / plant and 0.80, 0.65, 0.60 and 0.20 / plant respectively. The incidence of plume moth and blue butterfly didn't differ significantly in the T3 and T4. The pigeonpea intercropped with sunhemp witnessed more incidence of blister beetles. The treatment T3 and T4 recorded yield of 920 and 900 kgs/ha with a benefit cost ratio of 1.39 and 1.38 respectively.

S6.62: Status of chickpea diseases in Marathwada region of Maharashtra state

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Survey was conducted during *Rabi* 2021-22 to know the incidence of Chickpea diseases within Aurangabad, Jalna, Latur, Beed and Osmanabad districts of Marathwada region of Maharashtra state. The total 50 ha area were surveyed.During the survey, it was observed that in an initial stage *i.e.,* seedling stage crop was infected by collar rot in all Marathwada region, later on wilt incidence was increased and secondary infection by *Rhizoctonia* and *Macrophomina* causing dry root rot and blight disease respectively. The maximum average Collar rot incidence was recorded in Jalna (27.81 %) and minimum average was recorded in Osmanabad district (19.50 %). The maximum average dry root rot incidence was recorded in Latur (10.98 %) and minimum average was recorded in Aurangabad district (05.33 %). The maximum average wilt incidence was recorded in Latur (26.00 %) and minimum average was recorded in Osmanabad district (15.50 %). Loss due to biotic and abiotic stress in yield of chickpea is showing increasing trends where mostly field sanitization and soil health issues are prominent reasons behind it.

S6.63: Screening of chickpea genotypes against *Fusarium oxysporum* f.sp. *ciceri*

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Total 365 entries of chickpea were screened under different trials Projects, ICRISAT, State Multilocation Varietal and Station trails at Agricultural Research Station, Badnapur. Under project entries amongst all the tested entries (277) the total seventy three entries *viz.*, BRC 2021-09, RKG 19-1, RKG 21-1, IG 2021-01, BDNG 2020-68, JG 2021-71, BG 4031, Phule G 1302-3-5, Phule G 1314-3-27, IG 21-05, JG 2021-69, Phule G 181609, H 19-21, GJG 1907, IPC 2016-231, KCD 19-05, H 19-12, IG 2018-111, GNG 2513, RKG 21-2, RVSSG 105, GJG 1913, RVSSGG 109, BG 4032, PBC 590, JG 2021-67, Phule G 1216-10-17, KCD 19-05, Phule G 1221-2-6, GJG 1910, CSJ 138, GJG 1913, IG 2020-16, GNG 2518, RVSSG 108, RKGKD 17-09, Phule G 171313, IG 21-04, COC 18-02, Phule G 181312, RVSSG 96, KCK 20-9, GL 17020, GJG 1810, BDNGK 798, GL 19607, RLBGMH -6, Phule G 201114, RVSSG 110, RKG 21-9, KCMH 20-17, BGM 20211, Pant Gram 5, IPC 2017-351, RVG 204, GNG 2207, JG 2021-70, RG 2020-12, KAK 2, RLBGMH 5, IPC 2018-59, Phule G 05-17, H 18-08, IG 21-08, RVSSG 111, RKGM 20-1, NBeG 810, CSJ 174, Pusa 10216, JG 16 were shown resistant reaction against wilt disease. Three coded entries *viz.,* ICWRRN 1902, ICWRRN1930 and ICWRRN 1918 from ICRISAT trial were shown disease free reaction against wilt disease. Seven entries from SMVT (Rf.) *viz.*, Phule Vikram, Phule G 1327-10-12, PDKV Kanchan, AKG 1808, Phule G 1131-4, AKG 1809, Phule G 1221-2-6 and seven entries also from SMVT (Irr.) *viz.*, BDNG 2017-1, Phule 1221-2-6, Phule Vikrant, BDNG 2018-16, Phule Vikram, BDNG 2020-68, PDKV Kanak and Two entries *viz.,* PDKV 4 and AKGK 1710 from SMVT (K) were shown resistant reaction.

S6.64: Studies on Leaf Spot of Pigeonpea Caused by *Didymella* spp.

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In October 2021, Pigeonpea leaves having circular leaf spots with black pycnidial bodies were observed on 4-5 months old plant on the variety ICP883 of pigeonpea. Diseased leaves were collected, surface sterilized with 1% sodium hypochlorite 30 seconds and then washed thrice with sterilized distilled water and were placed in petriplates containing potato dextrose agar media for 2 to 3 days in BOD at temperature 24 °C. Greenish mycelia growth could be observed on the plates, colony was having regular margin with fluffy aerial growth. Black pycnidia formation occurred in media, these bodies were crushed on the slide to visualize pycnidiospores. Pycnidiospores were mostly single celled , hyaline and rod shaped. Pathogenicity tests were performed by spraying suspension from fungal mycelia on the plants of 3 to 4 leaf stage on varieties ICP 8863 and Bahar . Symptoms started appearing 5 days after inoculation and were similar to initial symptoms that we observed in the field. *Didymella* spp was found to grow fastest on oatmeal agar and on potato dextrose agar with different colony characteristics. *Didymella* spp. tested positive for production of amylase, cellulase, xylanase, polygalactournase and protease and laccase enzymes in pertiplate assays. ITS region of rDNA of the fungi was amplified by using ITS1 and ITS 4 primers and sequenced. The submitted sequence showed 97.59 % similarity with the sequence of Didymella spp. GenBank Accession No. MN912323.1. The ITS sequence of our isolate was submitted in NCBI with the GenBank Accession No. 506244.1.

S6.65: Impact of Triple layer bag on survivability of Pulse beetle *Callosobruchus maculatus*

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Urdbean, *Vigna mungo* (L) Hepper, is a member of the fabaceae family. It is also known as black gram, mash, etc. In India during 2020–21, black gram was cultivated over an area of 41.43 lakh ha and recorded a production of 22.30 lakh tonnes at a productivity level of 538 kg/ha. More than 200 species of insect pests have been recorded infesting pulses at different stages of crop during production and storage (CABI, 2007). Among them Pulse beetle an important storage pest which is very difficult to control belongs to sub family Bruchuninae under genus *Callosobruchus.* Proper packing and storage methods are to be followed for good storage stability. The majority of small farmers store in traditional methods or use normal bags such as jute, polypropylene to store their grains after seed harvest. Pulse beetle is one of the major insect pests to cause damage to different kinds of pulses in India both in field and storage conditions which causes great loss when the infested seeds stored in traditional methods. While assessing the impact of hermetic storage material in long run storage with six different sets of bags. By the end of sixth month, number of adults significantly differ between the bag types during six months storage period which ranged from 38.25 to 5.06. On the other hand highest number of live insects were present in cloth bag 66.32 fallowed by jute bag 43.36, polypropylene 41.24 and LDPE+ PP 39.21 which were on par with each other. Lowest number of live insects were in triple layer bag 5.06 followed by super bag 6.26 by the end of sixth month of storage.

S6.66: Effect of date of sowing on the seasonal abundance of spotted pod borer, *Maruca vitrata* (Fab.) on *Kharif* mungbean in Punjab

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Field experiments were conducted to study the effect of date of sowing on the seasonal abundance of spotted bod borer, *Maruca vitrata* on *Kharif* mungbean at Punjab Agricultural University, Ludhiana and Krishi Vigyan Kendra, Bahowal during 2022. Population dynamics of the pod borer was studied on two mungbean varieties (ML 2056 and ML 1808) sown at three dates of sowing-first fortnight of July, second fortnight of July and first week of August. The abundance of *M. vitrata* was recorded in terms of larvae per plant, webs per plant and pod damage (%). The results revealed that the pest incidence was significantly higher in crop sown during first fortnight of July. For both varieties, the peak larval population and webs was observed during 35th and 36th standard weeks at KVK, Bahowal and Ludhiana, respectively. Thereafter, the pest incidence (mean larval population) declined gradually and reached its minimum during 41st standard week at both the locations. Lowest pod damage and highest grain yield was recorded in mungbean sown in second fortnight of July in both the varieties as well as locations. Based on the lower abundance of the pod borer, second fortnight of July was the optimum date for sowing *kharif* mungbean in Punjab.

S6.69: Influence of root knot nematode on *Fusarium* wilt severity and yield in chick pea

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Chickpea (*Cicer arietinum* L.) a cool season food legume is known to be most important pulse crop of India. It suffers due to biotic as well as a biotic stresses. Among biotic stresses wilt disease caused by *Fusarium oxysporum* f sp. *ceceri* is the most widely occurring and devastating causing substantial yield losses. Association of wilt pathogen and root knot nematode (*Meloidogyne incognita*) is known to exacerbate the disease. India is the world's largest consumer and producer of chickpea, contributing over 70% of total global chickpea production in the world. A pot trial was conducted to determine the effect of sequential and concomitant inoculation with root-knot nematode (*Meloidogyne incognita*) and wilt fungus (*Fusarium oxysporum* f sp. *ceceri*) on chickpea. The sequential inoculations comprised of nematode prior to fungus (N'!F), fungus prior to nematode (F'!N) and nematode concomitant fungus (F+N). The severity of wilting (36%) significantly increased in the presence of root-knot nematode inoculated prior to fungus (N'!F) due to synergistic interaction between two pathogens. Severity of wilting (16%) was recorded in F'!N followed by F+N (16%) over control. Over all, maximum loss in plant growth parameter (41%) and yield (31%) of chick pea were recorded with the inoculation of *M. incognita* 3 days prior to *F. oxysporum* f. sp. *ceceri* followed by F'!N growth parameter (26%) and yield (25%). Minimum losses of plant growth parameter (10%) and yield (6%) were found in F+N over control. Among all the combinations, N'!F was recorded most destructive, followed by F'!N and F+N over control.

S6.71: *De novo* assembly, structural and functional annotation of the nematode egg parasitic fungus, *Purpureocillium lilacinum strain* IIPR-Pl-11

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The genome of the potential strain *Purpureocillium lilacinum* strain IIPR-Pl-11 (accession number: NAIMCC-F-04234) was sequenced using the Illumina Novaseq 6000 platform and the paired-end sequencing approach. The genome was assembled *de novo* using in-silico tools, namely Velvet 1.20, SSPACE Standard 3.0, and GapCloser-bin-v1-12 r6. The assembled genome was structurally and functionally annotated using the Funannotate annotation workflow. 792 contigs with an average length of 48436.32 bp were generated, and a 38.3 Mb draft genome assembly was constructed. N50 and L50 values were 235450 and 48 base pairs, while N90 and L90 values were 36097 and 185 base pairs, respectively. The GC percentage was determined to be 58.62%. There were 10656 predicted genes, 10558 of which coded for proteins and 98 for transfer RNAs. The average gene density and gene length are 278.22/Mb and 1610.39 bp, respectively. The proportion of the genome's repetitive sequence is 1.77 percent (680937 bp). About 97.1% of the predicted genes in the Hypocreales database were functionally annotated using the Benchmarking Universal Single Copy Orthologs (BUSCO) method (ODB10). The CAZy database predicted an aggregate of 451 (>2 tools) CAZymes: 251 belonged to the Glycoside Hydrolase family, 99 to the Glycosyl Transferase family, 75 to the Auxiliary Activity family, and 26 to other CAZYme families. Moreover, 27 chitinases belonging to the GH18 family were found. The draft genome sequence is an essential resource for further research on identifying nematicidal and economically important genes and understanding the molecular basis of nematode egg parasitism.

S6.72: Integrated Disease Management of Pigeon pea *Fusarium* wilt disease

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Pigeon pea [*Cajanus cajan* (L.) Millspaugh] suffers from many biotic stresses which significantly reduce yield. Among the all biotic stresses *Fusarium* wilt is major production constraint in all pigeon pea growing areas India. Treatments involving seed treatments with microbes and chemicals (*Azotobactor*, *Trichoderma*, Tebuconozole), soil application of *Trichoderma* and *Azotobactor* were used. Among the all treatments, the minimum disease severity was recorded in treatment involving (SA of *Trichoderma* through FYM ST with *Azotobactor*) treatment representing at 65 (03.11%), 85 (05.12%) and 105 (10.18%) DAS. Second best treatment was SA of *Trichoderma* through SMS+ST with Tebuconazole which resulted in wilt incidence of 04.20 %, 08.25% and 13.78 % at 65, 85, and 105 DAS, respectively. Maximum disease severity 16.11%, 27.70% and 41.96% at 65, 85 and 105 DAS respectively was recorded in control (untreated). Data on total phenol contents in leaves from different treatment indicate maximum 1.57, 2.03 and 2.42 mg/g of fresh leaves at 15, 20 and 25 days after pathogen inoculation, respectively. T_1-(SA of *Trichoderma* through FYM+ST with *Azotobactor*) treatment. Total phenol content in T_6 – (SA of *Trichoderma* through Spent Mushroom Substrate (SMS) +S. T. with Tebuconazole) treatment was 1.12, 2.10, and 2.42 mg/g of fresh leaves at 15, 20, and 25 days of after pathogen inoculation, respectively. From the data on effect of different treatments on disease reduction and total phenol contents it can be concluded that treatments increase phenol content in plant which in turn provided defense against the wilt pathogen.

S6.73: Development of IPM modules for management of major insect pests of mungbean crop

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Among the various grain legumes The mung bean (*Vigna radiata*), is one of the most important pulse crop in india and rajasthan. A field experiment was conducted on "Development of IPM modules for management of major insect pests of mungbean crop" during Kharif-2021 at Rajasthan Agricultural Research Institute (SKNAU:Jobner) Durgapura, Jaipur. The mungbean variety RMG-62 was sown in two blocks of 20 X 25 m (500 m^2) on 23.07.2021 with two modules. In Module first for management of moongbean pests seven treatments like (i) seed treatment with carbendazim @ 2.0 g, thiamethoxam 35FS @ 5.0 g and Rhizobium 25 g/kg seed, {FIR] (ii) grow one line of millet as trap crop around the field boundary as a barrier crop (iii) use *Helicoverpa armigera* pheromone trap @ 10/ha (iv) use yellow sticky trap 50 per ha. (v) Application of neem oil (1500 ppm) @ 1.5 ml/l at 30 days after sowing and followed by (vii) application of Chlorantarniliprole 18.5 SC @ 0.20ml/L after 10 days of first spray. In Module second farmer practices of zone were applied. The result show that the module- I was found more effective recorded high yield (705 kg/ ha.) and low pest population Mean Pop White Flies/ 10 plant (8.53), pod borer population/ 10 plant (9.01) and minimum percent pod borer damage (2.5 %) were found where as in modules- II found low yield (490 kg/ha.) and high percent pod borer damage (8.3 %) were recorded.

S6.74: Identification of Yellow Mosaic Disease resistance sources in moth bean under field conditions of western Rajasthan

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Moth bean [*Vigna aconitifolia* (Jacq.) Marechal], is affected by several pathogens causing substantial yield losses and quality losses to grain and straw. Among these, yellow mosaic disease (YMD) caused by mung bean yellow mosaic virus (MYMV), is the most destructive disease which may result in complete failure of the crop. YMD is transmitted by whitefly (*Bemisia tabaci* Genn) and caused by Gemini viruses. Therefore, genetic improvement for resistance to YMD is one of the major objective in moth bean. Hence, a germplasm set comprises 320 lines including four checks were evaluated in 2017 under field conditions at Jodhpur for YMD reaction and other agro-morphological traits. Thirty five promising genotypes were selected and were assessed further under field conditions for YMD incidence during i.e., 2018 and 2019. Standard scale was used to score the genotypes for YMD reaction (1-9). In all three years, the highest severity of the 7 score was observed. In the pooled analysis, the Area Under Disease Progress Curve (AUDPC) ranged up to 120. The incidence was recorded at two events, that is, 30 days after sowing and 60 days after sowing; and the minimum temperature and sunshine hours showed a significant positive and negative correlation, respectively, for the disease incidence at 30 days after sowing. These were strongly correspond to favourable weather for vector incidence for progressive spread of the disease in the next 30 days. AUDPC was higher in 2017 and 2018, while low in the third year but significant genotype and environmental interaction was found. Based on a pooled analysis of the stability index, two genotypes RMB 243 and IC 39697 showed consistence performance for disease susceptibility and 13 genotypes showed consistence performance for resistance, i.e. RMB series-39, 44, 45,47, 48, 49, 50, 223, 243, 279 and PLMO-14, IC 36032, IC 120986. These thirteen genotypes can be considered as valuable resources for improvement of moth bean against YMD resistance while RMB 243 and IC 39697 can be taken as susceptible parent for mapping population development to tag YMD resistant genes resting in moth bean.

S6.75: Begomoviruses: Are they seed-borne or seed-transmitted viruses?

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The presence of Begomoviruses in the seeds, especially the *Mungbean yellow mosaic virus* (MYMV) in mungbean seeds was first time detected in 2010 by our group from Navsari, Gujarat (India). However, its seed transmission was not observed, therefore, proposed its indirect route in 2015 by using whiteflies. Overlooking the differences between seed-borne and seed-transmission, a team from South Korea in 2015 claimed that *Sweet potato leaf curl virus* in sweet potato, and in 2016, the TYLCV in tomatoes are seed transmitted. Principally TYLCV was not the seed transmitted as required whiteflies for transmission. They used a cage to demonstrate it which needed validation. TNAU, in 2016 discussed that MYMV was seed-transmitted, but the emerging seedling remained asymptomatic. Why it was asymptomatic needs either correction or scientific justification. This overlooked fact has led to many claims of the erroneous first report of seed transmission of Begomovirus which has been thoroughly researched and rejected in 2020 and 2021. Misunderstanding needs clarification. Seed-borne term merely indicated that the pathogen and seed are associated, however, does not guarantee that the diseased seedling will be produced. It will be known as seed-transmitted if a seed-borne pathogen can give rise to infected seedlings. All the seed-transmitted viruses are seed-borne; however, all seed-borne viruses are not seed-transmitted. Accordingly, Begomovirus has been detected in the seeds, however, it has not been firmly explained that it can give rise to infected seedlings. Therefore, Begomoviruses are seed-borne but not seed-transmitted viruses and must be corrected in the future citation.

S6.76: Integrated disease management of powdery mildew in mung bean

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A field experiment was conducted during Rabi season,2021-2022 at Regional Research and Technology Transfer Station, Bhawanipatna under Odisha University of Agriculture and Technology to evaluate various fungicides against Powdery mildew of Mungbean. Mungbean variety IPM-02-14 which is susceptible to powdery mildew has been used for this trial under the supervision of different scientists of Centre for Pulses Research, OUAT, Berhampur. Treatments included the fungicides Thiophonate methyl @0.5gm/lt, Wettable Sulphur @0.5gm/lt, Trifloxystrobin + Tebuconazole@0.5gm/lt, Azoxystrobin + Difenaconazole @1ml/lt, *T.viride* @15gm/lt, *T.viride* +*P. fluorescens* @10gms each/lt, *Ampelomyces Quisqualis* @ 1ml/lt,. Among the treatments, Trifloxystrobin + Tebuconazole @0.5gm/lt, foliar spray 3times at 10days interval after disease initiation found to be best with lowest PDI(6.1), highest percent disease control (89.81%) and highest yield (864kg/ha) which is at par with Azoxystrobin + Difenaconazole @1ml/lt, foliar spray 3times at 10days interval after disease initiation with PDI(7.49), percent disease control (87.50%) and yield (818kg/ha). Followed by combine application of Wettable Sulphur @ 0.5gm/lt, *T.viride* +*P. fluorescens*@10gms each/lt and *Ampelomyces Quisqualis* @1ml/lt separately at 10days interval after disease initiation with PDI (9.87), percent disease control (83.52%) and yield (782kg/ha).

S6.77: Screening for Callose Mediated Resistance against *Botrytis* Grey Mould Disease in Chickpea (*Cicer arietinum* L.)

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The present investigation was conducted on 110 chickpea genotypes to identify BGM resistant genotypes through disease rating and Callose scoring. Screening of chickpea genotypes was done against Botrytis grey mould (BGM) disease in natural field condition for various morpho-physiological traits. Genetic diversity among experimental material was also estimated using hierarchical cluster analysis (HCA). Screening for disease reaction among 110 chickpea genotypes were done against BGM on the basis of callose deposition score using fluorescent microscopy and disease score in sick plot. The results of field screening against BGM disease revealed that out of 110 genotypes screened only five genotypes exhibited disease rating range of 4.5-5 (moderately resistant). The analysis of variance for 13 quantitative characters during all the studied years revealed significant differences among genotypes for different morphological traits *viz*., plant height, number of primary branches per plant, first pod height (cm), number of pods per plant, 100 seed weight (g), biological yield per plant (g) and seed yield per plant (g), and also among blocks. Genetic diversity analysis based on HCA grouped the genotypes in six different clusters. Microscopic investigation showed the presence of callose deposits in the cell wall in response to BGM infection. In the field screening, the response of genotypes was rated based on BGM symptoms. The five genotypes *viz*., ICC14429, ICC12429, ICC14454, ICC14470 and ICC16376 were identified having higher callose scores and lower disease scores.

S6.78: Consortium of Nematode Bio Control Agents for management of root knot nematode, *M. incognita* in pulses

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Plant-parasitic-nematodes are one of the major threat to the agricultural production of different crops worldwide. Many microorganism have been reported as potential nematode biocontrol agents and application of more than one microbes together is a reliable means of reducing the variability in biological control agents. In this background, we isolated, characterized and identified nematicidal potential strain of Actinobacteria (IIPR:KR01:03 *Streptomyces ginkgonis* (accession no: MN966860), *Purpureocillium lilacinum* (IIPR-Pl-11), *Trichoderma harzianum* (IIPR-Th-14), *T. asperellum* (IIPR-Ta-11) and *Bacillus cereus* (IIPR-Bc-14) against root knot nematode, *M. incognita.* In order to find out the ability for co-culturing of these strains we carried out Dual Plate Assay. The results showed that all the strains are mutually inclusive and compatible. We also carried out dual plate assay to test whether all identified strains with rhizobium from three crops viz., chickpea, field pea and lentil. The results indicated that the strains do not have any antagonism towards rhizobium and they are mutually inclusive. To identify single liquid media for co-culturing six media were evaluated (Potato Dextrose Broth (PDB, Nutrient Broth (NB), Starch Casein Broth (SCB), Yest Extract Malt Extract (YEME), PDB+NB, Tryptic Soy Broth (TSB)) and found TSB is suitable for culturing all the strains. *In vitro* bioassay on juvenile mortality with cultural filtrates of individual strains and consortium (co-cultured strains) revealed that consortium performed better than individual strains with LC_{50} value is $2.3x10^5$ ppm. Based on the results of the *in-vitro* evaluation, the consortium will be suitably formulated, further evaluated in field and used for nematodes management in pulses.

S6.79: Management of stored grain pests of pulses: Retrospects and prospects

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Stored pulses are often damaged by multitude of arthropod pests. These pests infest the crops from fields itself and get established in store houses due to favourable microclimate prevailing there. Early detection of pests is most crucial for their effective management. Assessment through pitfall traps, sieving, odour and quality of the grain are generally done. However, chitin analysis from grain samples and estimation of grain temperature are some of the novel approaches in practice. Hermetic storage structures are becoming popular as it prevents immigration by concealing the emanating volatiles. Heavy grade polyethylene and triple-bagging have been found effective against *Callosobruchus maculatus.* Modified atmospheric storage (O_2<3% and CO_2>50%) has been proven effective against *Rhizopertha dominica* in chickpea. Potent oxidizing agents like ozone (O_3) have been used successfully against phosphine resistant insect populations. Artificial heating techniques like microwave radiation (2,450 MHz) for 100s has been reported to cause complete mortality of *C. chinensis*. Various doses of gamma radiation significantly affect the fecundity of bruchids. Semio-chemicals, biocontrol agents including microbial pesticides, plant derivatives, fumigants and dusts have been successfully used against pulse and non-pulse pests. Similarly, very recently, nano technology and RNA interference (RNAi) are gaining popularity. Sustained research on chemical ecology and semio-chemicals, formulations and mass production of natural enemies, alternative and safer fumigants, strategies for bulk storage will certainly generate newer technologies for effective management of stored grain pests.

S6.81: Identification of pathogen associated with white mold disease of pole type purple colored bean (*Phaseolus vulgaris* L.) in Lushai hills of India

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Common Bean (*Phaseolus vulgaris*) is one of the important food legumes grown in India, in North East India farmers mostly grow pole type bean by intercropping with maize and other crops in the kitchen garden or backyard, or jhum field. In Mizoram, the french bean cultivar "Zorin Bean" (MZFB 48) is grown in a large area because of its characteristic purple color, anthocyanin-rich (8.32 ± 1.36 mg per 100 g of fresh pod weight) and high production potential under the diverse agro-ecosystems. In January 2021, white mold symptoms were noticed in farmers' fields at Kolasib, Mizoram, India with more than 45% disease incidence. The symptoms observed as water-soaked lesions, and cotton-like mold growth, accompanied by a watery soft rot on stem and pod. Black sclerotia are also found on the infected pod and stem tissues. Wilting also has been observed within the plant canopy. Based on the cultural and morphological parameters the pathogen was identified as *Sclerotinia species.* Further sequencing of rDNA internal transcribed spacer (ITS, 508 bp, GenBank Accession No. ON078499), and phylogenetic analysis confirmed the pathogen as *Sclerotinia sclerotiorum.* The pathogenicity test was also conducted and the pathogen was successfully reisolated, exhibiting cultural and morphological character similar to the original culture of *S. sclerotiorum*, confirming Koch's postulates. Findings from this study are significant as *S. sclerotiorum* may represent a serious constraint for bean production. We believe that information gathered in the present study will be useful in understanding fungal epidemiology for better management of this disease.

S6.82: Agronomic innovations in biotic stress management and its combined effect with abiotic stresses in crop production

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Insects, pathogens, nematodes, weeds among many others are the major pests of agricultural crops. These pests cause a serious threat to crop production and loss of produce to the tune of 20–40%. The synthetic chemical– based pest–management practices cause an environmental hazard, affect public health, and increases resistance to pesticides. Management aspects need to be evolved on avoiding the development of pests and weed resistance through the promotion of biological approaches, growing resistant varieties, and other eco–friendly agronomic measures such as soil solarization, summer ploughing, crop rotation, intercropping, time and method of planting, depth of sowing and planting density, fertilizer management, biological control, biofumigation, mulching, and organic soil amendments, trap and decoy crops, plant biostimulants, biopesticides among many others. These approaches are also particularly suited to integrated pest management for the present emerging production system. Other innovative methods of assessment and management of pests are remote sensing, artificial intelligence, use of nano–pesticides, use of thermal energy, infrared, microwaves, flames etc. Importantly, the influence of abiotic stress on various biotic stresses caused by these pests makes dynamic interaction on deciding the intensity of the damage of crops. This review focused on various agronomic practices and the influence of abiotic stress on biotic stresses for efficient pest management in agricultural crops.

S6.83: Management of Gram pod borer, *Helicoverpa armigera* (Hubner) by Evaluating different IPM Modules

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The field experiment to evaluate suitable and ecofriendly IPM modules was conducted at Turgarh village of Jhadol block of Udaipur district during Rabi 2018-19 and 2019-20 using 10 different modules. Results revealed that mean larval population of gram pod borer, *Helicoverpa armigera* was considerably low after evaluating sprays in different modules. The lowest larval population of insect (2.98 larvae /MRL) was recorded in Module 7, consissing of spinosad 2.5 SC @ 0.5 ml/l of water as 1st spray and indoxacarb 14.5% SC @ 1 ml/l of water as 2nd spray followed by module 1, consisting of clorfluazuron 5.4% EC @ 3 ml/l of water as 1st spray and indoxacarb 14.5% SC @ 1 ml/l of water as 2nd spray and module 2 consisting of spinosad 2.5 SC @ 0.5 ml/l of water as 1st spray and profenofos 50 EC @ 1.5 ml/l of water as 2nd spray in Rabi 2018-19 as well as in Rabi 19-20. Based on the benefit cost ratio module 6 Consisting of indoxacarb 14.5% SC @ 1 ml/l of water as 1st spray and profenofos 50 EC @ 1.5 ml/l of water as 2nd spray gave maximum return *i.*e. 1:2.04 & 1:2.12 respectively during first and second year, which proved more viable due to lower cultivation cost in both the seasons than all other modules evaluated during Rabi 2018-19 and Rabi 2019-20.

S6.84: Management of prevailing and emerging diseases of urdbean under Indian sub-continent.

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Urdbean (*Vigna mungo*) is an important food legume in Indian sub-continent with India the largest producer and consumer. Its productivity (570kg/ha) is low compared to the released varieties (10-15q/ha). Among various factors, diseases take a heavy toll of crop which may be managed by using chemicals. However, awareness regarding environmental pollution and health hazards restrict their use. Host resistance offers a cost effective, feasible and eco-friendly option for their management. Pathogens of major disease i.e. MYMV, anthracnose (*Colletotrichum trucatum*), and powdery mildew, PM (*Sphaerotheca fuligenea*) are highly variable; and MYMIV and MYMIV-VSKN strains have been reported. Genotypes i.e. DKU 6, 11, 82, 87, 90, 98, 102, 116, 118 etc. and varieties KUG 216, 540, IPU 2-33, 2-43, 94-1, Vamban 7 etc. showed stable resistance to MYMV and gene analogue markers YR4 and CYR1 were tightly linked with MYMIV resistance. Multiple resistance donors IPU 244, IPK 2K 21 (MYMV and CLS), IC 131044, 343936, PLU 710, IPU 99-52 (MYMV and PM), JB 233, PLU 1016, 190, 552, 819, 1025, 393, 557, IPU 99-213, 99-25, SDC 3175, UKS 3/SSC 7/21, NIC 15270, IC 1576 (MYMV and anthracnose), PLU 343 (Anthracnose, and CLS) were identified. Seed treatment and foliar applications of fungicides were effective. Prevalence and severity of diseases is increasing and web and macrophomina blight are emerging as potential threats. Hence, integrated disease management involving cultural practices, botanicals, host resistance and judicious use of pesticides is required.

S6.88: Efficacy of different phytoextracts against *Cercospora Canescens*

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Green gram is an important kharif pulse crop which is adversely affected by varoius fungal diseases. Leaf spot is one of the most important disease, caused by the fungus due to (C*ercospora canescens)* leads to much damage to production of green gram. Artificial fungicides made of chemicals are toxic and bad for the ecosystem since they ruin the ecosystem. In comparison to synthetic fungicides, phytoextracts including jasmonate, glucosinolates, quinones, and chitosan show strong antifungal activity. The antifungal activity of different medicinal and locally available plant extracts which are available in fields and surroundings of fields on (C*ercospora canescens*) were tested in lab conditions at college of Agriculture, Badnapur. It has been shown that certain phytoconstituents have strong antifungal capabilities, and the use of these extracts as bio-fungicides has been stressed within the larger framework of ecological sustainability. Many phytoextracts have been used, such as Neem, Garlic, Onion, Ginger, Tulsi, Ganeri, and Soapnut. Among that neem (*Azardiracta indica*) recorded highest average mycelial growth inhibition at both 10 and 20 percent concentration.

S6.89: Slow dispersal mechanism of nanoparticle encapsulated azadirachtin formulations for the management of groundnut bruchid *(Caryedon serratus)* coleoptera: bruchidae

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Slow dispersal mechanism in the process of controlling pests on stored grains is always been interesting and development of such formulations thereby is a challenging task to the scientific community. Encapsulation of principal chemical or its derivatives is gaining importance as helps in in slow releasing the chemical with the extended periods of time with relatively lower applied doses. Nanoscale (NS) pesticides are being used efficiently in agriculture and the present study is related to management of stored grain pest groundnut bruchid, *C. serratus* using NS Azadirachtin and NS NSKE formulations. A total of eight treatments *viz.,* NS ZnO encapsulated Azadirachtin 1000 ppm, NS ZnO encapsulated Azadirachtin 3000 ppm, NS chitosan encapsulated Azadirachtin 1000 ppm, NS chitosan encapsulated Azadirachtin 3000 ppm, NS ZnO encapsulated NSKE (5%), NS chitosan encapsulated NSKE (5%) and NS ZnO and NS chitosan were developed in the laboratory of Nanotechnology, Institute of Frontier Technology, Tirupathi, Andhra Pradesh, India and tested against *C. serratus* in groundnut. The stability of the molecule was revealed by Dynamic Light Scattering (DLS) which showed that the NS particles chitosan NS particles had mean size of 78.8 nm,. Azadirachtin was encapsulated (@ 3000 ppm where as NS zinc oxide particles @mean size 182.9 nm, NSKE encapsulated NS zinc oxide particles @ mean size 84.9 nm), respectively. The mean zeta potential -36.2 m was recorded for chitosan NS particles. Azadirachtin encapsulated (@ 3000 ppm exhibited -43.0 mV for, NS zinc oxide particles and NSKE encapsulated NS zinc oxide particles showed zeta potential of -39.4 mV. The lowest per cent pod damage by weight loss was seen in NS chitosan encapsulated NSKE (10.93) followed by NS ZnO particles (16.95). The NS ZnO encapsulated Azadirachtin treatments at both the doses (3000 and 1000 ppm) recorded 37.36 and 41.23 per cent pod damage by weight respectively. The per cent weight loss at 180 days was the lowest per cent weight loss (54.61) in NS chitosan encapsulated NSKE as against the maximum weight loss of 83.70 in untreated check.

S6.90: Genome-wide association studies for earliness and MYMIV resistance governing loci in mungbean (*Vigna radiata* L. Wilczek) using genotyping by sequencing approach

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Yellow mosaic disease (YMD) remains as a major constraint in mungbean [*Vigna radiata* (L.)] production. Short duration genotypes are beneficial as this allows multiple crops per year and also helps in escaping the terminal heat stress especially during summer cultivation. A set of 132 diverse mungbean genotypes were used for GBS and are also evaluated for various phenotypic traits including flowering time, area under disease progression curve (AUDPC) when infected with MYMIV, SPAD value, trichome density and leaf area. The range for various traits like AUDPC (0 to 1266.98), trichome density (1 to 4), leaf area (99.42 to 221.30 cm^2), days to first flowering (24 to 42 d), and SPAD value (29.33 to 62.32) showed great variability in the studied genotypes. The GBS assay could identify 31,953 high-quality SNPs on all the 11 chromosomes. Both GLM and MLM has identified 84 SNPs, of which 38 were significant. The candidate genes identified for the traits are flowering time (E3 ubiquitin protein ligase DRIP2, AT2G30580), MYMIV resistance (30S ribosomal protein S31, chloroplastic, AT2G21290), SPAD value (E3 ubiquitin protein ligase RIE1, AT2G01735), leaf area (nifU-like protein 1, chloroplastic, AT4G01940) and trichomes (LOB domain-containing protein 21 AT3G11090), respectively. Linkage disequilibrium (LD; r^2 =0.5) was estimated as 12.5 kb, while extensive LD decay was recorded, wherein r^2 decreased half of its maximum value at 500-1000 kb. Two genetically distinct population groups were observed using äK and second-order statistics. The results will help in marker assisted breeding of various economic traits on interest in mungbean.

S6.91: Shelf life improvement of recommended charcoal consortium biofertilizer: moving ahead to liquid biofertilizers with additives

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Application of microorganisms as biofertilizer for improving the availability of nutrients in plants is one of recommended agronomic practice for improving productivity in agricultural crops in sustainable manner. Among the biofertilizers nitrogen fixing *Rhizobium* plays a significant role in legumes through biological nitrogen fixation (BNF). PGPR based biofertilizers are commercialized recently to reduce the negative effects of chemical biofertilizers. Presently, charcoal based formulations are used as biofertilizer in India but their rate of consumption is not to the optimum level in comparison to agrochemical. Although the basic technology is known for mass sterilization of large volumes of carrier materials, majority of the production units ignore the carrier sterilization requirement. To combat this problem, liquid formulations (LFs) are being developed to assure better quality with improved shelf life, reduced size of pack and easy to use than the conventional carrier based biofertilizers. Recommended consortium of *Mesorhizobium* sp. (LGR33) and rhizobacterium (*Pseudomonas* sp. LPGPR1) were assessed for their viability with the supplementation of different additives *viz*., carboxymethylcellulose, 2% polyvinyl pyrollidone and 0.2% hydrogel. Treatment of consortium biofertilizer with 0.2% hydrogel revealed maximum viability up to 10 months of storage and retained plant growth promoting traits (P-solubilization, indole acetic acid, total protein content and ammonia production). Liquid consortium biofertilizer of LGR33+ RB-1 amended with 0.1% CMC improved the growth, biological nitrogen fixation, soil quality and yield in chickpea over recommended charcoal based biofertilizer.

S6.92: IPM modules for management of major insect pests of mungbean by minimum insecticide use

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Pulses are important sources of protein, fibre, vitamins and minerals. An array of insect pests attack on pulse crops causing considerable yield loss. It is reported that more than 250 insect pests are affect pulse crops in India and about 2.0 to 2.4 million tonnes of pulses are lost annually due to the damage caused by insect pests. Hence, an experiment was conducted to evaluate Integrated Pest Management (IPM) module against major insect pests of pulses. The IPM module consists of seed treatment with thiamethoxam 35 FS @ 5.0 g/kg and rhizobium inoculation, growing of maize as barrier crop, yellow sticky trap @ 50 per ha, sex pheromone traps @ 10 per ha, spraying of neem based insecticides at 30 days after sowing and need based application of inorganic insecticides during kharif and rabi 2021. Whitefly infestation in IPM plot was 2.8 and 1.9 per trifoliate leaves and it was 5.5 and 4.7 in farmers practice respectively during Kharif and Rabi 2021. In IPM plot, other pests viz., aphids, jassids, blister beetle, *Maruca vitrata* and pod bug population per plant was <25 & <25, 0.02 & 0.22, 0.12 & 0.32, 1.10 & 1.62 and 1.05 & 1.36 respectively whereas in farmers practice it was >50 & >50, 0.74 & 1.41, 1.35 & 3.42, 2.86 & 3.45 and 1.94 & 2.85 respectively during Kharif and Rabi 2021. The beneficial insect fauna *viz.,* coccinellids (3.05 & 1.74), rove beetle (1.26 & 0.85), ground beetle (0.05 & 0.32), assassin bug (0.05 & 0.04) and spiders (1.33 & 1.14) was also higher in IPM plot compared to control 1.44 & 0.68, 0.28 & 0.25, 0 & 0.2, 0 & 0 and 0.20 & 0.34 respectively during Kharif and Rabi 2021. The yield was also higher in IPM plot with 804.3 & 864.32 kg ha^{-1} compared to 685 & 667.5 kg ha^{-1} in farmers practice respectively during Kharif and Rabi 2021.

S6.93: Evaluation of different IPM modules against pod borer *Maruca vitrata* Geyer (Pyralidae: Lepidoptera) in cowpea

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Cowpea (*Vigna unguiculata*) is one of the important and nutritious legume crop grown for grains, tender pods and fodder in India and South East Asia. Spotted pod borer *Maruca vitrata* is a major borer pest causing significant damage up to 20-60% in cowpea. The control of pod borer relies on the use of conventional insecticides. Non-judicious and indiscriminate use of insecticides leads to resistance in insects, harmful pesticide residues and environmental hazards. The integration of different control methods reduces the harmful effects of pesticides and yield losses to a great extent. Keeping this in view, different IPM modules viz., biointensive, integrated modules were formulated and evaluated for their efficacy against pod borer in cowpea (cv DC 15) during Kharif season 2021 at ICAR-IIPR, RRS Dharwad. The first spray was done at the time of flowering. The results clearly indicate that among different IPM modules, the integrated module comprising of foliar application of chlorantraniliprole 18.5 SC@ 0.5 ml/l followed by spraying of azadirachtin 0.03 ppm @ 5ml/l and spraying of emmamectin benzoate 5 SG @ 0.5 gm/l at 10 days interval during flowering and pod formation stage was most effective and recorded lowest pod damage of 12.56 % by *M. vitrata* and highest per cent reduction of 65.22 % over untretaed control. The highest marketable grain yield (589.39 Kg/acre) was recorded in integrated module as compared to farmers practice and untreated control. Thus, the integrated module can be taken advantage for the management of pod borer in cowpea.

S6.94: Cowpea seed moth C*ydia ptychora* (meyrick) (Lepidoptera: Tortricidae): an emerging insect pest in transitional belt of Northern Karnataka

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Cowpea (*Vigna unguiculata*) is an important legume crop grown in the Southern peninsular region of India. Among various insect pests infesting cowpea, pod borers are important group causing significant damage. In recent times, Cowpea Seed Moth *Cydia ptychora* is an emerging pest problem during Kharif season in the transitional belt districts of Northern Karnataka. Emergence of this pest made it necessary to study the extent of damage done by *C. ptychora* in cowpea. A field experiment was conducted during Kharif season to study the incidence of *C. ptychora*, extent of damage and its natural enemies in cowpea (cv. DC-15) at IIPR-RRS, Dharwad in year 2021 and 2022. Cowpea seed moth *C ptychora* is a post-flowering pod borer and its peak activity was observed during August to November. *C. ptychora* female oviposit on senescent sepals and preffer young or maturing pods. Upon hatching, larvae enters the pod and feed on the seeds. In each pod on an average 2-4 larvae were observed. Larval development takes place within the pod. Mature larvae emerge out of pods by making small hole and pupate in the soil. The pod damage and seed damage in cowpea was around 47.11 % and 52.67 %, respectively. Among the natural enemies, two larval parasitoids of Braconid wasp were found to parasitise the pod borer larvae to the extent of 33.3 to 75 %. Detailed studies on its biology, host prefrerence, crop loss estimation is necessary for development of any management strategy for this new emerging pest in cowpea.

S6.95: Evaluation of urd bean varieties against major insect pests and their management

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The present investigations are on "Evaluation of urdbean varieties against major insect pests and their management" under field conditions during *Kharif* 2018 and 2019 at the Agricultural Research Farm and Insect Pest Management Laboratory at the Department of Entomology and Agricultural Zoology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP) during 2018 and 2019. Urdbean, *Vigna mungo* (L) Hepper, is a member of the fabaceae family. It is also known as blackgram, mash, mashkalai, black mapte, etc. In India during 2020–21, blackgram was cultivated over an area of 41.43 lakh ha and recorded a production of 22.30 lakh tonnes at a productivity level of 538 kg/ha. In Uttar Pradesh during 2020–21, blackgram was cultivated over an area of 5.54 lakh ha and recorded a production of 3.17 lakh tonnes at a productivity level of 573 kg/ha. The thirteen black gram varieties/genotypes were screened against whitefly, Yellow Mosaic Virus disease, leafhopper, flower thrips, and pod borer complex under field conditions during *Kharif* 2018 and 2019. The results of the study revealed that none of the varieties/genotypes were immune/highly resistant to the attack of the insect pests and YMV disease incidence. The varieties/genotypes Azad Urd-3, Pant Urd-31, Azad Urd-1, and Uttara were found to be least preferred by whitefly, leafhopper, and flower thrips, whereas BGP-247, UH-80-26, NEW-URD, and Azad Urd-1 are least preferred by the pod borer complex. The varieties/genotypes Azad Urd-3 and Pant Urd-31 were found resistant, whereas, Shekhar-1 and KU-99-12 were found susceptible to YMV disease incidence.

S6.96: Evaluation of insecticides against Pod borer complex in Pigeonpea

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Evaluation of insecticides against pod borer complex of pigeonpea was assessed in this trial comprising of seven treatments including untreated control for three years. Two applications of insecticides were made, first at 50 per cent flowering and second at pod development stage. Efficacy of insecticides against pod borer complex on pigeonpea was assessed on pod damage and grain damage due to *Helicoverpa armigera* and *Maruca vitrata*. Total pod damage and grain damage was shown in ranged between 8.07 and 24.02 and 6.71 and 21.18 per cent, respectively. Whereas, pod damage in different treatments decreasing order was chlorantraniliprole 18.5 SC fb flubendiamide 480 SC (4.91%), *Bt* (8.39%), azardirachtin 1500 ppm (8.57%), *M.anisopliae* (9.15%), *B.bassiana* (9.35%) and *L.lecanii* (12.10%). While, grain damage was recorded lowest in chlorantraniliprole 18.5 SC fb flubendiamide 480 SC (3.16%), azardirachtin 1500 ppm (4.28%) and *Bt* (5.25%). The significantly lowest (1.77%) grain damage by pod borers was recorded in treatment chlorantraniliprole 18.5 SC fb flubendiamide 480 SC followed by azardirachtin 1500 ppm (2.08%), *Bt* (2.50%), *M.anisopliae* (2.63%), *B.bassiana* (3.07%) and *L.lecanii* (3.28%). In case of pod fly, chlorantraniliprole 18.5 SC fb flubendiamide 480 SC was recorded the lowest grain damage by pod fly (4.94%) and it was at par with azardirachtin 1500 ppm (6.42%). The maximum grain yield (1955 kg/ha) was recorded in chlorantraniliprole 18.5 SC fb flubendiamide 480 SC and which was at par with azardirachtin 1500 ppm @ 50 ml/L (1735 kg/ha) and *Bt* @ 1 g/L (1604 kg/ha). As regards monetary returns, the maximum net monetary return was obtained from the treatment of chlorantraniliprole 18.5 SC @ 0.3 ml/L fb flubendiamide 480 SC @ 0.2 ml/L (Rs.32760=00/ha) followed by azardirachtin 1500 ppm @ 50 ml/L (Rs.23000=00/ha/ha) and *Bt* @ 1 g/L (Rs.17750=00/ha).

S6.97: Efficacy of Different Fungicide against *Cercospora canescens*

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Mungbean is popular due to its nutritive value, easy digestibility and suitability in multiple cropping system and is one of the major edible legume seed in Asia. It improves the fertility status of soil by fixing atmospheric nitrogen through symbiotic relationship with soil bacteria. Mungbean crop suffers from many fungal diseases, among them leaf spot caused by *Cercospora canescens* is one of the important disease in recent years. Hence with a view to generate information on management of diseases using chemicals *In vitro* evaluation of seven systemic fungicides were carried out against pathogen in College of Agriculture, Badnapur.In vitro evaluation of fungicides revealed that all the seven fungicides Carbendazim, Thiophanate methyl, Difenconazole, Azoxystrobin, Metalaxyl, Fosetyl and tebuconazole which were assessed at different concentration of @ 500,1000 and 1500 ppm were effective against *Cercospora canescens*. Among tested fungicides, the most effective at all three concentration with least average mycelial growth was recorded in fungicides viz., Thiophanate methyl, Difenconazole, Azoxystrobin and Tebuconazole, (0.00mm each) while the maximum colony diameter was recorded in fungicide Metalaxyl (25.82%), in case of mycelial inhibition the average mean mycelial inhibition was noticed maximum in fungicide viz. Thiophanate methyl, Difenconazole, Azoxystrobin and Tebuconazole (100 % each), while the least mycelial inhibition was noticed with fungicide Metalaxyl (71.28 %) respectively.

S6.98: Identification of *Ascochyta* blight resistant sources in *Kabuli* genotypes of chickpea and validation of identified QTLs

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Chickpea (*Cicer arietinum* L.) is an important edible food legume in the world after the common beans. It is highly nutritious as a rich source of proteins along with vitamins, minerals, fiber and also improves the physical properties of the soil. The low productivity of chickpea as compared to other *rabi* cereal crops is mainly because of its susceptibility to biotic and abiotic stresses. Among the biotic stresses, Ascochyta blight (*Ascochyta rabiei*) is quite damaging under favorable epiphytotic conditions causing serious losses in grain yield and quality. Sustained efforts are required to increase the yield potential of chickpea by identifying resistant sources and markers associated with QTLs in several populations. A total of 240 *kabuli* genotypes from different backgrounds/ locations were screened under artificial epiphytotic condition against AB during 2019-20 and 2020-21 at PAU, Ludhiana. Among them, 15 lines (GLK18091, GLK10-40, GLK20054, GLK20055, FLIP-09-256C-55, FLIP-07-314C-57, FLIP10-2434C, FLIP-09-194C, FLIP-08-104C, FLIP-04-219C, ICCV55233, ICCV55215, ICCV55135, ICCV55108 and ICCV155181) were found resistant over the years. The genomic DNA of all the resistant lines was extracted and for validation of already identified QTLs among the resistant lines, around 35 SSR markers associated with AB resistance were selected to conduct PCR. The PCR products were examined and the amplified SSR alleles were scored by identifying polymorphic and monomorphic sets. Nearly 20 SSR markers have shown polymorphism between resistant and susceptible lines. Therefore, these markers can be used with sufficient confidence in marker-assisted selection to develop superior lines for resistance to AB and also these resistant lines can serve as potential donors in the ongoing chickpea breeding programs.

S6.99: Disease resistance in different soybean genotypes against yellow mosaic virus disease

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Soybean (*Glycine maxx*. L. Merrill) is one of the most significant food legume and oil crops of the world. A variety of biotic factors negatively impact soybean production and productivity. One of the viruses causing yellow mosaic disease (YMD) significantly reduces the output of soybean and causes significant yield losses in India. Breeding of resistant variety against the viral diseases is the safest method of viral disease management. The goal of the current study was to find resistant genotypes among the 60 different soybean genotypes against the yellow mosaic disease (YMD). A trial was conducted to raise 60 genotypes in RBD design in the experimental field. In order to ensure proper spread of the disease and to maintain uniform pressure of it across the field, spreader rows of highly susceptible genotype (JS335) were grown as boarder rows. Genotypes of soybean were scored on '0' to '9' scale which represent 0 = HR (Highly resistant) and 9 = HS (Highly susceptible). As per disease scale of YMD, the minimum virus disease severity infection was recorded in 4 genotypes which were categorized as highly resistant (HR) viz., RVS 2012-01, EC602288, SP-37 and JS20-53 X JS20-34. 13 genotypes showed tolerance against YMV, however 7 genotypes were found susceptible viz., RVS 2011-21, Bragg, HIMSO-16, 5PS 1225, RSC1052, AMS243 and RVS 2001-04 against YMD. The maximum disease infection was found in Hardee, BAUS 102, PK 885 and JS 20-90 genotypes which represented highly susceptible genotypes of soybean.

S6.100: Epidemiology and management of fungal foliar diseases in Urdbean and Mungbean

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Urdbean and Mungbean are the most important and major contributing pulse crops in Tamil Nadu. Based on the seasonal influences, these crop affected by various fungal foliar diseases. Among them, powdery mildew involves the formation of white powdery patches on both sides of the leaves, tendrils, stem and pods. Symptoms of *Cercospora* leaf spot includes irregular to regular purplish brown spots with pale gray center. In case of anthracnose irregular brown spots on leaves followed by covered on entire leaf then shedding and drying. The transpiration and respiration of plant will be high especially during night and photosynthesis decreases. Only possible ways to reduce the yield loss due to these diseases are adopting the INM practices along with timely application of fungicides. A field experiment was carried out at National Pulses Research Centre, Vamban, Pudukkottai, Tamil Nadu during 2021- 22 with different seasons for studying the effect of different fungicides against fungal foliar diseases. The data on per cent disease index (PDI) was recorded at 10 days after second spray from the scale of disease scoring for the treatments during the experimentation. Based on the field experiments, seed treatment with Imidacloprid 600 FS 48%w/w @ 5ml/kg seed + Carbendazim 2g/kg seed followed by foliar spraying of Tebuconazole 50 %+ Trifloxystrobin 25 %WG @ 0.75g/lit of water at initial appearance of the disease symptom was found to be effective in reducing the powdery mildew, cercospora leaf spot and anthracnose diseases with increasing the grain yield in urdbean and mungbean.

S6.101: Assessment of powdery mildew incidence in blackgram under green house and open field conditions

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A field experiment was conducted at National Pulses Research, Tamil Nadu Agricultural University, Vamban from 2021-22 with the objective to assess the influence of microclimate on powdery mildew (*Erysiphe polygoni)* incidence of blackgram VBN 8 under shade net house (33% shade) and open field condition during summer and winter seasons. The percent disease index (PDI) was observed on the growth period of blackgram was partitioned into three stages *viz*. 20, 35, 50 days after sowing (DAS). The influence of environmental variables *viz*., temperature, relative humidity and light intensity were studied. In summer, the result showed that, the powdery mildew (*Erysiphe polygoni*) intensity was significantly higher under shade net house on 20, 35, 50 days after sowing when compare to field condition. The results showed plants in the earlier stage of growth with the lower rate of infection and the infections increased gradually from the second and third growth stage. The similar trend was also observed in winter season also. With regard to the seasons, summer season recorded comparatively lower incidence of powdery mildew than winter season. The disease is favored by low temperature (11-28ºC) and increased humidity (85-90%) and frost during winter season.

S6.102: New Sources of resistance and heritability to wilt/ root rot complex diseases in Kabuli chickpea

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Chickpea wilt/root rot complexes are the most important yield-limiting factors in spring planted chickpea in the Mediterranean region, south Asia, and East Africa highlands. In West Asia and North Africa, Fusarium wilt caused by *Fusarium oxysporum* f.sp. *ciceri* (*Foc*) is a dominant pathogen in the disease complex. ICARDA Kabuli chickpea breeding program evaluates breeding lines in sick plots dominated with *Foc* pathogen for global elite lines supplies. In the 2021–2022 growing season, 240 genotypes were evaluated in sick plots at Terbol ICARDA research station in Lebanon and naturally infested experimental field at Merchouch ICARDA research station in Morocco. The experiment was laid out in an alpha lattice design with two replications. Percent plant mortality was scored on plot bases once the average mortality of the susceptible line (ILC482) reached over 95%. The analysis of variance (ANOVA) analysis has indicated that the genetic variation among genotypes was caused by genetic variation as broad sense heritability was high (h2 = 0.76). However, only 51.3% of the changes were attributable to the genotypes, and only 10.0% to the environment (locations). Only four genotypes (S180005, S180022, S180071, and S180079) showed good levels of resistance (<20%) at both locations. These genotypes will be utilized for pyramiding additional resistance genes into other FW races and producing high-yield breeding varieties through the chickpea breeding program at ICARDA and will be shared with the national chickpea breeding programs in CWANA countries.

S6.104: Larval Parasitization of *Helicoverpa armigera* (Hubner) by *Campoletis chloridae* Uchida in chickpea intercropped with linseed

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Chickpea (*Cicer arietinum* Linnaeus) is an important legume crop of India. The damage caused by gram pod borer, *Helicoverpa armigera* (Hubner) is one of the major constraints in the cultivation of chickpea. The role of various cultural practices like adjustment of sowing dates and intercrops in chickpea make the crop environment less suitable for pest development. The experiments were conducted at research farm of Pulses Section, PAU, Ludhiana during *rabi* 2020-21 and 2021-22 to study the role of linseed as intercrop on *Helicoverpa armigera* in chickpea. The experiment has five treatments each of 8 x 8 m size plot sown in the ratio of chickpea: linseed as (10 : 1, 20 : 1, 10 : 2, 20 : 2 rows) and chickpea sole (24 rows). The crop was kept unsprayed during both the years. Data was recorded on the number of *H. armigera* larvae parasitized by *Campoletis chloridae* by collecting 15 larvae per treatment at 10 day interval during March-April and converted into per cent larval parasitization. Grain yield of chickpea as main crop and linseed as intercrop for each treatment was also recorded at harvest and converted into kg/ha. The mean per cent parasitisation ranged from 3.33-7.78 per cent in chickpea, where linseed was sown as intercrop as compared to 2.22 per cent in chickpea sole. Thus chickpea intercropped with linseed can be used as cultural practices in IPM strategy for the control of *Helicoverpa armigera* in chickpea.

S6.106: Ascertaining the extant of *Trichoderma* spp. and Fungicides against chickpea wilt acquired by *Fusarium oxysporum* f. sp. *ciceris*

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Fusarium wilt of chickpea is well known disease in India with 3-5 per cent of losses every year which may even reach up to 50 to 60 per cent under severe infestation. This study aims to cut down the cost of cultivation occurring due to use of non-effective chemicals and to provide hike in farmer's income. The experiment was conducted in Seed Breeding Farm, JNKVV, Jabalpur, followed Randomized Block Design with three replications in *Rabi* 2021-22 with resistant variety JG 16. Observations were taken after 20 days (Emergence count) and wilted plants were recorded at 30, 45 and 60 days and finally averaged. To assess the efficacy of some new fungicides and *Trichoderma* strain against *F. oxysporum* f. sp. *ciceris* causing wilt disease in chickpea by utilizing nine novel *Trichoderma* spp. one *Pseudomonas* spp. and two commercial fungicides. Under *in vivo* conditions, results showed that all the treatments with *P. fluorescens* (NBAIR-PFDWD) was most effective in minimizing wilt incidence (12.6%) followed by *Trichoderma* strain (UBSTH 501 NBAIM) and *T. asperellum* strain (NBAIR-TATP) with 12.9 and 13.5 per cent disease incidence as a significantly superior to the control (26.4%). *Trichoderma viridae*, *Trichoderma* mutant (T-8), *Trichoderma harzianum* (T-28), *Trichoderma harzianum* (T-6) and *Trichoderma* mutant (T-3) were the most effective and reduced the wilt incidence as compared to inoculated control *viz*., 14.9, 15.2, 15.3, 15.6, and 16.0 per cent disease incidence respectively. Highest incidence was observed in Propineb (16.3%), Mycobin (16.7%) and *Trichoderma harzianum* Liquid (17.0%).

S6.107: Screening of pigeon pea germplasms for *rangeeni* lac production

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Lac is a natural resin and is of great commercial importance. Baisakhi crop of *rangeeni* strain of lac insect, *Kerria lacca* (Ker) is most suitable for lac crop in late maturing varieties of pigeon pea. Potential of twenty-eight germplasms of pigeon pea were assessed for summer *rangeeni* (*baisakhi*) crop for three years. Germplasm RCMP 4, ICPR 2671, RCMP 8, KA 9-1, KA 9-2, RCMP 11, Assam local 2, MAL 31, RCMP 2 and Bahar had shown significant contribution towards brood lac production. Brood lac output ratio ranged from 1.6 to 3.9. Percent scraped lac was also significantly differed among germplasm. It varied from 16.95% (in ICPR 2671) to 35.65% (in IPA 9-1). After rearing lac insect on pigeon pea there was significant loss in 100 seed weight and grain yield per plant. The average loss in 100 seed weight and grain yield was recorded as 5.6 % and 13.9 %, respectively. Preference of *rangeeni* strain of lac insect varied with germplasm. Germplasm RCMP 4, ICPR 2671, RCMP 8, KA 9-1, KA 9-2, RCMP 11, Assam local 2, MAL 31, RCMP 2, Bahar and Assam local 1 had more than 60 percent contribution towards brood lac yield. Careful selection of pigeon pea germplasms will certainly help farmers to get good seed yield and lac crop.

S6.108: Genotypes X *Trichoderma* strains interactions and their effect on Plant growth and Wilt incidence in Chickpea

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The cultivation of chickpea (*Cicer arietinum* L.) is threatened by the biotic stresses, amongst these wilt caused by *Fusarium oxysporum* f. sp. *ciceris* is the major constraint. Seeds of twenty chickpea genotypes belonging to different categories were treated with three *Trichoderma* strains and one fungicide combination [Carboxin (37.5%) + Thiram (37.5%)]. In 'kabuli' types, maximum (94.02%) seed germination was in XIIth-82-511, while in 'desi' types 100 % germination was in JG-74, JG-315, C-104 and K-850. Maximum root length was found in chaffa (19.12 cm) treated with *T. harzianum* strain 1 and 2, whereas, in *T. viride* it was maximum (20.44 cm) in FLIP-10-243C. Seedling vigour was maximum 3883.37 in *T. harzianum* 2, followed by *T. harzianum* 1. At 30 and 60 days after sowing, significant differences in endophytic association of *Trichoderma* spp. were observed. At 30 days *T. harzianum* strain-2 had maximum 70.25 % association. Amongst the genotypes, the maximum association was in Chaffa (75.00%) followed by FLIP-07-183C (73.75%). At 60 days after sowing, *T. harzianum* strain 2 had highest 77.25% root association, followed by *T. viride* (76.00%) and *T. harzianum* strain 1 (73.50%). *In-vitro* efficacy revealed that *T. viride* inhibited the maximum (74.82 %) mycelial growth of Foc. Wilt incidence in 'kabuli' types was minimum 5.5 % in L 550 followed by 6.51 % in FLIP-10-, whereas, in 'desi' types Chaffa had a minimum wilt (6.96%). The present study revealed that the efficacy of *Trichoderma* spp. on plant growth and bio-control of wilt is dependent on the chickpea genotypes.

S6.109: *Fusarium chlamydosporum* as the causal agent of dry pod rot of mungbean [*Vigna radiata* (L.) Wilczek] in tarai region of Uttarakhand

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Vigna radiata is one of the most significant pulse crops in India, belonging to the *Fabaceae* family, and is commonly known as mungbean or green gram, or golden gram. Mungbean is a fast-growing short-term pulse crop grown in Kharif and Zayed seasons. During the field survey (2020-21) dry pod rot symptoms were observed on mungbean with 80-90% of disease incidence in Pantnagar (29.0222°N, 79.4908°E), Uttarakhand, India. Diseased pods were collected and brought to the laboratory for further study. The characteristic symptoms included white to salmon pink fungal growth over pods. Initially, water-soaked spots were observed which later turned into dry rot. The seeds from affected pods were shriveled with white fungal overgrowth. The Colony of the pathogenic fungus was initially white to light pink, aerial, and floccose with irregular margins. The fungal hyphae were hyaline branched and septate. Microconidia were mostly single-celled rarely bi-celled, ovoid to fusoid, and measuring 8-12 x 2-5 µm. Macroconidia were typically 3-5 septate, thick-walled, moderately curved, hyaline, and with an average dimension of 15-36 x 2-4 µm. Chlamydospores were intercalary, solitary or in the chain, globose to subglobose, and measuring 8-14 µm in diameter. Based on morphological characteristics, the pathogen was identified as *Fusarium chlamydosporum*. In the cultural study, it was found that the corn meal agar medium was suited best for mycelial growth but maximum sporulation was recorded on potato dextrose agar medium. The temperature of 30°C and pH 6.5 were found to be optimum for mycelial growth and sporulation of the pathogen.

S6.110: Screening of Genotypes Against Chick Pea Powdery Mildew

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Chickpea is the principal *rabi* pulse crop and important source of calories and protein in India which is predominantly grown in the vast rainfed areas of the country. Amongst the biotic stresses, powdery mildew is becoming severe in recent years. It is caused by *Leveillula taurica*, powdery mildew epidemic begins late in the season so yield components are usually less affected by the infection. However, early infections lead to more yield loss. Screening of the chickpea lines against the disease would be of a great help to identify the resistance source. Identification of resistant variety is one of the best management practices in the long run and there are hardly any resistant sources available against this pathogen. It would be of great help to chickpea growers to identify the stable resistant genotypes which lessens the cost of cultivation besides being environmentally safe. Out of 58 *Kabuli* genotypes screened, ten were found immune, seven genotypes resistant, eight genotypes found moderately resistant, fifteen genotypes showed moderately susceptible. Where as seventeen genotypes were found susceptible and only genotype found highly susceptible. Eighty six *desi* genotypes were tested against powdery mildew incidence. Among all tested genotypes two genotypes *viz.,* Magic-23 and Magic-80 are found immune. With respect to yield highest fruit yield was recorded by spraying Ametoctradin 300 g/l + Dimethomorph 225 g/l SC and Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (market sample) with 21.42 t/ha and 20.93 t/ha. Ametoctradin 300 g/l + Dimethomorph 225 g/l SC and Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (market sample) at 800 ml/ha was found to be next best treatment in terms of fruit yield. Where as unsprayed control recorded lowest yield (11.96 t/ha).

S6.113: Understanding differential pod borer, *Helicoverpa armigera* (Hübner) resistance in cultivated and mutation-derived chickpea genotypes

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The most significant pest of chickpea is the gram pod borer *Helicoverpa armigera* (Hübner). Many pesticides are used to control this pest; these chemicals not only leave harmful residues but also harm non-target organisms and the environment. In addition, the use of pesticides also leads to pest resurgence and the development of resistance to insecticides. Great amount of research has been carried out on screening the elite lines for pod borer resistance, but up until this point, no true resistant or tolerant lines for pod borer have been identified. In the present studies, we evaluated the mutant lines derived from ICCL 86111 (National resistant check) for pod borer damage assessment in field and laboratory conditions using detached leaf/pod bioassays. Based on three seasons of evaluation, we identified some notable mutant lines (M4 population), namely, ICCL 86111-B-8-4, ICCL 86111-B-688-10, ICCL 86111-B-638-8, ICCL 86111B-834-2, ICCL 86111-B-862-6, ICCL 86111-B-713-3, ICCL 86111-B-1066-2, ICCL 86111-B-1072-3, and ICCL 86111-B-1002-2, exhibiting lowest per cent larval survival and larval weight gain under lab bioassay and least pod damage under field conditions when compared to ICCL 86111(Non-mutant) and ICC 3137 (Susceptible check). Further research is being done to evaluate these mutant lines for morphological and biochemical characteristics, as well as to find secondary metabolites conferring resistance to pod borer.

S6.114: Proteome wide-identification of pathogen responsive Small Secreted Cysteine-rich Proteins in Pigeonpea (*Cajanus cajan* L)

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Small secreted cysteine-rich proteins (SSCPs) play an important role in modulating host-pathogen interactions. However, no SSCPs have been identified in pigeonpea. The NCBI database was used to retrieve *Cajanus cajan* predicted protein sequences (41,387), and 25,354 small proteins were sorted based on protein length of >300 amino acids. To obtain the small secretory proteins, protein sequences containing secretory signals were sorted using the Signal P 5.0 tool. The proteins with more than 5% cysteine residues were retrieved from these using the ProtParam (ExPASy) tool, yielding 62 small, secreted cysteine-rich proteins. Differential gene expression analysis of the 62 SSCPs in the pigeonpea wilt resistant (KPL44) and susceptible (Bahar) lines infected with *Fusarium udum* revealed 14 genes that were up regulated in the resistant variety (48 hpi), with four of them (SSCP 1-4) showing more than a five-fold up-regulation. These SSCPs were predicted to have potential antimicrobial properties when screened against the publicly available databases and thus offer high potential for future biotechnological applications. Among the four potential SSCPs, only SSCP1 was successfully cloned, expressed, and confirmed by western blotting and solubility testing (with the protein detected in the soluble fraction). Therefore, it may be stated that the identification of candidate SSCP (SSCP1), validation of its clone, and expression were successful. Additionally, it may be purified and evaluated for antimicrobial activity utilizing a variety of biochemical techniques.

S6.115: Unraveling the impact of weather parameters on *Phytophthora* stem blight disease development in Pigeonpea

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Pigeonpea (*Cajanus cajan* [L.] Millspaugh) is the second most important pulse crop in India. The crop represents ~5 % of global grain legume production, where India contributes more than 70 % of the total produce but the infestation of *Phytophthora* stem blight (PSB) is one of the major bottlenecks in achieving targeted yield. Weather conditions play a predominant role in determining the course and severity of *Phytophthora* stem blight development. Therefore, an attempt has been made to assess the complex relationship between weather parameters and *Phytophthora* infestation in pigeonpea. To accomplish the objective, periodical data on selected weather parameters such, temperature, rainfall, relative humidity (RH), and *Phytophthora* stem blight were collected from June-July, 2019 to October-November, 2022 along with native soil moisture. Experimental data revealed that, severity of *Phytophthora* blight was maximum in the last week of July (26-30) after heavy rains where maximum temperature (T_{max}) range was between 27.5 to 32.6. æ%C, RH was 76.8 % and content of soil moisture was 19-26%. The mortality gradually decreased with the scarcity of soil moisture along with progressive decline in RH. Correlation study revealed that rainfall and soil moisture is significantly interlinked with *Phytophthora* infestation by 0.43% and 0.53% respectively. Surprisingly, RH was found negatively correlate with *Phytophthora* with an average value of (-) ve 0.32. Henceforth, in the end the conclusion can be soil moisture and rainfalls are the determining factors in the development of *Phytophthora* stem blight disease in Pigeonpea.

S6.116: Molecular cloning and *in-silico* characterization of novel resistance gene analogue from lentil against Fusarium wilt

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Fusarium oxysporum f. sp. *lentis* (*Fol*) is the most devastating disease of lentil present worldwide and in India. Identification of multi-race Fusarium wilt resistance genes and incorporation into existing cultivar will help to manage the disease. In the present study, multi-race resistant lentil germplasms belonging to *Lens culinaris* sub sp. *culinaris*, *L. c* sub sp. *odemensis* and *L. nigricans* were identified through extensive screening during 2020-21 and 2021-22. The majority of resistance (R) gene has central nucleotide-binding site (NBS) domain flanking Toll/interleukin 1- like receptor (TIR) or coiled-coil (CC) at the N terminal and Leucine-rich repeats (LRR) at the C terminal. The degenerate primers designed from the NBS region amplifying P-loop to GLPLA motif isolated forty-five resistance gene analogues (RGA) from identified resistant accessions. The phylogenetic analysis grouped RGA into six classes, LRGA1 to LRGA6 determining the diversity of RGA present in the host. Grouping of RGA identified from *L. nigricans*, LnRGA 2, 9, 13 with I2 reveals a probable role in Fusarium resistance. The sequence alignment identified both classes of RGA, TIR and non-TIR based on the presence of Aspartate (D) and Tryptophan (W) at the end of the kinase motif respectively. The similarity index of 27.85 -86.98% was found among RGA and 26.83 - 49.41% between known R genes. Active binding sites within RGA were identified and ADP/ATP being the potential ligand determines ATP binding and ATP hydrolysis activity. Further, RGA identified can be used as a marker linked to functional R gene and to isolate the full-length gene.

S6.117: Identification of yellow mosaic disease resistant and early maturing soybean germplasm for enhanced productivity

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Yellow mosaic disease (YMD) is a serious disease of soybean *(Glycine max)* affecting soybean productivity in different areas. To meet his challenge, identification and deployment of resistant varieties offers an eco-friendly and cost effective solution. Though YMD resistant varieties have been developed in India, these are often late maturing. Therefore, 500 diverse accessions of Indian national genebank comprising of exotic collections from USA and indigenous collections were screened at New Delhi during *Kharif* 2019-20. Sufficient variation was recorded for different agro-morphological traits including YMD incidence. Resultantly, 20 putative resistant accessions were further evaluated in thrice replicated RBD under infector row technique using susceptible check as infector crop after every two rows. White fly count (WFC) and disease incidence (DI) over different phases of crop growth were also recorded. WFC showed significant positive correlation with leaf length, leaf width and plant height. However, DI did not show any association with WFC. Consequently, two accessions (EC993255 and EC1037786) showed prominent resistance despite high occurrence of white fly population on them. Besides resistance, both these accessions also expressed early maturity (~ 95 days) compared to late resistant checks at Delhi. The PCR mediated detection revealed the presence of Mungbean Yellow Mosaic Virus at New Delhi hot spot location. Furthermore, during *Kharif* 2022-23 the resistance of these accessions was also expressed and validated at Delhi, Ludhiana and Pantnagar locations. These germplasm accessions can be either good candidates for variety release or donor for developing early maturing and YMD resistant varieties for enhanced soybean productivity.

S6.119: Diversity profiling and characterization of indigenous *Trichoderma* isolates from pulses rhizosphere of India

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Pulses are known to improve soil health as they harbor beneficial microbes in their rhizosphere. Several *Trichoderma* isolates were collected from pulses rhizosphere and explored for its diversity and antagonistic potential through diverse characterization techniques. A total of 280 soil samples were collected from the rhizospheric soils of Chickpea, Pigeonpea, Lentil, Urdbean and Mungbean from 12 major pulse growing states (Uttar Pradesh, Bihar, Jharkhand, Madhya Pradesh, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu, Gujarat, Rajasthan, Telangana and Delhi) across the country, in which nine species (*T. harzianum T. longibrachiatum T. asperellum, T. afroharzianum, T. aureoviride, T. atrobreunum, T. brevicompactum, T. asperelloides & T. virens)* were identified from 160 *Trichoderma* isolates. Prevalence of *T. asperellum* was highest (47.5%) followed by *T. harzianum* (41.25%), *T. longibrachiatum* (6.85%) and *T. brevicompactum* (1.25%) and *T. afroharzianum* (1.25). For other species including *T. atrobreunum* (0.62%), *T. aureoviride* (0.62%), *T. virens* and *T. asperelloides* (0.62%) it was minimum. The prevalence of *T. asperellum* was higher in Andhra Pradesh followed by Karnataka and *T. harzianum and T. longibrachiatum* were prevalent in Tamil Nadu. Whereas, In Uttar Pradesh the prevalence of *Trichoderma asperellum* was more followed by *T. harzianum*. The characterization of these strains was carried out through morphological and biochemical observations and the amplification and sequencing of rDNA fragments (ITS regions), as well as the translation elongation factor 1-alpha (Tef 1-á), achieving the identification of isolates belonging to *Trichoderma* genus. Analysis of genetic diversity using molecular markers revealed intra-species diversity of isolated *Trichoderma* spp. The frequency of chickpea root colonization by *Trichoderma* spp. was found highest. These results provide precise information on prevalence and distribution of *Trichoderma* spp. across the country and helpful for soil and seed priming application in pulse crops for soil borne disease management as well as plant growth promotion.

S6.120: Unraveling epigenome modifications during abiotic stresses in chickpea

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Plants being sessile respond to changing environmental conditions for their survival. Plants evoke common and stress-specific molecular signatures that enable them to discriminate between stimuli and cope with different stresses. Chickpea is an important crop grown in developing countries, but their productivity is limited by various abiotic stresses. We analyzed epigenomic differences between different genotypes with contrasting phenotypes under salinity stress and drought stress, via generation of global DNA methylome maps and differential methylation patterns. The DNA methylation profiles revealed more hypermethylation in the salinity-tolerant genotypes and hypomethylation in drought tolerant genotypes. A positive correlation was observed between gene expression and CG context gene body methylation. The DMR-associated differentially expressed genes involved in root development or transport were majorly represented in the tolerant genotype. Further, we provide evidence for the role of smRNAs in inducing CHH context hypermethylation in TEs that may regulate the expression of associated genes. Overall, our studies identified several candidate genes showing differential DNA methylation that might function as epialleles in chickpea to serve as target candidate genes for epigenome modification for abiotic stress response/adaptation.

S6.121: Screening of chickpea germplasm against dry root rot disease

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Dry root rot disease in chickpea caused by *Rhizoctonia bataticola* (Taub.) Butler, is becoming a major threat to chickpea production in recent years. It is soil-inhabiting fungal pathogen capable of infecting chickpea at any crop stage, but most commonly at post reproductive stage and results in considerable yield losses that vary from 50 to 71 per cent particularly due to longer drought spells. In the present study, 168 germplasm lines were screened for their resistance to dry root rot in sick plot of Regional Agricultural Research Station, Vijayapur during 2021-22. Among 168 germplasm screened against dry root rot, only four germplasm (GPM111-1, GPM111-82, GPM111-100, GPM111-103) were found resistant, 44 germplasm were moderately resistant, 36 germplasm were moderately susceptible, 67 germplasm were susceptible and remaining germplasm were highly susceptible to the disease.

S6.123: Unravelling of collar rot (*Sclerotium rolfsii)* resistance and the underlying mechanisms in lentil (*Lens culinaris* Medik.)

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Collar rot (*Sclerotium rolfsii*) is a persistent problem for early sown lentil (*Lens culinaris* Medik.) in North-eastern plain zones of India under rice fallow system, as it is associated with significant yield losses every year. Management of this pathogen is very cumbersome due to high saprophytic survivability. The demand for lentil is increasing globally as it is a staple food of daily diets in developing and developed nations owing to its high nutritional status. However, collar rot compromises the lentil productivity which detrimentally affects the global need to meet the increasing demands. Development of collar rot resistant cultivars is one of the prudent ways to manoeuvre the risk. Therefore, identification of resistant sources followed by comprehensive understanding of the host pathogen interaction seeks immediate intervention. This present study sheds light in that direction through screening of 500 germplasm of lentil under field condition considering HUL-57 as susceptible and WBL-58 as resistant check at Gangetic New Alluvial Zone. Based on percent disease incidence and Area under Disease Progress curve (AUDPC), resistant lines (IC317520, IC0095652, IC241447 and IC0095660) were detected and further confirmed through artificial screening. The isolated pathogen was characterized at molecular level using Internal transcribed spacer (ITS) based marker. Histopathological and biochemical analysis were also integrated to unveil the lentil self-defence mechanism along with detection of the defense related enzymes. The identified resistant and susceptible lines can be useful for developing resistant cultivars towards achieving sustainable disease management in lentil.

S6.124: Screening of mungbean genotypes against thrips and associated tospovirus disease

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Mungbean (*Vigna radiata* (L.) Wilczek) is an important pulse crop in India and other Asian Countries. The yield production is limited by many insect pests, of which thrips and associated tospovirus disease (bud necrosis) are considered emerging threats to mungbean cultivation in India. However, there is less literature available on thrips and their association with bud necrosis disease in mungbean. In the present study, we generated basic information on thrips species and the population dynamics of thrips and bud necrosis. We screened 238 mungbean genotypes (155 mini core accessions, 74 breeding lines, 6 commercial checks, and 3 parental lines) availed from World Vegetable Center, South/Central Asia against thrips under field conditions at IARI, Pusa New Delhi during the spring (April-June) season of 2021 and 2022. We observed two thrips species (*Thrips palmi* Karny and *Scirtothrips dorsalis* Hood) occurring together at different stages of crop growth. Thrips infestation started from the first week after seedling emergence and higher density (4.83 thrips/shoot) was observed during the flowering to pod formation stage. Similarly, bud necrosis disease incidence started from the third week after sowing and cumulative disease incidence was observed up to 33.80 %. Among the 238 mungbean genotypes, 95 genotypes showed moderate resistance to thrips incidence during the spring season (2021). Subsequently, 95 genotypes were evaluated in the consecutive spring season, 2022; Out of which, 58 genotypes were resistant, 30 were found moderately resistant, and 7 were moderately susceptible against thrips incidence. The identified resistant genotypes will be further screened across different locations.

S6.127: *In vitro* evaluation of fungicides against *Rhizoctonia bataticola* causing dry root rot in chickpea

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Dry root rot in chickpea caused by *Rhizoctonia bataticola* (Taub.) Butler is a soil borne pathogenic fungi with diversified host range. *In vitro* efficacy of six combi-product fungicides against *R. bataticola* was evaluated at 500, 1000, 2000 and 3000 ppm concentrations. The data revealed that all the fungicides at each concentration reduced the mycelia growth of fungus when compared to control. Among the six combi-products evaluated against *R. bataticola*, Thiophanate methyl 45 % + Pyraclostrobin 5 % FS, Carbendazim 25 % + Mancozeb 50 %, Tebuconazole 50 % + Trifloxystrobin 25 % WG and Carbendazim 12 % + Mancozeb 63 % were found to be most effective and found significantly superior over all other fungicides, which inhibited cent per cent growth of *R. bataticola* at all the concentrations tested. This is followed by Carboxin 37.5 % + Thiram 37.5 % (77.43 %). Least inhibition of mycelial growth (60.80 %) was observed in Zineb 68 % + Hexaconazole 4 % WP and at 500 ppm concentration with the inhibition of 27.89 %.

S6.128: Bacterial endophyte, *Pseudomonas stutzeri* strain NIBSM_CaS37 induces endophyte mediated resistance against *Fusarium* wilt in Chickpea

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Chickpea (*Cicer arietinum* L.), an important legume crop, contributes about 40% of total pulses. Fusarium wilt caused by *Fusarium oxysporum* f.sp. *ciceri* is economically importance biotic stress. To control this deadly disease, endophytes have emerged as eco-friendly alternative approach. Endophytes are the microbes living inside the plant tissues and play a crucial role in plant growth, development and imparting resistance to various biotic and abiotic stresses. In this study, 119 bacterial endophytes were isolated from different tissues of chickpea. When screened for antimicrobial activities against *Fusarium,* 16 isolates showed potential of having pathogen growth inhibition (ranging from 31% to 60%) in dual culture assay and presence of lipopeptides genes - iturin, surfactin and bacilliomycin in PCR. On the basis of antagonistic activities, three isolates *viz.,* NIBSM_CaL1, NIBSM_CaS37 and NIBSM_CaS25 were used for *in planta* validation. Chickpea plants bio-primed with endophyte showed better survival rate against *Fusarium* infection with protection over control ranging from 57% to 75% and significant increase in plant biomass. Isolate *Pseudomonas stutzeri* strain NIBSM_CaS37 showed the best protection against *Fusarium.* Tri-partite (Chickpea- *Fusarium*- Endophyte) interaction was studied to identify differential expression of genes probably involved in imparting endophyte mediated resistance (EMR) using qPCR which showed an increased expression of Auxin binding protein ABP19a, NAC-TF, 14-3-3 like protein, Linoleate 9S-lipoxygenase and LRR protein genes in the endophyte bio-primed-pathogen inoculated plants in early stage of infection as compare to control thus indicating the role of EMR and may enhances the plant's immunity by modulating phytohormone and signalling pathways.

S6.129: Source with multiple disease resistance in urdbean (*Vigna mungo* L.)

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Urdbean (*Vigna mungo* L.), is a major pulse crop grown in India. The crop is inflicted by various diseases out of which mungbean Yellow mosaic virus (MYMV), anthracnose (Ant,), *Cercospora* leaf spot (CLS) and powdery mildew (PM) cause huge losses. The diseases can be effectively managed by cultivation varieties with multiple resistances to various diseases. Identification of donors with multiple resistance to various diseases is a pre-requisite for any successful breeding program, Keeping this in view, 275 promising genotypes of urdbean were evaluated against Anth,, CLS, and PM at Palampurand MYMV (Akrot). It was observed that 49, 13, 32 and 94 genotypes were resistant to PM, anth., CLS and MYMV, respectively. None of the genotypes were free from Anth, and CLS, Genotypes Mash 1-1, NBU 785 and OBG 32 were resistant/moderately resistant (DRd"5) to PM, anth., CLS and MYMV. Five genotypes i.e. DKU 131, NGU 14, 15, PK HPU 157, 557 and TU 94-2 were resistant to Anth. CLS and MYMV whereas, genotypes DKU 113, 123, 142, 15-7, HPBU 18, NGU13 and COBG953 were resistant to CLS, PM and MYMV and 10 genotypes were resistant/moderately resistant to Ant., CLS and PM. MYMV resistant genotypes will be registered with NBPGR and promising genotypes DKU 87, 90, 98 and 116 are being evaluated at farmers' fields. The genotypes with multiple resistances may prove useful donors to develop resistant varieties. The genotypes with moderately resistant genotypes may be deployed in disease prone areas after agronomic evaluation.

S6.130: Assessment of various packaging materials for pulse storage against pulse beetle (*Callasobruchus chinensis* L.)

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The present investigation on effectiveness of packaging materials and storage containers against pulse beetle (*Callasobruchus chinensis* L.)" was carried out by conducting a laboratory experiment by using various packaging materials viz. jute bag, gunny bag, polythene bag and cloth bag seeds of black gram in association with silica (2%) at Department of Entomology, Rajasthan College of Agriculture, MPUAT, Udaipur during 2020-2021. Polythene bags with silica (2%) was found to be best effective treatment among various packaging materials against pulse beetle during storage having minimum oviposition (21.33); seed damage (3.33%) and weight loss (7.93%) followed by gunny bags with silica (2%) (35.66, 4.60% and 11.67%); cloth bags with silica (2%) (39.53, 6.10% and 13.19%); Polythene bags without silica (41.86, 6.66% and 15.09%); jute bags with silica (2%) (43.86, 8.53% and 15.12%); gunny bags without silica (97.73, 17.40% and 27.86%); cloth bags without silica (109.26, 22.26% and 31.54%) and jute bags without silica (143.53, 27.86% and 37.89%).

S6.131: Disease resistance in different soybean genotypes against yellow mosaic virus disease

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Soybean (Glycine maxx. L. Merrill) is one of the most significant food legume and oil crops of the world. A variety of biotic factors negatively impact soybean production and productivity. One of the viruses causing yellow mosaic disease (YMD) significantly reduces the output of soybean and causes significant yield losses in India. Breeding of resistant variety against the viral diseases is the safest method of viral disease management. The goal of the current study was to find resistant genotypes among the 60 different soybean genotypes against the yellow mosaic disease (YMD). A trial was conducted to raise 60 genotypes in RBD design in the experimental field. In order to ensure proper spread of the disease and to maintain uniform pressure of it across the field, spreader rows of highly susceptible genotype (JS335) were grown as boarder rows. Genotypes of soybean were scored on '0' to '9' scale which represent 0 = HR (Highly resistant) and 9 = HS (Highly susceptible). As per disease scale of YMD, the minimum virus disease severity infection was recorded in 4 genotypes which were categorized as highly resistant (HR) viz., RVS 2012-01, EC602288, SP-37 and JS20-53 X JS20-34. 13 genotypes showed tolerance against YMV, however 7 genotypes were found susceptible viz., RVS 2011-21, Bragg, HIMSO-16, 5PS 1225, RSC1052 , AMS243 and RVS 2001-04 against YMD. The maximum disease infection was found in Hardee, BAUS 102, PK 885 and JS 20-90 genotypes which represented highly susceptible genotypes of soybean.

S6.132: Management of diseased sick plots during off season using herbicides

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Chickpea (*Cicer arietinum* L.) is prone to a number of soil borne fungal diseases, of which wilt caused by *Fusarium oxysporum* f. sp. *ciceri* (*Foc*) is a significant constraint to chickpea production worldwide. The wilt disease of chickpea has been managed well through wilt resistant varieties to a large extent. Since, development of varieties using diverse donors is a continuous process; the phenotyping of candidate varieties has to be taken up in sick plots. Once, wilt has been managed by exploiting host plant resistance, erstwhile minor diseases viz. collar rot (irrigated, normal sown condition) caused by *Sclerotium rolfsii* and dry root rot (normal sown rainfed, and late sown condition) caused by *Rhizoctonia bataticola* are emerging as new challenge in Central and Eastern Central India.

RLBCAU has developed sick plots for all three soil borne diseases to screen elite breeding lines and germplasm accessions to identify resistant donors through support from Indian Council of Agricultural Research-All India Coordinated Research Project on Chickpea (ICAR-AICRP). It is important to mention there is always a challenge to manage these sick plots which need to be kept fallow during the off season (rainy/summer season) to maintain the purity and load of the inoculums. Limited information is available for management of weed in the sick plot during the off season especially in rainy season. The accumulated weeds in fallow sick plots led in drain of nutrients from soils. There are reports in several crops that the herbicides such as glyphosate aggravate the multiplication of the pathogen. Accordingly, a study was planned in the laboratory conditions (for all the pathogens, i.e. wilt, collar rot and dry root rot) and simultaneously in the pots conditions (only for wilt) using two herbicides viz., pendimethalin and glyphosate at different concentrations i.e. 500 ppm, 1000 ppm, 1500 ppm, 2000 ppm and 2500 ppm. It was observed that in laboratory conditions, i.e. in petri plates the treatments with glyphosate at all the concentration hastened the growth of the fungal culture in all three pathogens and the production of micro- and macroconidia was initially observed at 2000 ppm. The results with use of pendimethalin were not very much convincing for Foc and *R. bataticola* as the fungal growth was restricted at all concentrations beyond 500 ppm. Though, the fungal growth was observed in case of *S. rolfsii.* However, the fastest growth was observed at 2000 ppm of glyphosate for *Foc* and *R. bataticola* and the growth of the *S. rolfsii* was equally fast when 1000-2500 ppm of glyphosate was used. In the treatment using glyphosate, the sclerotia were initiated first at 2000 and 2500 ppm both in case of *S. rolfsii* and *R. bataticola.* In pots, the soil was made sick by adding mass multiplied inoculum of Foc on sorghum grains. JG-62, wilt susceptible variety, was sown in the pots during rabi 2021-22. The weeds were allowed to grow in *Kharif* 2022 and the weeds were then suppressed using different conc. of selected herbicide i.e. glyphosate, based on the laboratory results. The spray of the herbicide before sowing of chickpea in the rabi 2022-23 did not show any toxic effect of the crop. The colonization of the chickpea tissue by Foc is being recorded in the current rabi season i.e. 2022-23 and the maximum mortality of the susceptible variety has been recorded at 2000 ppm in pots condition. It was thus concluded, that the use of a glyphosate did not prevent sporulation of the fungus and thus can be a useful for management of weeds in sick plots during the off season without affecting the inoculums load in the sick plot.

S6.134: Tapping of New Sources of *Fusarium* Wilt Resistant Chickpea (*Cicer arietinum* L.)

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Chickpea (*Cicer arietinum* L.) serves as a good source of dietary protein, vitamins and minerals and also improves soil fertility through symbiotic association with Rhizobium. A soil born disease, *Fusarium* wilt, is one of the major yield limiting factors of chickpea in central India. Breeding for host plant resistance is the most cost-efficient and eco-friendly strategy to control the disease. Most high yielding cultivars of chickpea in central India are prone to soil born diseases. Therefore, creating significant genetic diversity is a fundamental step to develop *Fusarium* wilt resistant genotype for sustainable agriculture. In this investigation, 500 chickpea accessions were evaluated with one susceptible check JG 62 and two resistant checks JG 12 and JG 315 against *Fusarium* wilt as well as yield and its attributing traits in *Rabi* 2021-2022 at Seed Breeding Farm, JNKVV, Jabalpur. Seventy-two accessions showed resistant against *Fusarium* wilt, out of which 35 accessions were found promising and resistant to *Fusarium* wilt having 3.76% disease incidence. These accessions had high yield per plant ranged between 11.5 – 18.7g, more total number of pods per plant (24 – 89) and effective pods per plant (20 – 37). These accessions also recorded high biological yield (20.3 – 40.0 g), harvest index (32.9 – 50.8%) and plant height (31.3 – 66.2 cm). These lines can be utilized as resistant source in the breeding programs for enhancing yield potential of chickpea.

New Vistas in Stress Resilience-Abiotic Stresses

S6.1: Problematic soil converted into profitable land with the intervention of salt tolerant Lentil variety under salt affected land

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Lentil (*Lens culinaris cv* Medikus; 2x = 24) is a self-pollinating crop plant with an approximately genome size of 4 *Gbp*. Lentil covers the area about 1.32 Mha with production 1.18 Mt and productivity of 894 kg/ha annually in India. First time in the history of lentil research, in the collaboration between ICAR-IARI, New Delhi and ICAR-CSSRI, Karnal (Haryana) released two variety PDL-1 and PSL-9 for salt tolerance. These two-variety released by classical breeding approach. PDL-1 gives 9-10.5 q/ha yield and PSL-9 gives 9.83 -10.50 q/ha yield under salt affected land upto 8 dS/m. Present investigation reports the transcriptome analysis of PDL-1 and PSL-9 give putative molecular mechanism in response to salt stress. The study revealed that active pathways for salt stress tolerance in lentil are phyto-hormones biosynthesis—predominantly through ABA signalling and secondary metabolism, which are also known to be actively involved in other abiotic stress response mechanisms. PDL-1 and PSL-9 showed pronounced tolerance towards salt stress compared to L-4076 (sensitive) owing to low accumulation of Na^+ and high accumulation of K^+ in both roots and shoots. The cultivar also maintained high cellular integrity and physio-cytological status under stress condition based on mitotic index, antioxidant production, osmolytes accumulation and membrane stability. These salt-tolerant genotypes of lentil will also have great potential to convert problematic areas into profitable and help enhance livelihood and nutritional security of the population living in such resource poor areas.

S6.2: Novel insights into the mechanism(s) of Silicon-induced drought stress tolerance in lentil plants as revealed through transcriptomic analysis

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Silicon (Si) is a beneficial element for plant growth and development, especially under stress conditions (Ma, 2003). Silicon plays a crucial role in alleviating drought stress in lentil plants (Biju *et al*., 2018, 2021). Although the physiological and biochemical mechanisms behind Si-mediated drought tolerance in lentil plants are known, the molecular mechanism is unknown. This study examined the differential expression of genes in response to Si-induced drought stress tolerance in two contrasting lentil genotypes (drought tolerant-ILL 6002 and drought-sensitive- ILLL 7537) via high-throughput RNA sequencing. A total of 7164 (3695 up-regulated; 3469 down-regulated) and 5576 (3077 up-regulated; 2499 down-regulated) differentially expressed genes (DEGs) were identified from drought-stressed ILL6002 and ILL7537, respectively, with Si treatment. Heatmap showed that DEGs responsible for osmotic stress response (Lc19777.1) were up-regulated along with the down regulation of proline biosynthetic gene (Lc19060.1) in both genotypes. Both the genotypes under Si-induced drought tolerance showed up-regulated DEGs related to chlorophyll biosynthetic processes (Lc09995.1), cell wall biogenesis (Lc17832.1), defence response (Lc21119.1) and drought recovery (Lc02021.1). Gene ontology (GO) enrichment analysis of DEGs displayed GO terms related to defence response, secondary metabolite production, and phytohormone biosynthesis in both tolerant and sensitive genotypes. The results suggest that a coordinated yet complex interplay between various metabolic pathways is required for Si to induce drought tolerance in lentil. DEGs uncovered in this study and their analyses shed new light on the mechanism of Si-induced drought stress tolerance in lentil and provide molecular material for further investigations of the role of Si under drought stress.

S6.6: Climatic resilient crop husbandry strategies to manage abiotic stresses in pulses

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Pulses, being rich in protein, minerals and vitamins, play a significant role in the nutritional security of Indian people, especially those below poverty line, who can ill-afford animal food products. However, per capita per day availability of pulses in India at present is about 45 g against the minimum recommended dose of 70 g/capita/day (Economic Survey, 2021-21). The productivity of pulses in India (~885 kg/ha) is very low as compared to other countries (2020-21). Biotic and abiotic stresses are the major barriers in realizing the yield potential, as about 87% of the area under pulses is rainfed and mainly confined to marginal and sub-marginal lands. Their cultivation in resource-scarce conditions exposes them to various abiotic and biotic stresses, leading to significant yield losses. Furthermore, climate change due to global warming has increased their vulnerability to emerging new insect pests and abiotic stresses that can become even more serious in the coming years.

S6.12: QTL-seq underpins major QTLs controlling heat tolerance in chickpea

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Rising events of heat stress due to global climate change have significantly caused global crop yield loss including chickpea. Aiming at discovering QTL/gene(s) contributing towards heat tolerance in chickpea, whole genome resequencing-based QTL-seq approach has been employed by selecting ten individuals showing high cell membrane stability value and high total pods/plant and ten individuals showing low cell membrane stability value and low total pods/plant from $F_{2:3}$ population developed from DCP 92-3 (heat sensitive) × ICCV 92944 (heat tolerant). Based on this approach, a total of three major QTLs *CaqH5.1, CaqH5.2* and *CaqH6.1* were identified. A total of sixty candidate genes were uncovered underlying these identified QTLs. Among the various candidate genes related to heat stress response/tolerance underlying these QTLs, *Ca_02170*, *Ca_16631*, *Ca_23016*, *Ca_09743,* and *Ca_25602* candidate genes showed differential expression through RT-PCR assay in vegetative and reproductive tissues of heat tolerant and heat sensitive parents. Thus, these candidate genes confirmed their significant role in heat tolerance and could be cloned for developing heat tolerance in chickpea.

S6.17: Dissipation behavior of glyphosate and aminomethyl phosphonic acid in soil and its residual effect on subsequent urdbean crop

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In intensive cropping system, mechanization is being promoted where glyphosate is applied to control weeds on non-cropped area before sowing of main crop. The major microbial degradation product of glyphosate is amino methyl phosphonic acid (AMPA), which has toxicity comparable to glyphosate. In this study, dissipation behavior of glyphosate and AMPA in soil was evaluated and their residual effect on subsequent urdbean crop was also studied. Field experiments were laid out in randomized complete block design with seven treatments and three replications, during 2022 kharif season at farm of ICAR-IIPR, Kanpur, India. Glyphosate was applied at the rate of 1.5 kg a.i./ha and 2.25 kg a.i/ha on weeds, which was followed by sowing of urdbean (IPU 13-1) after 7, 14, 20 days of waiting time. Soil samples were collected at different time interval and analyzed for residue status of glyphosate and AMPA by following alkali extraction technique in combination with HPLC-fluorescence detector (FD) analysis. Glyphosate persisted in soil for up to 45 and 60 days at application rate of 1.5 kg a.i./ha and 2.25 kg a.i/ha, respectively. Half-lives for glyphosate ranged 14.1 to 20.2 days in soil. AMPA persisted longer than glyphosate in soil, with half-lives ranging in between 45.2 to 66.5 days. Residues of glyphosate and AMPA were not detected in leaves and grains of subsequent urdbean crop at the time of harvest. The residues of glyphosate and AMPA did not influence germination, growth and yield of subsequent urdbean crop as compared to control.

S6.33: Salinity screening of black gram genotypes using hydroponics screening

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This study used ten black gram genotypes *viz.,* ADT 3, ADT 5, ADT 6, ADT 7, Co 6, VBG 13003, VBG 17007, VBG 19005, VBG 19010, and VBN 11 to investigate the salinity response using hydroponics. The Yoshida nutrient composition along with the salinity level of 13 dSm^{-1} was used to screen the ten genotypes. The salt imposition was carried out four times subsequentially at three days intervals to stimulate the challenging salinity condition. Based on survival rates, genotypes *viz.,* VBG 17007, and VBG 19010 as tolerant, and genotypes *viz.,* ADT 3, and VBN 11 as susceptible genotypes to salinity. These genotypes can be used to develop a mapping population to locate the QTLs responsible for salinity tolerance.

S6.34: Identification of donors for salinity tolerance at vegetative stage in blackgram [*Vigna mungo* (L.) Hepper]

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Salinity tolerance in blackgram was assessed at vegetative stage under hydroponics conditions. Pre-screening was carried out with five genotypes to determine the optimal salt concentration. Membership function value (MFV) was calculated for shoot length (cm), dry weight (g), survival percentage and salinity score. Based on the results, 13 dS/m salinity level was chosen as the ideal salt concentration for further screening. One hundred genotypes of blackgram were screened at 13 dS/m. Based on membership function value of survival per cent and salinity score, eight genotypes *viz.,* ACM BG 14-001, VBG 18-071, VBG 18-080, VBG 19-005, VBG 19-007, VBG 19-010, Vamban 3 and VBN 8 were identified as highly saline tolerant. These saline-tolerant genotypes could be utilized as donors in blackgram breeding programme.

S6.36: Drought attenuates the plant responses to multiple rhizospheric pathogens – a study based on dry root rot-associated disease complex in chickpea fields

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Dry root rot disease (DRR) in chickpeas is an emerging and enfeebling soilborne disease caused by the necrotrophic fungal pathogen *Macrophomina phaseolina* (Synonym: *Macrophomina phaseolina* (Maubl.) Ashby.). Under open field conditions, root rots were found to be complex infections (many fungal pathogen infections) that dramatically lower production. Literature on root rot disease complexes and their disease dynamics were not well studied under water stress. Drone imagery in survey studies across the chickpea fields of southern India showed large numbers of DRR-associated disease complexes among several other complexes. Analysis from fourteen different environments comprising two soil moisture regimes at seven locations showed drought to intensify disease incidence of disease complex causing a yield loss of 35 to 60% in susceptible genotypes. The whole genome metagenomic shotgun sequencing revealed the effect of drought on rhizospheric and root endo-microbial communities, especially root rot disease complex-associated pathogens. The root-pathogenic fungi are enriched in the chickpea rhizosphere. However, in infected chickpea roots, *M. phaseolina* dominantly infected the chickpea roots under well-watered and drought conditions, and also the symbiotic associations of chickpeas with nitrogen-fixing bacteria are suppressed under drought stress. LC-MS-based phytohormonal analysis of chickpea roots indicated a significant positive correlation of pathogen load with jasmonic acid alone in *M. phaseolina* infection alone, and salicylic acid and jasmonic acid together combined in multiple infections. Additionally, JA is found to have a highly significant negative correlation with abscisic acid attributing to feebler root functional defenses under drought stress contributing to higher infections.

S6.45: Morpho-physiological responses of chickpea genotypes (*Cicer arietinum* L.) to terminal drought

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Chickpea is predominantly grown as a rainfed crop in semi-arid regions that is prone to drought stress (DS), a major abiotic stress limiting chickpea growth and productivity. Deciphering the morpho-physiological traits of chickpea in response to DS will provide opportunities for improved adaptation and yield. An experiment was conducted under temperature-controlled glasshouse conditions in New Delhi, India. Six chickpea genotypes were selected for the study including QTL-hotspot donor parents (ICC 4958), high-yielding recurrent parents (Pusa 362 and RSG 888), their introgressed lines (BG 4005 and BGM 10218) and a drought-susceptible genotype (ICC 1882). PVC tubes (1m long, 15 cm in diameter) with 25 kg soil were used for growing the plants and their daily transpiration was recorded using a custom-made balance. After imposition of DS from early podding stage, all flowers and pods were tagged and counted. Seed yield and yield components of well-watered (WW) and DS plants were measured. Physiological parameters (e.g., leaf photosynthetic characteristics, pigments and osmotic adjustments, canopy temperature) were recorded on several occasions. Plant growth parameters such as shoot and root growth, pollen viability and germination were also recorded. Seed yields ranged from 8.6–30.1 g plant^{-1} under WW, and 1.2–15.1 g plant^{-1} under DS. DS decreased yield the most in ICC 1882 (86%) and the least in ICC 4958 (50%) relative to WW. The significant genotype × water treatment interaction for morpho-physiological traits was observed, which will assist in establishing the phenotype-genotype associations and better understanding of plant adaptation to DS.

S6.47: Drought tolerance indices in breeding for climate resilience in chickpea (*Cicer arietinum* L.)

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Drought is the major abiotic stress limiting the chickpea production around the world. There is an urgent need to develop the drought tolerant genotypes to enhance the productivity of the crop. It is also necessary to choose appropriate traits to enhance the precision of selection. Thirty four genotypes were evaluated for their drought tolerance under well-watered (WW) and low moisture stress (LMS) environments. Drought tolerance indices *viz.,* Drought and productivity index (DPI), drought susceptibility index (DSI), mean productivity (MP), tolerance to drought stress (TDS), drought tolerance efficiency (DTE), yield index (YI), relative reduction (RR) were calculated to complement the selection based on morpho-phenological and productivity traits. Analysis of variance for seed yield under both well-watered and low moisture stress condition showed significant difference indicating the presence of genetic variability. Based on the rank mean across the drought tolerant indices ICC4958 ranked first followed by JG11. Based on per cent reduction of yield under low moisture stress against well-watered condition, the genotypes ICCV 201202, ICC 4958, ICCX110053-8, ICCX-060157-11, ICCX 120044-31, M112, DIBG 205, ICCX 120041-67, BGD 111-1, ICCX-100106-9 were found to be superior for drought tolerance. Further, significant positive association of yield under WW and LMS with YI, DPI and MP was evident while significant negative association was noticed between DSI and TDS, DSI and DTE, RR and TDS, RR and DTE. These indices give additional information on drought tolerance and hence are very useful in enhancing selection efficiency.

S6.48: The *Auxin Responsive Factor* involved in lateral root formation and act as adoptive mechanism for seedling-water-logging tolerance in wild *Vigna umbellata* L.

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Mungbean is an important short duration grain legume. It is consumed as food and feed, fodder. It has a wider adaptability to an array of environmental conditions, shorter life cycle and improves the soil health through symbiosis. These features indicate that there is an ample scope of vertical and horizontal expansion of mungbean worldwide. However, it is much sensitive to various abiotic stresses, amongthem seedling waterlogging is major threat. The improvement in waterlogging tolerance required the potential donors. The crop wild relatives (CWRs) of *Vigna* possessed improved tolerance should be identified and introgressed in mungbean. The 32 *Vigna* accessions including cultivated and wild belong to nine different species were evaluated and two genotypes *namely* PRR 2008-2, and PRR 2008-2-1 demonstrated the unique feature of leteral root development under waterlogging. The histochemical staining indicated the lower cell death in leaves of PRR 2008-2 and formation of aerenchyma was also noticed. The expression of candidate genes and transcriptional revealed that the upregulation of ARF candidate upon 24-h after water logging in PRR 2008-2 seedlings. Besides, the upregulation of NAC, WRKY, and MAPK was also noticed at different time points under waterlogging stress. 26 ARF, and 19 VrAUX/IAA proteins were identified from its closely related model genome, *V. radiata*. The phyogeny and gene structure prediction revealed the significant structural diversity in *VrARF* candidates. The expression of selected candidates showed the differential regulation at diffrent time points in PRR 2008-2 seedlings indicated the possible involvement in the leteral root formation under waterlogging stress.

S6.50: Crafting Genetic Variability for Refined Moth Bean Plant Type Suitable for Hot Arid Climate through Mutagenesis

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Moth bean, a paramount legume, believed to be the most drought hardy climate resilient crop in arid zone. To confront the prevalent setback of narrow genetic base of the moth bean, mutation breeding has been contemplated worth utilizing in the present study for obtaining the desired mutants for more refined plant type suitable for hot arid climate of Rajasthan. Two varieties IPCMO-880 (late maturing) and GMO-2, treated with two mutagens viz; Gamma rays (200 Gray and 400 Gray) and EMS (0.3% and 0.5%) were sown in RBD along with their controls. No damage was observed in M1. M2 population consisting of 800 single plants to progeny rows were used to select desirable mutants. Accounting albino and sterile mutants, GMO-2 was more responsive to mutagenesis with higher frequency at 0.5% EMS and 400 Gy treatments. Zero sterility was observed in 0.3% EMS treatment in GMO-2, while 7 sterile lines in 0.5% EMS, 3 in 200 Gy and 5 in 400 Gy depicting 17.95%, 7.41% and 17.24% mutagenic frequency respectively, clearly portraying the proportional increase in mutation frequency with increase in dose of mutagen. In M3, five individual plants were selected from each line, considering visual and morpho-metric traits. The selected plants depicted wide range and diversity for all the traits. Moreover, three early flowering and maturing plants in M2 lines were selected from IPCMO-880 with a view to diversify source for early maturity. Hence, present study identified diverse mutant plants having erect growth habit, longer peduncle, compactness in plant type, more plant height and ultimately more yield, which could be further used in moth bean breeding programme.

S6.53: Evaluation of grasspea germplasm for below-ground traits and its relationship with ODAP under water-limited conditions.

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Exposure of plants to environmental stress affects numerous physiological processes which necessitates to look for crops with resistance to abiotic stresses to maintain food and nutritional security. Abiotic factors predominantly drought is a major threat to crop production in rainfed dry areas. Grasspea (*Lathyrus sativus* L.) is considered one of the climate-smart crops for its unique ability to withstand adverse environmental conditions. The present study focused on the below-ground traits of grasspea and their relationships with performance and ODAP content under water-limited conditions. Sixty-six diverse germplasm accessions representing ten *Lathyrus* species selected based on agronomic traits and ODAP content were screened under normal and water stress regimes employing three small-scale high-throughput phenotyping methods, namely a) non-paper roll, b) Clear pot, and c) Basket (Pasta strainer). Observations were recorded on root system architecture (RSA), root characteristics, agronomic traits, and ODAP content to establish relationships among RSA, drought, and ODAP content. The results from all three methods indicated IG *114935* and IG *115119* having wide root growth angle (RGA) and IG *64836,* IG *64839,* and IG *64861* having narrow RGA. Based on Water Stress Tolerance Index (WSTI), six genotypes showed tolerance to water stress with significantly higher grain yield and 12 genotypes tolerance to water stress with low ODAP content. One genotype, IG *64868* (*L. cicera)* was tolerant to water stress with high GY and low ODAP% compared to the checks, *Ratan* and *Wasie*. These results revealed significant association of ODAP content with root traits under water-stress conditions, which offers scope for utilizing this information to augment drought tolerance and grain yield with low ODAP content in grasspea varieties.

S6.54: Physiological dissection of blackgram germplasm for salinity stress tolerance

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Blackgram (*Vigna mungo*. L.) plays significant role in human nutrition and rich in phosphorus content, which is the 5–10 times richer than others pulses. The geographical range of legumes was constrained by high concentrations of Na^+ and Cl^- ions surrounding the root zone, which induces both osmotic and ionic stresses at all stages of its growth and development. Therefore, it is crucial to identify salt-tolerant cultivars and comprehend their physiological mechanism of adaptation to salt-stress. Through hydroponics experiment blackgram genotypes were treated with 130 mM NaCl for 6 days. Morphological, gas exchange and photosynthetic, water relation, antioxidant enzyme activity and cell membrane stability and nutrient uptake parameters were observed. By Pot culture experiment, salinity stress was imposed at flowering stage and pod filling stage separately by irrigating 130 mM NaCl salt water for 14 days and the end of stress period morphological, gas exchange and photosynthetic, water relation, antioxidant enzyme activity and cell membrane stability and yield parameters were recorded. Photosynthetic rate, Fv/Fm ratio, soluble protein, nitrate *reductase* activity, Relative Water Content, osmotic potential, ion content in leaves and root represented strong positive correlation with morphological traits. Numbers of pods, pod length, pod weight, and biomass represented strong positive correlation with yield at flowering and pod filling stage. Based on Principal component analysis and D value, the salt tolerant capacity of the blackgram genotypes is as follows VBG17007 > MDU1 > VBG13003 > VBN8 > CO6 > VBN11 > CO5 > CO2150 > ADT5 > LBG 653.

S6.56: Phytohormones response to heat stress in chickpea

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Chickpea is the major cool season pulse crop that serves as a source of plant-derived protein in human diet. India is the largest producer as well as consumer of chickpea. Terminal heat stress affects the growth and development of chickpea and ultimately reduces their yield. Phytohormones such as abscisic acid (ABA), gibberellic acid (GA3), and auxin (IAA: Indole acetic acid) play a crucial role in plant growth and development and also regulate the physiology and biochemistry of plants under stress. However, there are no reports on the response of phytohormones under heat stress in chickpea. Therefore, HPLC methods were standardized for estimation of these phytohormones in order to understand their response to heat stress in chickpea. Gibberellic acid (in flowers), auxin (in flowers, leaves, and roots) and ABA (in leaves and roots) were estimated in heat-tolerant and susceptible genotypes of chickpea under normal as well as heat stress condition. Higher GA3 and IAA content was observed in the flowers of heat-tolerant genotypes of chickpea as compared to heat susceptible genotypes. Under heat stress conditions, the GA3 and IAA content decreased in the flowers of heat tolerant as well as heat susceptible genotypes. The IAA content also decreased in leaves and roots of heat tolerant as well as heat susceptible genotypes. Higher ABA content was observed in roots as compared to the leaves of chickpea. Further, in response to heat stress, the ABA content increased in leaves and roots of heat tolerant as well as heat susceptible chickpea genotypes.

S6.67: Physiological Characterization of Pigeon Pea Genotypes for Cold Tolerance

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In north India, pigeon pea experiences low temperature stress during winter months (December-January). Information's regarding cold stress and its impact on morphological characters, physio-biochemical processes and yield attributes in pigeon pea crop is very limited. Keeping the above facts in to consideration, the experiment was formulated to screen suitable genotypes of pigeon pea tolerant to cold stress based on morpho-physiological and biochemical traits and ability to set flower and pods and yield performance. Based on the previous field screening for cold tolerance, field experiment with 04 cold tolerant (NDA-2, MAL-13, ICP-2275, IPACT-2),08 cold susceptible genotypes (IPA 15F, Dholi-D, JBT46/27, IPACT-6, IPACT-14, IPAC-1-17, IPACT-68, IPACT-22), 04 checks (IPA203, Bahar, NDA-1, ICPL 7035) and 14 breeding lines was conducted to study the effect of cold stress on morphological characters including flowers/pods retention %, NBI, Chlorophyll, Flavonols, anthocyanin and plant height were recorded periodically. Highest pod retention % after exposure of cold stress was observed in tolerant group (67.31%) among which MAL-13, NDA-2 and ICP 2275 recorded 70.3, 69.86 and 69.14% respectively. In susceptible group, the average % of retention of pod was 52.04 and varieties Like Dholi –D, IPACT 22 and IPAD 1-17 recorded 29.42, 45.93 and 51.92% respectively. Among the breeding crosses, the crosses of Bahar/ IPACT-79, IPACT-79/IPACT 80 and IPACT 79/IPACT 80 recorded 68.05, 68.18 and 67.21% pod retention respectively. Other crosses retained less than 67% Flower /pod set. In Plant efficiency parameters, including NDVI, photosynthetic rate, stomatal conductance and Transpiration Rate, no definite trend could be observed in tolerant, susceptible and crosses of pigeon pea. Moreover, tolerant group showed relatively higher stomatal conductance over susceptible group and might be considered as one of parameter for cold tolerance. Anti-oxidant enzymes including peroxidase and Super Oxide Dismutase showed higher activity in susceptible group as compare to tolerant group. Among the crosses no definite trend could be observed. Tolerant group of varieties showed higher 100 seed weight and grain yield per plant over susceptible group but no definite trend could be observed in breeding crosses evaluated.

S6.68: Physiological Characterization of Pigeon Pea Genotypes for Water Logging Tolerance.

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Water- logging stress is one of the important abiotic stress in pigeon pea crop especially in low lying areas in pigeon pea growing states. Being a rainy season crop, pigeon pea is invariably exposed to intermittent water-logging conditions for different durations from germination to early vegetative growth stages, which damage the crop partially and sometime eliminate the entire crop depending on intensity and duration of water stagnation. Keeping above facts in consideration the present research work was formulated to study the morphological, physio-biochemical characters and yield performance of water logging tolerant and susceptible pigeon pea genotypes. The experiment was conducted with 21 pigeon pea genotypes including checks, these were IPAC-79, ICPL-7035, ICPL-20241, ICPL-87051, ICPL-87091, ICP-2376, ICP-5028, ICPL-149, MA-3, MA-6, NDA-1, IPA-15F, Bahar, IPA-203, IPAC-211, IPAC-202, RCM/DD-17, WB-2019/25, WB-2019/26, WB-2019/27 and IPAC-212. Water logging stress was imposed for 24 h-48h-72h having minimum depth of water 12 inches at 30 DAS with 03 replications and a set of all genotypes sown under normal control. Meteorological data during water logging stress were recorded. Based on morphological characters' pigeon pea genotypes like ICPL-20241, ICPL-87091, ICP-5028, MA-6, NDA-1, Bahar, IPA-203 and IPAC-211 showed tolerance against water logging stress where as IPAC-202, RCM/DD-17, WB-2019/25, WB-2019/26, WB-2019/27 and IPAC-212 showed susceptibility against water logging stress. Tolerant group showed the formation of adventitious roots but susceptible group showed no adventitious roots. Physio-biochemical parameters including NBI, Chlorophyll, NDVI and photosynthetic efficiency were markedly reduced under water logging conditions over normal control. The Flavonols, anthocyanin's, anti-oxidant enzymes SOD, Peroxidase and soluble sugars in leaves were increased under water logging stress. Yield attributes and seed coat colour showed no definite trend and correlation with tolerance/susceptibility of pigeon pea genotypes against water logging stress.

S6.70: Temperature induction response technique: a screening tool for evaluation of urdbean genotypes for thermotolerance.

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Urdbean (*Vigna mungo*) is an important source of protein and widely used in daily diet. Pulses are more sensitive to high temperature stress. Screening and identification of cultivars for high temperature stress conditions is essential under changing environment. Temperature induction response (TIR) technique, is based on the principle of subjecting seedlings to sublethal temperatures and subsequent exposure to challenging temperatures, and further assessing growth and recovery. The standardization of induction temperature and lethal temperature is based on per cent growth reduction and survival percentage at the end of recovery period. The induction temperature was standardized at 36 to 46^{0}C for 3 h and the lethal temperature as 52^{0}C for 3 h. This study was conducted during 2020-2021 and 2021-2022 at Indian Institute of Pulses Research, Kanpur under laboratory conditions. A total of six selected urdbean genotypes were screened and evaluated for thermotolerance. By using standardized optimum induction and challenging temperature, cellular level tolerance was assessed in all the urdbean genotypes. Based on root length and shoot length of induced seedlings over control seedlings, the cellular level tolerance in terms of least reduction in growth and highest survival percentage was calculated. Thermotolerant genotypes PGRU 95014 and PGRU 95016 have shown intrinsic heat tolerance and therefore they can be explored as donor source in breeding programme aimed for global warming.

S6.80: Hydroponic aided evaluation of chickpea (*Cicer arietinum* L.) genotypes for high Aluminium stress tolerance

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Aluminum (Al) toxicity is a major emerging abiotic stress drastically hampering plant growth and crop productivity. In acid soils, the toxic form of aluminium, Al^{3+}, significantly inhibits root growth and elongation, due to less water and nutrient uptake. The present study evaluated a combination of landraces and advance genotypes for aluminium tolerance using a seedling-based hydroponic screening. The experiment was conducted to score root length trait in the presence of aluminum. Initially, two Al^{3+} concentrations (100 µM and 200µM) were used to test a panel of 150 chickpea genotypes. Genotypes were evaluated both for total root length under 100µM Al^{3+} and for root regrowth compared to a 0µM Al^{3+} control treatment. Considering both parameters of root length and root regrowth, we identiûed two tolerant chickpea genotypes (ILC8797, ILC180) and two susceptible genotypes (Pusa72, ILC0(Italy)) along with the tolerant and susceptible checks IPC92-39 and IPCK96-3 respectively. The tolerant lines had their root length under stress measured 15.00cm (ILC 8797) and 22.50cm (ILC 180).

S6.85: Discerning the morpho-physiological thermotolerance traits in Chickpea (*Cicer arietinum* L.) germplasm for high temperature stress under normal and late-sown conditions.

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The extremities of climate change and global warming necessitates the development of high yielding stress tolerant varieties. One among such stresses includes high temperature. In the current climate change scenario, the advancement of physiological plasticity governing thermo-tolerance in chickpea plays a critical role in improving chickpea production globally. The post-anthesis phase in Chickpea has been reported to be relatively more sensitive to high temperature stress. By keeping this aspect in mind, an experiment aiming towards the screening of different morpho-physiological traits of chickpea with varying dates of sowing, such as under normal and late-sowing conditions, has been carried out. The study has been conducted in 34 highly diverse chickpea germplasm accessions consisting of different agro-morphological traits such as leaf types such as simple leaf, compound imparipinnate and multipinnate leaves, as well as varying number of flowers per node (single and double) and pods per node (single and double). The work under consideration is likely to record morpho-physiological, and yield attributing components. Therefore, the traits contributing towards thermotolerance at different dates of sowing have been discerned.

S6.86: Delineating the role of plant stature towards heat stress tolerance in field pea (*Pisum sativum* L.)

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Terminal heat-stress severely affects field pea production in tropical climates. Identifying and characterizing of marker-trait(s) remain vital for breeding heat-tolerant cultivars of field pea. Field pea genotypes are highly variable for plant stature; however, the significance of plant stature for yield stability under high-temperature conditions is not yet well understood. The study aimed to investigate the sensitivity and significance of plant stature toward yield sustainability of field pea under high-temperature environments. A panel of 150 genotypes [dwarf (<50 cm), semi-dwarf (50-80 cm), medium-tall (80-150 cm)] grown under contrasting temperature environments *i.e.,* timely-sown non heat-stress environment (NSTE), moderately-late sown (15 days late) or heat-stress environment-I (HTE-I) and very-late sown (30 days late) or heat-stress environment II (HTE-II). Late-sown crops were exposed to high-temperature at flowering (+3.5 to +8.1°C) and grain filling (+3.3 to +6.1°C) over the NSTE. Medium-tall genotypes had longer grain-filling duration (11%), higher pod-bearing nodes (particularly upper nodes) and yield (22-62%), and lower yield losses (7-20%) over dwarf and semi-dwarf genotypes under moderate high-temperature environment (HTE-I). Plant height exhibited significant association with yield, yield loss, and heat-susceptibility index, which suggested the advantage of taller plants under high-temperature environment. GGEbiplot analysis revealed that the heat-tolerant genotypes were all tall type (mean=108 cm), while the heat-susceptible genotypes were mostly dwarf in stature (mean=45 cm). Tall height field pea genotypes have better adaptability under high-temperature environments. The breeding approach for high-temperature tolerance in field pea may be preferred in tall-type backgrounds over dwarf plant backgrounds.

S6.87: Physiological Mechanisms of Heat Tolerance in Lentil (*Lens culinaris* Medik.)

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Under changing climate, lentil crop encounters heat stress at flowering stage due to abrupt rise in temperature in the month of February/March in northern India which adversely affects the pod formation, development of grain and result in low yield. Production and productivity can be increased further by developing new varieties tolerant to high-temperature and having high early crop vigour along with high initial crop growth rate in terms of accumulation of higher biomass, production of more number of primary and secondary tillers, robust and healthy root system, maintains natural colour and cooler canopy during reproductive growth. Synchronization in flowering with higher pollen fertility and pod setting ability in terminal branches under high temperature conditions impart tolerance to heat stress. If a variety possesses these traits, it can withstand to changing climatic conditions. This will not only enable further increase in area under lentil under rice based cropping system but also help in improving the production and productivity of lentil grown after long duration rice varieties which matures by the month of November. Physiological characterization of a large number of contrasting genotypes for heat tolerance have indicated that high crop vigor, chlorophyll content, photosynthesis rate, MSI, cooler canopy, high pollen viability, pod formation in terminal branches, pod development and grain filling rate are the most important physiological parameters which was severely affected when temperature increased beyond 30 ^{0}C. Cooler canopy was found to be the most significant parameter which enables the plant to maintain its proper function at high temperatures.

S6.103: Phenotyping of lentil (*Lens culinaris* Medik.) germplasm against high temperature stress

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Lentil is very sensitive to even a slight increase in temperature during the reproductive stage. The objective of present study is to identify lentil germplasm with improved tolerance to extreme heat events during reproductive phase. In the present study 228 genotypes of lentil along with six checks (L-4076, IPL-220, BM-7, PDL-1, PSL-9, IPL-316) were sown in augmented design during *Rabi* season (2021-22) in late sown conditions in field at Seed and Research Farm at RLBCAU, Jhansi. Major traits studied for identifying suitable lines for heat stress tolerance were pollen viability, *in vitro* pollen germination and tube growth. Genotypes viz. ILL3271, EC78467, IC145268, IC520810 and ILL2922 showed pollen viability of 83.2%, 82.0%, 81.1%, 80.7%, 80.6% respectively. Genotypes viz. ILL2922, IC145268, IC520810, EC78467 and ILL3271 showed pollen germination of 76.82%, 76.25%, 75.62%, 74.35% and 73.1% respectively. These genotypes can serve as donor parents for breeding against heat stress. However, genotypes ILL3191, IC201580, FLIP 96-57, ILL1628, IC201766 were having comparable yield per plant with best check (BM-7). Correlation studies revealed that seed yield per plant was highly significant and positively correlated with number of filled pods per plant (0.69***), total no. of pods per plant (0.68***), yield per plant (0.28*), pollen viability (0.46**) and *in vitro* pollen germination (0.48**). Total number of pods, *in vitro* pollen germination, pollen viability, *in vitro* pollen tube growth, leaf area index, hundred seed weight and plant height had the highest direct and indirect effect on yield per plant in path analysis. Genotypes were classified into 4 clusters. Maximum inter cluster distance was obtained between cluster- I and cluster - III (6.962).

S6.105: Molecular mechanisms governing low temperature induced flower abortion in chickpea (*Cicer arietinum* L.)

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Chickpea (*Cicer arietinum* L.) is sensitive to low temperature (LT). Reproductive stage of chickpea is more sensitive to LT as compared to vegetative stage as LT at the reproductive stage leads to flower abortion that directly lowers yields of chickpea. LT induced abnormalities in anther and pollen development and mechanisms employed by tolerant genotypes to develop viable pollen under LT remain unknown. Following identification of flower and anther development stages in chickpea, impact of LT on different development stages in a LT-tolerant genotype and a LT-sensitive genotype was elucidated. LT disrupted microspore formation, gamete development, tapetum degradation, septum and stomium breakage and pollen viability. In contrast to LT-sensitive genotype, the LT-tolerant genotype maintained normal anther and pollen development under LT or showed less LT-induced disruption as compared to the sensitive genotype. LT induced pollen sterility was linked to disruption of carbohydrate and proline metabolism in anthers whereas pollen viability in tolerant genotype under LT was linked to the maintenance of starch, reducing sugars and proline levels and over-expression of UDP glucose pyrophosphorylase and cell wall invertase. All sucrose degradation genes of family, *cell wall invertase* (*CWIN*) were retrieved and identified in chickpea and expression of those studied in contrasting genotypes. Under LT, all *CWINs* overexpressed in the tolerant genotype but downregulated in the sensitive genotype revealing that *CWINs* played role in cold-tolerance in chickpea. The findings revealed molecular mechanisms governing pollen sterility and flower abortion under LT and strategies employed by the tolerant genotype to develop viable pollen under LT.

S6.111: Biochemical, and histochemical analysis for screening of salt stress tolerance in Horse gram (*Macrotyloma uniflorum*) germplasm

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Soil salinity is one of the biggest environmental problems affecting the production of many agricultural crops, having adverse effects on seed germination, plant growth, and yield. Horse gram has been considered relatively more salt tolerant than other legumes and has the potential as a pulse and fodder crop in salt affected areas. In the current study, 15 horse gram genotypes were screened under controlled environmental condition for the identification of salt tolerant and sensitive genotypes on the basis of percent reduction in root shoot length of ten days old seedling in petri plates containing 100 mM NaCl salt treatment. Based on the percent reduction in root shoot length, the genotypes DH-22 was identified as a highly salt tolerant and genotypes DH-11 was identified as a highly salt sensitive. The identified salt tolerant and sensitive genotypes were selected for further histochemical and biochemical analysis at 0, 50, 100, and 150 mM NaCl salt treatment. Biochemical analyses using the selected genotypes revealed that the tolerant genotype had lower lipid peroxidation (MDA content), higher ascorbate peroxidase (APX), catalase (CAT), glutathione reductase (GR), guaiacol peroxidase (GPX), superoxide dismutase (SOD) activity, high content of hydrogen peroxide (H_2O_2), and osmoprotectant; proline as compared to sensitive genotype upon exposure to varying degree of NaCl salt stress, which might play a vital role in cellular protection during salt stress tolerance. This study will facilitate identification of slat stress tolerance genes in horse gram and their network and pathways which further should assist in development of stress tolerant varieties.

S6.112: Genetic variation exists for heat tolerance in faba bean

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Faba bean is grown globally as a protein rich grain legume for food and animal feed. However, it is highly sensitive to heat stress during reproductive growth causing substantial yield losses. Selected elite lines from the faba bean breeding program at the University of Sydney were evaluated by exposing them to terminal heat stress in three sowing dates over two years. The late sown faba bean genotypes experienced above-optimal temperatures and increased solar radiation which accelerated flowering, podding and maturity, and shortened the grain filling duration. Terminal heat stress reduced plant growth and light interception causing 49–62% yield loss compared to the optimum sown condition. Heat stress resulted in short growing duration, decreased biomass production due to low assimilate production, high pod and flower abscission and poor partitioning. It also decreased seed weight, the number of seeds/pod and the number of pods/plant. Podding and grain filling were more affected by heat stress than flowering. A wide variation for heat tolerance was observed and the medium flowering genotypes performed the best under optimum as well as heat stress conditions possibly due to sufficient time for biomass accumulation for reproductive growth. Genotypes with high PAR interception and normalised difference vegetation index, taller plant stature and better photosynthetic efficiency produced higher yield. Among the genotypes, 12NF334a-7 recorded the lowest yield loss while PBA Warda-sel3 had the highest yield loss. Adaption to heat stress will require longer grain filling duration, early biomass production and high efficiency in partitioning to pods and seeds.

S6.118: Plasma technologies for green environment and smart agriculture methods

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Plasma Bioscience is an interdisciplinary field that combines the principles of plasma physics, material science, bioscience, medicine, agriculture, and environmental sciences towards the development of various future plasma-based innovative strategies. The study of plasma bioscience has yielded the development of new opportunities in the environment and agriculture fields. The objective of this talk is to present some research underlying nonthermal gas plasma methods useful in virus sterilization, microbial inactivation, food processing, decontamination, seed germination, plant growth, eradication of plant abiotic and biotic stress, and enhancement of aesthetic value, in the current scenario, challenges, and perspectives in environmental and agriculture sciences. At our Plasma Bioscience Research Center, we are focused on fundamental and applied studies on the characterization of the plasma sources applicable to the living organism, especially to plants and animals, and fundamental research of mutual interactions between the bio-plasma, water, organic/ inorganic materials, and nanomaterials. In the agriculture area, our other objectives are the development of plasma-based fertilizers (nitrogen fixation), food safety technologies, and plasma-based smart agriculture methods such as plasma-treated water for the aquaponic system for the improved growth of plants as well as healthy fish production. The knowledge that has arisen from studies in the plasma-based environmentally friendly or green agriculture methods area may translate into future innovations in the environment and agriculture industries.

S6.122: Chickpea: Role and responses under abiotic stress

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The chickpea is a significant legume crop that offers nutritional proteins to humans as well as animals. Among the abiotic stressors that limit chickpea yield are drought, heat and cold. Increased rates of genetic gain and the creation of cultivars that are more suited to abiotic stress conditions might result from the identification, validation and integration of agronomic, physiological and biochemical features into breeding programmes. Abiotic and biotic stress is common causes of external environmental stress for plants, including chickpea, which inhibits their ability to grow and develop. Due to these pressures, crop output is also greatly reduced. Plants, however, have a few defense mechanisms that might increase their resistance to them. The breeding effort for chickpeas has been further endangered by the genetic complexity of these abiotic challenges, a lack of appropriate screening, phenotyping and genotype-by-environment interaction approaches, and other factors. The scientists must thus comprehend the information gap concerning the physiological, biochemical, and molecular complex network of abiotic stressors mechanism in light of all depressing elements of abiotic stresses. In order to overcome the difficulties in producing chickpeas, breeders must first mine the "treasuring genes" from wild donors and create a genotype with "climate robust" genes.

S6.125: Physiological mechanism of drought tolerance in lentil (*Lens culinaris* Medik.)

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Lentil (*Lens culinaris*) is widely cultivated cool season legume crop. The crop faces intermittent drought in South Asian countries and terminal drought in West Asian and North African Mediterranean regions. Drought may lead to poor yield in lentil depending upon the severity of stress. Present study was conducted to understand the mechanism of drought tolerance in lentil. A set of diverse lentil germplasm (300 lines) was screened under rainfed conditions to identify novel donors for drought tolerance. Based on the screening, genotype IC560051, IC560032 and IC560246 were found drought tolerant and were investigated thoroughly under controlled conditions. Different physiological (seedling vigor, chlorophyll, stomatal conductance, canopy temperature, chlorophyll fluorescence), root traits (total root length, surface area, root diameter, primary root length, root dry weight), pollen load and viability, days to flowering and maturity and yield were recorded in selected lines. High seedling vigor, stomatal conductance, root length and branching, pollen load and early maturity lead to drought tolerance in selected genotypes. Identified genotypes can be used as donor in lentil improvement breeding for drought stress.

S6.126: Towards an integrated approach for improving drought tolerance in common beans: Linking roots with above-ground plant responses

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Roots are the hidden half of the plant that define plant productivity under stress conditions as they determine the resource acquisition, especially the mobile resources. Drought stress in common beans warrants selection of resilient varieties that withstand drought stress and such resilience will be mainly driven by better roots. We hypothesized that drought affects root system of common bean leading to decreased reproductive success, and a relationship exists between root traits, above-ground shoot traits, photosynthetic efficiency and reproductive success. In the present study we sought to quantify the effects of drought stress on various root, shoot traits and reproductive traits *viz*., pod set percentage in, and assess whether root traits had a relationship with reproductive success under drought. Weused various screening systems including agar based, PEG 6000 and column culture-based experiments. We found that root traits were significantly correlated with the above-ground response under water stress. Root angles ranged from 22.7 to 65.6^{o}Drought stress decreased rooting depth (14%), root biomass (29%), total root length (35%), volume (41%), pod set percentage (53%), and pod weight (43%). Among root traits we found that basal root angle and total root length were important root phenes whereas among above-ground traits, canopy temperature depression was an important surrogate trait for drought screening as selection for yield *per se* isnot so rewarding. We propose that basal root growth angle, total root length, CTD and pod set percentage should be used as an integrated selection index for improving drought tolerance in common beans.

S6.133: Screening of cultivated lentils (*Lens culinaris* ssp. *culinaris* Medik.) and its wild relatives against heat and water stress

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Lentil (*Lens culinaris* ssp. *culinaris* Medik.) is one of the most important cool-season food legume crops in the world, widely grown in rainfed dry areas where it encounters terminal heat and water stresses especially in South Asia, West Asia, and North Africa. Development of climate-smart varieties is one of the major breeding objectives. Keeping this in mind, we screened 30 cultivated and 50 wild accessions in four independent experiments following incomplete block design with three replications. These experiments represented heat stress (HS), water stress (50%IR), terminal drought (TD) and no water stress (100%IR). Analysis of variance and GGE biplot among accessions were followed under various environmental circumstances. Significant differences among lentil species were detected for major phenological and yield attributes under HS, TD and 50%IR treatments. Cultivated lentils had higher yield compared to wild lentils under heat stress while wild lentils performed better under drought conditions. For landraces, IG4400 had higher biological yield under 100%IR and 50%IR. IG137959 was identified as tolerant to heat as well as terminal drought. Three landraces, namely IG4400, IG156779, and IG1861 were the most stable genotypes in terms of grain yield under heat stress and are considered as heat tolerance. One accession each of *Lens ervoides* (IG72654) and *one L. orientalis* (IG137423) had the highest biological yield under full water irrigation, 50% IR and HS. *Lens oreintalis* accession IG136672 was the most drought tolerant while *Lens orientalis* accession IG72824 was moderately adapted to heat and drought. These results reveal the value of CWR in imparting climate smart traits to cultivated lentils.

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