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Extended Summaries and Abstracts

National Symposium on

Hybrid Technology for Enhancing Crop Productivity (NSHT)

8-10 January 2025

Venue: AP Shinde Symposium Hall, NASC, New Delhi-110 012

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Organizers

Trust for Advancement of Agricultural Sciences (TAAS), New Delhi
Indian Council of Agricultural Research (ICAR), New Delhi
International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Hyderabad
International Maize and Wheat Improvement Centre (CIMMYT), Mexico
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Foreword

I am pleased that a compilation of all the extended summaries of keynote and invited papers, and abstracts of rapid oral and poster presentations related to the **National Symposium on Hybrid Technology for Enhancing Crop Productivity**, being held from 8-10 January 2025 is being published. This symposium is being attended by a diverse group of experts, researchers, and industry professionals involved in exploring the transformative potential of crop hybrid technology in agriculture. It will provide a neutral platform to discuss the current status and future prospects of scaling hybrid technology for in evening production of food, fiber, and horticultural crops.

This publication encapsulates a wide array of research contributions presented at the symposium. It covers topics ranging from the present status of hybrid technology, germplasm management for hybrid crop breeding, advancements in genetic engineering and molecular breeding.

I thank the contributors for their invaluable insights into this area of crop improvement. My special acknowledgment is due to the editorial team for their meticulous efforts in bringing out this publication. It is expected that this publication will serve a useful reference for researchers, policymakers, and industry stakeholders, concerned with hybrid crop breeding.

RS Paroda
Chairman, TAAS

Preface

We are pleased to present compilation of extended summaries of keynote and invited paper and abstracts of rapid oral and paper presentations, submitted for the **National Symposium on Hybrid Technology for Enhancing Crop Productivity** (NSHT), being held on 8-10 January 2025. The Objectives of symposium are to (i) understand the current status of hybrid research in various crops; (ii) discuss and identity the current scientific and policy constraints in scaling hybrid breeding and seed production for increased productivity; (iii) foster closer public-private partnership for promoting hybrid breeding and seed production; and (iv) develop strategies and 'Way Forward' for accelerating adoption of hybrid technology on a large scale in the national interest.

The symposium features six technical sessions, two evening lecture, session, one panel discussion on way forward and a concluding session. A total of 32 keynote and invited lectures, two evening lectures, 20 rapid oral and 51 poster presentations are being made, covering a wide range of topics related to hybrid crop breeding.

The Extended Summaries and Abstracts cover wide spectrum of topics including the current status of hybrid research in various crops and scientific and policy constraints in scaling hybrid breeding and seed production for increased productivity. Suggestions on the 'Way Forward' for accelerating adoption of hybrid technology on a large scale are also included in this publication.

We express our sincere gratitude to all the contributors for their untiring efforts in making this compilation possible. We hope that this will serve as a valuable resource for researchers, faculty and students working in the field of hybrid crop breeding.

Editors

Acknowledgements

The organization of the **National Symposium on Hybrid Technology for Enhancing Crop Productivity** is made possible by the collaborative efforts of several organizations and individuals. We extend our heartfelt thanks to Dr RS Paroda, Chairman, Trust for Advancement of Agricultural Sciences (TAAS), New Delhi, for his visionary leadership in conceptualizing the organization of this important symposium. His foresight in identifying the need to accelerate the adoption of hybrid technology has been instrumental in shaping the agenda of this event. We extend our sincere gratitude to — TAAS, New Delhi; Indian Council of Agricultural Research (ICAR), New Delhi; International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad; International Maize and Wheat Improvement Centre (CIMMYT), Mexico; International Rice Research Institute (IRRI), the Philippines; and Indian Society of Plant Genetic Resources (ISPGR), New Delhi, for their technical and financial support. We are equally thankful to Co-Organizers and Sponsors - Federation of Seed Industry of India (FSII); Maharashtra Hybrid Seed Company (MAHYCO); Rasi Seeds (P) Limited; and Bayer Crop Science Limited; National Seed Association of India (NSAI); ACSEN Agriscience (P) Limited (ACSEN); and SeedWorks International (P) Limited whose contributions were instrumental in facilitating this event including the financial support.

We express our heartfelt thanks to the session chairpersons, speakers both from public and private sector organizations, authors and participants for agreeing to participate in the event and making valuable contributions included in this publication. Their expertise will enrich the symposium and make it a resounding success for which we express our sincere appreciation.

Core Organizing Committee

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Technical Session I

Hybrid Crops Research and Development – An overview

- **Extended Summaries of Keynote and Invited Presentations**

TS-I-KP-01

Accelerating hybrid crop breeding: CIMMYT's experiences and general perspective

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Plant breeders are now faced with a strong challenge: ensuring food and nutritional security while reorienting breeding strategies for greater efficiency, increasing genetic gain, and producing more with lesser natural resources. Exploiting heterosis, together with integration of modern breeding tools/approaches, including doubled haploidy (DH), molecular marker-assisted selection, and genomic selection/prediction, are integral to modern maize breeding programs. In addition, evolution of experimental designs, quantitative genetic methodologies, and breeding data analytics is facilitating use of sparse testcrossing and sparse phenotyping in CIMMYT's maize breeding pipelines in Africa, Asia, and Latin America.

CIMMYT's tropicalized haploid inducers with high haploid induction rate (10-13%) using marker-assisted breeding have been widely disseminated and being used globally to accelerate hybrid breeding. CIMMYT has also established centralized platforms offering maize DH development service to CIMMYT breeders as well as NARES and SME seed companies in Africa (at Kiboko, Kenya), Latin America (at Agua Fria, Mexico), and Asia (at Kunigal, India). Over 80% of lines used in CIMMYT's maize breeding pipelines are DH lines. The CIMMYT-operated Maize DH Facility at Kunigal, India, have developed and disseminated over 20,000 maize DH lines to the national maize breeding programs in India within the first two years of its operations. At CIMMYT, increasing genetic gains by using DH in combination with breeder-ready markers for specific traits, and rapid-cycle genomic selection for complex trait improvement have enabled shortening of the time required for recycling elite lines in breeding pipelines.

Hybrid seed production requires a scalable and cost-effective way of managing pollination between parents. Achieving commercially viable hybrid seed production is much easier in a crop like maize, while it remains challenging for many self-pollinating crops (e.g., wheat and rice despite their potential and decades of research. The potential avenues include a) reducing breeding costs by increasing the efficiency of breeding programs (e.g., speed breeding, heterotic grouping, recurrent population improvement, genomic prediction); b) rendering the seed production process cost-effective by improving the scalability of existing male sterility systems; and c) generating hybrid varieties with higher and more stable yields across multiple diverse environments. In maize, several recent studies have shed new light on the regulation of cytoplasmic male sterility (CMS) and indicate potential molecular targets for hybrid breeding. CIMMYT is also partnering with Corteva in Africa on a novel seed production technology for hybrid maize, based on *Ms44*-based genetic male sterility system.

Genome editing could facilitate further acceleration of hybrid breeding by generation of mutant male sterile lines (e.g., in crops like maize, rice, wheat, sorghum, tomato), induce haploid formation (e.g., in sorghum, tomato, rice, wheat, carrot, cabbage) and by use of apomixis for the clonal propagation of elite hybrids (e.g., in rice). As we gain increasing insights on the molecular bases of heterosis, including heterosis-associated genes and mechanisms in crop plants like rice, maize, and tomato, the optimal haplotypes that dosage-sensitively balance the crop maturity, plant height, and grain yield could be created or assembled by genome editing in the future.

Predictive breeding started in the 1930s when superior double-cross maize hybrids were identified based on the mean of the four nonparental single crosses. The advent of recurrent selection in the 1940s led to methods to predict the mean of the next cycle of selection. The shift to single-cross hybrids in the 1960s necessitated methods to predict their performance. Genomic best linear unbiased prediction (GBLUP) was developed in 1994 for predicting single-cross performance for yield and other agronomic traits. In the 1990s, rapid-cycle recurrent selection with molecular markers led to the use of multiple regression for predicting the performance of individual plants undergoing selection. With Meuwissen *et al.*'s (2001) landmark article on genome-wide selection, prediction methods shifted from multiple regression with fixed marker effects to ridge regression and Bayesian models with random marker effects. Over the last 7-8 years, CIMMYT published a series of research articles on rapid-cycling genomic selection (RCGS) in both biparental and multiparent populations and mainstreamed the strategy in breeding pipelines. Very few institutions in India have so far utilized the power of predictive breeding. This capacity needs to be rapidly ramped by overcoming various limitations, including: (a) lack of well-defined breeding schemes; (b) limited funding to cover genotyping costs; (c) awareness about when and how to apply genomic prediction; (d) lack of computational expertise, etc. There is also tremendous scope to strengthen data management and analytics, besides application of deep/machine learning capacities to dynamically process large datasets (phenotypic, genotypic, pedigree, environmental, and farmers' management) to effectively aid selection decisions and product targeting.

Crop breeding institutions across the global south need to not only intensify efforts on breeding climate-resilient and nutritionally enriched hybrid varieties, but also ensure that these hybrid varieties are adopted by the resource-constrained smallholders. This warrants innovative public-private partnerships and product licensing models.

TS-I-IP-01

Hybrid crops research by private sector: recent advances

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The seed industry is undergoing a technological revolution, with advancements impacting every stage from research and development to market delivery. Private sector companies, both Indian and MNCs, are playing an increasingly important role in driving innovation in the seed industry. Their established research programs and significant investments in R&D are leading to:

- **Development of Advanced Technologies:** Funding the development and deployment of AI-powered breeding tools, automated phenotyping systems, and other cutting-edge technologies.
- **Breeding of Improved Varieties:** Developing new crop varieties with enhanced traits, such as disease resistance, drought tolerance, and improved yield potential.
- **Market-driven Innovation:** Focusing on developing varieties that meet the specific needs and preferences of farmers and consumers.

Some of the advances made by private seed companies in seed R&D are:

1. Breeding Innovation

- **AI-Powered Precision:** Artificial intelligence and machine learning algorithms are transforming plant breeding. By analysing vast datasets on plant genetics, environmental factors, and historical performance, AI can:
  - *Accelerate breeding cycles*: Predict the outcomes of breeding crosses more accurately, reducing the time and resources required to develop new varieties.
  - *Enhance genetic gain*: Identify superior genetic combinations and optimize breeding strategies for desired traits like yield, disease resistance, and drought tolerance.
  - *Improve decision-making*: Provide breeders with data-driven insights to make more informed decisions about which plants to select for the next generation.
- **The Human-AI Synergy:** While AI offers powerful analytical capabilities, human expertise remains crucial. Breeders' deep understanding of plant biology, field

conditions, and market demands is essential to guide AI models and interpret their results effectively. Private seed companies who have well established R&D Program employ highly experienced breeders and are leveraging the combined power of human intelligence and advanced technology.

2. Automated Phenotyping

- **High-Throughput Trait Analysis:** Traditional methods of measuring plant traits are time-consuming and labour-intensive. Automated phenotyping systems, incorporating robotics, computer vision, and machine learning, can:
    - *Increase efficiency:* Rapidly assess many plants for various traits, such as plant height, leaf area, and disease symptoms.
    - *Improve accuracy*: Minimize human error and provide more objective and consistent measurements.
    - *Generate comprehensive datasets:* Collect detailed information on plant growth and development over time, enabling a deeper understanding of plant performance.
- **Applications in Precision Agriculture:** Private seed companies with well-established research program are integrating automated phenotyping data with other data sources, such as weather and soil information, to optimize resource management in precision agriculture. This is leading to more efficient use of water, fertilizers, and other inputs, reducing costs and environmental impact making research program much more efficient and sustainable.

3. Remote Sensing and Drone Technology

- **Precision Crop Monitoring:** Drones equipped with sensors can capture high-resolution images and data on crop health, soil moisture, and other factors. This information can be used to:
    - *Monitor crop development*: Track plant growth, identify stress factors, and detect early signs of disease or nutrient deficiencies.
    - *Optimize irrigation and fertilization*: Apply water and nutrients precisely where and when they are needed, reducing waste and improving resource efficiency.
    - *Improve disease management*: Implement targeted disease control measures, minimizing the use of pesticides and reducing environmental impact.
- **Hybrid Performance Monitoring:** Private seed companies with well-established research program are using remote sensing to assess the performance of different crop hybrids in various field conditions, providing valuable data for breeding programs and seed selection.

4. Addressing Key Challenges

- **Weed Control in Rice:** The development of herbicide-tolerant (Ht) rice varieties is a significant breakthrough in weed control. These varieties, combined with the direct-seeded rice (DSR) technique, can:
  - *Reduce weed-related yield losses*: Significantly minimize the impact of weeds on rice production, leading to higher yields and improved farm incomes.
  - *Promote water conservation*: DSR can reduce water consumption compared to traditional transplanting methods.
  - *Enhance sustainability*: Reduce the reliance on herbicides, promoting more environmentally friendly farming practices.
- **High-Density Planting Systems for Cotton:** HDPS can increase cotton yields by maximizing plant density per unit area. However, it requires specific crop varieties with:
  - *Early maturity*: To ensure crop completion within the shorter growing season often associated with rainfed conditions.
  - *Compact plant architecture*: To facilitate optimal light penetration and air circulation within the dense canopy.
  - *Synchronous boll opening*: To ensure efficient harvesting and minimize yield losses.

Private seed companies with established research program are investing heavily in HPDS, HT Rice and DSR to provide a much better value proposition to farmers.

5. GM Crops in India

The Indian GM crop sector has experienced substantial growth, primarily fuelled by the successful commercialization of Bt cotton, which spurred increased private sector investment in agricultural biotechnology research and development (R&D). Indian companies are actively engaged in R&D efforts, adopting advanced technologies and exploring innovative breeding approaches to enhance crop productivity while addressing public concerns. Key Developments in Indian GM crop sector include:

- *Bt Cotton Success*: The widespread adoption of Bt cotton in India has significantly stimulated private sector R&D within the agricultural biotechnology domain. Private seed companies with established research program have responded by increasing R&D expenditures, modernizing their infrastructure, and developing in-house capabilities for genetic transformation.
- *GM Crop Imports*: Private Indian seed companies and public research institutions also possess import permits for various GM traits in rice, including insect resistance, herbicide tolerance, and abiotic stress tolerance.

- *Emergence of New Technologies*: Private Indian companies are actively embracing modern technologies such as RNA interference (RNAi) for developing traits that confer resistance to pests and diseases in key crops. Furthermore, collaborative research initiatives between domestic companies and public research institutions, are focused on developing disease-resistant traits in vegetable crops.
- *Growing Interest in Novel Breeding Techniques*: Private seed companies are increasingly interested in novel breeding techniques that can potentially mitigate public concerns associated with GM crops, particularly those stemming from the use of transgenes. These emerging techniques include marker-free plant transformations, cisgenesis, intragenesis, and genome editing.

Overall, the Indian GM crop sector is a dynamic landscape. Private seed companies are actively contributing to the field through R&D investments, technological advancements, and collaborative partnerships. The increasing focus on novel breeding techniques demonstrates a commitment to addressing public concerns and developing sustainable and innovative agricultural solutions.

Conclusion

The convergence of advanced technologies, such as AI, machine learning, robotics, and remote sensing, is transforming the seed industry. By embracing these innovations, the industry can accelerate breeding progress, improve crop productivity, enhance sustainability, and ensure food security for a growing global population. However, it is crucial to ensure that these technologies are developed and deployed responsibly, considering ethical and environmental implications.

Technical Session II

Germplasm Management for Hybrid Crop Breeding

- Extended Summaries of Keynote and Invited Presentations

TS-II-KP-01

Genetic resources for hybrid development

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Plant genetic resources (PGR) contribute significantly to multiple sustainable development goals of the United Nations, towards achieving food, feed, nutritional and environmental security. Diverse landraces, exotics and wild relatives of crops hold a wealth of genes/alleles which, if included in breeding programs, can help increase yield and enhance stress resilience of agronomically superior cultivars. Globally, 7.4 million accessions are conserved in more than 1,750 genebanks. However, scant use (<1%) of assembled germplasm in breeding programs is a major concern, as genetic bases of crop gene pools continue to be narrowed by intensive selection among small numbers of genotypes. Genetically uniform modern varieties and hybrids are often closely related and planted in large areas, making them vulnerable to new pests, diseases, climatic conditions, and changes in market needs. The main reasons for low use of genetic resources are the large size of collections and lack of reliable data on traits of economic importance, noting that such traits show high genotype x environment interaction and require extensive testing. These problems can be mitigated by developing 'core' (10% of entire collection, Frankel 1984) and 'mini core' (10% of core or 1% of entire collection, Upadhyaya and Ortiz, 2001) collections, sampling the diversity in a collection. Our research revealed that mini cores selected using phenotypic traits were as good as those based on simple sequence repeat DNA markers. In cross pollinated crops such as pearl millet it is important to consider both inter- and intra-accession variability in forming core/mini core collections. Mini core collections often meet the needs of plant breeders for variation in multiple traits. Mini core collections have been used for genome wide association studies and can be employed for combining ability studies for traits of economic importance. Systematic evaluation of mini core collections has resulted in identification of a number of germplasm lines with agronomically and nutritionally beneficial traits in addition to resistance/tolerance to abiotic and biotic stresses in both selfing (chickpea, groundnut) and outcrossing crops (sorghum, pearl millet) which can be used for developing agronomically superior varieties and hybrids. Use of diverse germplasm lines identified from a groundnut mini core resulted in developing exceptionally high oil (up to 63%, compared to ~48% in control cultivar) and high-yielding breeding lines, indicating that new germplasm sources contribute to enhancing genetic gains. Systematic and sustained efforts are required to infuse diversity from wild relatives. Groundnut TxAG 6, an amphiploid developed in 1993 has been successfully used to enhance 100-seed weight (up to 87 g, cultivated parent ~ 40g), pod yield (up to 27% more than cultivated) and drought tolerance components such as specific leaf area and SPAD chlorophyll meter reading. Similarly, in sorghum, recombinant inbred lines of *S. bicolor* x *S. propinquum* were crossed as pollen parents with four cultivars, Teshale, Macia, Lata and BTx 623. Hybrids flowered earlier and 15 of them yielded more (up to 22%) than the elite parent (BTx 623). One RIL, 234, which has 75% of *S. bicolor* and 25% *S. propinquum* alleles, increased seed yield in F_1 combinations with all four cultivars. This was not an artifact of poor yield of the RIL itself, as 234 was among the highest yielding RILs.

TS-II-IP-01

Hybrid-oriented source germplasm for improvement of hybrids

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Sustaining crop productivity with impending changing climate is a challenge for crop researchers across the globe especially India, where there is a need to increase production to meet the energy and nutritional requirements of our ever-growing population. As there is no option to increase the area under cultivation for increasing the production, developing nutritionally enhanced crop hybrids adapted to various stresses is a viable option for improving productivity with enhanced quality. This necessitates prospecting germplasm, mapping traits and its introgression through judicious use of genetic and genomic resources. Landraces are genetically dynamic and display equilibrium with the environment and the stresses prevailing an eco-geographic region. Crops are endowed with diverse germplasm and landraces possessing unique traits including genetic variability for plant architecture, biotic/ abiotic stresses and grain quality traits. Prospecting germplasm is important to identify genotypes possessing valuable alleles for plant type, resistance to stresses as well as for grain and nutritional quality. The wealth of genomic resources in different crops such as rice, maize, pearl millet, pigeon pea, Indian mustard and wheat not only aids in mapping the QTLs/ gene(s) governing the useful traits through GWAS/ linkage mapping but also mine novel valuable alleles governing the target traits. Through effective integration of genetic and genomic resources, useful donors for plant type, tolerance/ resistance to abiotic/ abiotic and nutritional quality traits in crops been identified from the germplasm. The assessment of the germplasm has been helpful in identification of unique variations which have been validated and utilized in improvement of parental lines in crops. Molecular breeding is a valuable strategy for development of hybrid-oriented source germplasm, which have been used for development of elite parents, which in turn can help in improvement of hybrids in crops. The effective utilization of genetic resources has enabled development of elite parents with unique plant architecture, tolerance/ resistance to abiotic/ biotic stresses, enhanced grain and nutritional quality, which can help in sustaining crop production and profitability. Progress in developing hybrid-oriented germplasm in rice, maize, pearl millet, pigeon pea, Indian mustard and wheat and its prospects in improvement of hybrids in these crops will be discussed with examples.

TS-II-IP-02

Consortia approach for germplasm improvement and hybrid development in South Asia

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Background

Crop breeding is one of the key pillars for agrifood research and development institutions to make an impact. Breeding is important for ensuring food security by developing new varieties that are nutritious, higher yielding, disease resistant, drought and heat tolerant, and regionally adapted to different environments and growing conditions. For plant breeding to succeed, rigorous breeding and testing pipelines are required. In classical line breeding, the breeding workflow starts by creating variability from which the selection is operated; the advanced lines are sequentially evaluated through hierarchical stages from within the breeding programs on-station, and downstream into Multi-Environment Trials i.e., METs. The METs are the *sine qua non* testing step allowing the breeder to assess the adaptability of the plant materials to the target production environments. In India, superior products from METs are nominated for on-farm evaluation for state-wise release purposes, and All India Coordinated Research Project (AICRP).

Major Challenges and Proposed Strategy

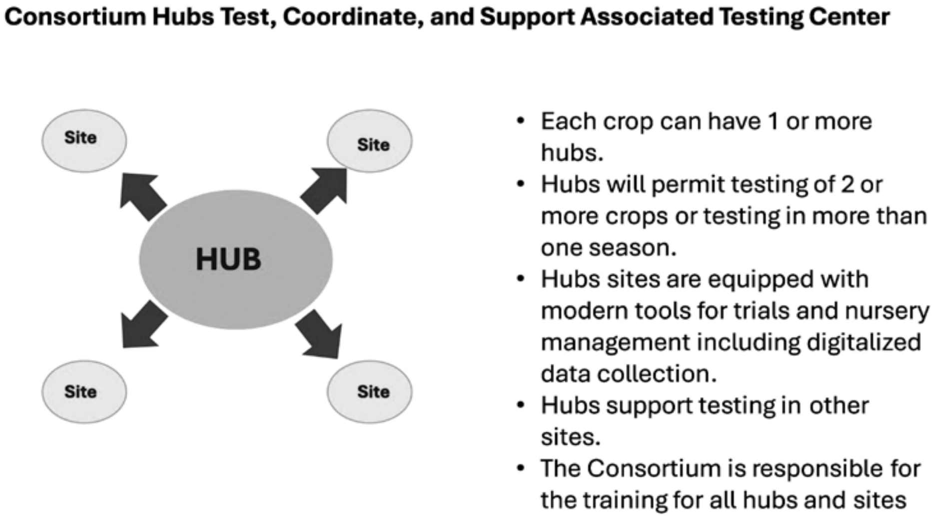
In cultivar development, international and national agricultural research systems (NARS) collaborate for variety release. However, the collaboration is currently mainly in terms of materials exchange, particularly through the Hybrid Parents Research Consortium platform. To run METs individual breeders rely on personal relationships with some NARS, some private companies, and some agricultural universities. Such collaboration is not sustainable because it depends on the availability of resources and the priorities of the moment at the NARS end. On the other hand, NARS partners have long experience in extension research and would provide reliable data, but they lack the resources and technology to run the trials appropriately, and they do not have technicians to monitor and phenotype the trials. The consortium should therefore agree and deliberate on the modalities for supporting NARS and for the functioning of the reciprocal responsibilities of the consortium members.

Consortium Design

A sound strategy for population improvement should be put in place to cyclically improve the germplasm as a source of the future superior line varieties and parental lines of future superior hybrids. Early generation recycling should be the rule in order to shorten the breeding cycle and increase the genetic gain (GG). Sparse testing using genomic prediction can be efficiently used for this purpose and for increasing the number of testing environments while maintaining selection intensity in the early yield testing stage without increasing the breeding budget. Sparse testing leverages information generated within and across environments, and hence its accuracy in METs relies heavily on genetic correlations between environments and genomic relationships of lines across environments. GBLUP is currently viewed as the best predictor of true breeding value, and can therefore be used as a selection decision metric in the early yield testing stages, and for advancement decisions by breeding programs. The GG (expected and realized) should be one of the major KPIs to measure the success of the Consortium. To evaluate the realized GG, the consortium should adopt a good strategy to maintain connectivity among checks across years. The identification of target population of environments (TPEs) and testing hubs (Fig. 1) within consortium's TPEs and standardizing yield testing protocols will significantly improve the data quality and the power of decision making to achieve a higher rate of genetic gain.

Expected Outcomes from the Consortium

(1) Creation of an extension research platform for varietal release, and evaluation of GG and the efficiency of crop breeding research programs. (2) Improved genetic gain for the crop species of interest. (3) Enhanced collaboration breeding R&D instittutions in India and outside of India (Fig. 2). (4) High-quality data (high repeatability) across institutions' METs. (5) Sustained release of superior varieties statewide, across India, and outside of India.



Consortium Hubs Test, Coordinate, and Support Associated Testing Center

- Each crop can have 1 or more hubs.
- Hubs will permit testing of 2 or more crops or testing in more than one season.
- Hubs sites are equipped with modern tools for trials and nursery management including digitalized data collection.
- Hubs support testing in other sites.
- The Consortium is responsible for the training for all hubs and sites

Figure 1. *Consortium hubs design for producing quality data*

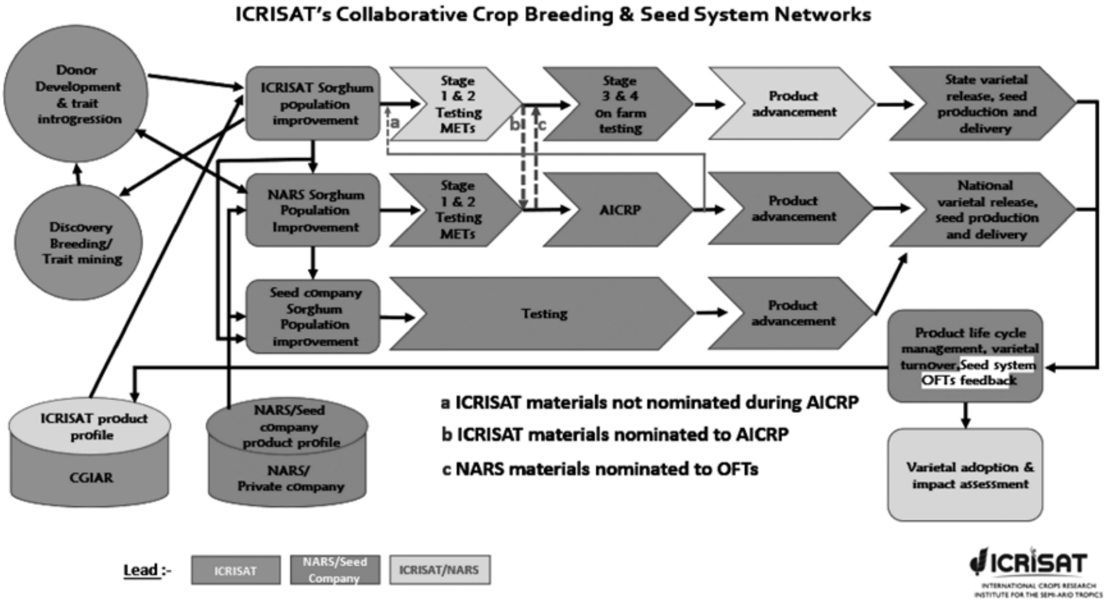


Figure 2. *Collaborative Crop Breeding and Seed Systems Networks*

Technical Session II

Germplasm Management for Hybrid Crop Breeding

- Abstracts of Rapid Oral Presentations

TS II-OP-01

Development and Characterization of *lpa1* and *lpa2*-based low phytate double mutants for kernel quality, yield, and agro-morphological traits for utilization in low phytate maize hybrid breeding

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Reducing phytic acid is crucial for enhancing micronutrient bioavailability. Low phytate maize hybrids can sustainability alleviate micronutrient malnutrition by enhancing the bioavailability of Fe and Zn. This study aimed to develop and characterize *lpa1-1* and *lpa2-1*-based low phytate double mutants for their potential utilization in hybrid breeding. Seven *lpa1-1* and *lpa2-1*-based NILs were intercrossed to generate double mutants (*lpa1/lpa2*) which were then evaluated for grain quality, yield, and agronomic performance for two seasons. ANOVA revealed wide genetic variation for phytic acid, inorganic phosphorus, grain yield, and agronomic traits with lesser contribution of G × E interactions. Phytic acid reduction in double (*lpa1/lpa2*) mutants (41%) was more than the *lpa1* (36%) and *lpa2* (30%) alone. Phytic acid content of double mutants (1.73 mg/g) was much lower than wild-type lines (2.92 mg/g). Double mutant lines were comparable to wild-type lines for grain yield and agronomic traits indicating no adverse effects of combining two mutations into a single genetic background. The mean plant and ear height of double mutants was 167 cm and 68 cm. Similarly, for days to male and female flowering, double mutants (56 and 58 days) performed statistically similar to the wild-type lines. Average grain yield of double mutants (2775 kg/ha) was at par with grain yield of wild type lines (2807 kg/ha). Across different genetic backgrounds and seasons, PMI-PV5 recorded highest grain yield. The newly developed double mutants are potential genetic resources for low phytate hybrid breeding as they have greater reduction in phytic acid and similar grain yield and agronomic performance. This is the first report of low phytate double mutants in maize for improving nutritional quality of food and feed.

TS II-OP-02

Expanding the arsenal of male sterile germplasm for accelerating hybrid pigeonpea research and breeding

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The exploitation of hybrid vigour could overcome the barriers plateauing yield gain in pigeonpea. In this context, cytoplasmic male sterility (CMS) has demonstrated to be an excellent genetic mechanism to control pollination for commercial production of hybrid seed. Recently, researchers at ICAR-Indian Institute of Pulses Research (IIPR), Kanpur have developed two short-duration pigeonpea hybrids (IPH 09-5 and IPH 15-03) using CMS technology. Diversity of CMS lines and their stable fertility restoration is an essential prerequisite for harnessing the potential of heterosis or hybrid vigour. To enhance the availability of diverse CMS lines in pigeonpea, we attempted a number of crosses to combine the organelle genomes of a pollen-sterile seed parent with the nucleus of a pollen-fertile pollen parent i.e. elite agronomic bases. After five backcrosses (BC5F1), the standard practice of introducing a sterility-inducing cytoplasm to different genetic (nuclear) backgrounds could recover lines that carry only 1.6% nuclear genome of the original pollen-sterile seed parent and more than 98% nuclear genome of the recurrent pollen-fertile parent while retaining the sterile pollen phenotype in each generation. By following this standard practice, we have developed a set of 14 new CMS lines viz. Pusa 992A, AL 201A, ICPL 7148A, Pusa 2002-2A, MN 5A, PAU 881A, ICPL 20340A, ICPL 88034A, ICPL 11244A, ICPL 11301A, ICPL 20325A, ICPL 20326A, ICPL 20327A and ICPL 20329A. Except Pusa 992A with *Cajanus cajanifolius* (A4) cytoplasm, all CMS line carry *Cajanus scarabaeoides* (A2) cytoplasm. The CMS lines ICPA 2089 (A4), ICPL 88039A (A2) and GT 288A (A2) were used as cytoplasmic donors in the backcross scheme. All CMS lines have attained homozygosity with complete pollen sterility and phenotypic stability. Except pollen sterility trait, the newly developed CMS lines have retained almost all phenotypic traits of the recurrent parent. Non-functionality of the pollen has been confirmed by visual inspection and a variety of pollen-staining techniques. We have also identified potential restorers (R-lines) of these lines to demonstrate their immediate utility in the pigeonpea hybrid research and breeding.

TS II-OP-03

Development of popcorn DH lines for augmenting popcorn germplasm base and development of high yielding popcorn hybrids

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In the past few decades, popcorn has emerged is an important cash crop in India and area under popcorn cultivation has seen a progressive increase. The seed market however is dominated by foreign-bred varieties, though public-bred popcorn hybrids are gradually beginning to make their presence. Popcorn germplasm is inherently narrow and lack of dedicated breeding programmes to augment the indigenous popcorn germplasm base have left the public breeding programmes with very limited superior germplasm for use in the development of high yielding popcorn hybrids with desired consumer quality traits. Concerted efforts therefore need to be undertaken for expeditious augmentation of indigenous popcorn germplasm employing different breeding approaches.

Doubled haploid (DH) lines, completely homozygous lines that can be produced in substantially less time than conventional inbreds, are a quick means of enriching genetic diversity in hybrid breeding programs. In maize, *in vivo* maternal haploid induction is the most widely used method of generating DH lines on account of operational ease. Development of field corn, sweet corn and biofortifed corn lines is being widely undertaken in major breeding programs worldwide both is public- and private-breeding programs. However, use of doubled haploidy for developing popcorn DH lines has not yet received much attention. The present study reports development of popcorn DH lines using two public-bred popcorn hybrids (LPCH-3 and LPCH-4) as the source populations. A total of 87 DH lines derived from the two source populations were evaluated for important agronomic and quality parameters. The popular popcorn composite VL Amber Popcorn was used as the check. The developed popcorn DH lines exhibited significant variation for important agronomic traits [maturity days (95.2-105.6), plant height (90.8-185.6), cob length (11.2-18.2), cob girth (8.5-10.6), test wt. (134.2-152.6)] as well as quality parameters such as popping percentage (73-99) and expansion ratio (10.3-28.9).

The variability exhibited by popcorn DH lines used in this study will significantly contribute to broadening and diversifying the existing popcorn germplasm pool. The DH lines showing superior performance for popcorn traits will be useful as donors and for synthesizing new source populations for developing superior popcorn DH lines in future. DH lines showing performance comparable to or better than the check may be of direct use in popcorn hybrid development programs.

TS II-OP-04

Mapping BMR trait and introgression into different genetic backgrounds for developing low lignin and high biomass pearl millet genotypes

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The brown midrib (bmr) mutants are associated with reduced lignin content in pearl millet and other C4 grasses, as they modify the lignin biosynthesis pathway. This reduction in lignin content, in turn, improves in vitro dry matter digestibility (IVDMD) and enhances milk production in cattle. Since the bmr gene(s) is recessive and exhibits pleiotropic effects, identifying markers linked to this gene will facilitate marker-assisted selection. The F5 mapping population was developed by crossing two contrasting parents, ICBbmr07 (the bmr mutant) and ICBP19 (the non-bmr mutant). A bulk segregant analysis approach was used, where 660 SSR primers were screened, and 99 SSR markers showed polymorphism between the parents. Further screening of these 99 SSR markers in the parents and the bmr and non-bmr bulks revealed that one marker, *Xpsmp* 2077, showed polymorphism between the parents and the bulks. SSR marker *Xpsmp* 2077 is located on linkage group 2 and was validated for its association with the bmr trait through selective genotyping in the F5 mapping population. This marker effectively differentiated bmr and non-bmr lines in the mapping population. Furthermore, this marker was used for screening and selecting segregating generations developed by crossing bmr lines with high biomass-yielding cultivars such as Moti bajra, Giant bajra, Baif bajra 1, and IP2269. Using this approach, we generated S2 generation bmr lines in the background of high forage-yielding genotypes. The selected diverse S2 generation bmr lines were then crossed to develop composites of bmr pearl millet OPVs with high biomass and improved regrowth ability. This is the first report of mapping the bmr gene in pearl millet. Through marker-assisted selection, we can accelerate the development of high-biomass, low-lignin cultivars in pearl millet.

Technical Session II

Germplasm Management for Hybrid Crop Breeding

- ✦ Abstracts of Poster Presentations

TS II-PP-01

Development of sub-tropically adapted *indeterminate gametophyte1* (*ig1*)-based paternal haploid inducer line for CMS conversion in maize hybrids

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Doubled haploid (DH) technology has been an important tool for accelerating the development of inbreds in maize globally. The wild-type *Indeterminate gametophyte1 (Ig1)* gene functions as a Lateral Organ Boundaries (LOB) domain transcription factor in maize. While, its mutant allele (*ig1*) is a loss of function allele due to insertion of *Hopscotch* transposable element in exon-1. When used as female parent, *ig1*-based haploid inducer (HI) lines induce paternal haploids with cytoplasm from maternal side. This phenomenon is a valuable tool for conversion of maize inbreds into its male sterile form. Such *ig1*-based paternal haploid inducer lines are available for temperate environment. There has been no report of such lines in subtropical background. Here, a *ig1*-based temperate lines were crossed with a set of sub-tropically adapted maize inbreds to develop F_2 populations. The segregating generations were genotyped using a functional marker (MGU-IG1-Hopscotch) to identify *Hopscotch* insertion in the mutant *ig1* gene. Severe segregation distortion was observed in all the F_2 populations. Majority of the identified *ig1ig1* plants showed male sterility. The fertile *ig1ig1* plants could be maintained and advanced by selfing. These newly developed *ig1*-based paternal haploid inducer lines possessed *R1-nj* gene for identification of haploids at seed level. These sub-tropically adapted *ig1*-based lines serve as an invaluable tool for rapid conversion of maize inbreds to their CMS form, thereby accelerating the hybrid breeding program.

TS II-PP-02

Exploring variability in LOX activity to enhance germplasm for developing rancid-free high-oil maize hybrids for superior bioavailability of fat-soluble vitamins

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Increasing the oil content in maize kernels is essential for enhancing the bioavailability of fat-soluble vitamins. Recent breeding programs have focused on developing maize hybrids with increased oil content and multi-vitamin biofortification. However, the endogenous enzyme lipoxygenase (LOX) oxidizes the pentadiene motif in free fatty acids, undermining the goal of achieving high oil content and, consequently, the enhanced bioavailability of fat-soluble vitamins. Genetic variation in a favorable direction for lipoxygenase activity in the parental inbreds is a prerequisite in developing low- or non-rancid maize hybrids to realize improved bioavailability. Therefore, this study has analyzed the lipoxygenase activity among a set of 48 maize inbreds through spectrophotometric analysis using linoleic acid as a substrate at optimum pH. Parental maize inbreds possessing favorable alleles for various fat-soluble vitamins such as *crtRB1*, *lcyE*, and *vte4* and oil content such as *dgat1-2* and *fatb* have revealed significant variation for kernel lipoxygenase activity which dispersed from lower to higher extreme. Our study suggests that future investigations into favorable haplotype variation in the alleles of lipoxygenase genes, using sequencing-based allele mining techniques, could facilitate the development of superior parental inbreds. These inbreds could then be combined to create improved maize hybrids with enhanced bioavailability of fat-soluble vitamins, which play a crucial role in addressing malnutrition through food and feed, thereby contributing significantly to global nutritional security.

TS II-PP-03

Identification of specific combining inbred lines under coastal ecological conditions

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In a study on 44 crosses along with parents evaluated for combining ability revealed significant differences through analysis of variance for combining ability by parents *vs* crosses for all the traits indicating the presence of variability in the genetic material. Out of 44 crosses, significant high *sca* effect in desirable direction was recorded by the cross PI 14 x LM13 for ear length, and grain yield plant-1; PI 303 x LM13 for kernel rows ear-1 and ear placement height; PI 9 x CL02450 for 100-kernel weight; PI 8 x CML451 for protein content and PI 215 x CML451 for grain yield per plant. The high *sca* effects for most of the crosses were resulted due to parental *gca* combinations with low x low, high x low and low x high. The ratio of GCA variance to SCA variance for most of the traits was less than unity indicating the predominance of non- additive gene action whereas, it was more than unity for days to 50% silking, plant height and no. of kernels/row indicating the predominance of additive gene action in the inheritance of these traits. Parents PI 9 exhibited significant *gca* effect in desirable direction for days to 50% anthesis, days to 50% silking, days to maturity; PI 21 for ear height, 100 kernel weight, grain yield per plant and PI 8 for ear length, kernel rows ear-1 and no. of kernels/row in desirable direction. Among the testers, LM13 recorded significant high *gca* effect in desirable direction for the traits *viz*., days to 50% anthesis, days to 50% silking, days to maturity; CML451 for plant height, grain yield per plant; CL02450 for ear height, kernel rows/ear and CML581 for 100-kernel weight.

TS II-PP-04

Mapping phenomic variability for yield attributing & quality traits in saffron (*Crocus sativus* L.)

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Saffron (*Crocus sativus* L.) is a prime spice harvested from flowers of stigmas from crocus species. The investigation comprised of 264 saffron germplasm clones laid out in an augmented block design during Kharif, 2021 at ARSSSS, SKUAST-Pampore, J&K. Observations were recorded for different agro morphological and quality traits included crocin (%), safranal (%) & picrocrocin (%). The results indicated that highest coefficient of variation was recorded with respect to WDH (19.51) followed by weight of corm (15.14) while lowest was recorded in quality parameter, crocin (2.93). Heatmap plot revealed the overall phenotypic diversity present in the available saffron germplasm with respect to different quantitative traits and it was found that crocin content (%) had significant variability as compared to other traits like picrocrocin, safranal, leaf length and WDH. Phenotypic traits like NFPC, NLPC and WC revealed marginally very low range of variability. The principal component analysis identified first 4 component characters with a eigen value greater than one explaining cumulative variance of 64.01 per cent of the total variance. The remaining 5 components contributed 35.99 % of total variation. PCA contribution revealed that PC1 with a high positive loading for NFPC (0.882) and PC2 with a highest positive loading for WC (0.595) followed by WDH (0.551). Phenotypic variability was highest for crocin content followed by safranal and picrocrocin. Based on the results, the identified elite genotypes exhibiting high saffron yield and better quality could be used in the saffron breeding program for the development of saffron varieties.

TS II-PP-05

Determination of the critical stage for the fertile-sterile phase in rice TGMS lines under a controlled environment

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The rapidly increasing population and the continuous decrease in rice-growing areas have created pressure to increase rice production and productivity. The use of hybrid rice has proved to be an effective and economical way to increase rice productivity. Thermo-sensitive genic male-sterility (TGMS), does not require the third line for sterile line production, as the same genotype can alter sterility and fertility phases depending on the environment is exposed. These systems are simple and effective for production of hybrid seed in rice. Here, we aimed to determine the critical temperature for sterile-fertile phases in 10 TGMS lines. The ten TGMS lines were planted in growth chambers, each subjected to varying conditions of low and high temperatures. The different temperature regimes to which lines were exposed were: 17-22°C (12 h), 19-24°C (12 h), 21-26°C (12 h), 23-28°C (12 h), 25-30 °C and ambient temperature. We found that the critical stage for most of the TGMS lines expressed normal fertility at low temperatures and variable sterility at high temperatures. TGMS lines Pusa 119s, Pusa 125s, Pusa 129s, Pusa 182s, Pusa 209s, Pusa 210s, Pusa 212s, Pusa 240s, Pusa 1s, and Pusa 28s were identified to have critical sterility point (CSP) at a mean temperature of above 28°C. These lines showed complete sterility at a high temperature. Critical fertility point (CFP) of the lines ranged between 19 to 21 °C. A narrow band of sterile-fertile phase was found among five lines, while five other lines had broader temperature band. The stability of these lines for fertility-sterility suggested their potential utilization in hybrid seed production in rice. Evaluating TGMS lines using this new strategy was found to be more stable in terms of sterility expression and these lines can be effectively used to increase the overall productivity of rice.

TS II-PP-06

Genetic variation of folate composition and accumulation pattern in developing kernels of maize (*Zea mays* L.) inbreds

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Humans require folate (vitamin B9) for proper growth and development. Folate deficiency (FD) has emerged as a global problem in both developing and underdeveloped countries, resulting in major health issues such as neural tube defects. The recommended daily folate intake is 400 µg for individuals and 600 µg for pregnant women. The biofortification of natural folates in maize, a folate-poor crop, provides a practical and sustainable strategy. In the present study, 48 maize inbreds were evaluated for folate and its major derivatives, at three stages of kernel development-15, 30, and 45 days after pollination (DAP). ANOVA revealed significant variability for 5-methyltetrahydrofolate (5-MTHF), 5-formyltetrahydrofolate (5-FTHF) and total folate content among the genotypes, across the different stages of kernel development, highlighting strong genetic control over folate accumulation. The mean folate content across the stages was 75.0 µg/100g, ranged from 22.7(PMI-PC101) to 133.1(PMI-SWT016) µg/100g. Folate levels of genotypes exhibited a declining trend throughout kernel development stages (15 DAP: 96.3 µg/100g, 30 DAP: 71.6 µg/100g, 45 DAP: 56.9 µg/100g). Significant effects of genotype, DAP stage and genotype × DAP stage interactions were observed for 5-MTHF, 5-FTHF and total folate content. The high folate lines identified such as PMI-SWT016, PMI-PV7, MGU213wx, PMI-SWT020 and MGU203W can be used as donor lines for maize folate biofortification programmes. This is the first research effort in the country dealing with characterization of the maize genotypes for folate accumulation.

TS II-PP-07

Evaluation of inbred lines and F_1 hybrids of periwinkle (*Catharanthus roseus* (L.) G. Don) for their growth and flowering characteristics

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Periwinkle is a widely recognized herbaceous plant. While it is valued for its medicinal properties, its potential as an ornamental plant has been somewhat underexplored. Despite its limited ornamental use, periwinkle has significant promise as a valuable flowering annual, particularly in tropical and subtropical climates. This study aimed to evaluate the growth and flowering characteristics of periwinkle to explore its suitability as an ornamental crop and contribute to the development of improved cultivars for commercial use. Eight distinct inbred lines with unique plant characteristics and flower colours (Magenta with white centre, Magenta, Cherry Pink, Peach, Purple, Pink with dark pink centre, Light Pink with white centre, and White with red spot) were selected for this study. The inbred lines were then crossed in a half-diallel mating design, resulting in the production of twenty-eight F1 hybrids, which were evaluated for various growth and flowering parameters. The results of the study demonstrated that the F_1 hybrids exhibited superior performance over the parental lines in several important growth and ornamental traits. Notably, the F1 hybrids flowered earlier, had a longer flowering duration, and produced more flowers per plant. In addition, the plants were taller and spreading, number of flowering branches was increased and the flower diameter was larger in the hybrids compared to the parental lines. These enhancements are particularly valuable for ornamental plant breeding, as they contribute to a longer blooming period, a key characteristic for ornamental plants used in landscaping and decorative purposes. The increased number of flowers per plant and the larger flower size make the F_1 hybrids more visually appealing and suitable for use in gardens and as potted plants. The findings of this study offer important insights into the ornamental potential of F_1 hybrids of periwinkle. This study thus contributes to expanding the potential use of periwinkle beyond its medicinal applications, offering new possibilities for its commercial and decorative use.

TS II-PP-08

Molecular screening of bacterial blight resistance genes in improved CMS line of rice

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Hybrid rice can substantially enhance rice productivity. To realize the actual potential of hybrids , incorporating resistance to major biotic and abiotic stresses as well as acceptable grain quality is vital. In Punjab, the hybrids have a great scope but limited area because of their susceptibility to bacterial blight, false smut, non-acceptable milling quality and lodging. Thus, there is a need to develop improved parental lines with bacterial blight (BB) resistance and desirable grain quality. BB , caused by *Xanthomonas oryzae* pv. *oryzae*, is one of the most destructive diseases threatening rice production. Presently, there are 10 pathotypes of BB prevalent in Punjab and none of the CMS lines is resistant to all the pathotypes. Earlier studies have indicated that single gene might not be effective in controlling the pathogen. Therefore, pyramiding of BB resistance gene(s) in parental lines of hybrid rice is important for developing hybrids with durable resistance.

An elite breeding line, PAU5942-1-1-1-1-1-1 possessing BB resistance genes *viz*., *Xa*4, *Xa* 21 and *Xa*38 was crossed with maintainer line PCMS16B (susceptible to BB) for transfer of BB resistance genes using marker assisted backcross breeding. A set of 183 BC4F4 derived lines from the above cross were selected on phenotypic basis for molecular characterization of BB resistance genes during 2022-23. These lines were screened for the presence of *Xa*4, *Xa*21 and *Xa*38 using gene specific markers i.e. MP4, pTA248 and Os04g53050-1, respectively.

The results of molecular analysis showed that out of 183 lines tested, 156 lines had *Xa*4 gene, 26 lines had *Xa*21 gene and 31 lines had *Xa*38 gene. The gene combination *Xa*4+*Xa*21 was present in 21 lines; *Xa*4+*Xa*38 in 26 lines and *Xa*21+*Xa*38 in 5 lines. The three gene combination (*Xa*4+*Xa*21+*Xa*38) was present in four lines. Developing CMS lines with three resistance genes will offer broad resistance to bacterial blight, aiding in the creation of BB-resistant hybrids using various restorers.

TS II-PP-09

Heterotic grouping of germplasm lines using diversified testers in maize

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Narrow genetic base is one of the most important limiting factors for yield improvement and is a bottleneck in any of the breeding programs. Information on heterotic groups is very useful in inbred line development and help breeders to utilize their germplasm in a more efficient and consistent manner through exploitation of complementary lines for maximizing the outcomes of a hybrid breeding programme. Maize, being a highly cross-pollinated crop, heterosis exploited to a great extent. Development of highly heterotic hybrid is dependent on the choice of parents that combine well and this step is very crucial. The selection of parents can be aided by heterotic grouping of germplasm, where in genetically diverse groups are established.

The experiment was conducted at Agricultural Research station, PJTAU, Karimnagar during *Kharif*, 2021 ,*Rabi,* 2021-22 and *Kharif*, 2022 to classify newly developed inbred lines into different heterotic groups. The experimental material included 134 single cross experimental hybrids obtained by crossing 68 lines with two opposite heterotic group testers, viz., LM-13 and LM-14 in L × T fashion during *Kharif,* 2021 and evaluated in *Rabi,* 2021-22, along with lines and testers for grain yield . Heterotic grouping was done based on HSGCA (heterotic group specific general combining ability) proposed by Fan *et al.* (2009).

During *Rabi,* 2021-22, 134 single cross hybrids along with 68 lines and two testers were evaluated for grain yield. Based on HSGCA method classified lines into three distinct groups (A, B and un known group). Twenty seven lines were common in group A (LM-13 group) and 25 inbreds in B group (LM-14 group) and remaining lines in un known group . This study successfully classified inbred lines into heterotic groups based on their combining ability. The resulted heterotic groups, each with unique genetic characteristics and combining ability patterns. These groups can be used to develop high yielding and superior hybrids, exploiting heterosis to improve maize production.

TS II-PP-10

Combining ability analysis and heterotic grouping of medium maturity field corn inbreds under non-stress and drought stress environment

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Maize is the third important cereal crop in India used for food, feed, fodder and biofuels. Among abiotic stresses drought is one of the serious stress that greatly affect the production and productivity of maize. Combining ability analysis and heterotic grouping of germplasm is an effective breeding tool to classify germplasm and identify heterotic parents to develop high yielding maize hybrids and also to identify source germplasm for further breeding programme of drought stress tolerance. A set of 306 experimental hybrids generated by crossing 103 medium maturity maize inbreds with two diverse testers LM 13 and LM 14 in line × tester design along with four commercial checks was evaluated under non-stress and under managed drought stress environment during Rabi 2020-21 and 2021-22 at RMR&SPC, Begusarai. Forty-three inbred lines under drought stress and 41 inbreds under non-stress showed positive and significant General Combining Ability (GCA) effects for grain yield. Fifty-six hybrid under drought stress and 46 hybrids under non-stress showed positive and significant Specific Combining Ability (SCA) effects for grain yield. Based on Mean, GCA and SCA 41 inbreds in heterotic group "A" and 45 inbreds in heterotic group "B" under drought stress and 17 in group "A" and 36 in group "B" were classified. On the basis of HSGCA, 57 inbreds in heterotic group "A" and 43 inbreds in heterotic group "B" under drought and 37 in group "A" and 26 in group "B" under non-stress were grouped. Inbreds in both the groups were ranked based on HSGCA value and top ten inbreds in each heterotic group were selected to constitute a heterotic base population for extraction of next generation drought stress tolerant maize inbred lines. The top ranking inbreds in each heterotic group may be utilized to develop heterotic hybrids for non-stress and drought stress environment.

TS II-PP-11

Exploring genetic variability for waterlogging tolerance related traits in early-generation maize

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Climate change has increased the frequency of abiotic stresses, such as waterlogging (WL), caused by heavy, unpredictable rainfall in compacted soils. Waterlogging is a severe abiotic stress that adversely affects the growth and yield of maize (Zea mays L.). To breed waterlogging-tolerant maize hybrid, understanding genetic variability for WL tolerance traits in source germplasm is critical. This study, conducted at Punjab Agricultural University, Ludhiana, involved two experiments to evaluate F_2:$_3$ maize populations (derived from WL tolerant and WL susceptible line) for physiological and root traits in pots and yield-related traits in the field giving WL treatment for a week at V_{4-5} stage. The aim was to decipher variability for waterlogging-tolerant traits viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance (GA) and selection potential. In Experiment I, traits as root dry weight (RDW), shoot dry weight (SDW), root surface area (RSA), and root diameter (RD) exhibited high heritability and genetic advance, making them promising for improving waterlogging tolerance lines in later generation. Traits like chlorophyll content before treatment in potted plants (CCBT-P) and chlorophyll content after treatment in potted plants (CCAT-P), which showed lower heritability, require further investigation. In Experiment II, yield-associated traits like ear height (EH), plant height (PH), and ear yield (YLD) demonstrated moderate to high heritability, making the lines suitable for selection in breeding programs. Although waterlogging tolerance coefficient (WTC) showed lower heritability, it may still be enhanced under specific conditions. The study emphasizes prioritizing traits with high genetic potential to develop waterlogging-tolerant maize varieties, bridging productivity gaps, and ensuring sustainable maize farming in waterlogging-prone areas in Northern regions of India.

TS II-PP-12

Phenotypic evaluation of fall armyworm resistance in F_2 maize populations: Unveiling the path to pest-resilient crops

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Maize production is hampered by a variety of issues, viz. biotic and abiotic stresses throughout the lifecycle. In the maize crop, about 250 species of insects and mites have been identified but spotted stem borer, shoot fly and pink stem borer are the most common pests, causing yield losses of 25-80 per cent in extreme cases. Fall armyworm (FAW), Spodoptera frugiperda (J.E. Smith) is a lepidopteran polyphagous, highly mobile and destructive pest. It causes significant damage to maize crops, leading to reduced yields and compromised quality. To start any breeding program, it is imperative to study genetics involved in the expression of various traits. For this, the development of different generations viz., F 1 and F 2. Three crosses have been made to study the genetics against FAW-related traits. Out of these crosses, one parent is resistant and the other is susceptible as CML71, CML67 and CML72 are tolerant to FAW and LM23 and EML 220 are moderately susceptible. The F_2 population mean generated from these crosses was analysed and found that the mean cob injury rating was higher for CML 71 X LM 23 (3.5) followed by CML72 X LM23 (2.4) and CML67 X EML220 (2.3). Most of these crosses shows continuous distribution curve this suggest that oligo to polygenes are regulating these traits against FAW.

Technical Session III

Biotechnology for Accelerating Hybrid Crop Breeding

- Extended Summaries of Keynote and Invited Presentations

TS-III-IP-01

Disruptive innovations in hybrid breeding

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Hybrid breeding has revolutionized agriculture and cultivar improvement, delivering significant gains in crop yield, resistance to pests and pathogens, and adaptation to diverse environmental conditions. However, as the global population continues to grow and the climate becomes increasingly unpredictable, traditional hybrid breeding methods face limitations. In the context of hybrid plant breeding, disruptive innovation involves introducing breakthrough technologies—such as genome editing, predictive breeding, digital phenotyping, speed breeding, big data driven trait analysis, synthetic biology—that reshape traditional breeding methods. These technologies promise to accelerate breeding cycles, enhance genetic diversity, and tailor crops to specific needs, ushering in a new era of agricultural productivity and sustainability.

- **(i) Genome Editing- Precision Breeding at Scale*:*** CRISPR-Cas genome editing has transformed hybrid breeding by enabling precise modifications to plant genomes. Unlike traditional methods, it allows targeted changes to enhance traits like drought tolerance, pest resistance, and nutritional value. This accelerates the development of high-yielding hybrids that are resilient to environmental stressors and aids in overcoming challenges like self-incompatibility and male sterility in hybrid seed systems.
- **(ii) Predictive Breeding Through Big Data*:*** Genomic selection (GS) uses genetic profiles and machine learning to predict plant breeding values with high accuracy, minimizing the need for extensive field trials. This approach is particularly effective for complex traits like yield and stress tolerance. When combined with high-throughput phenotyping, GS identifies elite hybrids, optimizing performance across diverse conditions and transforming breeding into a precise, predictive science.
- **(iii) Digital Phenotyping*:*** Advanced imaging, sensors, and AI technologies enable the accurate measurement of traits such as growth, canopy structure, and root architecture. This ensures breeders can select and quantify traits contributing to hybrid vigor, enhancing heterosis.
- **(iv) Synthetic Biology - Engineering Novel Traits*:*** Synthetic biology designs novel genetic circuits and pathways to create new traits beyond traditional breeding's scope. Applications include engineering photosynthesis for better carbon

fixation, nitrogen-fixing cereals, and designer parent lines with complementary traits. It also enables biosensors for real-time monitoring of plant health, further optimizing hybrid performance. In my talk, I will focus on how recent innovations in *in planta* haploid induction could revolutionize hybrid plant breeding.

(a) *Cybrids through paternal haploids*: Cytoplasmic inheritance, governed by organelle genomes such as mitochondria and chloroplasts, plays a vital role in determining traits like male sterility, stress tolerance, and photosynthetic efficiency. Traditional methods of transferring cytoplasmic traits between lines can be labour-intensive and time-consuming, as they often involve repeated backcrossing to achieve the desired nuclear and cytoplasmic combinations. The use of paternal haploids offers a streamlined alternative. Paternal haploids are generated by inducing uniparental genome elimination, where only the paternal genome contributes to the zygote, effectively replacing the maternal cytoplasm with the paternal counterpart, a feat not possible by in vitro production of haploids. This method allows breeders to transfer cytoplasmic traits rapidly and efficiently while maintaining the desired nuclear genome. CENH3 haploid inducers are instrumental in creating paternal haploids, enabling breeders to bypass the complexities of traditional methods. This approach also reduces the genetic drag associated with traditional cytoplasmic transfer methods, preserving the vigor and productivity of hybrid lines.

(b) *HI (Haploid induction)-edit*: In this process, the haploid inducer (HI) carrying CRISPR-Cas machinery enables genome editing during fertilization, and the edited haploid genome is doubled to create homozygous diploids with desired traits. The combination of paternal haploids and HI-Edit offers a transformative toolkit for modern hybrid breeding by enabling cytoplasmic trait transfer, like CMS system establishment. The absence of inherited transgenes alleviates regulatory and consumer concerns, facilitating rapid adoption.

(c) *Analytical breeding for ploidy reduction in polyploids*: Analytical breeding offers innovative strategies for reducing the ploidy of polyploid crops, enabling their genetic simplification while retaining desirable traits. This targeted approach facilitates the development of diploid or lower-ploidy varieties with enhanced hybrid performance, improved genetic stability, and optimized agronomic traits. CENH3 based haploid in planta haploid induction system can be exploited for practicing analytical breeding. By integrating genomic selection, chromosome engineering, and advanced genome-editing tools like CRISPR-Cas, breeders can selectively eliminate excess chromosome sets and streamline complex polyploid genomes.

(d) *Reverse breeding*: It is another innovative technique enabling the recreation of parental lines from hybrids by suppressing meiotic recombination. This method facilitates the recovery of non-recombinant haploid gametes, which can be doubled to generate homozygous parental lines. Reverse breeding overcomes the challenges of traditional breeding by preserving specific allele combinations responsible for hybrid vigor, ensuring consistent performance across generations. It holds immense potential for producing tailored parental lines for hybrid seed systems.

Integrative Approaches: The Future of Hybrid Breeding: The true potential of disruptive innovations lies in their integration into cohesive breeding strategies. Combining genome editing, genomic selection, digital phenotyping, in vivo haploid induction with HI- edit and synthetic biology creates a holistic framework for hybrid breeding. For example, genome editing can be used to introduce key traits into parental lines, while genomic selection identifies optimal crosses. Digital phenotyping validates the performance of hybrids, and synthetic biology adds novel functionalities. Such integrative approaches enable the development of hybrids tailored to specific agro-ecological zones, market demands, and consumer preferences. They also promote sustainability by reducing the need for chemical inputs and enhancing resource use efficiency.

Challenges and Ethical Considerations: Despite their promise, disruptive innovations in hybrid plant breeding face several challenges. Regulatory hurdles, public acceptance, and the high cost of implementation are significant barriers. Ethical concerns regarding the ownership and control of genetic resources must also be addressed to ensure equitable access and benefit-sharing. Investments in capacity building, infrastructure, and collaborative research are essential to bridge this gap and promote inclusive innovation.

TS-III-IP-02

Data-driven predictive breeding in hybrid crops – progress and prospects

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Across a range of Grain and Oilseed crops, global productivity has increased roughly 35% over the past 25 years. Hybrid technology has certainly been one of the key contributors to this productivity enhancement and successfully prevented over

500 million acres from entering production. Along with regular crop improvement approaches, high density genotyping platforms, high throughput phenotyping techniques, doubled haploids and breeding informatics form the core of modern plant breeding programs nowadays. Integrating these modern tools in time and resource efficient manner is critical to accelerating genetic gains especially in the regions that are experiencing intense and adverse climate change effects such as rising temperatures, frequent droughts, excess rainfall as well as evolving biotic stresses. Both specific marker- based approaches such as QTL mapping and genome-wide association studies (GWAS) as well as whole genome-based prediction strategies offer unprecedented opportunities for improvement of simple as well as complex traits under challenging array of growing environments. While billions of genotypic and phenotypic datapoints are generated in a cost-efficient manner, converting them into meaningful selection units that breeders can act upon is turning out to be a challenge in breeding programs. Genome editing is another new tool that promises great potential and opens up a lot of newer avenues. Here, the recent developments with respect to various hybrid-based crop improvement strategies, tools and their applicability to plant breeding programs with few illustrations from tropical corn and hybrid rice are reviewed. Various challenges and infrastructural bottlenecks that impede the wide-scale adoption of hybrid technology such as efficient seed production at scale in developing regions of the world and opportunities to overcome them are highlighted.

TS-III-IP-03

Learnings from apomictic grasses towards fixation of hybrid vigour

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Apomixis is a mode of asexual production through seeds. Apomicts produce progeny that are genetic copies (clones) of themselves, thus preserving the maternal characters (genotype). It is one of the highly desired features in agriculture by virtue of its capacity to ‘fix’ the hybrid vigour, as there would be no segregation in advance generations and the farmers can use their own seeds for subsequent sowing, and could continuously perpetuate and harvest the advantages of hybrid varieties. This will also significantly reduce the cost of hybrid seeds. In nature, apomixis is widespread but infrequent: it occurs in around 10% of the 400 families of flowering plants, but only in 1% of the 40,000 species that make up those families. Apomixis is most frequent in Gramineae (the cereal family), Compositae (which includes sunflower), Rosaceae (which includes many fruit trees) and Asterceae (the dandelion family). Only a handful of crops are apomictic: citrus, mango, some tropical forages and a few others, however, apomixis doesn't occur naturally in important cereals such as wheat, rice, maize, pearl millet and other important crop plants.

Apomictic crops breed true because meiosis and segregation are bypassed, and the seed produced is exactly like the mother. An 'Evaluation and Synthesis' is being followed to eventually develop hybrids reproducing through apomixis. Naturally occurring apomixis systems (eg., *Panicum*, *Pennisetum*, *Paspalum*, *Hieracium*, *Boechera*, *Taraxacum*, *Tripsacum*, *Erigeron* etc.) are studied to decipher the genes and genetic mechanisms responsible for apomixis in the 'Evaluation' component. The information thus gained, is utilized in 'Synthesis' approach, to introgress, mutate or induce apomixis into target sexually reproducing crop plants.

The process of apomictic seed development is complex and comprises three distinct components, *viz.*, apomeiosis (leading to formation of unreduced egg cell), parthenogenesis (development of embryo without fertilization) and functional endosperm development. These three components should function in unison to develop apomictic seed. However, in many crops, these three components are reported to be governed independently by unlinked genes wherein genetic recombination is possible, leading to their uncoupling/partitioning. Such uncoupling events generate higher frequency of triploids and/or haploids progeny from a diploid maternal parent. Multiple cycles of self-pollination, suitably supplemented with hybridization, provide a cytogenetic tool to manipulate ploidy levels. We termed this approach as Hybridization-supplemented Apomixis-components Partitioning Approach (HAPA) and demonstrated this in guinea grass (*Panicum maximum*) wherein from a single tetraploid (2n=4x=32) progenitor, worlds' largest ploidy series in a crop plant was generated represented by 3x, 4x, 5x, 6x, 7x, 8x, 9x and 11x cytotypes, by manipulating reproductive pathways. Similarly, genome addition was obtained in other species such as *Pennisetum orientale* and its tri-species hybrids with *P. glaucum* and *P. squamulatum*. Polyploids and haploids thus generated contribute towards better understanding of the apomixis phenomenon, as the trait is largely affected by the ploidy levels. Possible consequences leading to diversity in seed developmental pathways, resources to understand apomixis, inheritance and identification of candidate gene(s) for partitioned components, as well as generation of variability are added contributions from HAPA. It also helped us to understand endosperm development and imprinting effects, endosperm being the most economically important component of cereal grains.

Detailed molecular analysis of genomic regions governing apomixis in natural apomictic systems led to the identification, characterization and isolation of key genes involved in apomictic reproduction *per se* or its components. These include genes controlling apomeiosis, such as *APOLLO*, *HAPPY*, *HpARI*, those controlling parthenogenesis, such as *ASGR-BBML*, as well as that modulating endosperm development, such as *PsORC3a* and *AutE*.

Recently, we also demonstrated potential of an Apomixis Mediated Genome Addition (AMGA) strategy suitable for breeding of crops belonging to agamic complexes. Through AMGA, the sexuality of one species could be successfully utilized to 'release' the 'frozen' variability embedded in another species. Subsequently, the hybrids representing desirable trait combinations could be again 'fixed' utilizing the apomixis alleles from the male parent in a back-and-forth apomixis-sexual selection cycle. As a proof of concept, we recently demonstrated the potential of AMGA in breeding forage type pearl millet. Contrasting reproductive capacities (sexuality and apomixis) of pearl millet and the wild *P. squamulatum* were used to access the otherwise un-available variability embedded in *P. squamulatum*. Segregating population of inter-specific hybrids exhibited significant variability and heterosis for desired morphological, agronomical and nutritional traits such as higher crude protein content, biomass, tillering and regeneration as well as improved nutritional, digestibility and other cattle preference traits. Elite apomictic and perennial hybrids were evaluated in breeding trials, and eventually a novel grass cultivar was released for commercial cultivation in India. The performance of newly developed cultivar was superior to other adapted perennial grasses of arid and semi-arid rangelands. In another perspective, AMGA derived hybrids also exhibited a potential for domesticating CWRs of crop plants belonging to agamic complexes.

A synergy is thus desired between the information generated from natural apomictic systems and its subsequent utilization in sexually reproducing systems to harness the full potential of fixing hybrid vigour through apomixis technology.

Technical Session III

Biotechnology for Accelerating Hybrid Crop Breeding

✦ Abstracts of Rapid Oral Presentations

TS III-OP-01

Revisiting *floury2* gene after 50 years: Development of subtropically adapted maize hybrids with enhanced methionine in maize kernels using genomics-assisted breeding

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Quality protein maize (QPM) contains high lysine and tryptophan but sulfur-containing amino acid methionine remains deficient in maize grain. To overcome methionine deficiency in maize-based feeds, cost-intensive synthetic methionine is used as a racemic mixture. Mutation in *floury2 (fl2)* gene is associated with increased methionine and lysine. Here, we targeted to improve a popular biofortified maize hybrid, 'Pusa HQPM-5 Improved' (PMI-PV5 × PMI-PV6) for methionine accumulation using genomics-assisted breeding. Sequencing of *fl2* gene in eight wild-type and two mutant inbreds detected a significant transversion of C (wild-type allele) to T (mutant allele) position leading to substitution of alanine by valine in *fl2* mutant lines. We developed a PCR-based functional marker (*FL-SNP-CT*), that was successfully used to genotype BC1F1, BC2F1, and BC2F2 populations. Background selection using >100 SSRs led to recovery of >90% recurrent parent genome (RPG) among the progenies. The reconstituted hybrids accumulated higher methionine (>0.320% in flour) compared to 0.185% in the original hybrids. Reconstituted hybrids also possessed high lysine (>0.350%), tryptophan (>0.070%) and provitamin-A (>8 ppm) due to presence of *opaque2, crtRB1* and *lcyE* genes. The high yielding reconstituted hybrids with high methionine, lysine, tryptophan and provitamin-A good agronomy developed in the study through accelerated genomics-assisted breeding hold immense significance for farmers and feed industry. The is the first report on the study of effect of *fl2* mutation on methionine enhancement among sub-tropically adapted maize and assumes great importance to alleviate malnutrition, especially in developing countries.

TS III-OP-02

Introgression of *Pi9*, a broad spectrum gene into elite rice cultivar of CO 51+*Pi54* through marker-assisted selection

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Blast disease is a highly destructive disease and causes significant yield losses in rice. To address this issue, this study was chosen and focused on stacking the *Pi9* along with CO 51+*Pi54*, which provides broad-spectrum resistance to blast pathogens. This study demonstrated that stacking of the *Pi9* gene from donor parent #562-4 into CO 51 along with *Pi54*, against blast disease resistance. Marker Assisted Selection has been employed to stack *Pi9* and *Pi54* genes into CO 51 through functional markers of NBS4 and Pi54MAS respectively. Thirty-six advanced breeding lines were developed from CO 51 X 562-4 and evaluated for blast disease resistance in a natural hotspot region over two growing seasons (*kharif* 2021 and *Kharif* 2022). The recurrent parent, CO 51 recorded an IRRI SES score of 3.1 in *Kharif* 2021 and an SES score of 3.15 in *Kharif* 2022 as moderately resistant while Backcross Inbred Line (BILs) of CO 51 with *Pi9*+*Pi54* genes displayed a blast score of 0<2, indicating strong resistance. All 36 progenies revealed the genetic potential of the stacked genes into CO 51 genetic background and exhibited an immune reaction to blast pathogen *Magnaporthe oryzae* in *Kharif* 2021 and *Kharif* 2022. The average yield of a single plant has increased by 0.28 % to 35.05 % in BILs of CO 51. A maximum single plant yield of 35.05 % was recorded in progeny #20x6-5-11-121 which was followed by progeny #20x6-5-11-125 (31.65 %). Phenotypic traits such as the number of productive tillers per plant, panicle length, thousand-grain weight, and grain yield per plant exhibited transgressive segregation in comparison to the CO 51 parent.

TS III-OP-03

Making sweetcorn hybrids healthier with vitamins, amino acids and antioxidants through genomics-assisted breeding

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Sweet corn has emerged as a popular choice in worldwide markets due to its distinct flavour and delightful taste. However, the nutritional value of traditional sweet corn is quite low. Here, we improved four elite lines (PMI-PVE-5, PMI-PVE-6, PMI-PVE-7, and PMI-PVE-8) that were the parents of four hybrids (APTQH-1, APTQH-4, APTQH-5 and APTQH-7) through genomics-assisted breeding. Genes such as *brittle2* (for sweetness), *crtRB1* and *lcyE* (for provitamin-A), *vte4* (for vitamin-E) and *opaque2* (for lysine and tryptophan), *Anthocyanin1 (A1)*, *Purple1 (Pr1)*, *Colour1 (C1)* and *Red1 (R1)* (for anthocyanin) were combined. Gene-based markers were successfully used for foreground selection in BC1F1, BC2F1 and BC2F2 populations. In order to recover the recurrent parent genome (RPG), >100 SSRs were used for background selection which led to the recovery of >90% RPG among the introgrssed inbreds. The newly developed sweet corn genotypes possessed significantly higher vitamin-A (>15 ppm), vitamin-E (>15 ppm), lysine (>0.350%), tryptophan (>0.075%) and anthocyanin (>300 ppm) through genomics-assisted breeding. The newly developed biofortified sweet corn genotypes also possessed high kernel sweetness (>18% brix). These multinutrient-rich sweet corn genotypes are the first of its kind effort across the globe and assume great significance in maintaining a sound health and alleviating malnutrition.

Technical Session III

Biotechnology for Accelerating Hybrid Crop Breeding

- Abstracts of Poster Presentations
- Evening Lecture I

TS III-PP-01

Maintaining genetic purity in grains of maize hybrids through utilization of *Gametophyte factor-2* gene

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Maize is one of the leading staple food crops of world with multiple uses including food, feed, fodder and bioenergy. Being a highly cross-pollinated crop, maize pollen can travel easily to one field to the silk of the nearby field. Such contamination with unwanted foreign pollen is a major issue in maintaining genetic purity of maize grains of biofortified maize hybrids. *Gametophyte factor (Ga-2)* is a crossing barrier gene which restricts fertilization from foreign pollen. Here, *Ga-2* was introgressed in to the parental line of 'Pusa Vivek QPM9 Improved' using molecular breeding. Foreground selection for *Ga-2* along *opaque2* and *crtRB1* genes have been carried out with gene-based markers in BC_1F_1 generation. Background selection with >90 SSR markers has led to the recovery of >77% recurrent parent genome (RPG) in BC_1F_1 generation. The selected progenies have been forwarded to raise the BC_2F_1 generation. These novel biofortified maize hybrid with unilateral cross incompatibility system would aid in the maintenance of genetic purity without isolation distance.

TS III-PP-02

Genotyping and phenotyping of ToLCD resistant backcross lines of tomato for processing traits

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Tomato (*Solanum lycopersicum* L.) 2n=2x=24 is one of the most widely grown warm season vegetable crop grown throughout the world both for fresh consumption and

processing. The present study entitled "Genotyping and phenotyping of Tomato leaf curl disease (ToLCD) resistant backcross lines of tomato for processing traits" with the aim to evaluate the backcross derived ToLCD resistant genotypes for superiority for higher yield, multiple disease resistance, fruit quality and tomato processing traits. A total of 46 genotypes were genotyped with disease resistance gene(s) linked molecular markers including ToLCD (*Ty-1, Ty-2, Ty-3, Ty-4, ty-5* and *Ty-6*); late blight (*Ph-2* and *Ph-3*); and fruit quality traits, fruit shape *ovate* gene (SlOvate). Simultaneously, the genotypes were subjected to agro-morphological analysis for fruit quality traits (fruits shape, FSI, pH, acidity and TSS) including juice recovery (%) puree (9 °Brix) and paste (25 °Brix) yield and its nutritional analysis, fruit shape index (FSI) for fruit shape *ovate* gene and phyto nutraceutical (lycopene and beta carotene) and minerals (Zn, Mg, Ca and Fe) and fruit yield per hectare. Genotypes having superior promising processing qualities along with *Ty-3* gene for ToLCD resistance [Pusa Tomato Hybrid-6 (PTH-6) and DTH-6 Delhi Tomato Hybrid-6, (DTH-162)] also carrying resistant allele for late blight disease resistance gene *Ph-3* also superior over the check (Punjab Chhuahra). Among the genotypes evaluated PTH-6 with high processibility was found most promising for dual purpose segment. The present study indicated at the availability of promising breeding lines and hybrids suitable for tomato juice puree and paste with multiple disease resistance and high fruit yield for upscaling indigenous Indian tomato-based processing industry.

TS III-PP-03

Molecular characterization of *Phytase1* gene governing phytase activity in contrasting inbreds for developing maize hybrids with higher bioavailable phosphorus and minerals

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Phytic acid-$C_6H_{18}O_{24}P_6$ (IP_6) is an unavailable form of P present in all plant parts. It is a negatively charged reactive compound that forms complexes with positively charged minerals, thereby limiting the bioavailability of the same in the gastrointestinal tracts of monogastric animals. Hydrolysis of phytic acid into bioavailable inorganic P can be accomplished by enhanced phytase activity in the seeds of maize. Based on variation for phytase activity, five extremely high (>880-1000 U/kg) inbreds, PMI-Q1, PMI-CMT193, CML408, PMI-CMT200 and UMI1220 and five extremely low (<750-860 U/kg) inbreds, PMI-PV1, PMI-PV3, PMI-PV8, PMI-Q2 and CML489 were selected. Furthermore, we characterized the full-length gene sequence of *Phytase1* gene of 4695 bp located on the long arm of chromosome 3. Multiple sequence analysis of 10 inbreds identified 206 polymorphic sites including 9 InDels, which separated into eight haplotypes with a diversity index (Hd) of 0.927. Twelve synonymous and five non-synonymous SNPs in the CDS region are found which replaces five amino acids. The phylogenetic tree based on nucleotide and protein sequences grouped wild- and mutant-inbreds into two clusters for the *Phytase1* gene. Sequence polymorphisms among wild- and mutant-inbreds were further exploited to study InDel-based gene diversity in 48 diverse maize inbreds. InDel-markers specific to *Phytase1* grouped the diverse maize inbreds into two distinct clusters with a mean PIC of 0.45. Screening inbreds for phytase activity and identifying allelic variation of contrasting high and low phytase inbreds resulted in the development of gene-based InDel-markers. Hence, introgression of high phytase trait into parental inbreds of high-yielding maize hybrids using marker-assisted selection results in genetic enhancement of maize genotypes for phytase activity. The identified inbreds with increased phytase activity in maize germplasm could provide higher bioavailability of nutrients in food and feed.

TS III-PP-04

Development of multi-nutrient rich 'blue maize' hybrids through marker-assisted breeding

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Blue maize rich in anthocyanins possesses numerous health benefits as antioxidants and anti-diabetic activity. Traditional yellow and white-coloured maize kernels are devoid of anthocyanins. Besides, traditional maize also lacks an adequate concentration of lysine, tryptophan, provitamin-A, and vitamin-E in the endosperm. The recessive *opaque2* gene enhances lysine and tryptophan, whereas the mutation in the *vte4* gene increases vitamin-E in the maize kernel. Higher levels of provitamin-A accumulate in the presence of mutant *crtRB1* and *lcyE* genes. While, *A1*, *Pr1*, *C1* and *R1* genes are responsible for the accumulation of anthocyanins in the endosperm of the maize kernel. A genomics-

assisted breeding strategy was employed to combine *opaque2, vte4, crtRB1, lcyE, A1, Pr1, C1* and *R1* genes into four elite parents. The BC_1F_1, BC_2F_1, and BC_2F_2 generations comprised of 90-120 individuals for foreground selection using gene-based markers associated with *opaque2, crtRB1, lcyE, vte4. The presence of anthocyanin governing genes were also confirmed in selected pigmented progenies.* Background selection using >100 SSRs led to recovery of >90% recurrent parent genome (RPG) among the progenies. The introgressed inbreds possessed high levels of lysine (0.290 to 0.340%), tryptophan (0.078 to 0.086%), vitamin-E (14 to 20 ppm), provitamin-A (8 to 12 ppm) and anthocyanins (~250 to 400 ppm). These newly developed multi-nutrient-rich blue maize hybrids would serve as a superfood for human consumption. This is a first-of-its-kind report to develop biofortified 'blue maize' using marker-assisted backcross breeding.

TS III-PP-05

Introgression of *shrunken2* gene for development of super sweet corn hybrids using marker-assisted breeding

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Sweet corn is under huge demand, owing to its growing popularity as fresh and processed food worldwide. The major lacuna in the area of sweet corn hybrid breeding is the unavailability of superior and diverse inbred parents. *Shrunken2 (sh2+)* gene located on chromosome-3, encodes for large subunit of ADP-glucose pyrophosphorylase (AGPase), which catalyzes the rate-limiting step in starch biosynthesis. In recessive *sh2* mutant, structural alteration in the gene leads to a 6-fold increase in sucrose and reducing sugar levels compared to the wild-type *sh2+*. Here, we targeted to introgress the recessive *sh2* gene into four elite parental lines (UMI-1200, UMI-1201, UMI-1205 and UMI-1230), which are the parents of three single cross maize hybrids (COHM-6, COHM-8 and COHM-9) developed at TNAU, Coimbatore. We used PMI-SWT-019 developed at IARI, New Delhi as a donor for *sh2*. F_1 hybrids were generated and subsequently backcrossed to their respective recurrent parents. BC_1F_1 and BC_2F_1 populations were genotyped using the *sh2*-based SNP marker (SNP_AG1). A dCAPS marker (MGU-SC-dCAPs-T/C) was further designed to validate the selection. Background recovery using >90 SSR markers led to the high recovery of RPG (>78% in BC1F1, >85% BC_2F_1 generations). BC_2F_1 plants have been selfed to generate

BC_2F_2 populations. The introgressed lines with *sh2* and high background recovery would be selected for further advancement. The *sh2*-based sweet corn inbreds show significant potential for developing into high-yielding sweet corn hybrids.

TS III-PP-06

Development and assessment of training population lines for genomic prediction in Basmati rice

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Hybrid rice is primarily based on three-line system including a cytoplasmic male sterile line (A line), its maintainer line (B line), and a restorer line (R line). Development of heterotic pools can help in prediction of heterotic combinations. However, heterotic pool development in self- pollinated crop like rice is one of least explored areas in crop improvement research. Towards achieving this, diverse restorer and maintainer pools were developed, which laid the foundation for long-term improvement of the parental lines aimed at development of Basmati hybrids. To enhance the genetic gain, 28 restorers and 10 maintainer founders were selected based on *per se* performance, molecular diversity, population structure, testcross performance to develop within-pool inter-crosses resulting in 125 populations, which were advanced to develop 31,887 improved lines. A training population was constituted with 256 improved lines were evaluated across four environments to assess the *per se* performance for various agro-morphological traits, as well as grain and cooking quality characteristics. These lines showed significant improvement in grain yield as compared to the founder parents. Additionally, the improved lines showed significant G × E interaction for grain yield. GGE biplot analysis revealed that two lines from the maintainer populations and 12 lines from the restorer populations were stable as well as superior over the founders across four environments. Assessment of grain and cooking traits revealed that majority of the lines (221 lines) from both pools cleared the minimum quality standards for Basmati. Further, there was significant improvement

in allelic frequencies of resistance alleles of *xa13*, *Xa21*, *Pi2,* and *Pi54* genes over the founder parents. The present study signifies that there is an improvement in the *per se* performance of the parental lines over the founder through recurrent selection within the pools which can help in improving heterosis in Basmati rice.

TS III-PP-07

Development of biofortified waxy maize hybrids through marker-assisted selection of *waxy1*, *opaque2*, and *crtRB1* genes

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In addition to being biofortified, increasing amylopectin in maize helps in achieving both food security and industrial applications. Maize starch contains more amylopectin due to the mutant *waxy* (*wx1*) allele, which has numerous dietary and industrial uses. As compared to normal maize which has a modest amount of amylopectin (70–75%), waxy maize, with favorable *wx1* allele, has ~95–100% amylopectin. In the present study, the *wx1* allele was introgressed into multi-nutrient-rich maize inbreds viz. PMI-PV9 and PMI-PV5 have recessive *crtRB1* and *opaque2* genes. These parental inbreds are parents of the hybrid, APQH8 that possesses high provitamin-A, lysine, and tryptophan. From three backcross generations BC1F1, BC2F1, and BC2F2 desirable gene segregants were selected using gene-specific markers. High recovery of recurrent parent genomes was observed among selected backcross progenies (94.8–96.8%). Compared to original inbreds (mean: 74.7%), genomics-assisted backcross-generated inbreds showed higher amylopectin content (mean: 98.0%). Amylopectin levels in the reconstituted waxy hybrids were higher (mean: 98.4%) than in the original hybrid (mean: 72.7%). Similar to the original hybrid (lysine: 0.330%, tryptophan: 0.079%, and proA: 10.4 ppm), the reconstituted hybrids

likewise showed increased levels of lysine (mean: 0.382%), tryptophan (mean: 0.092%), and provitamin-A (mean: 10.4 ppm). A comparable agro-morphological trait and grain yield were examined in introgressed inbreds and reconstituted hybrids. Biofortified waxy maize hybrids that are rich in provitamin A, lysine, and tryptophan, with enhanced amylopectin content, offer significant benefits for both industrial- and nutritional-value.

TS III-PP-08

Identification of promising three-line hybrids through heterosis and grain quality assessment in rice (*Oryza sativa* L.)

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The exploitation of heterosis in rice, a global staple crop, is vital to address worldwide demographic expansion. The heterotic potential of 70 three-line hybrids, derived from crosses between five CMS lines and 14 diverse testers, was assessed at the Paddy Breeding Station, Tamil Nadu Agricultural University during *kharif*, 2023. Standard heterosis over the checks, CORH 3 (short duration) and CORH 4 (long duration), was estimated for 13 biometrical traits. Hybrids showing significant negative standard heterosis for days to 50% flowering included TNAU CMS 2A x CO 51, TNAU CMS 2A x CBSN 517, COMS 25A x CO 51, and COMS 25A x CBSN 510, indicating potential for short-duration hybrid development. Five hybrids *viz*., COMS 24A x CBSN 511, COMS 25A x CBSN 511, COMS 24A x WGL 32100, COMS 23A x IR64 DRT, and COMS 25A x CBSN 517 exhibited significant standard heterosis for single-plant yield. Among these, COMS 24A x CBSN 511 and COMS 25A x CBSN 511, derived from the WRM derivative CBSN 511, recorded yield increases of 39.40% and 23.50%, respectively, over CORH 4, showcasing the utility of wild rice for yield enhancement. Other hybrids, COMS 24A x WGL 32100, COMS 25A x CBSN 517, and COMS 23A x IR64 DRT, recorded yield increase of 19.10%, 12.70%, and 15.60%, respectively, with desirable heterosis for yield traits. All five hybrids possessed medium slender grain type which is predominantly preferred by South Indian states. COMS 23A x IR64 DRT was characterized by intermediate amylose content, soft gel consistency, and medium gelatinization temperature. COMS 25A x CBSN

511 and COMS 25A x CBSN 517 exhibited intermediate amylose content, medium gel consistency, and low gelatinization temperature. These medium-slender hybrids with good grain quality hold promise for commercial cultivation in South India.

TS III-PP-09

Development of multi-vitamin-rich maize hybrids with high kernel oil and better fatty acid composition through genomics-assisted stacking of *dgat1-2, fatb, crtRB1, lcyE, vte4*, and *opaque2* genes

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Maize oil is a sustainable resource for human and livestock diets and a raw material for diverse industries. Owing to its unique health benefits, high calorific values, and enhanced bioavailability of fat-soluble vitamins, increasing oil content and tailoring fatty acid composition have gained momentum in maize research. Traditional maize kernels possess ~4% oil, with over 80% being unsaturated fatty acids. However, the complex nature of this trait makes phenotypic-based selection challenging for plant breeders. Here, we targeted to introgress favorable alleles of *dgat1-2* and *fatb* into parental lines of four popular multi-nutrient-rich maize hybrids (APTQH1, APTQH4, APTQH5, and APTQH7) through genomics-assisted stacking. The parental lines possessed high lysine, tryptophan, provitamin-A, and vitamin-E due to the presence of favorable alleles of *opaque2*, *crtRB1*, *lcyE,* and *vte4* genes. Gene-based markers of all six target genes were used for foreground selection in BC_1F_1, BC_2F_1, and BC_2F_2 generations. Background selection using genome-wide distributed SSRs led to >95% recovery of recurrent-parent-genome and high phenotypic resemblance with their original versions. The oil content was significantly enhanced among introgressed progenies and hybrids (>6.0%) compared to original parents/hybrids. Palmitic acid was significantly reduced from 20.5% to 14.2%, whereas oleic acid was increased from 26.4% to 40.5% in introgressed progenies. Thus, MAS-derived genotypes possessed a >35% increment in oil content and >50% increment in oleic acid with a >30% reduction in palmitic acid over their original versions, while possessing higher

provitamin-A, vitamin-E, lysine, and tryptophan. Multilocation evaluations revealed that these hybrids maintained similar plant architecture and high-yielding abilities as the original hybrids. Further, these newly developed genotypes possessed better fatty acid ratios, and health and nutritional properties over original versions. These novel high-oil and better FA profile-based multi-nutrient-rich maize hybrids hold immense significance in nutritional security including alleviation of malnutrition sustainably in a fast-track manner.

TS III-PP-10

Restructuring leaf angle in biofortified maize hybrids through molecular breeding for high plant density

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Boosting productivity gain in maize remains the primary goal to meet rising food, feed and bioenergy demands. High plant density is a less exploited approach, since wide-canopied maize hybrids are prone to lodging and yield penalties in higher plant densities. Here, we targeted to reduce the canopy leaf angle to increase the plant density along with enhanced photosynthetic efficiency by minimizing shading and competition. In the present study, we identified a 130 bp insertion in the mutant *liguleless1* (*lg1*) gene leading to narrow leaf angle. We have altered the leaf angle of two popular biofortified hybrids, 'Pusa Vivek QPM9 Improved' (PMI-PV1 × PMI-PV2) and 'Pusa Vivek Hybrid-27 Improved' (PMI-PV3 × PMI-PV4) through introgression of *lg1* allele in to the respective parents. The co-dominant functional marker (MGU-InDel-lg1) targeting the *InDel* within *lg1* gene was successfully developed, and used in genotyping of BC1F1, BC2F1 and BC2F2 populations. More than 90 SSR markers were used for background selection that led to the recovery of >90% recurrent parent genome (RPG). The reconstituted *lg1*-based hybrids possessed narrow leaf angle of ~8-12o as against 45-50o in the original hybrids. These *lg1*-hybrids also possessed high provitamin-A (~8-10 ppm), lysine (~0.265-0.350%) and tryptophan (~0.070-0.095%) due to the selection of *crtRB1* and *opaque2* genes. The newly derived hybrids with narrow leaf angle will play a pivotal role in enhancing the productivity of maize through high-density planting.

TS III-PP-11

Identification of genomic segments and candidate genes conferring yield heterosis in *Brassica carinata*-derived *Brassica juncea* introgression lines

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Indian mustard, being a crop of national importance, remains indispensable for achieving national edible oil security, therefore, needs to improve its seed and oil yields. Interspecific hybridization is a valuable tool for introgression of desirable traits between species. To improve productivity, efforts have been made to develop *B. carinata*-derived *B. juncea* introgression lines (ILs). A set of 40 homozygous and cytogenetically stable (2n=18II) ILs, expressing a wide range of variations for agro-morphological traits was used to identify heterotic genomic segments. To assess the effect of introgression in the heterozygote state, these ILs were hybridized with their respective genetic backgrounds (DRMRIJ 31 and Pusa Mustard 30) as well as with the common tester (SEJ 8) to generate Introgression Line Hybrids (ILHs) and Test Hybrids (THs), respectively. Ten ILs with significant mid-parent heterosis in ILHs and significant standard heterosis in THs for seed yield were used to dissect heterotic genomic segments. A total of 254 and 335 heterotic segments were identified in the heterotic ILs developed from DRMRIJ 31 and Pusa Mustard 30, respectively. This investigation identified potential genes such as *PUB10*, *glutathione S transferase*, *TT4*, *SGT*, *FLA3*, *AP2/ERF*, *SANT4*, *MYB*, and *UDP-glucosyl transferase 73B3* that were previously reported to regulate yield-related traits. The heterozygosity of the *FLA3* gene significantly enhanced siliqua length and seed count per siliqua in ILHs of Pusa Mustard 30. The increase in 1000 seed weight (g) in ILHs as compared to ILs in the genetic background of DRMRIJ 31, was due to heterozygosity of *glutathione s transferase*, *TT4*, *SGT*, *BRI 1* and *ARFs* genes. The current study demonstrated the value of interspecific hybridization in introducing genetic variability and improving the level of heterosis in cultivated species.

Evening Lecture I

Hybrid Breeding for Unstoppable Genetic Gains

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Twentieth century has witnessed several revolutions especially in hybrid technology in Corn in U.S. Europe China, and other countries; Green revolution in wheat, rice in Asia; Information technology; Commercial exploitation of genetically modified crops; Human genome sequence and later genome sequencing of some crop species; Livestock revolution and country specific success stories milk and Bt. Cotton in India. The topic I am to discuss is very challenging and will certainly need support and collaboration of different disciplines both in public and private institutions nationally and internationally. To achieve continuing genetic gains it is absolutely essential to have a robust germplasm base utilizing potentially useful materials in existence in the program. It is equally important to have an appropriate germplasm management strategy in place to have a continuous flow of materials from the lower performing group to the higher performing group including accessions from the germplasm bank. Since hybrid development is now being practiced in many crops the decision rests with the breeder. From this point onwards I shall concentrate on maize sharing my decades of experience at CIMMYT and also working closely with NARs in many developing countries. My preference will be to use two-tier system consisting of gene pools and populations classified as backup and advanced unit materials. Appropriate breeding schemes will be discussed in such materials that will be discussed in the presentation. For hybrid development one should use improved germplasm that has tolerance to inbreeding, good combining ability and possess traits that are needed in pollen parent and seed parent inbreds. Options for developing inbreds will be discussed highlighting procedures that are easy, cost-effective and will require much less storage space. Evaluation of lines for *per se* performance and combining ability will be discussed using different procedural options. For stress traits field conditions as well as inoculation and infestation techniques must be used that have given good results. Exotic materials improved for biotic and abiotic traits if available should be procured and adapted under your ecological environment rather than developing your own that may require special testing and evaluation facilities. Heterotic grouping, patterns and modeling of maize germplasm will be discussed giving examples from my own experience. Conscious research efforts are needed for identifying tester lines belonging to different populations. Time jumping strategies be deployed wherever possible to reduce breeding cycle. Some suggestions will be made in this regard in my presentation. Indirect strategies such as conducting inbred line evaluation nurseries in different environments and for different traits can provide solutions to some of the complex problems. CIMMYT data supporting this strategy will be presented. Development of pedigree populations and their subsequent handling will be discussed. Perhaps a new initiative be launched by distributing S3 bulks to all breeders for promoting public private partnership. Trends in type of hybrids to be developed and commercialized will be discussed emphasizing shift to two-parent single cross hybrids. Progress from various research projects be measured periodically and analyzed for factors contributing to genetic gains. Conventional breeding procedures need to be blended with new tools and biotechnologies such as marker assisted selection, genomic selection and genome editing for precise, targeted and accelerated genetic improvement in the future.

Technical Session IV

Current Status and Future Prospects in Hybrid Crop Breeding I
(Food and Fiber Crops)

- Extended Summaries of Keynote and Invited Presentations

TS-IV-KP-01

Advances in hybrid rice breeding

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Hybrid rice technology is the most viable option for increasing rice production, especially in the face of climate change. Rice hybrids assure >25% heterosis over the best-inbred checks. IRRI has been advancing and promoting this technology in Asia and Africa through the Hybrid Rice Development Consortium (HRDC). However, deploying hybrid rice technology has been slow for many reasons. The hybrid rice area in India has stagnated at around 3.5-4.0 m ha for several years. Outside China, the current hybrid rice area is around nine m ha. The key challenges for widescale adoption of hybrid rice technology are primarily the level of heterosis with yield stability over best-inbred checks (<20%) to attract farmers, rice hybrids are susceptible to biotic and abiotic stresses, poor market and consumer acceptance of grain and eating quality of rice hybrids. Seed producibility of hybrid rice seeds is about < 2.0 t/ha, and reducing the cost of hybrid rice seeds is becoming difficult. To overcome these challenges, IRRI systematically increased grain yield heterosis by >25% with stability by carrying out genomic selection within the heterotic pool, further improved the GCA of parental lines, and developed market-driven two-line hybrids (Figure 1). IRRI capitalized on its research advances under the Green Super Rice project by utilizing climate-resilient inbred varieties as parental lines for the two-line rice hybrids. We developed many multi-stress-tolerant parental lines for different biotic and abiotic stresses matching market needs. Breeding parental lines and developing hybrids that match the consumer grain and cooking quality for other target regions. Improving grain yield stability for superior performance of hybrids by precision breeding approaches involving informatics on genomics, high throughput digital phenotyping, and speed breed facility. Selecting specific crosses through genomic predictions and artificial intelligence & machine learning (AI & ML). Identifying superior heterotic combinations most efficiently through our newly launched AI-Hybrid Rice Intelligence Platform at IRRI. Identifying heterotic hybrids with higher hybrid seed producibility of >3t/ha and narrow flowering differences (< 5 days) between the parents is of utmost importance for the seed industry.

We are trying to reduce the cost of hybrid rice seeds by introducing highly advanced two-line technology using stable temperature-sensitive genic male sterile (TGMS) lines with low-critical sterility temperature points (>24°C). IRRI is promoting two-line hybrid

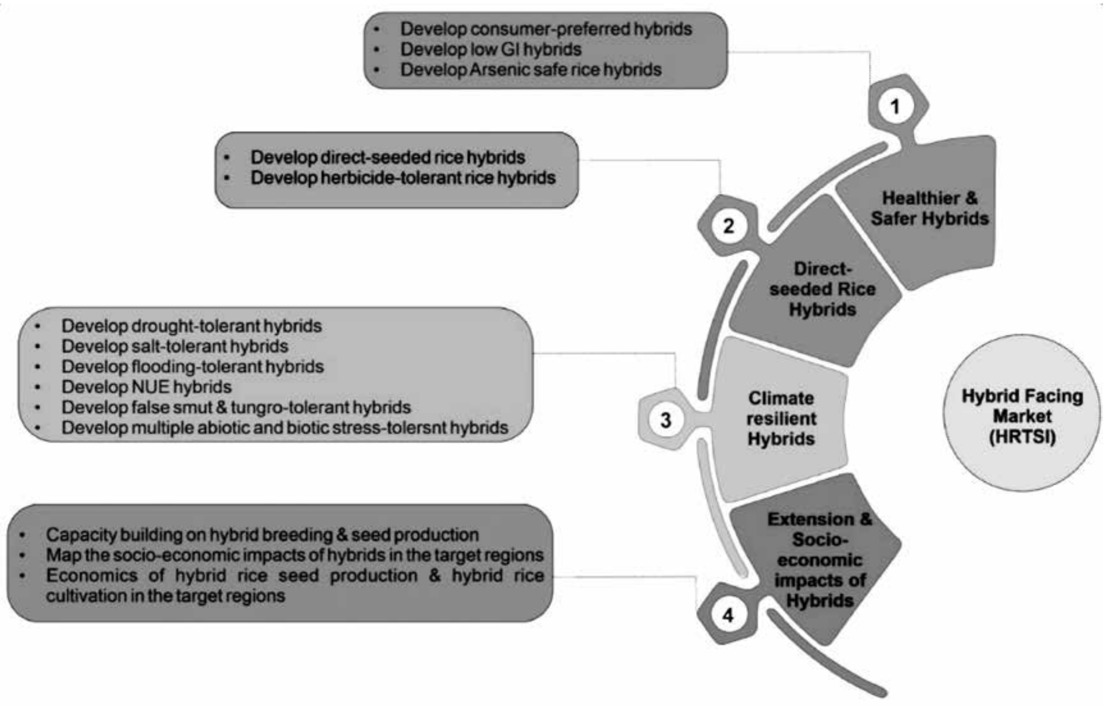

Figure 1. *IRRI's Hybrid Rice Breeding Program*

rice technology through the sponsored Two-Line Study Group (TLSG) initiative from 2019 onwards. Under this initiative, IRRI has shared more than 15 TGMS lines, 35 pollen parents, and 15 two-line hybrids to its members. Two-line technology with improved heterosis levels of >30% and superior grain quality (>60% Head Rice Recovery and >70% Milling Recovery). Two two-line hybrids with superior yields have been identified with more than 12t/ha at IRRI and high hybrid seed production levels (>3t/ha). Recently, IRRI successfully developed the Super Stigma-TGMS line, which has the longest bifid stigma that protrudes evenly across all the spikelets, ensuring higher outcrossing with more than 3.5t/ha seed production (Figure 2). As a game changer, this trait ensures higher seed producibility and attracts the attention of the seed industry for higher returns and reduced hybrid seed costs. Farmers inclined to adopt 2-line hybrids with higher grain yields and superior grain quality (high HRR and MR).

Among the diseases, the Rice False Smut (RFS) is becoming a significant threat in the rice-growing regions of Asia. IRRI has developed four highly resistant lines to RFS under controlled conditions. IRRI is sharing multiple abiotic and biotic stress tolerant lines with the TLSG and HRDC members to augment the ongoing efforts to promote the hybrid rice technology. IRRI's OneRice Breeding Strategy (ORBS) is based on elite x elite crosses adopting genomic selection across all breeding pipelines, and these elite inbred materials

Figure 2. *Newly developed Super Stigma-TGMS line for enhanced hybrid seed producibility*

regularly flows to hybrid breeding programs. ORBS focuses on ten breeding pipelines, six overlapping with hybrid rice market segments. Four hybrid breeding pipelines are transplanted, two for direct seeded conditions. Recently, IRRI's hybrid program will develop hybrids for the transplanted-Late maturity, medium, slender grain, and a soft texture on cooking segment with BPT5204 as check. There lies a significant market opportunity with 11mha for spreading the rice hybrids to South India. IRRI is closely working with UC Davis and CIRAD to develop synthetic apomictic hybrids. However, it will take another five years before this technology is fully mature and could be commercialized. Recent advances in hybrid rice technology will augment the hybrid adoption area and expand globally to provide sustainable food security coverage in the face of climate change.

TS-IV-IP-01

India's maize improvement program: challenges, progress, and roadmap

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Maize is the important versatile crop also known as 'Queen of cereals' due to its highest yield potential among the cereals. It is a relatively climate resilient crop and can be grown around in tropical, subtropical, and temperate climates from sea level to 3000 metres above sea level. Since beginning, abiotic and biotic stresses, upscaling of improved PoP at farmers' fields, availability of quality seeds and inputs at affordable prices, coverage under single cross hybrids, post-harvest losses, and market volatility have remained major challenges in maize. Before 1957, the India's maize productivity was only 547 kg/ha. As a result, the organized research on maize in India started in 1957 with the establishment of India's 1st AICRP in Maize which led to several breakthroughs, including the first set of double-cross hybrids in 1961 (Ganga 1, Ganga 101, Ranjit and Deccan); the first OPV Jawahar in 1967; further another set of hybrids (Hi-starch, Ganga 5, Ganga Safed 2) in 1969; better quality protein varieties, such as Shakti, Rattan, and Protina with *opaque2* in 1971; first single cross hybrid Paras in 1995 and first marker-assisted hybrid Vivek QPM 9 in 2008 with high lysine and tryptophan. Due to low seed yield and challenges in hybrids seed production, the composite breeding began in 1967 and continued until 1988. By systematic crossing of exotic and native germplasm populations, six composite cultivars such as Vijay, Kisan, Amber, Vikram, Sona, and Jawahar were released for cultivation which became much popular in farmers' fields.

Thereafter, in 1988 in which the new seed policy came into existence, again the hybrid programs particularly single cross hybrids (SCHs) were introduced and promoted in the country. As a result, the first single cross hybrid 'Paras' was released by the Punjab Agricultural University, Ludhiana in 1995. Due this intervention, there was significant increase in maize productivity from 1988-1996 to 1997-2006. The maize yield significantly increased after 2000 and this was due to the replacement of composites by single-cross hybrid and adoption of improved packages of practices. India produced 1.73 million tonnes of maize in 1950-51 from 3.16 million hectares land with a productivity of 547 kg per hectare. Presently (2022-23), nearly 38 million tonnes of maize are produced from 10.7 million hectares with a productivity of 3551 kg/ha. There has been a significant increase in maize production and productivity in the country. The production of maize has increased by 22 times, productivity has increased by 6.5 times, and area has increased by 3.4 times since 1950-51. The adoption of single cross hybrid maize technology (~65% coverage), best management practices, and effective insect and pest control along with the policy support have contributed significantly to this success. The per day productivity of maize in India is currently comparable or nearer to that of the USA in selected districts of the country. The state like Tamil Nadu has 7.3 t/ha Kharif, and West Bengal 8.0 t/ha Rabi state average maize productivity where 100 % area is under hybrid maize cultivation.

Currently, maize is an important crop of India and being used as feed (poultry-47%, animal- 13%), starch and export (18%), direct (13%) and processed food (7%) etc. t present

Government has decided to use as major feedstock for bio-ethanol production. By 2030, we need nearly 65 million tonnes for meeting out the domestic requirements. Considering it, there is the strong needs of increasing the maize production and productivity in the country by developing high yielding climate resilient maize hybrids with better ethanol recovery, improving quality of by-products (reducing aflatoxin, improving nutritional quality) from maize ethanol, making ethanol extraction process more efficient and integrating innovative tools such as gene editing, DH, genomic selection and markers-assisted selection for accelerating genetic gain of ongoing improvement programme. Further there is need of diversifying the maize growing ecology and seed hubs, upscaling improved package of practices for bridging yield gap, developing storage, drying and transport infrastructure for proper handling of maize harvest.

TS-IV-IP-02

Development and scaling of hybrid rice by private sector in India

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The current world population exceeds 8 billion and will reach 9 billion in 2035. it is important that one of the ways to solve the food shortage problem is to greatly enhance the yield level of food crops per unit land area through the advance of science and technology. Rice is a main food crop. It feeds more than half the world population. It has been estimated that the world will have to produce 60 percent more rice by 2030 than it produced in 1995. Therefore, the increase in rice production plays a very important role in food security and poverty alleviation. For many years there has been evidence that hybrid rice has a more than 20 percent yield advantage over improved inbred varieties. Hybrid rice has proved a very effective approach to greatly increasing yield, (L Youn 2004). The development and scaling of hybrid rice in India have seen significant contributions from both the public and private sectors. The private sector, in particular, has played a crucial role in advancing hybrid rice technology and expanding its cultivation

Hybrid Rice History in India: Though the hybrid rice technology was developed and used in The People Republic of China during 1980s. The National Agricultural Research System took longer than anticipated time to adopt and develop this technology for India, Although the hybrid rice research was initiated during 1980 , the serious commitment was made during 1988-89 (Virmani S S 1993). Rice breeding was a monopoly of the Public sector in most countries till the 1980, however there were 16 private breeders in the world by 1993 . In India Mahyco, Pioneer (PHI Biogene) and Proagro were one of the early private companies involved in Hybrid rice breeding (Pray, 1993). Later EID Parry, Cargill seeds. In fact Cargill was one of the first companies along with Ring Around to collaborate with China since 1980 for global expansion of Hybrid rice technology. Many of the Japanese companies and were also collaborating with China during that period. (Siddiq, 1993). Apart from the seed companies, the initial support to the private sector were started by Mahyco research foundation (B R Barwale 1993). EID parry India was one of the companies which had direct collaboration with China National Rice Research Institute during 1994. PHI Biogene, (now Corteva) was a major player in the private sector seed industry, involved in the development and commercialization of hybrid rice in India. They have contributed to the advancement of hybrid rice technology by developing high-yielding and disease-resistant varieties. One of their first hybrid PHB 71 was notified for all India and was sold for a decade since it's launch in 1990. Along with PHB 71, Proagro' s PA6201, was one of the first hybrids to be in the market for a long time. Companies like Sandoz (Now Syngenta), Bioseed and ITC-Zeneca (now Advanta) started their work during 1990s

Companies Involved in Hybrid Rice Research in India: The private sector has developed numerous hybrid rice varieties tailored to different agro-climatic conditions. n India, there are 80 private seed companies actively involved in hybrid rice research and development. These companies play a crucial role in advancing hybrid rice technology and contributing to the country's rice production. As of recent reports, out of the 127 rice hybrids released in India, 89 have been developed by private companies. A survey by IFPRI (international food policy research Institute) about 90 percent of the hybrid rice farmers procured their required seed from private seed companies (Negi *et al*, 2020) Some of the leading hybrids from the private sector include as per the table below:

Company	Maturity segment	Hybrid Names
Bayer	Medium	Arize 6444 Gold, Arize8433DT
	Late	Arize Dhani,
Corteva	Mid Early	27 P 31 27P37 22P22
	Medium	28P67
Syngenta	Mid Early	S 4001
	Medium	S7002
	Late	S1001

Company	Maturity segment	Hybrid Names
VNR Seeds	Early	VNR 2111
	Mid Early	VNR 2222
Seed Works	Mid Early	US 312
Advanta	Early	PAC 207 Plus
	Mid Early	PAC 837 Plus
Kaveri	Mid Early	KPH468
Mahindra Agritech	Mid Early	MP3030
Tata Rallis	Mid Early	DRH 834
Savannah Seeds	Early	Sava 127, Vijeta, Sava300
	Mid Early	Sava 134, Sava 7501, Sava 7301
Pan Seeds	Mid Early	PAN 2423
Bioseed	Mid Early	Tana Tan

Impact and Growth of Hybrid Rice: Hybrid rice is cultivated on approximately 3 million hectares in India, with a significant portion of this area being managed by private sector initiatives. States like Uttar Pradesh, Jharkhand, Chhattisgarh, Madhya Pradesh, Odisha, and Haryana are major contributors. Hybrid rice technology is considered a sustainable option for boosting productivity growth. The adoption rate of hybrid rice technology, however, has remained sluggish. Hence a survey was conducted in 2020 by international food policy research Institute, which concluded that, the benefits from hybrid rice technology do not seem significant enough to incentivize its widespread adoption in India. Some of the reasons that the survey mentioned that hampers widespread adoption of hybrid seed technology was that

1. Hybrid rice is often grown in India under irrigated conditions but on poor soils.
2. A greater cost of irrigation as well as other inputs, such as fertilizers, essential for plant growth.
3. Lack of access to information on hybrids.
4. Lack of access to financial resources for frequent purchases of hybrid seeds, which are much costlier than the seeds of inbred varieties (Negi *et al*, 2020)

Yield and Economic Benefits: Hybrid rice varieties typically offer a 20-30% yield advantage over traditional high-yielding varieties (HYVs). This yield boost translates into higher income for farmers and contributes to food security[2.]

Public-private Partnerships: The success of hybrid rice in India is also attributed to effective public-private partnerships. These collaborations have facilitated the commercialization of hybrid seeds and the dissemination of best practices for hybrid rice cultivation.

Challenges and Prospects: Despite the progress, challenges such as unfavorable monsoons, inadequate yield heterosis, and the need for specific agro-management practices persist. Ongoing research and development efforts aim to address these issues and further enhance the adoption of hybrid rice1.

The private sector's involvement has been instrumental in making hybrid rice a viable and profitable option for Indian farmers, contributing significantly to the country's agricultural productivity and sustainability.

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Breeding for nutritional quality traits in maize: status and prospects

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Malnutrition has emerged as a major health issue worldwide. Consumption of food unbalanced in nutritional qualities affects metabolism, therefore affects normal growth and development. Malnutrition also causes increased morbidity, disability, abnormal physical and mental health, and contributes to poor socio-economic development. Poor quality diet can lead to different forms of malnutrition, including under-nutrition, micronutrient deficiencies, overweight and obesity. World leaders at United Nations framed several Sustainable Development Goals (SDGs) to provide the current nourishment needs and safeguard future generations. Among various approaches, 'Crop biofortification' – a process of increasing nutrient density in edible seeds through breeding, has emerged as the most promising approach. Compared to other approaches, biofortification offers several advantages *viz.*, (i) most sustainable (ii) cost-effective, and (iii) provides nutrients in natural form to alleviate malnutrition. Maize has emerged as the most important cereal crop of the globe. Apart from food and feed usage, maize also provides raw materials to corn syrup, emulsifier, textile-, paper- and adhesive- industries. However, traditional maize grain is poor in nutritional qualities such as protein quality (lysine, tryptophan and methionine), provitamin-A, vitamin-E, anthocyanins, iron and zinc. Availability of molecular markers associated with the target genes for nutritional quality provides great opportunity to accelerate the breeding cycle by involving nearly half of the time required in conventional breeding.

Biofortification in Maize

Maize protein is deficient in lysine and tryptophan, which is less than half of the recommended dose specified for human nutrition. Lysine and tryptophan serve as precursors for several neuro-transmitters and metabolic regulators, and their deficiency leads to reduced appetite, delayed growth, impaired skeletal development and aberrant behaviour in humans. The recessive allele of the *Opaque2* (*O2*) gene located on chromosome-7 causes doubling of lysine and tryptophan. Several *o2*-based Quality Protein Maize (QPM) hybrids have been developed through conventional breeding in India. However, with the advent of molecular markers, QPM hybrids have been developed through marker-assisted selection (MAS) as well. 'Vivek QPM9' released during 2008 is country's first MAS-derived maize hybrid. Later, several MAS-derived QPM hybrids *viz*., 'Pusa HM4 Improved' (2017), 'Pusa HM8 Improved' (2017), 'Pusa HM9 Improved' (2017), 'VL QPM Hybrid-45' (2022) and 'QPMH-6' (2024) have been developed for commercial cultivation. Further, a recessive *opaque16* gene present on chromosome-8 has also been found to increase nutritional value in maize. In addition, methionine an essential amino acid is also present in low concentration in maize grains. The deficiency of methionine is associated with fatty liver, atherosclerosis, neurological disorders, and tumorigenesis. Among several candidate genes, *floury2* located in chromosome-4 has been found to accumulate more methionine in maize. Breeders have now developed high methionine maize through MAS.

Vitamin-A is essential for normal body function such as proper visibility, maintenance of cell function, epithelial integrity, red blood cell production, immunity and reproductive systems. Though yellow maize possesses tremendous natural variation for carotenoids, it is predominated by lutein and zeaxanthin. Two genes, *lcyE* on chromosome-8 and *crtRB1* on chromosome-10 have been shown to regulate the accumulation of provitamin-A compounds. Several, provitamin-A rich hybrids *viz*., 'Pusa Vivek Hybrid-27 Improved' (2020), 'VL Vita' (2023) and 'PVAPMH-1' (2024) have been developed using MAS. Vitamin-E or tocopherol is an essential micronutrient for reproduction and quenches free radicals in cell membrane. It protects the humans from cardiovascular disease, Alzheimer disease, neurological disorder and many age-related degenerations. Maize kernels are rich in total tocopherol of which, γ-tocopherol constitutes ~80% and α-tocopherol accounts ~20% of the total pool. Due to favourable interaction with the receptor, α-tocopherol is present 10 times more than γ-tocopherol in plasma of humans. A favourable allele of *vte4* (chromosome-5) accumulates α-tocopherol by 3.2-fold. In India, 'Pusa Biofortified Maize Hybrid-5' (2024) and 'APTQH-1' (2024) possessing high α-tocopherol have been developed through MAS.

Anthocyanins are water soluble pigment with high antioxidant activity. It prevents several chronic diseases such as cancer, and reduces the risk of cardiovascular diseases, and obesity, besides improving visual and neurological health. Traditional maize grains are poor in nutritional quality as they do not contain anthocyanins required for proper growth and development in humans. Among various genes, *A1* gene (chromosome-3) has been identified as one of the major structural genes involved in the development of anthocyanin in endosperm and aleurone layer. Several experimental hybrids with ~150-450 ppm of anthocyanins in endosperm have been developed.

Humans require iron for basic cellular functions and proper functioning of the muscle, brain and red blood cells. Zinc is an essential mineral for humans, animals and plants for many biological functions. It plays a crucial role for more than 300 enzymes in the human body for the synthesis and degradation of carbohydrates, lipids, proteins and nucleic acids. However, phytic acid present in maize kernels reduces the bioavailability of iron and zinc as it chelates positively charged ions. Two mutations namely *lpa1* (chromosome-1) and *lpa2* (chromosome-1) possessing 66% and 50% less phytic acid compared to wild types, respectively have been used in the breeding programme. Three hybrids *viz*., 'PMH-1-LP' (2022), 'ALPQH-1' (2024) and 'ALQH-9' (2024) with low phytate have been developed through MAS strategy.

Several hybrids with combination of nutritional quality traits developed by MAS, have been released in India. 'Pusa Vivek QPM-9' (2017) earns the distinction of being world's first provitamin-A rich QPM maize cultivar. Similarly, 'Pusa HQPM-5 Improved' (2020), 'Pusa HQPM-7 Improved' (2020), 'Pusa HQPM-1 Improved' (2021), 'Pusa Biofortified Maize Hybrid-1' (2021), 'Pusa Biofortified Maize Hybrid-2' (2022), 'Pusa Biofortified Maize Hybrid-3' (2022) and Pusa Biofortified Maize Hybrid-4 (2024) were also rich in protein quality (lysine and tryptophan) and provitamin-A, and released for commercial cultivation in India. 'Pusa Biofortified Maize Hybrid-5' and 'APTQH-1' rich in protein quality, provitamin-A and vitamin-E have been identified for release in India.

Challenges

Despite the development of large number of QPM hybrids, its area remains small worldwide. QPM cultivars account for only 1% or less of 90 million hectares grown in Mexico, Latin America, Sub-Saharan Africa and Asia. India is also not an exception in this regard, despite the availability of diverse QPM hybrids. Successful adoption of biofortified maize cultivars depends on various factors related to research and development, socio-economic issues and policy interventions. Some of the factors that warrant urgent attention is mentioned below. It is perceived that nutritionally enriched crops possess low yielding potential. QPM, provitamin-A, vitamin-E, anthocyanins, iron and zinc do not have any yield penalty, and nutritionally enriched maize for these traits can provide grain yield similar to normal maize. However, germplasm base of nutritionally enriched maize is quite narrow, primarily due to the fact that very few breeding centres have active quality breeding. Therefore, strengthening of research collaborations among various national partners of the National Agricultural Research System (NARS) and international research organizations like CIMMYT and HarvestPlus would help in sharing novel germplasm and expertise for the development of biofortified maize. Attractive labelling and suitable branding highlighting the health benefits on products made from biofortified maize would help the consumers to choose more nutritious foods over conventionally available ones. To meet the industrial requirement, biofortified maize grains need to be systematically evaluated, and 'contract farming with buy-back policy' would ensure continuous supply of grains to the industry. Strong extension activities may play a major role in the popularization of biofortified crops. Further, specific training of extension workers and volunteers, arrangement of community drama, radio broadcasts, and other activities such as field days, training for grandmothers and community leaders, and market promotion events would help in the promotion of biofortified maize. Policy supports from the government are essential for the successful adoption of biofortified maize cultivars. Intensive awareness campaign supported by the government would help in popularization of biofortified maize for its nutritional value. The available biofortified maize can potentially contribute to the nutritional security especially in the North-Eastern states and tribal areas in India. Inclusion of biofortified maize in the government sponsored programs would help in further popularization. Enhanced minimum support price (MSP) should be provided to biofortified grains over traditional maize, as value of the nutritional quality should also be included while calculating MSP.

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Hybrid Wheat Breeding: Current status, challenges and way forward strategies

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Increasing human population of India around 1.5 billion in 2030 and 1.6 billion by 2050 (World Bank, 2020b), growing need for food and consumption by 4% per year (Gandhi *et al.,* 2012) bring about the necessity of improving crop yield by new ways. One of the most promising options is hybrid breeding, which offers advantages over inbred lines, such as higher yield potential due to heterosis, improved yield stability, biotic and abiotic stress tolerance, and nutrient use efficiency (Jordaan 1999; Longin *et al.*, 2013; Muhleisen *et al.*, 2014; Miedaner *et al.,* 2017).

Current status of hybrid wheat research, challenges and solutions: Hybrid wheat is commercially planted in some parts of USA, Europe and Asia, and accounts for less than 1% of the global wheat area (Gowda et al. 2012; Kempe et al. 2014). Area under hybrid wheat in Europe was increased from 100,000 ha in 2002 to 560,000 ha in the year 2017–2018 (Gupta et al. 2019). During 2009–2012, hybrid wheat varieties in China were grown on ~ 66,700 ha with an average yield improvement of 15.7% in 11 provinces. In India, the first hybrid wheat (Pratham 7070) was introduced by Mahyco in 2001 using CGMS system for cultivation under low input conditions of central and peninsular India, which is still under cultivation in area of about 10000 ha.

Major Factors affecting the Success of a Hybrid Program

(i) *Degree of heterosis*: Wheat hybrids exhibited an average yield advantage of up to 2.05 t/ha (10–20%) over the highest yielding pure line (Kempe and Gils 2011; Gowda *et al.,* 2012; Longin *et al.,* 2013), higher stability (Gowda *et al.,* 2010; Mühleisen et al. 2014), around 10% in Western Europe (Longin *et al*., 2013), 6–20% in the US Great Plains (Adhikari *et al.,* 2020b; Easterly *et al.,* 2020), 12% or 1.3 t/ha in about 6% of hybrids in Germany and France and 6.2–9.5% or 0.43–0.68 t/ha in CIMMYT, Obregon, Mexico, 10% in Mexico and 15% in India in best hybrids. In a survey done in India from 2001 to 2005 by a Maharashtra-based company Mahyco, hybrid wheat provided a yield advantage of over 0.9 t/ha on an area of 16,000–23,000 ha of small holder farmers field (Matuschke *et al.,* 2007). These examples clearly illustrate the potential of hybrid wheat in the context of climate change and future food security, but to ensure widespread adoption by farmers, the grain yield heterosis must be high enough to offset hybrid seed costs. Genome-wide approaches revealed role of genetic distance between parents and adaptability of parental lines (Melchinger and Gumber 1998), additive-by-additive epistasis (Yong Jiang *et al*., 2017, Philipp *et al*., 2020) and combining ability (Philipp, 2018) in driving heterosis in wheat. It may be desirable to identify and pyramid multiple dominant alleles of most favorable yield genes/QTL for heterosis (Gowda *et al.,* 2013; Zhao *et al.,* 2013; Jiang *et al.,* 2017). Genomic prediction of hybrid performance has been reported for grain yield (Zhao *et al.,* 2013; Zhao *et al.,* 2015), grain quality traits (Liu *et al.,* 2016) and flowering time and grain yield (Basnet *et al.,* 2018). In future, hopefully, further progress will allow genomic prediction of superior wheat hybrids with improved accuracy.

(ii) *Hybrid seed production system and ease of control pollination*: Production of commercial hybrids requires hybridization or cross-pollination between male and female parents with minimum manual intervention. This is mainly achieved through any of the following approaches, which are available in wheat: (1) cytoplasmic genetic male sterility; (2) artificial induction through chemical hybridization agent (CHA) or photoperiod /temperature treatment; (3) genetic male sterility.

(iii) *Availability/development of heterotic pools*: Heterotic groups are of major importance for the success of a hybrid breeding in the long run but are not yet available in wheat. Boeven *et al*. (2016b) proposed the HyBFrame approach to accelerate hybrid breeding and the establishment of heterotic groups by reciprocal recurrent selection with use of genome-wide marker profile with phenotypic data and genetic distance between groups.

(iv) *Female and male floral traits*: The crucial traits for male-female compatibility are plant height and flowering time. Females should flower about two days earlier than males to allow the florets to gap (Pickett, 1993). Males should be taller than females to facilitate pollen flow and to optimize female seed set (Virmani and Edwards, 1983; Pickett, 1993). Phenotypic selection assisted by molecular markers for candidate genes (Rht-D1a for tall plant, Rht-D1b and Rht24 for reduced height), could be effectively used to fine-tune plant height in the male and female parents. However, little is known about the genetic architecture and inheritance of floral traits of interest and further research is required.

(v) *Seed set and cost of hybrid seed production*: The seed set on female plants in hybrid seed production is the crucial parameter for the success of a hybrid wheat breeding as it determines seed costs and the competitiveness with line breeding. Seed set in hybrid crossing blocks is influenced by female traits (stigma size, exsertion or receptivity) and male traits (anther extrusion, pollen mass), environmental conditions (like temperature, relative humidity or daytime, wind) with suitable production locations, planting configuration, optimization of male–female ratio and nick adjustment (male is two to three days later in days-to-heading than the female to maximize seed set). Further research is required for phenotypic traits, genetic control, markers and genomic prediction of floral traits and its correlation for seed set, which can be used for female and male pools development. POWERPOLLEN^{TM} technology, proposed in maize, could also be useful in hybrid seed production in wheat and rice for pollination.

(vi) *Quantity of seed requirement for sowing per unit area*: Hybrids can tolerate and respond slightly reduced seeding rates compared to local practices for cultivars due to better seedling vigour and the ability to support slightly higher tillering capacity than cultivars. However, standardization of seed rate for hybrid wheat is an area that deserves more attention.

Way Forward Strategies for Hybrid Wheat Technology

Over the years, a significant progress in scientific understanding of hybrid wheat systems, in terms of genetics of heterosis, heterotic pool development, seed production dynamics, markers development and prediction of heterosis have been made. The key task now is putting all these together to design and develop commercially viable hybrid wheat varieties in a sustainable way by focusing on Public-Private Partnership for Hybrid – Parent Research and Development Consortium for female and male parental lines development, development of female and male heterotic pools with high GCA, desirable traits, floral traits, wider adaptability, genetic diversity in different hybrid production system, optimization of female to male ratio, nicking requirement, mapping of suitable production locations, standardization of seed rate for hybrid for different agro-climatic regions and conditions, marker development for desirable agronomic traits and floral traits, identification and pyramiding of multiple alleles for yield genes/QTL and heterosis, genomics based prediction model for hybrid performance with high accuracy, gene editing for important agronomic and floral traits, Speed breeding and doubled haploid (DH) / DH inducer technology to speed up breeding cycles.

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Hybrid millets and sorghum breeding

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Millets pioneered the hybrid development in India and the first hybrids were developed in sorghum (1964) and pearl millet (1965) which further led to the evolution of the hybrids seed industry in the country. The hybrids in these two millets have enhanced the productivity and contributed to sustained area under the cultivation while the area under varieties came down drastically due to lower productivity.

Pearl millet is a climate smart crop suitable for diverse ecologies. Highest annual yield gains of >5% have been reported due to exploitation of its outcrossing nature in developing commercial single cross hybrids. To date a total of 207 hybrids and 66 varieties are released for cultivation in diverse agro-ecologies. Of the total pearl millet cultivated area, the hybrids occupy majority of the area having an annual rainfall of >400 mm, sandy loam to moderately heavy soils and with adequate number of inputs. The varieties are confined to drought or heat prone ecologies lacking suitable climatic and agronomic conditions. Also, decade-long trial data from the Indian national cultivar release system have indicated that hybrids have shown yield superiority of about 25% over landraces/OPVs in highly drought-prone ecologies. Hybrid breeding provides ample opportunity to utilize diversity to harness maximum heterosis, and yet produce a cultivar with a high degree of morphological uniformity. After release of first hybrid HB1 in 1965, only 5 hybrids were released till 1969, due to downy mildew epidemic caused due to narrow variability in the cultivated cultivars. Due to strong hybrid programs both in the public and private sectors, there is significant diversity in the parental lines and hybrids with about 70–80 hybrids cultivate on the farmers' field at any point in time in India. This along with high hybrid replacement rate has contained downy mildew (Gupta *et al*., 2024). Currently, India is the largest grower of pearl millet in the world on 7.0 m ha of which dual-purpose hybrids occupy about 4.5-5.0 m ha.

In the last four decades, hybrid breeding has received a very high priority in India, using genetically diverse parental lines targeting various production ecologies. Product profiles are those defined by breeders to replace existing products in a particular ecology. Most of the pearl millet breeding programs in the public and private sectors in India have developed and working on their product profiles, depending on the need of their target mega-environment. For hybrid cultivars, high grain yield, pest and disease resistance, benchmark levels of Fe and Zn, and maturity duration of 75–85 days, as per the agro-ecological requirements, have been accorded the highest priority in pearl millet.

Diverse CMS sources are available in pearl millet, of which A_1 CMS system is extensively used by the public and private sector breeding programs. The other alternate CMS systems, A_4 and A_5, could not be exploited on a large scale due to lack of sufficient restorers. Studies assessing molecular diversity classified inbred lines into genetically distinct groups and confirmed the existence of two broad-based pools in hybrid parents—one for seed parents and another for restorer parents and these behave as two separate broad heterotic pools.

In sorghum, commercial exploitation of heterosis has been possible owing to the availability of a stable and heritable CMS mechanism which enables large-scale, economic hybrid seed production. Systematic effort for the improvement of sorghum in India started during 1960s by manipulating the genes controlling height and maturity by introducing American germplasm. The first hybrid, CSH 1, developed by crossing the MS line CK 60 (Milo (A_1) cytoplasm) with the germplasm line, IS 84, was an early duration dwarf hybrid released in 1964 for cultivation that resulted in quantum jump in the productivity. CSH 1 became most popular as it had high yield potential, suited to light soils and low rainfall areas. Remarkable progress was achieved during the next five decades by diversifying the parental lines for yield, maturity, height, disease and insect tolerance, and quality by utilizing indigenous and exotic germplasm. New hybrids with diverse genetic background such as 2077A, 2219A and 296A recorded substantial increase in yield and adaptability. Genetic improvement in plant type and resistance to stresses in a systematic manner has resulted in the development and release of high yielding grain hybrids (3.0-4.2 t ha^{-1}) and varieties (2.8-3.8 t/ha) gradually over a period of five decades. Next set of hybrids were based on newer female parents specifically for *kharif* and *rabi* adapted hybrids, forage sorghum and sweet sorghum, including from alternate cytoplasm such as in A_2 background. The greater contribution of hybrids to yield, compared to improved and landrace varieties has been demonstrated in almost every situation/condition. To date, AICRP on Sorghum has released 48 hybrids and 52 varieties under different product types such as grain, forage and sweet sorghum types. In *kharif*, high productivity, grain mold resistance and possibly mechanical combine harvest may minimize losses and keep sorghum competitive.

For the development of forage sorghum hybrids, sorghum lines with forage traits and Sudangrass introgression lines were used as male parents. The CMS lines possessing A3 cytoplasm were reported to be good combiners for important fodder yield and quality traits, indicating that A3 cytoplasm based female lines can also be used as hybrid parents, diversifying the male sterility source of forage sorghum hybrids. hybrids New female parents for sweet-stalked sorghum hybrids for biofuel purpose were also developed that led to 15-20% more potential bioethanol yields over varieties.

Although several hybrids have been developed and released for *rabi* season cultivation, the area covered with hybrids in rabi season is almost negligible due to low levels of heterosis and grain types that are not preferred by consumers. Consumer preference revolves around bold, round and lustrous seed as that of local variety *Maldandi*. Therefore, there is a dire need for developing new hybrid parents for *rabi* that not only exhibit good adaptation and yield potential than the varieties and also match the varieties in consumer preferences for the grain.

Genomic prediction can be used in breeding programs of hybrid development in millets based on estimated breeding values from genome-wide sets of markers for rapid development of desired genotypes through genomic selection. It is also found that for the purpose of genomic selection, a small number of selected single nucleotide polymorphisms (SNPs) can achieve relatively high prediction accuracy in the pearl millet population. Genomics and genomics-assisted breeding can help improve the precision and efficiency of the hybrid breeding program.

TS-IV-IP-06

Hybrid pigeonpea breeding in India: retrospect, status and prospects

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Pigeonpea is an important food legume crop of the semi-arid tropics. It is cultivated in 6 mha area producing 5.3 mt annually, with an average yield of 861.2 kg/ha (FAOSTAT, 2022). More than 80% of the global pigeonpea area is in India followed by Myanmar (7.4%), Malawi (4.3%), Kenya (2.4%) and Tanzania (2.4%). In India, 3.4 mt of pigeonpea is produced annually (DAFW, 2024). Consistent research efforts have been made to enhance the yield levels of pigeonpea. In this context, exploitation of heterosis remains a promising approach to improve crop performance owing to the often-cross pollinated nature of the crop.

Since the first case of male sterility was documented in pigeonpea (Deshmukh 1959), a variety of male sterility systems have been reported as a genetic mechanism to facilitate hybrid breeding and seed production in pigeonpea. Discovery of male sterility in pigeonpea gave an impetus to its hybrid breeding program. Unlike previous male-sterile plants showing several floral abnormalities, Reddy et al. (1978) found male-sterile mutant plants in pigeonpea that exhibited normal floral characteristics except translucent anthers, and the ability to maintain these male-sterile plants paved the way for production of hybrids in pigeonpea. Based on the genic male sterility (GMS) system, six hybrids were released between 1991 and 1998 in India which showed varying level of heterosis e.g., ICPH 8 (30-40%), PPH 4 (14%), CoH 1 (19-22%), CoH 2 (35%), AKPH 4104 (64%) and AKPH 2022 (25-35%). However, identification of the fertile sibs, which account for half of the population in the maintenance block (*Msms* × *msms*), could not be proven economically-viable and the entire process of removing undesirable plants contributed to substantially increase the seed production cost. Due to challenges in seed production, the pigeonpea hybrid breeding witnessed a shift towards the use of cytoplasmic genetic male sterility (CMS) technology for production of commercial hybrids.

Nine sterility-inducing cytoplasms (designated as A_1-A_9) have been reported in pigeonpea, of which only two derived from *Cajanus scerabaeoides* and *Cajanus cajanifolius* have been used for production of hybrids (Bohra *et al*., 2022). In India, seven pigeonpea hybrids have been released so far by using CMS technology, which include GTH-1 (2006), ICPH 2671 (2014), ICPH 2740 (2015), ICPH 3762 (2014), IPH 15-03 (2019), IPH 09-5 (2020), and most recently, Pusa Arhar Hybrid 5 (Pusa Arhar Yamuna) (2022). The hybrid IPH 15-03 was the first early pigeonpea hybrid released for north-western plain zone (NWPZ) by ICAR-Indian Institute of Pulses Research (IIPR), Kanpur. The two hybrids developed at ICAR-IIPR *i.e*. IPH 15-03 and IPH 09-5 have the yield potentials of 2,426 kg/ha and 2,293 kg/ha, respectively with 28.3% and 30.5% superiority over the best check. High yields, disease resistance and early maturity (<150 days) of the two pigeonpea hybrids make them highly suitable for use in pigeonpea-wheat rotation system. In the NWPZ region, the pigeonpea-wheat rotation system enabled by the two early pigeonpea hybrids has the potential to replace the existing wheat-rice cropping system (RWCS), which because of its intensive nature (labour, water, capital and energy) has been facing increasing challenges in terms of profits, production and sustainability. Given the uniqueness of the advantages offered by the two pigeonpea hybrids IPH 15-03 and IPH 09-5, the two hybrids featured among the 35 unique crop varieties dedicated to nation on September 28, 2021 by our honorable Prime Minister, Shri Narendra Modi ji (https://krishijagran.com/agripedia/complete-details-of-35-crop-varieties-released-by-pm-modi/). At ICAR-IIPR, Kanpur, several new CMS lines have also been developed in diverse genetic backgrounds for application in hybrid breeding and potential pollen donors have been identified that could restore complete fertility in the hybrids derived from these CMS lines (Bohra *et al*., 2017a).

Quest for a more efficient system for seed production has also led to the identification of alternative genetic systems for pollen sterility in pigeonpea, such as temperature-sensitive genic male sterility (TGMS). A preliminary report suggests that the temperature-sensitive lines derived from the cross between its wild relative (*Cajanus sericeus*) and a cultivated type/accession (ICPA 85010) show marked changes in their fertility status based on the temperature regimes (Saxena 2014). The lines Envs S-1, Envs S-2, Envs S-3 and Envs S-5 produce fertile pollen grains at ≤24°C while remain completely male sterile at ≥24°C. Further diversification of the sources for male sterility in pigeonpea calls for investigating the fertility transitions according to photoperiod lengths as well. Availability of such robust and efficient environment-sensitive genetic systems of pollen sterility will help circumvent the need for maintaining a sterile line while overcoming the dependency on the fertility restorers for hybrid production.

Large-scale seed production remains a herculean challenge given the need for isolation distance in seed production plots. To ensure widespread use of the new pigeonpea hybrids, ICAR-IIPR, Kanpur has made significant efforts to license with several private seed companies. There is also a need to use modern genomic and breeding tools to make hybrid breeding of pigeonpea more efficient. The utility of DNA marker technology (e.g., simple sequence repeats) for testing the genetic purity of hybrids and parental lines has been demonstrated in recent studies and the low-cost and rapid molecular assays have emerged as a great support to the traditional grow-out-test (Bohra *et al.*, 2017b; Saxena *et al.*, 2010). Also, the DNA markers tightly associated with CMS-restoration trait are useful not only for rapid identification of potential restorer lines but also to enable rapid and precise introgression of fertility restorer gene (*Rf*)/ *Rf*-containing genomic segments to good agronomic bases, thus speedily converting these elite lines into restorers for hybrid development (Bohra *et al.*, 2016). In absence of these DNA markers identification of restorers necessitates extensive field-testing of progenies derived from A × R crosses and the phenotypic assays cannot be performed before the onset of flowering. Similarly, genetic marker technologies may be helpful in prediction of genetic worth of a large number of untested hybrid combinations (Saxena *et al.*, 2021). Long-term gains from hybrid breeding in pigeonpea would require implementation of genomic prediction for the establishment of heterotic groups and identification of high heterotic patterns.

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TS-IV-IP-07

The hybrid mustard breakthrough: Bridging innovation and farmer profitability

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India is the world's third-largest producer of rapeseed-mustard, contributing 12% to global production and playing a pivotal role in the country's agricultural economy, especially in oil seed. Accounting for nearly one-third of India's edible oil production, the crop is a critical source of income for small and marginal farmers, especially in rain-fed regions. However, a significant gap between domestic production and consumption persists, necessitating substantial edible oil imports. Enhancing domestic production offers significant potential for import substitution, reducing dependency on imports.

To address this challenge, development and introduction of mustard hybrids during early part of the century met with limited success due to unreliable seed production system. During the subsequent decade, a series of comprehensive and integrated interventions by private sector led to rapid adoption of hybrid technology by farmers from 2010 onwards. The evolution of hybrid mustard over the past decade has been driven by a combination of market needs, technological advancements, and focused product development strategies. Key factors contributing to this success include higher yield potential, enhanced oil content, improved hybrid purity, and robust resistance to biotic stresses. Critical milestones such as the development of cytoplasmic male sterility (CMS) systems, efficient restorers, and targeted production improvements have strengthened the foundation of hybrid mustard. Strategic market development initiatives, with a focus on priority districts and economic benefits under low commodity price scenarios, have further expanded its adoption.

Based on market feedback, future improvements in hybrid mustard focus on addressing biotic stresses such as resistance to sclerotinia, Striga, and Alternaria, while also targeting a 3–4% increase in oil percentage and improved oil quality with reduced glucosinolates. Yield-contributing traits such as larger seed size, enhanced test weight, shorter internodal lengths, increased siliqua numbers, and optimized pod branching are also identified as critical areas of improvement. Abiotic stress tolerance, including frost and drought resilience, alongside secondary traits like aphid tolerance, remain key targets for genetic enhancement.

To ensure sustained growth, the following strategies are recommended:

- Accelerated breeding programs emphasizing genetic diversity and access to novel germplasm and resistance sources.
- Marker-assisted selection (MAS) for biotic and abiotic stress traits.
- Gene-editing technologies for critical traits, including disease tolerance, herbicide tolerance, and improvements in oil quality and quantity.
- Optimization of production locations to improve seed yield and the development of new products tailored to underserved markets or delayed-season cultivation.

This multi-pronged approach underscores the potential of hybrid mustard as a resilient, high-value crop capable of addressing emerging challenges and expanding its contribution to the agricultural economy.

TS-IV-IP-08

Heterosis breeding in oilseeds crops

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The vegetable oils are indispensable in the human food as also in several industrial uses. The oilseed sector constitutes an important determinant of agricultural economy in India. Oilseeds are the second largest agricultural commodity in India after cereals occupying about 13-14% gross cropped area. They account for 1.4% of gross domestic product (GDP) and 7% of value of all agricultural products (2021-22). About 14 million farmers are involved in oilseeds production and processing. India ranks first in the production of castor, safflower and niger, third in rape-seed mustard, sesame, fourth in linseed, fifth in soybean and seventh in sunflower in the world. Currently, India accounts for 12-15% of world's oilseeds area, 7-8% of world's oilseeds output, 6-7% of world's vegetable oil production, 9-12% of world's vegetable oil import and 9-10% of world's vegetable oil consumption. The diverse agro-ecological conditions in the country are favourable for growing all the nine annual oilseeds, which include seven edible oilseeds *viz.,* groundnut, rapeseed – mustard, soybean, sunflower, sesame, safflower, niger and two non-edible sources *viz*., castor, linseed. One or more oilseed crops are cultivated in every state in the country. Madhya Pradesh, Gujarat, Rajasthan, Andhra Pradesh, Maharashtra, Karnataka, Tamil Nadu and Uttar Pradesh account for nearly 90% of oilseeds area and production in the country.

Hybrid Technology in Oilseeds

Heterosis is a prevalent genetic phenomenon utilized extensively in sunflower, castor and safflower. The unique floral biology of these oilseeds has resulted in developed of male sterile lines with genetic male sterile system, environment driven male sterile and cytoplasmic male sterile system. Currently, large number of hybrids in sunflower, castor and safflower are being commercially cultivated in the country.

Sunflower: Sunflower (*Helianthus annuus* L.) is an important edible oilseed crop of the *Asteraceae* family. It is well suited for hybrid breeding due to its cross-pollinated nature. Hybrid sunflower became a reality with the discovery of cytoplasmic male sterility and effective male fertility restoration system during 1970. Due to ever increasing supply demand gap for edible oilseeds, heterosis breeding is being viewed as a main driving force for productivity enhancement and has been commercially exploited in sunflower. In the world, the first CMS-based commercial sunflower hybrids were made available in 1972 in the USA. In India, the first CMS based hybrid (BSH-1) was released for commercial cultivation in 1980. Till now more than 60 hybrids have been released from the public as well as private sectors. Majority of the released hybrids are location specific and are highly susceptible to downy mildew disease. From ICAR-IIOR, Hyderabad recently two hybrids (TilhanTec-SUNH-1 and TilhanTec-SUNH-2) have been released for commercial cultivation. Both the hybrids having high seed and oil yield potential and resistant to downy mildew and moderately resistant to leafhoppers. Nearly 95% of the area in the crop is covered by hybrids due to high yield potential, suitability to intensive management conditions, resistance to major diseases, high autogamy (%), uniformity in crop stand, and maturity.

Three biological requirements for successful hybrid seed production include the presence of hybrid vigour, elimination of fertile pollen in the female parent, and adequate pollination by the male parent. Once a new hybrid is released, only a small quantity of nucleus seed of released population or A, B, and R lines of F_1 hybrid is available with the breeder for further multiplication. Seed production or multiplication is a very specialized activity as it often requires specific season and areas for seed production, supplementary pollination by manual hand pollination, adequate isolation distance, staggered sowing of male and female parents, planting methods, planting ratio of seed as well as pollen lines, rouging, and field inspection. Hence, a rigorous practical knowledge of climatic requirements, crop biology, and pollination techniques is the basic requirement for under taking quality hybrid seed production of sunflower.

Castor: Castor is a typical cross pollinated crop due to monoecious inflorescence, nevertheless, pollen can fertilize the female flower of the same plant. Heterosis or hybrid vigour upto 80% for seed yield is documented which is largely due high number of female flowers in the spikes, number of effective spikes per plant, 100 seed weight and number of capsules per spike.

The first castor hybrid, GCH-3 based on the exotic pistillate line, Texas stable Pistillate (TSP)-10R was released in 1968. Development of indigenous pistillate line, VP-1 based on TSP-10R gave new impetus to hybrid castor development programmes in the country. The release of GAUCH-1 in 1973 has transformed castor cultivation in the state of Gujarat. This hybrid became popular even in the rainfed areas of Telangana, Andhra Pradesh, Maharashtra, Orissa, and Karnataka due to its high yield potential and tolerance to intermittent dry spells during monsoon which is a common feature.

The research efforts initiated during the latter part of 70's resulted in the development of first ever wilt resistant hybrid *viz.,* GCH-4 which was released in 1986 for commercial cultivation in entire castor growing areas of the country. During later part of 1990's, several other high yielding hybrids *viz.,* DCH-32, DCH-77, GCH-5, GCH-

6, GCH-7, DCH-519, GCH-8, PCH-1, YRCH-1, ICH-66, ICH-5 and ICH-6 were released for rainfed and irrigated regions of castor cultivation.

Hybrid seed production in castor is mainly based on exploitation of environmentally sensitive polymorphic pistillate expression of N, S and NES-type. Sex expression in castor is polymorphic and varies from monoecious, pistillate, pistillate with ISF, sex reversion etc. Female promoting environment (F) includes mean day temperatures <32°C, young age, irrigation and good nutrition. Maintenance of pistillate lines in hybrid seed production with pistillate lines with environmentally sensitive genes for production of ISF as a pollen source in summer season. Seed production standards have been revised to suit the refined method of maintenance of pistillate line as it results in 98% genetic purity, less labour cost for roughing and low cost of production.

Safflower: Safflower (*Carthamaus tinctorius*) is predominantly a self-pollinated crop, however, some extent of cross-pollination occurs mainly through honeybee indicating the scope to develop hybrid technology. The discovery of genetic male sterility (GMS), both dominant and recessive types encouraged safflower breeders to initiate development of commercial hybrids. Genetic male sterile line produces both male sterile and fertile plants. Several GMS lines were available in safflower. In the existing GMS lines, the male sterile and fertile sister plants can be differentiated only at flowering stage. Flowers in male sterile plants appear like a pinched brush and are devoid of pollen, whereas flowers in fertile plants have normal appearance and produce abundant pollen.

The first GMS-based safflower hybrid DSH 129 was released (Anjani 1998) for commercial cultivation in India. Genetic male sterility (GMS), and thermo sensitive genetic male sterility (TGMS) lines were developed in India. Development of agronomically superior genetic male-sterile lines in safflower in India have resulted in the development and release of spiny safflower hybrids DSH-129 and MKH-11 in 1997 and NARI-H-15 in 2005, the first nonspiny hybrid safflower NARI-NH-1 in 2001. These hybrids in general exhibit an increase of 20 to 25% increase in seed and oil yield over the national check A-1.

However, hybrid seed production of GMS based hybrids at a commercial level is constrained because of incomplete or delayed rogueing of fertile plants from the female parent population. This compelled the development of cytoplasmic-genic male sterile lines that would overcome these constraints and facilitate hybrid seed production. Cytoplasmic-genic male sterile lines were developed an interspecific cross was made between *Carthamaus oxyacantha* and the cultivated species *C. tinctorius* to develop a cytoplasmic-genic male sterility (CMS) system in safflower. *C. oxyacantha* was the donor of sterile cytoplasm (Anjani 2005). A CGMS based hybrid DSH-185 with a yield advantage of 1430 (rainfed) - 1740 (irrigated) has been released for all India cultivation during 2018 from ICAR-IIOR.

Challenges in Hybrid Breeding

One of the major challenges would be to develop newer hybrids for diverse situations and superior to those presently grown in terms of seed and oil yield to sustain the competitive ability of sunflower vis-a-vis other crops. A major lacuna in the present Indian breeding programme has been the lack of strong approach to develop large number of inbred lines and evaluate them for their nicking ability and convert the promising ones into stable male sterile lines. Maintenance of genetic purity of the parental lines of the released hybrids is one of the most difficult aspects and this has not received adequate attention till now.

Future Thrust

- Development of stable non revertant pistillate lines with environmentally sensitive genes for ISF expression in castor
- Development of pistillate lines resistant to biotic stress like gerymold, jassids, semi -looper and capsule borer in castor, resistance to powdery mildew, *Alternaria* leaf spot in sunflower and safflower
- Diversification of CMS sources and synthesis of diverse and heterotic gene pools and identification of good maintainers and restorer lines
- Development of agronomically superior CMS lines with dwarfness, early maturity, to fit into different copping system and high density cropping pattern
- Exploitation of the full potential of the hybrids in rainfed conditions for castor and safflower.

Conclusion

The demand for high-yielding hybrids of oilseeds has increased due to the government's pressure to curtail the import of edible oils. For the sustenance of these crops in the future, it is an obligation to develop agronomically superior hybrids of sunflower, castor, and safflower which can fit into different cropping patterns across diverse agro-ecological cropping systems.

List of commercially potential hybrids

Crop	Hybrids	Special features
Sunflower	**KBSH-88 (2021)** Gujarat, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu and Telangana	♦ Days to maturity (91-95 days); Yield (1600-2200 kh/ha) Oil content (35-37%) ♦ Resistant to downy mildew disease and moderately resistant to leafhoppers
	Tilhan SUNH-1 (2021) Uttarakhand and Jammu & Kashmir, Gujarat, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu and Telangana	♦ Days to maturity (92-96 days); Yield (1648-2411 kh/ha) Oil content (35-37%) ♦ Resistant to downy mildew disease and moderately resistant to leafhoppers
	KBSH-88 (2024) Uttarakhand and Jammu & Kashmir, Gujarat, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu and Telangana	♦ Days to maturity (86-88 days); Yield (1600-2200 kh/ha) Oil content (35-36%) ♦ Resistant to downy mildew disease and moderately resistant to leafhoppers
	Tilhan SUNH-2 (2024) Gujarat, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu and Telangana	♦ Days to maturity (89-91 days); Yield (1519-1657 kh/ha) Oil content (37-40%) ♦ Resistant to downy mildew disease and moderately resistant to leafhoppers
Castor	**GCH-8 (2018)** Gujarat, Rajasthan, Haryana, Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Odisha and Maharashtra	♦ Yield (1500-1895 kg/ha); Oil content (48 %) ♦ Resistant to *Fusarium* wilt, *Macrophomina* root rot and leafhopper
	ICH-66 (2019) Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Odisha and Maharashtra	♦ Yield (1560-1750 kh/ha); Oil content (46-49 %) ♦ Resistant to *Fusarium* wilt, *Macrophomina* root rot and leafhopper
	ICH-5 (2021) Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Odisha and Maharashtra	♦ Yield (1671 kh/ha); Oil content (48 %) ♦ Resistant to *Fusarium* wilt, *Macrophomina* root rot and leafhopper
	ICH-5 (2024) Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Odisha and Maharashtra	♦ Yield (1516 kh/ha); Oil content (47 %) ♦ Resistant to *Fusarium* wilt, *Macrophomina* root rot and leafhopper

Crop	Hybrids	Special features
Safflower	**DSH-185 (2013):** Maharashtra, Karanataka, Telangana, Madhya Pradesh and Chhattisgarh.	♦ Rainfed yield 1430 kg/ha; Irrigated yield - 1740 kg/ha; Oil content (28-29 %)
	ISH-402 (2019) Maharashtra, Karanataka, Telangana, Madhya Pradesh and Chhattisgarh.	♦ Irrigated yield - 2325 kg/ha; Oil content (28-30%)

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TS-IV-IP-09

GM cotton hybrid breeding

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Cotton cultivation is crucial to India's agricultural economy and textile industry, contributing about 25% of global cotton output. It supports 6 million farmers and generates 10 million jobs in the textile sector. The cotton industry contributes 2-3% to India's GDP and drives substantial export revenues, exceeding 580 billion rupees annually. With India's population projected to reach 1.5 billion by 2030, cotton consumption is expected to rise. To meet this demand, cotton lint production must double by 2030, requiring improved yields and better agronomy practices to break the yield plateau.

Overview on Global Lint Productivity

India's lint productivity is significantly lower compared to leading cotton-producing countries like Australia, Brazil, China and the United States (Table 1).

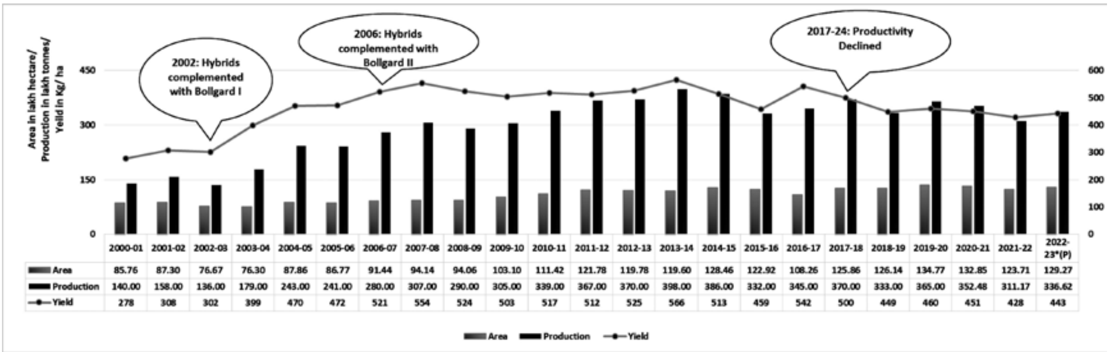
Table 1. The lint productivity (kg per hectare) for cotton in the top cotton-producing countries

Country	Lint Productivity (kg/ha)	Lint Percent Range
Australia	~1,800	41.0 – 45.0
Brazil	~1,500	40.0 – 45.5
China	~1,200	37.5 – 41.2
United States	~900	40.0 – 45.0
India	~500	33.0 – 35.0

The gap in productivity is largely due to majority of cotton production area (around 65% of cotton cultivation) lies in rainfed region coupled with light shallow soil with poor soil fertility, differences in ability of genotypes to lint yield per hectare, farming practices, access to technology, irrigation, Trade policy and overall infrastructure. Increasing India's lint productivity will require focused efforts to develope better genotypes, improving agricultural practices, introducing advanced technology and enhancing irrigation facilities.

Crop Improvement Phases in Enhancing Indian Cotton Yield

Before 1970, cotton productivity in India was below one bale per hectare due to traditional varieties and limited crop management knowledge. In 1970, Dr. C.T. Patel introduced the first cotton hybrid, 'H 4' (Sankar-4), which significantly increased productivity, reaching 340 kg of lint per hectare. Hybrid cotton area expanded from



	2000-01	2001-02	2002-03	2003-04	2004-05	2005-06	2006-07	2007-08	2008-09	2009-10	2010-11	2011-12	2012-13	2013-14	2014-15	2015-16	2016-17	2017-18	2018-19	2019-20	2020-21	2021-22	2022-23*(P)
▬ Area	85.76	87.30	76.67	76.30	87.86	86.77	91.44	94.14	94.06	103.10	111.42	121.78	119.78	119.60	128.46	122.92	108.26	125.86	126.14	134.77	132.85	123.71	129.27
▬ Production	140.00	158.00	136.00	179.00	243.00	241.00	280.00	307.00	290.00	305.00	339.00	367.00	370.00	398.00	386.00	332.00	345.00	370.00	333.00	365.00	352.48	311.17	336.62
—●— Yield	278	308	302	399	470	472	521	554	524	503	517	512	525	566	513	459	542	500	449	460	451	428	443

Source: https://cotcorp.org.in/statistics.Aspx

3% in 1975 to 40% by 1997. The introduction of *Bt* technology in 2002 ensured the potential yields, peaking at 566 kg per hectare in 2013-14. Bt cotton hybrids, which covered 94% of India's cotton area by 2021, reduced pest damage, pesticide use and improved farmers' income.

Advantages of Hybrids

Hybridization is a powerful technique to break yield barriers, cotton hybrids yield 50% more than traditional varieties due to heterotic potential. Hybrids offer a broader genetic base and wider adaptability, combining the genetic traits of both parent lines for better performance in diverse environments. In India, hybrids thrive in rainfed areas with poor soil and limited irrigation due to their early vigour and response to optimized crop management. They integrate multiple traits, such as higher yields and improved fiber quality. Hybrids also show resilience to biotic and abiotic stresses, making them a valuable choice for farmers, especially those with marginal land holdings.

Challenges in Cotton Production

Since 2017, Indian cotton productivity has sharply declined to 429 kg/ha due to several factors. Pink bollworm (PBW) resistance to Bt cotton, lack of new technology adoption, climate change, including erratic rainfall and temperature fluctuations, limited germplasm, insufficient agronomic practices, diseases like boll rot, low mechanization, and poor ginning out turn have further contributed to the decline in cotton production. This combination of biological, environmental, and technological factors has created a challenging landscape for cotton production, necessitating urgent action and innovation to address these issues effectively.

Breeding Strategies and Selection Methods

Breeding strategies and selection methods have significantly advanced with the development of genetic technologies, improving both time and cost efficiency in crop improvement. Traditional breeding relied on phenotypic selection was slow and resource-intensive due to long generation cycles and large-scale field trials. In contrast, molecular breeding using techniques like marker-assisted selection (MAS) enables earlier selection based on genetic potential, also helps in reducing time and costs by avoiding lengthy field trials.

Genetic transformation in cotton, including *Bt* cotton, herbicide resistance, and RNA interference (RNAi), has revolutionized cotton improvement. *Bt* cotton, which incorporates genes from *Bacillus thuringiensis*, provides resistance to key pests like bollworms, reducing pesticide use and preventing yields loss. Herbicide-resistant cotton enables farmers to manage weeds more effectively. RNAi technology offers potential for silencing specific genes to control pests or improve disease resistance. Gene editing tools like CRISPR-Cas9 further enhance precision, allowing for targeted modifications to improve traits such as drought tolerance, fiber quality, and pest resistance for ensuring sustainable cotton production

Speed breeding further accelerates the process by manipulating environmental factors such as light and temperature to hasten plant growth. This allows multiple breeding cycles within a year, improving time efficiency while reducing resource usage. Speed breeding optimizes space and labour, lowering long-term costs.

Genomic selection takes molecular breeding a step further by using genome-wide data to predict plant performance for multiple traits such as yield and resistance. It reduces the need for extensive field trials, allowing quicker identification of superior plants, facilitates faster responses to market demands and environmental changes. Genomic selection also integrates high-throughput phenotyping, further reducing time and costs by enabling large-scale, cost-effective trait analysis.

The potential of haploid inducer line development and the double haploid technique in cotton breeding is highly promising and remains largely untapped. The successful implementation of these technologies is expected to transform the speed and efficiency of developing new cotton cultivars.

The integration of double haploid technology, genomic selection, gene editing, and high-throughput phenotyping holds immense potential for accelerating cotton improvement and integration these technologies can revolutionize cotton breeding.

Breeding Objectives

Breeding objectives in cotton focus on developing new cotton hybrids with specific traits and characteristics that address the needs and challenges of cotton production. The specific breeding objectives in cotton vary by region and over time, but some common goals include the development of early to medium-duration hybrids, enhancing CLCuVD and TSV tolerance, improved resistance to sucking pests, improved resistance to the bollworm complex, enhancing disease resistance, stay-green and para-wilt tolerance, improving tolerance to environmental stresses, improving fiber yield with varying fiber quality parameters, and adapting to different agronomic practices such as closer spacing and high-density planting systems (HDPS). These objectives are designed to develop more productive, resilient and sustainable cotton hybrids that align with market demands and environmental considerations.

Strategies for Strengthening Global Competitiveness, Enhancing Cotton Productivity and Profitability in India

India is the second-largest cotton producer and exporter globally, cultivating cotton on approximately 130 lakh hectares, with an annual production of 53.8 lakh tonnes. Despite these numbers, India ranks 44th in cotton productivity, with growth stagnating over the last 5-7 years. This productivity gap negatively impacts cotton farmers and the textile industry.

Challenges hindering cotton production include labour scarcity, rising wages and increased input costs which is forcing many long-term cotton farmers to abandon cultivation. To overcome these challenges and enhance cotton's profitability, mechanization and advanced agronomy practices are highly crucial. Cotton picking is a labour-intensive process which accounts for 30-35% of cultivation costs. Mechanization especially in planting, spraying and harvesting can address labour shortages and rising production costs.

However, small land holdings and tall cotton hybrids make mechanization difficult in India. The adoption of High Density Planting System (HDPS) can help by using short-duration, semi-compact cotton hybrids planted at high densities (60,000–75,000 plants/ha). This system optimizes mechanical operations and increases yield by maximizing boll production per unit area, leading to higher productivity.

Improving the Ginning Out-Turn (GOT) from 35% to 42% can further boost profitability by increasing usable fiber. This will improve India's competitiveness in the global market, support sustainable farming and stabilize cotton production. These strategies aim to enhance productivity, making cotton a more profitable and sustainable crop benefiting both farmers and the broader economy, while strengthening India's position in the global cotton industry.

HDPS Hybrids Development Strategy

The preferred cotton ideotype for HDPS hybrids include early to early-medium maturity (140-150 days), with compact, semi-compact and erect plant types ranging from semi-dwarf to medium-tall (80-120 cm height, ≤60 cm width). The stem should be flexible but not prone to breakage with sparse hair to glabrous. Leaves should be small to medium with upward or erect angles and sparse trichome density exhibiting natural senescence. Small to medium bracts and high boll retention are desirable. The first sympodia should be above 20 cm and the boll should be large, uniform with high locule retention. Ginning percentage should be above 40%. High response to PGRs and defoliants along with tolerance to pests (Jassid, Thrips, Whitefly, Bollworm) and diseases (CLCuVD, TSVD and various wilts) are essential. The plant should also tolerate abiotic stresses like drought, salinity and para wilt.

The female line development focuses on creating agronomically superior, early to medium duration with synchronized maturity, GMS integrated and should exhibit wide adaptability and enhanced tolerance to both biotic and abiotic stresses for good producibility and seed recovery. The male line development aims to incorporate essential traits for High-Density Planting Systems (HDPS), including early, synchronized maturity, compact or semi-compact plant types and high boll retention. These male lines also feature large, fluffy-opening bolls, high ginning percentage and strong responsiveness to plant growth regulators and defoliants. The resulting hybrids are evaluated for suitability to HDPS practice, yield advantage and its stability across the environment.

Government Intervention Needed through Policy

The following government interventions and strategies are essential for advancing cotton breeding and production in India:

(i) **Collaboration with Public Institutions:** Partner with public institutions working on transgenic technologies to test and promote novel transgenic events that are effective against Pink Bollworm (PBW).

(ii) **Development of HDPS Ecosystem:** Establish a cost-effective ecosystem for High-Density Planting System (HDPS) including affordable planters, harvesters, pre-cleaners and standardized protocols for canopy management and defoliation, ensuring effective implementation of HDPS and mechanical harvesting.

(iii) **Lint-Based Market and High GoT Development:** Develop markets for lint-based cotton and varieties with High Ginning Outturn (GoT) combined with high productivity.

(iv) **Public-Private Partnerships (PPP):** Foster PPPs for germplasm improvement, focusing on pre-breeding for climate resilience and resistance to biotic factors.

(v) **Simplified Germplasm Sharing:** Implement simplified mechanisms for the sharing of germplasm materials to encourage innovation and collaboration.

(vi) **Development of ELS Cotton:** Focus on the development of Extra Long Staple (ELS) cotton based on specific market requirements.

(vii) **Genome Editing Guidelines:** Establish clear guidelines and regulations for genome editing, ensuring its safe and ethical use in cotton breeding.

These interventions can enhance the efficiency, sustainability and profitability of cotton cultivation by addressing the challenges posed by climate change, pests and market demands.

Conclusion

Advancing cotton hybrid breeding in India is critical for improving productivity, profitability, and sustainability in the cotton sector. By focusing on developing high-yielding, resilient hybrids, adopting mechanization, India can address current challenges such as pest resistance, climate change, and labour shortages. Government intervention through supportive policies, infrastructure development and public-private partnerships will further strengthen India's position as a global cotton leader, ensuring long-term growth and economic benefits for farmers and the textile industry. Sustainable and efficient cotton cultivation will drive India's competitiveness in the global market.

TS-IV-IP-10

Hybrid rice in India: Public sector perspectives

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In India, excellent progress has been made in hybrid rice research and development and because of concerted efforts over the last three decades, 162 hybrids have been released for commercial cultivation in different rice growing states across the country. Among these, 42 hybrids have been developed by the public sector, while the remaining 95 have been developed by the private sector. The area planted to hybrid rice in the country during *Kharif* 2023 was around 3.5 m.ha. (8% of total rice area) & has contributed 5-6 m.t. of additional rice to the total rice production and more than 80% of the total hybrid rice area is in the states of Uttar Pradesh, Jharkhand, Chhattisgarh, Madhya Pradesh, Odisha and Haryana. However, its adoption is rather slow than the expected level. The main reasons for this are marginal heterosis, narrow genetic base of the parental lines, high seed cost because of seed production issues. All these issues are addressed through systematic research initiatives, and significant progress has been made in the development of hybrid rice parental lines both female and male parents with good floral traits. The female parental lines are being improved for traits like stigma exsertion and high outcrossing that helps in higher seed yields, thereby reducing the hybrid seed cost. Many newly developed parental lines are being fortified with resistance genes for major diseases such as BB, and blast that will help in the development of hybrids having resistance to major diseases. Careful analysis of the grain quality characters of the recently released hybrids clearly indicate significant improvement in their grain quality traits. The major limitations of the technology are technology constraints (inadequate yield heterosis, narrow genetic base of the parental lines, diversified consumer preferences, and susceptibility of hybrids to major diseases and insects; social, economic constraints (high seed cost, lower market price offered and discrimination against hybrid rice produce by millers/traders); besides certain policy constraints from the Government. In this paper, status of hybrid rice research and development in India's public sector is presented.

Hybrid rice research is being carried out in a network project mode 'Consortia Research Platform on Hybrid Crops – Hybrid Rice and is funded by the Indian Council of Agricultural Research (ICAR), since 2015. In this network, nine centers spread across the country (ICAR-Indian Institute of Rice Research, Hyderabad (as Lead Center); ICAR-Indian Agricultural Research Institute, New Delhi; ICAR-National Rice Research Institute. Cuttack; Tamil Nadu Agricultural University-PBS, Coimbatore; Acharya NG Ranga Agricultural University-RARS, Maruteru; Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur; Rice Research Station, Karjat (KKV, Dapoli); University of Agricultural Sciences-ZARS, Mandya; and Punjab Agricultural University, Ludhiana, are working on various aspects of hybrid rice research and development, as detailed below:

(i) Development of new hybrids for both favourable and unfavourable ecologies

(ii) Diversification of CMS sources and restorer/maintainer improvement

(iii) Two-line breeding system

Development of New Hybrids: More than fifty new hybrids were evaluated in national AICRPR trials and four promising ones are identified and released for commercial cultivation. ICAR-IIRR has developed and released the world's first public sector aerobic rice hybrid DRRH 4 for Punjab, Odisha, Chhattisgarh, Tripura and Gujarat (Senguttuvel P *et al*., 2023). ICAR-IIRR also developed DRRH 5, world's first coastal salinity hybrid for the states of Andhra Pradesh, West Bengal, Goa and Gujarat. ICAR-IIRR has developed early duration hybrid with tropical japonica restorer and released for Odisha and Uttar Pradesh states. ICAR-NRRI released two long duration rice hybrids *viz*., CR Dhan 702 and CR Dhan 703, for Odisha state (ICAR-NRRI Annual Report 2022). These hybrids are suitable for irrigated as well as shallow low land ecologies. CR Dhan 703 was found suitable for Boro areas in the state of Odisha, Bihar, Assam as well. ICAR-IARI in collaboration with JNKVV, Jabalpur has developed and released the first public sector two-line hybrid Pusa JRH 56 for the state of Madhya Pradesh.One more two-line hybrid (from TNAU) TNTRH 55 was released as CORH 5 during 2024.

Diversification of CMS Sources: All the hybrids released in the country are based on a single source of cytoplasmic male sterility (CMS) *viz*., Wild Abortive (WA) system. Wild species of rice such as *Oryza nivara; Oryza rufipogon; Oryza perennis* were already found to have alternate cyto-sterility sources, but their commercial exploitation was limited by the fact that no good restorers are available for these CMS sources like WA system. Intensive efforts are being made to identify suitable restorers for these various sterility sources. Another sterility source Kalinga I and a CMS line CRMS 32A is developed using this source and a hybrid *viz*., Rajalaxmi has also been developed from this new source (ICAR-NRRI, Cuttack). Two new CMS line CRMS 55A (medium duration)(ICAR-NRRI Annual Report 2017-18); CRMS 56A (mid late duration; (ICAR-NRRI Annual Report 2018-19) are also developed using this Kalinga 1 source.

Genetic Improvement of Maintainer and Restorer Lines: One of the major limitations of the hybrid rice technology is the higher seed cost and it's acting as deterrent in wide spread adoption of hybrid rice cultivation in the country. This can be overcome by developing CMS and maintainer lines with good floral traits such as high outcrossing ability etc. Two promising maintainer lines *viz*., APMS 6B, IR 68897B were improved for stigma exsertion trait through back cross breeding approach with donor genotypes *viz*., BF 16B and BF 2096. APMS 6B has been fortified Phosphorus uptake (Pup1) and BB (Xa21, Xa38) resistance through marker-assisted backcross breeding strategy (Madhusudan *et al*., 2022).

By adopting inter sub-specific *(indica* × *tropical japonica)* hybridization approach, a set of improved restorers were developed and among these unique restorer lines with combinations of major fertility restorer genes (*Rf*3, *Rf*4) and wide compatibility genes (S5n) (Sruthi *et al*., 2023; Pradeep *et al*., 2023). These restorer lines are helping in development of hybrids with high yield heterosis. Similarly, restorer lines in New Plant Type (NPT) background are developed. A set of novel iso-cytoplasmic restorer lines (from an elite rice hybrid KRH 2) were developed and are being used in the development of superior hybrid combinations (Kulkarni *et al*., 2022).

Development of Parental Lines and Hybrids with Tolerance to Salinity and Suitability to Aerobic Situations: It is essential to develop hybrids for water limiting solutions (aerobic) keeping in view of the dwindling freshwater resources in coming years. A set of improved restorer lines including RP 63340-NRR 25, (in the background of KMR3R - possessing qDTY12.1, qDTY2.3, qDTY1.1 and qDTY6.1 and Rf3 & Rf4 genes) are developed and they are found to have reproductive stage drought tolerance. Another set of restorer lines possessing Saltol QTL were developed and are using in the development of hybrids for saline conditions.

Development of Heterotic Gene Pools: A concept, well exploited in corn in development of gene pools that led to development of highly heterotic hybrids, is being explored in the improvement of hybrid rice parental lines. In continuation to this study, under consortium research platform on hybrid technology (CRPHT) scheme, for heterotic grouping purpose, around 150 parental lines (Restorers and Maintainers) from six hybrid rice centers (PAU, Ludhiana; IARI, New Delhi; JNKVV, Jabalpur; ZARS, Mandhya; RARS, Karjat and ICAR-IIRR, Hyderabad) were collected. Genetic distance based grouping of these 150 parental lines has been done based on molecular [GCP-SSRs@50 and SNPs (1K RICA@Intertek)] and morphological characterization under three environments (Sruthi *et al*., 2019).

Two-line Breeding System: TGMS trait was successfully transferred in the background of IR58025B, a female parent of widely used one of the three-line hybrid system in India. Efforts are on to transfer TGMS traits in the background of mega varieties like BPT 5204, Swarna, CR 1009 and a CMS maintainer line IR68897B are under progress at ICAR-IARI.A new TGMS line TNAU 60S was developed at TNAU with wider sterility period and has been utilized in hybridization and many heterotic hybrids were developed. This line was registered with NPBGR for its unique TGMS trait as IC 0622805 and INGRI 17028.ICAR-IARI in collaboration with JNKVV; Jabalpur has developed and released the first public sector two-line hybrid Pusa JRH 56 for the state of Madhya Pradesh. One more two-line hybrid (from TNAU) TNTRH 55 as CORH5 is released for Tamil Nadu state.

Key strategies and policy options to promote hybrid rice development

Research Strategies: An expanded network project on hybrid rice will be implemented to intensify the research efforts on hybrid rice development. The major emphasis will be on:

(i) Development of parental lines that can produce highly heterotic rice hybrids

(ii) Development of heterotic gene pools (a concept well exploited in corn will be explored in hybrid rice development)

(iii) Diversification of CMS sources

(iv) Identification of alternate sources suitable for hybrid seed production

(v) Human resource development through exposure visits and training programmes.

Seed Production Strategies

(i) Refining the seed production technology to enhance the seed yields, so that cost of hybrid rice seed can be reduced.

(ii) Involvement of seed agencies in the public sector, NGOs, farmers cooperatives along with private seed sector which is already doing its best, to meet the increased demand for hybrid seed in the years to come.

(iii) Strengthening of the existing institutional mechanism for the production and supply of breeder, foundation, and certified seed. The National Seed Corporation, State Farm Seed Corporation, and State Seed Corporations need to be strengthened with competent plant breeders.

Technology Transfer Strategies

(i) Transfer of hybrid rice technology from the research farms to the farmers' field is as important as developing the hybrids. Extension agencies have to play greater role in creating much needed awareness among the farmers about the advantages of cultivating hybrid rice through various innovative strategies.

(ii) Identification and popularization of promising hybrids for different states from the available released and notified hybrids.

Policy Options

(i) Providing adequate funding support and human resources to the hybrid rice research and development in the country.

(ii) Encourage the contract farming models involving hybrid rice cultivation in different parts of the country.

(iii) Providing a strong interface between the public sector and private seed sector for popularization of the technology.

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TS-IV-IP-11

Hybrid breeding for quality protein maize (QPM) and other traits for bio-fortification

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Quality Protein Maize (QPM) has emerged as a critical solution to malnutrition in maize-dependent regions of the world. Traditional maize varieties are deficient in essential amino acids like lysine and tryptophan, which are crucial for human health. The development of QPM, particularly through the introgression of the *opaque2* (*o2*) gene and its associated modifier genes, has greatly improved maize's amino acid profile. The *opaque2* gene increases the availability of lysine and tryptophan in the maize kernel and when combined with modifiers, it ensures that the grain maintains a suitable texture, hardness, and agronomic performance. Over the years, QPM hybrids have played a vital role in alleviating malnutrition, especially in regions where maize is a staple food. QPM significantly enhances human and poultry nutrition due to its enriched lysine and tryptophan content. It addresses human protein-energy malnutrition, promoting better growth, immunity and cognitive development, particularly in children and pregnant women. For poultry, QPM reduces the reliance on synthetic lysine supplements, improving feed efficiency, growth rates, and egg production whereas lowering feed costs. By naturally enhancing amino acid availability, QPM supports improved health outcomes for vulnerable populations and contributes to sustainable and cost-effective livestock nutrition systems.

Breeding QPM hybrids involves a combination of conventional and modern approaches to enhance nutritional and agronomic traits. Traditional breeding strategies like backcrossing, where the *opaque2* gene is introgressed into high-yielding maize inbreds, have been fundamental in QPM hybrid development. Recurrent selection for the stabilization of modifiers ensures the retention of traits like kernel hardness and improved protein quality. In parallel, modern techniques such as doubled haploid (DH) technology allow for the rapid development of homozygous lines, ensuring the stability of desired traits. Additionally, marker-assisted selection (MAS) has been a game-changer, enabling precise selection for the *opaque2* gene and associated loci, thus speeding up the breeding process and ensuring the development of high-quality hybrids.

However, the development of QPM hybrids faces several challenges, such as the yield gap compared to conventional maize hybrids and the environmental instability of modifiers. Balancing the nutritional quality of the maize with its agronomic traits, such as kernel hardness and yield, remains a significant challenge. Despite these hurdles, QPM breeding has continued to make significant strides thanks to genomic tools and innovative breeding strategies. Genome-wide association studies (GWAS) are helping identify key loci associated with protein quality, whereas genomic selection (GS) allows breeders to select for multiple traits simultaneously, improving breeding efficiency. Moreover, emerging technologies like CRISPR-Cas9 genome editing hold the potential to fine-tune QPM-related genes, enabling breeders to overcome existing limitations and create more resilient, nutrient-rich hybrids.

ICAR-VPKAS, Almora, has pioneered the development of QPM hybrids, particularly in India. The institute made a remarkable contribution by developing India's first marker-assisted quality maize hybrid, Vivek QPM 9, which signifies the commitment of ICAR-VPKAS towards ensuring nutritional security through innovative breeding and research. This hybrid has been instrumental in improving the nutritional quality of maize in India, as it exhibits significantly enhanced levels of lysine and tryptophan. Since then, ICAR-VPKAS has developed seven high-yielding QPM hybrids, with one of them being a QPM hybrid that includes provitamin A and low phytate, further enhancing its nutritional value and addressing multiple micronutrient deficiencies.

The impact of QPM hybrids, particularly those developed by ICAR-VPKAS, has been profound, especially in the context of food and nutritional security. These hybrids have contributed to enhanced nutritional quality and improved farmers' livelihoods, particularly in maize-dependent regions like the Himalayan states of India. These regions benefit from biofortified hybrids that increase the nutritional value of staple foods, thus addressing both protein and micronutrient deficiencies. Integrating high-yielding, biofortified hybrids into the farming system is a key strategy to improve food security and combat malnutrition.

The future of QPM hybrid breeding holds tremendous potential, with innovations on the horizon such as enhanced drought tolerance, pest resistance, and the fortification of additional micronutrients. By incorporating traits like provitamin A, low phytate and vitamin E, QPM hybrids can address multiple forms of malnutrition simultaneously. Scaling up the adoption of these hybrids will require robust seed production systems, farmer-participatory approaches, and stronger linkages between research institutions, policymakers, and extension services. Collaboration across these sectors will be essential for improving the accessibility and adoption of QPM hybrids, particularly in underserved areas.

In conclusion, QPM hybrid breeding has significantly improved the nutritional quality of maize, thereby contributing to global efforts to address malnutrition and food insecurity. Various research and breeding efforts demonstrate the vital role of science and technology in advancing food and nutritional security. Through continued innovation, collaborative efforts, and the application of cutting-edge breeding tools, QPM promises to make significant contributions to global agricultural and nutritional sustainability.

Technical Session IV

Current Status and Future Prospects in Hybrid Crop Breeding I (Food and Fiber Crops)

- Abstracts of Rapid Oral Presentations

TS IV-OP-01

Maize hybrid development for high density planting with ideal plant architecture and climate resilience

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Maize (*Zea mays* L.) is an important food, feed and industrial cropacross the globe. Increasing demand has led to the adoption of high density planting of maize hybrids for enhanced production. However, productivity is constrained by factors such as charcoal rot disease, lodging, weak root systems and shading effects. To address these challenges, 40 diverse tropical and temperate inbred lines, were grouped using two diverse testers (CML 286 and CML 41) by HSGCA (Heterotic grouping by general and specific combining ability) method for grain yield. Eleven inbred lines belonging to two heterotic groups (Group A comprising of tropical PFSR 393, PFSR 204, GP 327, PFSR 145 and GP 82 and temperate GP 329 lines; Group B comprising of tropical GP 36, GP 69, GP 86 and temperate GP 83 and GP 107 lines) were crossed in line × tester (6 × 5) mating design to produce 30 single cross hybrids (G1-G30) during *Kharif* 2022-23.These hybrids were evaluated during *Rabi* 2022-23 under normal planting density (NDP, 83,333 plants/ha) and high density planting (HDP, 1,11,111 plants/ha) at three locations (Hyderabad, Karimnagar and Madhira) in Telangana state. Overall, the hybrids have showed high yield performance in HDP compared to NDP with seven hybrids recording grain yield over 13,000 kg/ha and two hybrids G13 (GP 329 × GP 83; 13570 kg/ha) and G14 (GP 329 × GP 86; 13485 kg/ha) were identified as highest yielders. The AMMI Stability Value and Genotype Stability Index identified the hybrid G13 (GP 329 × GP 83) as the most ideal and stablehigh-yielding genotype followed by the hybrids G5 (PFSR 393×GP 107), G14 (GP 329×GP 86) and G28 (GP 82×GP 83) as desirable genotypes. The key traits contributing to high yield performance of the hybrids included erect leaf angles (72°-80°), early flowering (50% tasseling in 52-55 days), medium plant height (165-175 cm), ear height (82-84 cm), reduced tassel branches (5-6). In conclusion, these traits along with resistance to charcoal rot are essential for enhancing the maize hybrid performance under high-density planting conditions.

TS IV-OP-02

Utilizing genomics-assisted breeding to develop provitamin A-rich low phytate quality protein maize (QPM) hybrids

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Addressing deficiencies in iron (Fe) and zinc (Zn) is significant otherwise which can lead to health issues like stunted growth, pregnancy-related complications, cognitive impairments, and increased risks of illness and mortality. Improving the levels of these nutrients in maize is essential; however, maize grains naturally contain high levels of phytic acid, an anti-nutritional compound that binds to Fe and Zn, reducing their bioavailability by 80-90%. Additionally, traditional maize varieties tend to have lower levels of provitamin A, lysine, and tryptophan. In our study, we utilized genomics-assisted breeding to lower phytic acid levels and boost the content of provitamin A, lysine, and tryptophan. This was achieved by stacking the *lpa1-1*, *crtRB1*, and *opaque2* (*o2*) genes into four elite maize inbreds: PMI-PV5, PMI-PV6, PMI-PV7, and PMI-PV8, which serve as parents for four commercial biofortified maize hybrids. We used *InDel* and SSR markers related to the *crtRB1* and *o2* genes, respectively, and SNP markers linked to the *lpa1-1* gene for the BC1F1, BC2F1, and BC2F2 generations. Using over 100 SSR markers and phenotypic evaluations, we developed introgressed inbreds with beneficial alleles and agronomic performance. These inbreds were then utilized to develop hybrids, which were assessed for grain yield, agronomic traits, and quality parameters such as kernel phytic acid, lysine, tryptophan, and provitamin A at three locations: Bajaura, Delhi, and Jhansi. Compared to the original inbreds (2.78 mg/g and 91%), the *lpa1-1*-introgressed inbreds had a much lower PA (1.77 mg/g) and PA: TP ratio (64%). With their great potential for grain yield and low phytic acid content, the elite *lpa1-1* introgressed lines may prove to be useful donors in upcoming breeding initiatives. The newly developed maize hybrids, leveraging genomics-assisted breeding, could pave the way for a comprehensive strategy to combat malnutrition effectively.

TS IV-OP-03

Transforming agriculture with hybrid pigeonpea: A success story

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In response to the challenge of low pigeonpea yields and food insecurity, ICAR-IIPR, Kanpur has developed an innovative hybrid pigeonpea varieties namely IPH 15-03 and IPH 09-5 and gazette notified in 2020 and 2021 respectively for cultivation in the North West Plain Zone of India. The hybrid IPH 15-3 and IPH 09-5, characterized by its high-yield potential (2,426 kg/ha and 2293 kg/ha respectively) and resilience to wilt and phytophthora stem blight, was a breakthrough in agricultural science. Cytoplasmic Male Sterility based hybrid breeding techniques and cutting-edge agronomic practices were employed in its creation. Over a span of three years, the hybrid pigeonpea was popularized in Haryana (Karnal, Mahendragarh, Ambala districts), Delhi NCR region, Uttar Pradesh (Gautam Budh Nagar, Aligarh, Kanpur Dehat, Fatehpur, Hamirpur districts), and introduced through adoptive trials in Madhya Pradesh (Bhopal, Sehore districts), Maharashtra (Badnapur, Akola, Rahuri Districts), Gujarat (Banaskantha, Junagadh Districts), Odisha (Berhampur), Chhattisgarh (Raipur), Karnataka (Bengaluru, Dharwad, Kalaburgi) and Telangana (Warangal) states. A total of 98 hectares of Front-Line Demonstrations and two seed production training programs to the Farmers Participatory Organizations (FPO's) and Seed industries were conducted to equip the stake holders with the necessary skills and knowledge. The introduction of hybrid pigeonpea led to a remarkable 28-30% increase in average pigeonpea yields. Economic analysis showed a substantial boost in farmer net incomes (Rs.95997/ha), enhancing food security in the FLDs conducted districts. Additionally, the hybrid pigeonpea fostered community resilience and sustainability. This success story highlights the transformative power of hybrid pigeonpea. With the potential for widespread adoption, hybrid pigeonpea stands poised to revolutionize agricultural productivity and food security on a larger scale.

TS IV-OP-04

A comprehensive meta-QTL analysis for selected nutritional traits in maize

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Developing superior maize genotypes with enhanced nutritional quality is a primary goal of current breeding programs. However, the complex genetic architecture of these traits, influenced by multiple genes with small effects, poses a significant challenge. The inconsistency and instability of previously identified QTLs across different genetic backgrounds and environments hinder their effective application in maize breeding programs. Meta-QTL (MQTL) analysis is as a powerful approach to identify stable and reliable QTLs across diverse genetic backgrounds and populations. It enhances the precision and accuracy of QTLs from different studies while reducing their confidence intervals (CIs). A comprehensive MQTL analysis was conducted to identify stable and reliable QTLs for selected polygenic nutritional traits in maize, such as grain zinc (GZn), grain iron (GFe), kernel oil (KO), and protein content (PC). Study identified 34 stable MQTLs from 308 initial QTLs collected from 29 studies across diverse genetic backgrounds and populations. The average CI was significantly reduced from 22.36 cM to 4.59 cM, representing a 4.86-fold decrease. The percentage of phenotypic variance explained (PVE %) of MQTLs varied from 6.3% to 49%, with an average of 17.8 %. Additionally, we identified 591 candidate genes (CGs) within the MQTL regions. Gene ontology analysis revealed that these genes encode a diverse array of proteins, including transcription factors, transporters, and enzymes, implicated in various biological processes and pathways. Notably, 8 CGs with known roles in key biological functions, including Zn and Fe homeostasis (*GRMZM2G168747*, *GRMZM2G135877*, *GRMZM2G065635*, *GRMZM2G142063*, *GRMZM2G442791*), kernel oil biosynthesis (*GRMZM2G164318*) protein content and protein quality (GRMZM2G102878 and *GRMZM2G047129*), were identified within the MQTL regions. Overall, current studies highlight the value of MQTL analysis in maize breeding, revealing stable genomic regions linked to multiple nutritional quality traits, which can contribute significantly in quality traits improvement.

Technical Session IV

Current Status and Future Prospects in Hybrid Crop Breeding I (Food and Fiber Crops)

- **Abstracts of Poster Presentations**

TS IV-PP-01

Teosinte (*Zea mays* ssp. *parviglumis*) as a source for protein enhancement in maize

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Protein is of the most important components of diet, as it not only provides energy, it is an integral part of cellular membranes and enzyme activity. Protein-energy malnutrition (PEM) accounts the highest number of deaths worldwide. Quality Protein Maize (QPM) enhances nutritional value with higher levels of essential amino acids, lysine, and tryptophan in the kernel endosperm due to the recessive *opaque2* gene coupled with endosperm modifiers. Despite improved protein quality, QPM retains the 8-10% protein as traditional maize. In contrast, teosinte (*Zea mays subsp. parviglumis*), the wild progenitor possesses protein content of 20-30%. Teosinte-introgressed lines have shown great promise for higher protein content in maize breeding programme. Identification of candidate gene followed by its validation would lead to development of high protein lines through molecular breeding. At IARI, a set of teosinte-introgressed lines were found superior for protein content over traditional maize lines. These lines are currently being used to enhance protein content in popular maize hybrids.

TS IV-PP-02

Predicting the hybrid performance in sunflower based on mixed model analysis incorporating relationship information

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Sunflower is a cross-pollinated crop, and identifying heterotic combinations is crucial for improving hybrid performance. However, creating and evaluating hybrid combinations is a resource-intensive process, and often it is not possible to evaluate

all the hybrid combinations. While traditional methods, such as estimating combining ability and assessing parental diversity, have contributed to identifying inbreds that might yield superior cross combinations, their effectiveness has been limited. A more efficient approach could involve predicting the performance of cross combinations using genetic relationship information. This method would aid in selecting the best parent combinations, even when a subset of cross combinations have been evaluated. Eighteen hybrids were evaluated during spring 2024 at Sunflower Experimental Area, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana for seed yield. The parental lines of these crosses included four CMS lines and 14 restorer lines. The relationship (additive) matrix based on pedigree was constructed using AGHmatrix package of R software and the relationship information with respect to parents was derived out of it. Mixed model analysis was done using the model $y = 1\mu + W\theta + Z_1u_1 + Z_2u_2 + Z_3u_3 + e$ as mentioned by Caamal-Pat *et al.* 2021. The regression coefficient among observed and predicted values was 0.72 which was statistically significant. The higher value of R_2 and adjusted R_2 of 84.64% and 84.18% respectively suggest that the model holds good for predicting the performance of hybrids. The estimated variance components for the parents and hybrids were 162780 and 43446 respectively. The heritability was estimated as per Covarrubias-Pazaran (2016), using the formula $h_2 = (\sigma^2_1 + \sigma^2_2)/ (\sigma^2_1 + \sigma^2_2 + \sigma^2e)$, which came out to be 67.61%. Based on the BLUP values the top ranking hybrids for grain yield were 38AxOPH137, 103Ax47R, 67Ax160R, 82Ax107R and 103Ax137R. Among the top ranking hybrid combinations based on predictions were 38Ax137R, 38Ax138R, 38AxOPH81, 38AxOPH75, 103Ax138R, 103AxOPH81, 103AxOPH75 and 103AxOPH137.

TS IV-PP-03

Genotype × environment interaction and stability analysis of baby corn hybrids for grain yield using AMMI and GGE Biplot

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In response to the growing demand for baby corn, the development of dual-purpose hybrid varieties with both high yield potential and genetic stability is critical to ensure

consistent production across multiple growing seasons. Accordingly, the present study aimed for multi-location testing of ninety-two baby corn hybrids along with three checks in two replications across three environments *viz.,* Hyderabad, Ludhiana and Hazaribagh during *rabi*, 2022-23. Analysis of variance highlighted the significant impact of genotype (G) and environment (E), for days to 50% silking; whereas significant effect of environment was noticed for the trait baby corn yield (BCY) without husk and significant effect of both environment and GE interaction was noticed for BCY with husk. The environment remained as the most important source of variation for all the traits, followed by GE (0.09-0.89%) and G (0.22-0.82%). The first two principal components explained 89.88%, 77.46% and 77.08% of the total variation for DS, BCY without husk and BCY with husk, respectively. Classification of the three locations into three distinct mega-environments revealed no relationship between the environments which means genotypes that performed well in one environment might exhibit poor performance in another and *vice-versa*. Based on the GGE biplot and AMMI analysis, genotypes T81, T64 and T26 exhibited superior performance and stability across all the three locations for BCY without husk.

TS IV-PP-04

Study of gene actions and mapping quantitative trait loci (QTLs) for resistance to maydis leaf blight and flowering in maize (*Zea Mays* L.)

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Maydis leaf blight (MLB), a serious foliar fungal disease of maize, may cause up to 40% losses in yield. The present studies were undertaken to understand the genetics, development of recombinant inbred lines (RILs) population, and identify quantitative trait loci (QTL) for MLB resistance, days to anthesis and silking in maize. For this, initially 112 diverse inbred lines were evaluated to identify the extreme genotypes for targeted traits. The crosses were attempted between resistant lines with long duration and susceptible with short duration in all possible combinations. The generation

mean analysis revealed, predominantly dominance effects with additive x additive gene interaction for MLB resistance and dominance with dominance x dominance interaction for flowering traits in maize. Further one cross of resistant and long duration (CML 269-1) with the susceptible and short duration (HKI 4C4B) were carried forward to develop RIL mapping population. Total 198 RILs with two parental lines were phenotyped for flowering and MLB disease at 8 different environments during 2020-2023. The disease screening was done under artificial inoculated conditions at hot-spot locations (Delhi, Karnal, Ludhiana, Dholi). The disease symptom was recorded using 1-9 scale and then percent disease incidence (PDI) value was calculated for each genotype. Genotyping of 198 RILs and their two parents was undertaken using ddRAD-seq (double digest restriction-site sequencing) approach. A genetic linkage map with 6527 SNP markers spanning over 2,124.30 cM was used for QTL interval mapping. Using genotypic and phenotypic data, a total of 12 QTLs were mapped of which 5 were for MLB, 3 for days to anthesis and 4 were for days to silking. These QTLs were distributed on 5 different maize chromosomes (1, 3, 5, 6, 8). LOD scores of these QTLs was ranging from 3.4 to 5.8 and explaining up to 16.9% of the phenotypic variation. The QTL identified in this study can be used in marker-assisted breeding for MLB disease resistance in maize.

TS IV-PP-05

Exploitation of heterosis for productivity enhancement in pigeonpea (*Cajanus cajan* L. Millspaugh)

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Consortia Research Project on Pigeonpea Hybrid Technology funded by ICAR is running since 2015-16 with ICAR-IARI, New Delhi as lead center with other 3 centers across the states *viz*., ICAR-IIPR, Kanpur, Punjab Agricultural University, Ludhiana and ARS, Badnapur (MAU, Parbhani) for the exploitation of heterosis in pigeonpea. The objectives under this project are developing new diverse A and R lines with good combining ability with superior *per se* performance, broadening the genetic base of A and R lines, developing highly heterotic hybrids, developing heterotic pools, identification of molecular markers for testing genetic purity of parental lines and identification of molecular markers tightly linked to QTLs governing male fertility restoration.

With respect to broadening of the parental lines, diverse crosses are being generated and inter-specific crosses are also being utilized. Large number of new diverse stable A and R lines of short and medium duration maturity have been developed by the centers. 'A' lines having built in resistance to *Fusarium wilt*, Phytophthora blight and pod borer are also being developed. Diversification of the restorer lines is also an important aspect in hybrid breeding program. In order to enable efficient transfer of the male fertility restorer gene(s) it is important to identify tightly linked molecular markers. Thus, molecular markers have been utilized for mapping of QTLs governing male fertility restoration with respect to A_2 cytoplasm and this work is under progress. Identification of polymorphic hyper-variable SSR markers between A and R parental lines is also underway.

Large number of test-crosses are being generated by each of the center and are tested for male fertility restoration, standard heterosis and high *per se* grain yield, 100 seed weight and days to maturity. Every year, promising hybrids developed by each center are being evaluated in CRPHT multi-location hybrid trial which led to identification of the superior hybrids. These superior hybrids were submitted for evaluation in AICRP multi-location trials *viz*., IHT followed by AHT-1 and AHT-2. Two short duration hybrids IPH 15-03 and IPH 09-5 having heterosis ranging from 28.3% to 30.05% for grain yield over the best check variety UPAS 120 were released and notified in 2020 for the commercial cultivation in the NWPZ of the country comprising of Punjab, Haryana, Delhi, Uttarakand and Western UP. Another hybrid Pusa Arhar Hybrid 5(PAH 5) was released for Delhi and NCT in the year 2023 and was notified in the year 2024. PAH 5 had 24.6% superiority for grain yield over the check variety Pusa 992, based on the Zonal mean over the locations of NWPZ (base on mean over two years 2018-19 and 2019-20 over NWPZ) in IHT (E) (2018-19) and AHT-1(E) (2019-20). Another hybrid of medium duration maturity *viz*., BDNPH 2018-05 was released for Central Zone in 2024. This medium duration hybrid had the standard heterosis of 20.76%, 34.46%, 34.80% and 32.04% over the checks PT-0012, BDN-711, GTH-1 and CoRG-9701, respectively. Every year all the centers are contributing their promising hybrid for the IHT multi-location trial of AICRP. Several hybrids have also been promoted to the advanced multi-location trials of AICRP.

TS IV-PP-06

Large scale combining ability analysis of test cross hybrids of maize to foster food grain production in maize (*Zea mays* L.)

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Globally, Maize is highly valued for its multifarious use as food, feed, fodder and raw material for large number of industrial products. Single Cross Hybrid technology offers an easy, viable and economical option to the farmers and are the most productive among the other types of hybrids and composite varieties. Single cross hybrids have shown better adaptability to new set of cropping systems and management practices. Pertaining to this context, the present study was conceptualized to identify potential single cross hybrids exhibiting high yields at Agricultural Research Station, Karimnagar during *Rabi* 2021-22 and *Kharif* 2022.

The present study was conducted at Agricultural Research Station, Karimnagar, Telangana, India during *Rabi* 2021-22 and *Kharif*, 2022. Around 40 lines were crossed with 6 testers and obtained 216 crosses which were evaluated during *Kharif,* 2022. During *Kharif,* 2022, 216 Entries forming into 54 Entries + 6 checks in four sets were evaluated in 2 replications in Randomized Block Design at 60 x 20 cm spacing in two rows of 3 m length. Data pertaining to Plant stand (Initial and final), Plant height (cm), Ear height (cm), Total no. of ears harvested per plot, Total grain yield per plot (g), Ear length (cm), Ear diameter (cm), No. of kernel rows/ear, No. of kernels / row, Grain yield (kg/ha), Shelling (%), Test weight (g) and Moisture % were recorded. In the present study, among the hybrids, the hybrid KMH-422813 (9354 kg/ha) has out yielded the check yield of Bio-9544 (8140 kg/ha) with a superiority of 14.9 %. In maize, single cross hybrids have highest genetic potential for yield, hence, development of high yielding hybrids with stable performance will give good returns to the farmer and thus the development of climate resilient single cross hybrids has been the focus of Indian maize programme.

TS IV-PP-07

Advancing hybrid maize breeding: accelerating nutritional enhancement through multi-trait doubled haploid lines

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Maize, the third most important global staple crop, is nutritionally constrained by deficiencies in essential amino acids and micronutrients, posing significant challenges to food and nutritional security. Addressing these challenges, this study leveraged doubled haploid (DH) technology to accelerate the development of nutritionally enhanced maize lines. DH technology enables rapid fixation of homozygosity and enhances genetic diversity, making it a transformative approach in hybrid maize breeding. A total of 151 DH lines were developed from multi-trait source populations combining high tryptophan, lysine, and micronutrient content: MTC 4 (PVD 3-2 × BS 24-2-5), MTC 8 (PVE 44-11 × BS 24-2-5), and CML161 × Bajim-06-15. Nutritional profiling revealed significant variability in kernel nutrient content, with Fe ranging from 29.4–47.6 ppm, Zn from 26.5–42.7 ppm, Ca from 1,042–4,189 ppm, Mg from 554.6–2,436.7 ppm, K from 3,102–5,701 ppm, and tryptophan from 0.59–0.82%. Positive correlations were observed among Fe, Zn, Ca, Mg, K, and tryptophan, underscoring the synergistic potential of these traits in quality protein maize (QPM) backgrounds. Factor analysis partitioned the total variability into three components, explaining 64.5% of the variation. Transgressive segregation was observed in several elite lines, surpassing parental traits for key nutrients. Prominent DH lines included MTC8-DH-96 and CMBDH-34 (Zn >36 ppm), MTC8-DH-52 (Ca >3,500 ppm), MTC8-DH-122 (Mg >2,000 ppm), and MTC8-DH-150 (K >5,500 ppm), while 42 lines exhibited high tryptophan content (>0.70%). This first comprehensive study on DH lines demonstrates their potential as multi-trait donors for biofortification and direct use in hybrid maize development. By integrating nutritional enhancement with breeding efficiency, this research offers a scalable solution to combat global malnutrition and ensure sustainable food security.

TS IV-PP-08

Breeding superior stable popcorn hybrids by combining exotic and indigenous popcorn germplasm for a sustainable popcorn breeding program

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Breeding programs in popcorn, involve a multifaceted emphasis on yield and popping quality traits. The economic significance of popcorn in both global and Indian markets requires the utilization of promising exotic germplasm to diversify the genetic base and develop superior stable hybrids. In this study, promising inbreds derived from exotic landraces were crossed to parents of superior popcorn hybrids, in a line × tester mating design. The effects due to crosses, lines, testers, and location × line × tester were highly significant when the hybrids were subjected to multi-location evaluation for agro-morphological and popping quality traits across diverse maize-based agro-climatic zones. Popping quality traits, such as total flake volume, popping expansion volume, and popping rate were found to be primarily governed by additive genetic variance (VA), while agro-morphological traits had a prevalence of dominance genetic variance (VD), implying that the parents should be selected based on favorable performance for popping quality. The GGE biplot methodology applied as line main effect plus line × tester interaction analysis identified the inbred Dpcl-15-90 as an ideal tester for GY alone, while the testers PMI-PC-101 and PMI-PC-104 were ideal and highly discriminating the lines for popping quality traits. Hybrids PMI-PC-205×PMI-PC-104, PMI-PC-203× PMI-PC-104, and PMI-PC-203 × PMI-PC-101were identified as superior and stable for popping quality traits and grain yield. Therefore, the crosses with high GCA parents and high SCA effects are useful for population improvement and recycling of inbreds to provide heterotic lines. Breeders should exploit VD for genetic improvement in grain yield, simultaneously using VA for improvement in the popping quality traits. The results imply promising utilization of exotic germplasm to establish a sustainable popcorn breeding program through the development of highly heterotic popcorn hybrids in India.

TS IV-PP-09

Estimation of heterosis, combining ability and gene effects for forage quantity and quality traits in maize

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Maize is an important crop with diverse uses such food, feed, fodder (green, hay and silage) and biofuel. The understanding of the genetic mechanisms conditioning the inheritance of forage quantity and quality traits is essential in the development of superior maize genotypes (hybrids/composites). In this study, 190 hybrids derived from diallelic crosses among twenty inbreds of maize were evaluated for twelve forage quantity and five forage quality traits during *kharif* 2023. The better parent heterosis was ranged from 37.5 to 112.7%, 25.3 to 109.9%, -7.4 to 11.0%, -8.0 to 7.7%, -13.3 to 9.4%, -8.2 to 6.7% and -11.8 to 12.4% for green fodder yield (GFY), dry fodder yield (DFY), crude protein, NDF, ADF, ADL and dry matter digestibility (DMD), respectively. These findings of heterosis indicated the potential of heterosis breeding in improving the fodder yield and quality in maize. The GCA and SCA effects were significant for all the forage quantity and quality traits. The greater relative proportion of SCA to GCA for most of the forage quantity and quality traits suggested the importance of non-additive gene effects in inheritance of these traits. Inbreds IGMI-2, IGMI-9 and IGMI-20 were best general combiner for GFY, while inbreds IGMI-2, IGMI-11, IGMI-19 and IGMI-20 were best general combiner for DFY. For crude protein and dry matter digestibility, inbreds IGMI-2, IGMI-6 and IGMI-11, and IGMI-9, IGMI-15 and IGMI-20 showed significant positive GCA effects, respectively. Based on the SCA values, crosses IGMI-2 × IGMI-5, IGMI-3 × IGMI-11, IGMI-6 × IGMI-11, IGMI-9 × IGMI-18 and IGMI-9 × IGMI-20 were identified as the best hybrids for GFY, and crosses IGMI-3 × IGMI-11, IGMI-9 × IGMI-18, IGMI-14 × IGMI-20 and IGMI-17 × IGMI-19 for DFY. For crude protein and dry matter digestibility, the best hybrids were IGMI-7 × IGMI-11 and IGMI-5 × IGMI-11, and IGMI-3 × IGMI-19 and IGMI-9 × IGMI-20, respectively. These hybrids can be used for exploiting hybrid vigour for forage yield and quality in maize.

TS IV-PP-10

Hybrid research in sunflower: progress and future thrusts

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Sunflower (*Helianthus annuus* L.) is one of the important oilseed crops cultivated worldwide for its healthy oil, ornamental and confectionary purposes. Due to cross pollinated nature of the crop, it is well suited for heterosis breeding. In case of sunflower up to 200% heterosis for seed yield and 25-30% for oil content has been recorded and documented. Based on yield, oil content and stability over locations, the first CMS based sunflower hybrid BSH-1 was released for commercial cultivation in 1980. Since then, development of hybrids base in this crop has been widened through the extension of hybrid breeding work in many research centres. Till now, a total of 38 hybrids have been released from public sector for commercial cultivation. Sunflower crop is mainly grown in marginal land hence; full potential of hybrids could not be realized. To achieve further quantum jump in large areas, production of superior hybrids is essential. In this context, recently two hybrids (TilhanTec-SUNH-1 & TilhanTec-SUNH-2) have been released from ICAR-IIOR, Hyderabad. These hybrids have high seed (>20 q/ha) and oil yield (>700 kg/ha) potential coupled with resistance to downy mildew and moderate resistance to leafhoppers. These hybrids have been recommended for most of the sunflower growing states under rainfed condition. Despite success in heterosis breeding, there are some challenges like broadening the genetic diversity, diversification of CMS sources and synthesis of diverse and heterotic gene pools and identification of good maintainers and restorer lines remain the need of the hour. Further, to keep pace with the new challenges, diversification of genetic base of male sterility as well as restorer lines for development of superior hybrids and maintenance of genetic purity of the parental lines of the released hybrids for exploitation of maximum heterosis assume importance in sunflower heterosis breeding.

TS-IV-PP-11

Prediction of silage quality traits in maize using near-infrared reflectance spectroscopy in an F_1 hybrid population

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Maize silage is a heterogeneous fodder from maize plants converted into succulent feed through anaerobic fermentation and emerging as an enterprise for the dairy sector. Estimating silage quality is important in the breeding programs for breeders to develop superior hybrids. Although conventional wet chemistry-based estimations use standard analytical chemistry methods and offer precise quantitative data, it is both time and resource-intensive, therefore the potential of near-infrared reflectance spectroscopy (NIRS) as a rapid and reliable method for estimating quality variables for silage maize is dissected through this study. For this experiment, an F_1 hybrid population (358 hybrids) is generated by diallel crosses and NC II designs using 25 tropical and 17 temperate inbred parents and evaluated in two replications at two locations from February to May 2024. 1600 samples were collected and scanned using NIRS from 400 to 2500 nm, of which 70 samples were selected to calibrate estimated contents and validate the derived equations. Predictions of traits in this study showed satisfactory accuracy. Calibration models for NIRS measurements gave multivariate correlation coefficients of determination (R^2) and the range of variables as 0.95 (86.96 - 90.90), 0.94 (2.18 - 10.12), 0.97 (0.53 - 1.62), 0.97 (43.32 - 73.64), 0.97 (18.40 - 41.39) and 0.87 (1.86 - 5.10), 0.93 (6.73 - 9.66), 0.93 (45.81 - 63.80) for dry matter (DM), ash, nitrogen (N), neutral detergent fibre (NDF), acid detergent fibre (ADF), acid detergent lignin (ADL), metabolizable energy (ME) and *in vitro* organic matter digestibility (IVOMD) on a dry weight basis respectively. The results show the ability of NIRS to predict the chemical composition of maize silage samples as a routine method in breeding programs.

Technical Session V

Current Status and Future Prospects in Hybrid Crop Breeding II (Horticultural Crops)

- Extended Summaries of Keynote and Invited Presentations

TS-V-KP-01

Hybrid research in horticultural crops

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Application of research on exploitation of heterosis in horticultural crops in India has grown rapidly since 1980s. At present, F1 hybrid varieties are available for many horticultural crops in India. The development and commercialization of F1 hybrids is more common in vegetable crops and is at the level similar to field crops. The present lead lecture on 'hybrid research in horticultural crops' will focus on the achievements, status and potential areas of hybrid research in vegetable, fruit and flower crops.

Vegetable Crops: The application of heterosis was first proposed in cucumber. Ever since the discovery of the male sterility in onion and self-incompatibility mechanisms in cabbage, various genetic and non-genetic mechanisms have been developed. In the recent past, discovery of male sterility in vegetable cowpea has opened up prospects of exploitation of heterosis in leguminous vegetable crops as well. These mechanisms have been utilized to develop commercial F1 hybrids in Solanaceae, Cruciferae and Cucurbitaceae vegetables. The hybrids in these crops exhibit uniformity, vigour, earliness, yield, stress tolerance and adaption to varied production environments.

At present, the most important vegetables grown in India that have highest share of hybrid cultivars include tomato, chilli, okra, capsicum, watermelon, melon, cucumber, bitter gourd, cabbage and tropical cauliflower. Very successful hybrids with multiple disease resistance, superior yield and quality have been delivered so far. The hybrids are replacing open-pollinated varieties in these important vegetable crops.

The hybrid research is being undertaken by both public sector institutions and private sector on the following lines.

- Development of superior inbred lines with multiple disease resistance and high temperature tolerance
- Focus on market segmentation
- Mechanisms of hybridization such as male sterility and gynoecium
- Double haploid production and utilization
- Genome editing for trait manipulation
- Genome editing for male sterility

Fruit Crops: Developments of fruit varieties through hybridisation has also been underway in some fruit crops at different centres under National Agriculture Research system. These efforts have resulted in several varieties of which many are grown commercially. The hybridization has been successfully exploited in fruits crops such as apple, apricot, almond, ber, custard apple, grape, mango, guava, papaya, peach, passion fruit and pomegranate.

Hybridisation in general has resulted in better shelf-life, early maturity, high dessert quality, better colour, sweet fruits, disease resistance and climatic adaptation in fruit crops. The hybridisation in apple and almond have led to development of low chilling varieties. Similarly, apricot improvement has been instrumental in evolving variety that escape spring frost. A variety of custard apple, Arka Sahan (Gem x Mammoth) has been released from IIHR, Bengaluru and has gained popularity throughout the country for size, pulp content, high TSS and low seed content. Hybridization work in grape has delivered varieties that could be trained on head system suitable for juice and wine purposes. Also, seedless varieties of grape.

In guava, hybridization has been undertaken at various centres of NARS has resulted in the development and release of soft seeded and large fruited varieties in both white and red fleshed varieties. The systematic hybridization work in mango resulted in release of more than 30 hybrid cultivars by various institutes in India. In mango, major emphasis has been given to development of regular and precocious bearing, dwarf, large fruited varieties with good keeping quality and freedom from spongy tissue disorder. Systematic work on breeding of papaya varieties with high yield and good quality for wider adaptability is underway. Kaveri, a hybrid passion fruit bred at IIHR, Chethalli by crossing green and purple varieties can endure rains and has better keeping quality. It is now extensively cultivated in the N.E. regions. Similarly, hybridisation work has been useful in releasing varieties in Peach and pomegranate.

Flower Crops: Hybrids in flower crops can be categorized into multiple types. Flower crops such as rose, gerbera, gladiolus, and tuberose are vegetatively propagated. Hybrid development in these crops involves crossing selected parents, which are generally heterozygous. This hybridsation produces hybrid progeny populations that are both heterozygous and heterogeneous. Through selection from these populations, followed by rigorous evaluation, hybrids are identified based on the specific objectives of the breeding program. Such hybrid development programs are actively pursued by several public sector organizations under the National Agricultural Research System (NARS), including universities, IARI, IIHR, and DFR.

For seed-propagated flower crops, F1 hybrids—are highly sought after, especially for landscaping purposes. These hybrids emphasize uniformity in traits such as plant stature, height, flowering duration, and flower forms. Crops like petunia and antirrhinum are examples where such F_1 hyrbids are sought after. Indo-American Hybrid Seeds was the first private entity to focus on Petunia hybrids. A few other private seed companies are involved in the hybrid seed sector; however, most of them depend on imported breeding lines and prioritize seed export. Currently, flower seed production in India covers approximately 600–800 hectares, with significant activity in states such as Punjab, Haryana, Karnataka, Himachal Pradesh and West Bengal.

One of the most sought after F_1 hybrid seeds for commercial flower cultivation by Indian farmers are that of Marigold. F_1 hybrid development in marigold presents unique challenges. Unlike F1 hybrids in vegetables or field crops, marigold hybrids must be sterile and exhibit full flower forms. Currently, marigold cultivation spans about 87.07 thousand hectares, and there is a growing demand for F_1 hybrid seeds both for flower production and carotenoid extraction. Most hybrid seeds are imported from countries like China and Thailand by private seed companies. ICAR-IIHR has pioneered public-sector research in this area, identifying multiple male-sterile lines and releasing four F_1 hybrids that cater to the needs of flower growers and the commercial demand for carotenoids.

In addition to crop specific achievements and status of hybrid research, the lead lecture will focus on the recent trends in double haploids, progress in exploitation of male sterility, gynoecy, application of markers and genome editing.

TS-V-IP-01

Hybrid breeding in fruit crops: Current status and future prospects

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Hybrid breeding in fruit crops is a transformative approach to enhancing essential traits such as yield, quality, pest resistance, and climate adaptability. This strategy has achieved significant progress through both traditional methods and modern technologies, resulting in the development of hybrids that meet diverse agricultural and consumer needs. Traditional methods like clonal selection have significantly unlocked the genetic potential of various fruit crops, leading to substantial advancements. Examples include Aonla varieties such as Krishna Kanchan and Goma Aishwarya, Bael selections like Banarasi and Pant Shivani, and improved banana varieties like Udayam and Phule Pride. In Grapes, varieties such as Manjari Naveen and Manjari Kishmish stand out, while guava selections like Lalit and Shweta, sapota variety PKM-1, and litchi selection Swarna Madhu with small-seeded characteristics represent significant progress. Improvement in Citrus crops with Mudkhed Seedless Mandarin, Balaji and Sai Sharbati acid lime. Similarly, Ber varieties like Goma Kirti and Thar Bhubharaj, along with farmer selections such as Lakshmana in tamarind for enhanced pulp recovery and Siddhu and Shankara in jackfruit for superior fruit colour and quality, have achieved widespread acceptance.

Hybridization further accelerated the progress like, mango hybrids such as Arka Udaya, Arunika and Pusa Lalima stand out for their regular bearing, superior fruit quality, and export potential. Similarly, guava hybrids like Arka Kiran, enriched with lycopene and vitamin C, and papaya hybrids such as Arka Prabhat, known for enhanced sweetness and extended shelf life, have made significant contributions, alongside the Co series hybrids from TNAU, with emphasis on yield and quality improvement. Other prominent hybrids include Kaveri Kanchan in banana (Nendran × Cultivar Rose) and Arka Sahan in custard apple (*A. atemoya* × *A. squamosa*), both showcasing advancements in yield, quality, and pest resistance. In apple, hybrids such as Ammol, Pride, and Priame demonstrate scab resistance and excellent fruit quality, while walnut hybrids like CITH-W-12 and CITH-W-121 offer improved nut yield and size. Additionally, mutation breeding has led to innovations such as dwarf papaya (Pusa Nanha), highlighting the potential of modern techniques in enhancing crop performance and expanding genetic diversity. However, the success is often-slow and time consuming.

Modern technologies are helpful in accelerated hybrid breeding efforts. Availability of whole genome sequence information, next generation sequencing (NGS) techniques, identification of QTLs and DNA markers associated with traits, Marker-assisted selection (MAS), tissue culture, and genomic tools have significantly improved genetic diversity and hybrid development in crops such as mangoes, grapes, and strawberries. Techniques like mutation breeding and embryo rescue have expanded the genetic base for desirable traits. However, challenges persist, including the perennial nature of fruit crops, long breeding cycles, heterozygosity and complex inheritance patterns.

Looking ahead, innovations such as CRISPR/Cas9 genome editing, gene pyramiding, and speed breeding hold immense promise. These advanced technologies enable the rapid development of climate-resilient, nutrient-rich, and consumer-focused varieties with improved shelf life and reduced environmental impact in short span of time. Achieving these goals requires sustained investments, collaborative research, and supportive policies. Strengthening public-private partnerships and addressing consumer acceptance will ensure hybrid breeding continues to contribute to global food security and sustainable agriculture.

TS-V-IP-02

Breeding tomorrow's vegetables: Integrating technology, nutrition, and sustainability

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Vegetables play a critical role in addressing global nutritional challenges, acting as a primary source of essential vitamins, minerals, and dietary fiber required for human health. As populations grow and dietary patterns shift, the importance of vegetables in promoting health and preventing malnutrition continues to increase. However, the vegetable seed industry faces multifaceted challenges due to rapidly changing environmental conditions, evolving consumer preferences, and shifting market dynamics. Addressing these challenges requires a forward-thinking approach, integrating technology, nutrition, and sustainability into vegetable breeding.

Challenges in Vegetable Breeding

The impacts of climate change are among the most pressing issues confronting vegetable production today. Erratic rainfall, temperature fluctuations, and other extreme weather events exacerbate abiotic stresses, reducing yields and compromising crop quality. Vegetables, being sensitive to environmental conditions, are particularly vulnerable to such stressors, which can manifest as stunted growth, reduced flowering, or lower nutrient density. In addition to climatic pressures, emerging biotic stresses such as pest infestations and disease outbreaks pose significant risks. These challenges are further compounded by the rapid evolution of pathogens and pests, which often outpace conventional breeding efforts. As a result, vegetable breeders must constantly innovate to develop varieties that are not only high-yielding but also resilient to these threats. Meanwhile, consumer preferences are shifting. Today's consumers demand vegetables that are not only nutritious but also align with environmental sustainability and traceability standards. There is a growing emphasis on transparency regarding production practices, pesticide usage, and carbon footprints. Meeting these expectations requires breeders to deliver varieties that balance nutrition, yield, resilience, and market appeal.

Integrating Advanced Technologies in Breeding

To address these challenges, advanced tools and technologies are reshaping vegetable breeding, offering transformative solutions that were previously unimaginable. Among these, artificial intelligence (AI) is leading the way, revolutionizing the processes of data analysis and decision-making. AI-driven phenotyping allows breeders to identify and measure plant traits with remarkable precision, while predictive modeling enables the optimization of key attributes such as yield, disease resistance, and nutrient density. The integration of AI expedites hybridization processes, allowing breeders to make informed decisions about parental selection. This technology reduces the time and resources required to develop superior varieties, accelerating the pace of innovation in the vegetable seed industry. Furthermore, AI's ability to analyze vast datasets opens new opportunities for understanding complex traits, paving the way for multi-trait improvement in vegetable crops. Biotechnology tools have also transformed the genetic landscape of vegetable breeding. Techniques like CRISPR-Cas systems allow precise gene editing, enabling targeted improvements in traits such as drought tolerance, pest resistance, and enhanced nutrition. Marker-assisted selection (MAS) facilitates the identification of desirable genes, ensuring their inclusion in breeding programs. Together, these tools significantly shorten the breeding cycle while ensuring the development of robust and high-performing cultivars.

One area of increasing interest is the breeding of rootstocks for grafted vegetables. Rootstocks enhance plant resilience by conferring resistance to both biotic and abiotic stresses. This approach has gained traction in crops such as tomatoes, peppers, and cucurbits, where grafting onto specialized rootstocks can improve productivity and adaptability under challenging conditions. Rootstock breeding exemplifies how innovation can bridge the gap between traditional practices and modern technological advancements.

Speed breeding, another revolutionary technique, utilizes controlled environments to accelerate plant growth and reproduction. By optimizing conditions such as light intensity, temperature, and photoperiod, breeders can achieve multiple generations within a single year. This approach not only reduces the time required to develop new varieties but also enhances the capacity to respond to emerging challenges, such as new pest outbreaks or changing climate patterns.

Innovations in Urban Agriculture

As urbanization continues to expand, the demand for fresh produce in cities is rising. Innovations in urban agriculture, such as vertical gardening and aeroponics, are addressing this need while promoting space-efficient cultivation. These systems integrate seamlessly with urban environments, allowing vegetables to be grown in areas with limited arable land. Breeding efforts are increasingly focusing on developing varieties suited for these systems, with traits such as compact growth, high yield, and adaptability to controlled environments. Urban agriculture also plays a role in reducing the environmental impact of food production. By minimizing transportation distances and utilizing resources efficiently, these systems contribute to sustainability goals while providing consumers with access to fresh, nutritious vegetables.

Advancing Genomics in Vegetable Breeding

Genomic tools are at the forefront of vegetable breeding, enabling a deeper understanding of plant genetics and their relationship with agronomic traits. Genome sequencing and genome-wide mapping are powerful tools that identify loci associated with critical attributes such as stress tolerance, nutrient content, and disease resistance. These insights allow breeders to make informed decisions when selecting parent lines, ensuring that desired traits are passed on to subsequent generations. Mapping efforts also aid in the conservation and sustainable utilization of germplasm resources. By exploring genetic diversity within and across vegetable species, breeders can identify unique traits that may be valuable in future breeding programs. This approach not only enhances the genetic base of cultivated crops but also ensures their adaptability to changing environmental and market conditions.

Consumer-Centric Breeding Approaches

Today's consumers are highly informed and selective, prioritizing vegetables that align with their health and ethical values. Breeders are responding by developing varieties that cater to these preferences. High-nutrient vegetables, such as those rich in vitamins, antioxidants, and phytonutrients, are becoming increasingly popular. Similarly, efforts are being made to reduce the bitterness or pungency of certain vegetables, making them more appealing to diverse consumer groups. In addition to nutrition, sustainability and traceability are key consumer concerns. Breeders are addressing these by reducing the need for chemical inputs, such as pesticides and fertilizers, through the development of pest-resistant and nutrient-efficient varieties. These innovations not only enhance the environmental sustainability of vegetable production but also align with consumer demands for safer and more eco-friendly food options.

Transforming the Vegetable Seed Industry

The convergence of advanced technologies and innovative cultivation systems is ushering in a new era for the vegetable seed industry. By integrating AI, biotechnology, speed breeding, and urban agriculture, breeders are developing vegetables that meet the multifaceted demands of the 21st century. These advancements ensure that vegetables are not only high-quality and nutrient-dense but also resilient to stress and aligned with sustainability goals. The potential impact of these innovations extends beyond the vegetable seed industry. By improving the availability and accessibility of nutritious vegetables, these efforts contribute to global nutritional security. They also play a crucial role in supporting the livelihoods of farmers by offering high-yielding and market-relevant varieties that enhance profitability. In conclusion, the vegetable seed industry stands at the crossroads of tradition and innovation. By embracing cutting-edge tools and addressing consumer and environmental needs, it has the opportunity to transform vegetable production systems into robust contributors to global health and sustainability. The journey toward breeding tomorrow's vegetables is not just about meeting today's challenges—it is about shaping a future where nutritious, resilient, and sustainable vegetables are accessible to all.

Keywords: Vegetables, Nutrition, AI in Breeding, Biotechnology, Rootstocks, Speed Breeding, Genome Mapping, Consumer Preferences, Climate Resilience.

TS-V-IP-03

Breeding for new hybrids in flower crops

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Flowers hold significant cultural and emotional value and play a key role in various social and religious ceremonies. Floriculture industry is one of the profitable enterprises that contribute Rs.25000 cr from domestic trade and about Rs.700 cr through exports to Indian economy. Floriculture industry predominantly deals with the cultivation, processing and marketing of annuals, biennials and perennial ornamentals. Most of the annuals are predominantly propagated through seeds.

Global flower seed industry is valued at USD 7.64 Billion with major contributions from Netherlands (USD 2.13B), United States (USD 1.1B), France (USD 646M), Germany (UDS 609M), Denmark (USD 405M). The major importers of flower seeds include The Netherlands (USD 725M), United States (USD 616M), France (USD 462M), Germany (USD 450M), Spain (USD 439M). India also imports flower seeds worth USD 88M which are used for raising flower crops for seed production besides local trade.

India contributes USD 123 M to the global seed industry by producing a wide range of flower crop seeds including African and French marigold, annual chrysanthemum, balsam, calendula, candytuft, coreopsis, cornflower, cosmos, dahlia, echium, gaillardia, helichrysum, linum, lupin, marigold, nasturtium, nigella, pansy, petunia, phlox, poppy, portulaca, salvia, statice, sunflower, sweet pea, verbena, zinnia. The flower seed industry is mostly in the hands of private players which is mostly concentrated in the states of Punjab, Haryana, Karnataka, West Bengal and Maharashtra.

Research on hybrid development in flower crops was initiated initially at ICAR-IARI, New Delhi followed by ICAR-IIHR, Bengaluru and later on at ICAR-DFR, Pune (after its inception in 2009). AICRP on Floriculture played a pivotal role in evaluating the hybrids developed in NAREES. A large number of hybrids are developed in Rose, chrysanthemum, gladiolus, marigold, tuberose, aster and bougainvillea, *etc.* not only by ICAR institutes, some of the State Agricultural Universities and CSIR laboratories like CSIR-NBRI, Lucknow and CSIR-IHBT, Palampur.

In private sector, initial work on hybrid seed production in flower crops was started by M/S Indo American Hybrid Seeds (India) Pvt. Bangaluru. The company used to produce F1 hybrid seeds of Petunia for 100% export during 60’s.

Production of seeds of open pollinated flower crops was started by M/S Beauscape Farms, Sangrur, Punjab who started flower seed production involving farmers on large scale. A number of companies including M/S Namdhari, M/s Sutton Seeds, M/S East West, M/S Pochas, M/S Syngenta, M/S Sakata etc., have started producing seed on large scale for export to Holland, UK, USA, France, Germany, and Japan etc.

Realizing the potential of F1 hybrids in flower crops, ICAR launched a Network project on F1 Hybrids in Flower crops during 2000 in ICAR institutes and some of the SAU’s to lay the required foundation. Concerted efforts have resulted in development of promising hybrids in Aster, Marigold, Pansy, Chrysanthemum, ornamental Kale, tuberose, gladiolus, gerbera, crossandra, lilium, etc in recent times.

Hybrid production relies on several factors like plant, pollinator, and environmental factors that influence either individually or in interactive way. Hence, understanding these components coupled with agronomic crop management could be a game changer in the hybrid seed production of annual flower crops. Heterosis between two diverse genotypes can be harnessed not only for the crop improvement but also develop climate resilient varieties that caters to the needs of the flower industry. Hybrid development in flower crops is hindered by a number of challenges that include self-incompatibility, male sterility, development of inbreds and prolonged dormancy, *etc.*, this paper shall discuss such challenges and possible strategies to overcome them.

Technical Session V

Current Status and Future Prospects in Hybrid Crop Breeding II (Horticultural Crops)

- Abstracts of Rapid Oral Presentations

TS V-OP-01

Exploitation of CMS line in hybrid development in long-day onion (*Allium cepa* L.) at ICAR-VPKAS, Almora

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Onion (*Allium cepa* L.) is a major bulbous crop among cultivated vegetables. The productivity of onion in India is 12.5 t/ha, much lower than the productivity of the USA (41.12 t/ha). The higher productivity of onion in the USA is due to the cultivation of the long day hybrids. The lower productivity of onion in India could be attributed to the limited availability of F_1 quality seed. The lack of hybrids in onion is the major limiting factor. The discovery of male sterility in onion led to a rapid change to F_1 hybrids, possibly due to simplicity and the low cost of seed production. Hybrids have a higher yield with a larger and more uniform bulb size than open-pollinated cultivars. Robust CMS line i.e. VL In. 31-1A (Female) & VL In. 31-1B (Maintainer) was developed by deploying DNA markers in an intermediate day-length Indian onion population. The first onion CMS line (INGR 22084) suited for intermediate/long day conditions has been registered as genetic stock with ICAR-NBPGR.

It is very well suited to develop an F1 hybrid for the Rabi season for the Plan, mid hills (Intermediate day length), and high hills (long day length). It has already been utilised in the heterosis breeding programme at ICAR-VPKAS, Almora. One F1 (VLP-68) is in the final year of testing in the All-India Network Research Project on Onion & Garlic (AVT II, Long day conditions during 2023-24). At present, not a single F1 hybrid is recommended for cultivation under mid-hills and long-day conditions. This CMS line will strengthen the country's hybrid development programme.

TS V-OP-02

Quantitative trait loci mapping for horticultural traits in melon (*Cucumis melo* L.) using a genotyping-by-sequencing-based genetic map

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Muskmelon (*Cucumis melo L.*) is an economically important vegetable crop, valued for its nutritional benefits and diverse genetic variability. Fruit quality traits, such as size, weight, maturity and flavor, significantly influence consumer preference and market value. These traits are governed by multiple genes, which are modulated by environmental and genetic factors. Understanding the molecular basis of these traits is crucial for effective crop improvement programs. In this study, we performed quantitative trait loci (QTL) mapping to identify the genetic factors controlling key horticultural traits in muskmelon. We utilized a Genotyping-by-Sequencing (GBS) approach to construct a high-resolution genetic linkage map in an $F_{2:4}$ population of 110 individuals, derived from a cross between muskmelon variety *Punjab Sunehri* and snapmelon accession SM2012-1. The F_4 population was phenotyped across two growing seasons (spring and rainy) in 2023. A total of 1962 single nucleotide polymorphism (SNP) markers were used to construct a genetic map with 13 linkage groups, which facilitated the detection of QTLs for nine important horticultural traits: days to first male flower, fruit maturity, fruit weight, fruit length, fruit width, flesh thickness, cavity length, cavity width and total soluble solids (TSS). In total, 60 QTLs were identified, which were distributed across all chromosomes except chromosome 8. The identified QTLs explained 6% to 32% of the phenotypic variance (PVE), with logarithm of odds (LOD) scores ranging from 2.5 to 42.7. Seventeen overlapping QTLs were observed, affecting multiple traits on chromosomes 1, 2, 3, 5, 7 and 10. These findings provide valuable insights into the genetic architecture of melon fruit quality traits and highlight potential markers for marker-assisted selection (MAS). The results of this study will serve as a foundation for future fine-mapping efforts and the application of MAS in melon breeding programs aimed at improving fruit quality and enhancing overall productivity.

TS-V-OP-03

Current status and future prospects of hybrid breeding in Indian cauliflower for higher yield, nutraceuticals and disease resistance

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Cauliflower is sixth important vegetable crop in India and reached all across the country. It has been transformed from 'crop of aristocrats' to 'food of commoners', particularly after development of Indian tropical cauliflowers and streamlining of commercial production. India (9.58 million tonnes) become the second largest producer of cauliflower after China (9.78 million tonnes) and both are almost equal contributors (36.94%; 30.01%) in the global production (26.47 million tonnes). In terms of average productivity of cauliflower, India (19.4 t/ha) has surpassed the world (18.8 t/ha). The cauliflower scenario has improved due to development of hybrids in different maturity groups. The hybrids showed pronounced heterosis in earliness, curd weight, yield besides tolerance to diseases and heat stress and uniformity. Three sterile cytoplasms (*Ogura*, *Can* and *Tour*) were deployed and developed cytoplasmic male sterile (CMS) lines in different maturity groups besides stabilizing self-incompatible (SI) lines. Both genetic mechanisms were exploited for hybrid breeding and three SI based hybrids (Pusa Kartik Sankar, Pusa Hybrid 2, Pusa Cauliflower Hybrid 101) and two CMS based hybrids (Pusa Cauliflower Hybrid 102, Pusa Cauliflower Hybrid 3) by IARI, New Delhi. Three more hybrids Pusa Snowball Hybrid 1, Pusa Snowball Hybrid 2, Pusa Cauliflower Hybrid 301 were developed by IARI Regional Station, Katrain using *Ogura* CMS system. These hybrids have higher yield (30-45%) than OP varieties of respective maturity groups. New resistance sources with single dominant genes for black rot (*Xccbo1*) and downy mildew (*Ppa3*) which imparted disease resistance to hybrids. The *Or* gene (for ß-carotene) and *Pr* gene (anthocyanin) were introgressed through marker-assisted breeding in Indian cauliflower and developed 11 and 16 lines, respectively. Some of these lines were found promising in hybrid combinations for ß-carotene or anthocyanin and marketable curds. The hybrid breeding could facilitate commercial utilization of *Or* gene. In future, cauliflower hybrid breeding aims to diversify sterile cytoplasm, develop hybrids with multiple disease resistance, wider curding plasticity, less pesticide retention, higher dietary nutrients and desirable levels of functional compounds (glucosinolates, anthocyanin and ß-carotene) to benefit the farmers and increase per capita cauliflower availability across the country.

TS V-OP-04

Combining ability studies in ridge gourd [*Luffa acutangula* (L.) Roxb.] for harnessing better parents and hybrids

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Ridge gourd is an important vegetable crop in India. It is monoecious and highly cross-pollinated, so developing hybrids for yield and improvement is easy and rewarding. Combing ability is the ability of genotypes to transfer their good performance to their progeny, so it is a better way to identify better parents as well as promising crosses. This study was carried out at Navsari Agricultural University, Navsari during *Late Kharif* -2021-22 using seven parents which were crosses in diallel fashion excluding reciprocals and 21 crosses are generated. Analysis of variance for combining ability of study revealed that the σ2sca was higher than σ2 gca for all characters denoting a preponderance of non-additive gene action for these characters and it is confirmed by σ2 gca/ σ2sca ratio which was less than unity. The results of general combining ability effects revealed that among seven two parents possessing significant GCA effect for fruit yield per plant were GLC-1 and GLC-3. Along with fruit yield, GLC-1 was found to be a good general combiner for fruits per plant, days to first female flower, vine length (m), fruit length (cm) and crude fiber (g/100g) and parent GLC-3 was good general combiner for days to first female flower, days to first male flower, vine length (m), fruit girth (cm) and days to marketable maturity. SCA effects did not show any specific trend for the GCA of the parents. The crosses with desirable SCA effect involved all types of combinations *viz*., Good × Good, Average × Good, Poor × Good, Average × Average, Average × Poor, Poor × Poor of the parents. Genotypes GLC-5, GLC-3 and GLC-1 can be recommended for use as one of the parents to generate high-yielding and better-quality hybrid due to high GCA effects and good *per se* performance.

TS-V-OP-05

Development of CMS lines and hybrids of early cauliflower for better curd quality, shorter duration and higher yield

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Cauliflower (*Brassica oleracea* var. *botrytis* L.) is an important cool season cross-pollinated vegetable crop. The early maturity group which comes to curd harvesting during mid-September to mid-November is an important market segment in North India plains because of its tropical nature fetching remunerative price. As environment during the period is hot (27-30°C) and humid, uniform crop establishment, better curd quality (white, compact and delayed-bursting) and improved yield are the target traits. Hence, the robust CMS system and parental lines with better crop ideotype plays a crucial role in development of hybrids and seed production at commercial scale. Cauliflower improvement programme is carried out at ICAR-IIVR, Varanasi, UP targeting early group. A number of lines with different plant morphology (semi-spreading, semi-erect) and curd parameters (compactness, size, curd colour) have been developed through bud pollination and sibmating. Cytoplasmic male sterility of Ogura CMS source has been transferred to the promising lines through backcrossing. A total of 35 F_1 hybrids were developed and evaluated, comprising five robust male sterile Ogura CMS lines (confirmed through P1 dominant marker with ~450bp specific to orf138) and seven pollen parents vis-a vis leading hybrid of early segment Syn-1522 which holds major market share of over 50% with excellent curd compactness (very compact curd with >0.410 CCI), white coloured curd, marketable curd percentage of 96.5%, marketable curd weight of 427 g, yield potential of 185 q/ha and 88 days of maturity. Among 35 hybrids evaluated, three F_1s namely VRCFH-407, VRCFH-408 and VRCFH-410 were found to be promising for curd compactness (compact curd with CCI of 0.381, 0.388 & 0.395); off-white coloured curds; marketable curd percentage of 89.2, 90.7 & 92.8%; marketable curd weight of 473, 496 & 465 g; yield potential of 190, 202 & 194 q/ha; and 78, 80 & 82 days of maturity. The newly developed hybrids are significantly shorter in duration, and higher in marketable curd weight than the leading hybrid and have the potential to increase the choice among farmers.

Technical Session V

Current Status and Future Prospects in Hybrid Crop Breeding II (Horticultural Crops)

- Abstracts of Poster Presentations
- Evening Lecture II

TS-V-PP-01

Improvement of cucumber (*Cucumis sativus* L.) through heterosis breeding

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The present study was conducted during 2023 to 2024 at the Experimental Research Farm, Department of Vegetable Science, COHF, Neri, Hamirpur (HP). 6 inbred lines of cucumber along with 15 F_1s, using half diallel design and 1 check “CODE-CU01” were evaluated in Randomized Complete Block Design with 3 replications to assess the extent of heterosis, GCA & SCA and gene action. Analysis of variance indicated significant differences among the various genotypes with respect to all the traits studied. Experimental results revealed that 3 lines viz., CU-COHF-LC-1, Solan Srijan and Punjab Naveen were found superior based on their mean performance for fruit yield per plant and also promising for number of fruits per plant and stem diameter. Parent CU-COHF-LC-1 showed best desirable GCA effect for the fruit yield per plant. 3 cross combinations *viz*., Japanese Long Green × CU-COHF-LC-3, Solan Srijan × Japanese Long Green and CU-COHF-LC-1 × CU-COHF-LC-2 were found promising in terms of performance of hybrids for the most economic traits like fruit yield per plant and fruit length. The same hybrids also exhibited best desirable SCA effects for the character fruit yield per plant. Superior values for heterobeltiosis and heterosis over standard check were recorded by 3 cross combinations *viz*., Japanese Long Green × CU-COHF-LC-3, Solan Srijan × Japanese Long Green and Punjab Naveen × Japanese Long Green (CU-COHF-LC-1 × CU-COHF-LC-2 equivalent value to Punjab Naveen × Japanese Long Green for heterobeltiosis only) for fruit yield per plant and fruit length, respectively. Gene action studies revealed the predominance of non-additive gene action in governing most of the traits indicating that exploitation of hybrid vigour along with hybridization, as a better tool for improvement.

TS-V-PP-02

Combining ability studies in ridge gourd [*Luffa acutangula* (L.) Roxb.] for identifying better parents and hybrids

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Ridge gourd is an important vegetable crop in India. It is monoecious and highly cross-pollinated, so developing hybrids for yield and improvement is easy and rewarding. Combing ability is the ability of genotypes to transfer their good performance to their progeny, so it is a better way to identify better parents as well as promising crosses. This study was carried out at Navsari Agricultural University, Navsari during *Late Kharif* -2021-22 using seven parents which were crosses in diallel fashion excluding reciprocals and 21 crosses are generated. Analysis of variance for combining ability of study revealed that the σ2sca was higher than σ2 gca for all characters denoting a preponderance of non-additive gene action for these characters and it is confirmed by σ2 gca/ σ2sca ratio which was less than unity. The results of general combining ability effects revealed that among seven two parents possessing significant GCA effect for fruit yield per plant were GLC-1 and GLC-3. Along with fruit yield, GLC-1 was found to be a good general combiner for fruits per plant, days to first female flower, vine length (m), fruit length (cm) and crude fiber (g/100g) and parent GLC-3 was good general combiner for days to first female flower, days to first male flower, vine length (m), fruit girth (cm) and days to marketable maturity. SCA effects did not show any specific trend for the GCA of the parents. The crosses with desirable SCA effect involved all types of combinations *viz*., Good × Good, Average × Good, Poor × Good, Average × Average, Average × Poor, Poor × Poor of the parents. Genotypes GLC-5, GLC-3 and GLC-1 can be recommended for use as one of the parents to generate high-yielding and better-quality hybrid due to high GCA effects and good *per se* performance.

TS-V-PP-03

Nutritional Profiling and Antioxidant Activity of Carotenoids in Papaya (*Carica papaya* L.) Hybrids

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Papaya (*Carica papaya* L.), native to Central and South America, ranks as India's fourth most important fruit crop and is widely cultivated in tropical and subtropical regions globally. India leads worldwide papaya production, followed by Brazil, Mexico, and Nigeria. Papaya's exceptional nutritional profile, ranking first among 38 common fruits, has contributed to its increasing consumption due to associated health benefits. The fruit is rich in bioactive compounds and antioxidants, particularly carotenoids and vitamin C. It exhibits diverse medicinal properties, including antihelmintic, antiprotozoan, antibacterial, antifungal, antiviral, anti-inflammatory, antihypertensive, hypoglycemic, hypolipidemic, wound healing, antitumor, free-radical scavenging, antisickling, neuroprotective, diuretic, abortifacient, and anti-fertility effects. Papaya consumption can prevent vitamin A deficiency, a leading cause of night blindness in tropical and subtropical developing nations. Despite its importance, limited research has been conducted on identifying and quantifying key bioactive compounds and antioxidant activities in Indian papaya hybrids. A study of nine papaya hybrids revealed that hybrid P-9-12 × P-7-2 contained the highest total carotenoids (4.88 mg/100g). LC-MS analysis identified 18 carotenoids and carotenoid esters in papaya pulp, including three hydrocarbon carotenoids, five free xanthophylls, nine xanthophyll esters, and one carotenal. Five of these carotenoid fractions were quantified using LC-MS. This research contributes to our understanding of papaya's nutritional composition and potential health benefits, highlighting the need for further investigation into diverse papaya hybrids to optimize their cultivation and utilization in India and globally.

TS-V-PP-04

Principle component analysis in field pea (*Pisum Sativum* L.) germplasm

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Hybridization followed by selection is a cornerstone of plant breeding, with the choice of appropriate parental lines being crucial for enhancing genetic recombination and improving yield potential. The study of diverse morphological traits within germplasm collections is essential for evaluating genetic diversity and breeding potential. However, the assessment of numerous traits often includes variables with limited discriminatory power, complicating the evaluation process. Principal Component Analysis (PCA) offers a robust solution, allowing for the reduction of redundant data and the identification of key patterns within complex datasets. As a multivariate statistical tool, PCA simplifies inter-relationships among a large set of variables into a smaller number of components, while preserving essential information. This study evaluated 132 field pea genotypes focusing on yield, starch, crude protein content, and contributing traits using PCA to assess genetic diversity. PCA revealed that the first five principal components, each with an eigenvalue greater than 1, explained 69.03% of the total variation. PC1 accounts for 21.14% of the variation and PC2 accounts for 17.38% of the variation. The PCA biplot highlighted strong positive correlations among pod width, 100-seed weight, and yield per plant, while traits such as plant height and starch percentage demonstrated a negative relationship. Growth traits like primary branches per plant, days to 50% flowering, and days to maturity were closely aligned, indicating positive associations. Weak correlations were observed between certain trait pairs, such as primary branches per plant & yield per plant, and plant height & starch percentage. These findings underscore the value of PCA in germplasm characterization, facilitating the selection of optimal parental lines for crop breeding programs.

TS-V-PP-05

Impact of genotype innovation on physiological parameters of ber (*Ziziphus mauritiana* Lamk.) in the Awadh region

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Ber (*Ziziphus mauritiana* Lamk.), popularly known as ber, the generic name is derived from '*Zizouf*', which is the arabic name of the fruit of *Z. lotus* Lamk. It is a member of the Rhamanaceae family and has a basic chromosome no x=12. The species *Z. mauritiana* Lamk. Is indigenous to India and is tetraploid (2n=48) to *Z. jujuba* Mill is indigenous to China and is diploid (2n=24). Due to its nutritional value, good taste, and affordable price, this fruit is quite popular among people of all social classes. During 2020-2021 Eleven cultivars of ber, Banarasi Karaka, Mehrun, Gola, Chhuhara, Kaithli and Illaichi, Goma Kirti, Narendra ber were collected from NDUAT in the vicinity of Lucknow, at fully uniform ripe stage in February, which were collected from trees present on the Horticultural Research Farm of Department of Horticulture, Babasaheb Bhimrao Ambedkar University, Lucknow. During analysis of some germplasm of ber fruits variability in various physico - chemical characters viz. fruit shape (oval, oblong oval, ovate, subspherical, apple shape), length, surface colour at maturity (brownish, radish brown, yellowish red, yellowish green yellowish surface with red-ting, half green, half-red), flesh colour (yellow, creamy-yellow, white, yellowish white), texture, TSS, Ascorbic acid, Acidity, total sugar, reducing sugar and non-reducing sugar was observed. Wider variability in stone shape (round, spherical, painted at both ends) and size was also observed. Narendra ber selection - 1 is superior in mostly parameters like as fruit length, fruit width, fruit weight, specific gravity and pulp weight, which were all statistically almost equivalent.

TS-V-PP-06

Heterosis and combining ability studies in tomato (*Solanum lycopersicum* L.)

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This study was conducted at the Experimental Farm, Department of Vegetable Science, COH&F, Neri, Hamirpur (HP), during the Kharif season of 2023. Seven parental lines viz. Arka Vikas, Solan Lalima, Punjab Sartaj, Punjab Gaurav, Punjab Swarna, Palam Pride, and 12-1 were crossed in a half-diallel design, yielding twenty-one hybrid combinations. These combinations were evaluated alongside the parents and a check variety (Palam Tomato Hybrid-1) for various qualitative and quantitative traits using a Randomized Complete Block Design (RCBD) in summer 2024. The cross Arka Vikas × Solan Lalima recorded the highest yield per plant, surpassing the check, followed by Punjab Sartaj × Punjab Gaurav and Solan Lalima × Punjab Gaurav. For traits such as fruit weight and seed count, Solan Lalima × 12-1 and Arka Vikas × Solan Lalima excelled. Heterosis analysis revealed that Arka Vikas × Solan Lalima displayed the highest significant heterosis for yield over both the better parent and the standard check, followed by Solan Lalima × Punjab Swarna and Solan Lalima × Palam Pride. Additionally, Solan Lalima × Punjab Swarna exhibited significant heterobeltiosis for ascorbic acid, while Punjab Gaurav × 12-1 showed high heterosis over the standard check. Traits such as days to 50% flowering, number of fruits per plant, and yield per plot identified 12-1, Punjab Sartaj, and Solan Lalima as good general combiners. Additive gene action was predominant across most traits which shows effective heterosis. This study highlights promising cross combinations like Arka Vikas × Solan Lalima and Solan Lalima × Punjab Gaurav for improving yield and quality traits in tomatoes, providing a strong foundation for future breeding programs. The findings will serve as a valuable resource for tomato breeders aiming to enhance productivity and nutritional quality in their cultivars.

TS-V-PP-07

Development of tomatoes against high temperature in context to climate change

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Climate change, a consequence of global warming is a major warning for crop productivity and food security as it threatens to increase the frequency and intensity of extreme weather events such as heat waves. Temperature projection increases range from 2°- 5°C by the end of the 21st century (IPCC, 2014). Rising temperature above optimal due to global warming directly reduce yield in crops like rice, groundnut, cowpea, *etc*. More than any other crops, vegetables, especially tomatoes are highly sensitive to temperature. Tomato crops can survive under heat stress through anatomical, morphological, physiological, phenological and molecular responses; yet, the high temperature has an extensive effect on the reproductive stage and yield. As per CRISIL, in June, tomato prices increased by 30% compared to the previous year as a result of high temperatures in key growing regions of India. In this climatic scenario, breeding for heat tolerance in tomato is essential to ensuring food security. Several wild and local species exhibit heat stress tolerance by generating metabolites, osmoprotectants, heat shock proteins (HSPs) as well as changes in leaf number, transpiration rate, photosynthesis rate, plant height and pollen tube growth. More knowledge of these mechanisms will help in the development of novel tomato varieties that can survive under high temperatures. Conventional breeding is time consuming process but it can be improved up by working with advanced breeding techniques like genetic engineering especially with *CRISPR Cas*, marker assisted selection, mutation breeding, speed breeding, etc. Heat tolerance genes are polygenic in nature and have low heritability but trait-specific breeding will be made possible by the identification of QTLs and genetic mapping. A comprehensive approach is essential to fully understand the reasons of tomato susceptibility to heat stress and the development of heat-

resistant varieties in the interfaces of constantly rising global temperatures. Genetic engineering, genetic resource collection, preservation and exploitation would allow researchers and breeders to develop heat tolerant tomato varieties that can survive under high temperatures for a long period of time.

Evening Lecture II

Technological advances for hybrid crop breeding to ensure food and nutrition security

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The three big developments in plant breeding in the 20^{th} century were dwarf wheat, dwarf rice and hybrid maize (corn). The first two developments were the saviours of humankind from mass starvation in the 1950s and 60s in developing countries and the third development improved dietary intake in developed countries. Corn is the quintessential crop for understanding heterosis breeding. George H Shull introduced the term heterosis in 1914. Heterosis can be described as the superior performance of the hybrids over the mid-parent value or the better parent. Heterosis can manifest as superior biomass or grain yield or both.

Maize is a monoecious plant but bears separate male (tassel) and female (ear) flowers. One of the parental lines is detasseled manually and the seed collected from this line is the hybrid seed. As a cross-pollinated crop, maize populations contain many undesirable recessive alleles. The initial inbred lines were too weak and two-way crosses had to be made. It was only when single-cross hybrids became available that hybrid corn spread dramatically. Hybrid breeding in corn was a success story from the US, the next success was from China in rice – a self-pollinated crop. Hybridization between two divergent lines in self-pollinated crops with the male and female organs in each flower requires a pollination control mechanism allowing only cross-pollination. This pollination control system could be a CMS-based three-line system (A, male sterile; B, near-isogenic of A but male fertile maintainer line; and R, divergent line with fertility restorer gene) or nuclear-encoded temperature and/or photoperiod-sensitive male sterility (GMS). Three-line and two-line systems have been extensively used for hybrid seed production in rice and other crops. Many labs have reported third-generation pollination control systems that use new breeding technologies – genome editing and genetic engineering (reviewed by Liu *et al*. 2024. *iScience* 27: 108901). However, these systems are yet to be deployed commercially.

Besides maize and rice, heterosis breeding has been used in nutri-cereals, oil seed crops - sunflower and rapeseed, and many vegetables. Both rapeseed (*Brassica* *napus*) and mustard (*B. juncea*) are self-compatible, but cross-pollination mediated by insects like honeybees occurs readily. Rapeseed crops in Canada, Europe, and China are predominantly hybrids. Europe uses CMS systems, China uses a PTGMS system, and Canada, Australia, and the US use the GM barnase/ barstar system for pollination control.

Our group has done extensive work on heterosis breeding in mustard. In 1993 we showed two divergent gene pools in oilseed mustard, the Indian gene pool, and the East European gene pool. Hybrids between the two gene pool lines were heterotic for yield (Pradhan *et al*., 1993. *Euphytica* 69: 219-229). The challenge thereafter was to develop a robust pollination control system to exploit this finding. We tried to improve some of the alloplasmic CMS systems i.e., *tour* and *oxy* available in India by somatic cell hybridization. While the male sterile lines could be improved, no restorer lines could be developed or found. We developed and tested a new CMS named 126-1 (Sodhi *et al*., 2006. *Theor. Appl. Genet*. 114: 93-99) in mustard and used this to develop hybrid DMH-1 which is serving as a national check in hybrid trials by ICAR-AICRP on rapeseed and mustard. However, 126-1 is stable only in one Indian gene pool line Pusa bold, and therefore has limitations on its use.

We developed transgenic male sterile and fertility restorer lines using the barnase/ barstar transgenes (Jagannath *et al*. 2002. *Curr. Sci*. 82: 46-52) and have found this to be the ideal system for high-purity hybrid seed production in mustard. The barnase/ barstar-based pollination control system and the first hybrid DMH-11, a cross between Indian gene pool line Varuna and East European line EH2, were ready for testing in 2002. All the currently stipulated biosafety tests were initiated in 2005 and completed by 2010. The environmental release by the Government of India only came through in October 2022. The release is now stuck in the Supreme Court of India due to a 2005 PIL by anti-GM activists.

Earlier work on corn and other crops had shown heterosis to be due to three different phenomena – dominance, over-dominance, and epistasis. Recent work in genomics and other omics has shown that heterosis in maize and rice is due to many minor-value positive epistatic interactions. The same has been confirmed in rapeseed and mustard (Aakansha *et al*. 2021. *Front. Plant Sci*. 12: 721631). Therefore, hybrids between genetically divergent lines will always increase yield over the pure lines used as combiners for developing hybrids. The challenge in mustard is to improve the combiners without sacrificing divergence. The main theme of my talk would be to present our work on QTL mapping of yield-influencing traits in DH populations derived from multiple bi-parental crosses and by Association mapping and describe what needs to be done to improve pure lines that would combine well to provide hybrids with a yield advantage of 10-20% over the leading pure line varieties.

Technical Session VI

Strategies for Hybrid Seed Production and Management

- Extended Summaries of Keynote and Invited Presentations

TS-VI-IP-01

National initiatives in hybrid seed production

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Hybrid seed production is expected to play a transformative role in shaping the future of agriculture in India. With agriculture contributing 18.2% to the GDP and employing 42.3% of the workforce, ensuring consistent productivity and food security is paramount. The presentation on National Initiatives in Hybrid Seed Production delves into the state of hybrid seed production, the challenges faced, opportunities, and strategic way ahead for growth in India.

The Agricultural Landscape in India: India's unique agro-climatic conditions, spanning 15 prominent climates and 46 of the world's 50 soil types, make it a powerhouse of agricultural potential. The country ranks as the second-largest in arable land (160 million hectares). Despite this, agriculture faces critical challenges such as low mechanization, fragmented landholdings, declining natural resources, and yield stagnation. India must increase food production by 4%, 45%, and 55% to meet the population's demand in 2030, 2050, and 2065, respectively.

Current Status of Hybrid Seed Technology: Hybrid seeds, known for their yield advantages due to heterosis, have seen varied adoption rates across crops. While hybrids dominate in cotton (97%) and castor (94%), adoption remains limited in staples like paddy (9%), sorghum (35%), and maize (65%). India's hybrid seed market, valued at USD 1.44 billion, underscores the untapped potential for further penetration. In vegetable crops, hybrids account for over 80% of seed usage, with okra, tomato, and peppers leading the market. Large seed companies, including Bayer, Syngenta, and Advanta, invest 6-10% of their turnover in R&D, releasing over 500 hybrids in the past two decades. However, more than 80% of these companies depend on public institutions for breeder seeds. Public sector institutions focus on socially driven objectives such as providing affordable quality seeds to smallholder farmers. Hybrid varieties like KRH-2 (paddy) and DMRH series (maize) have been developed. However, their reach is limited due to poor commercialization policies and insufficient marketing efforts.

Challenges in Hybrid Seed Sector

(i) **High Costs:** The cost of hybrid seed production remains high due to labor-intensive processes and complex breeding techniques. For instance, maize hybrid seeds cost Rs. 200-250/kg from the public sector and Rs. 300-600/kg from the private sector.

(ii) **Climate Change:** Extreme weather, rising temperatures, and new pest outbreaks adversely impact hybrid seed yields.

(iii) **Consumer Preferences:** Hybrids often lack the taste, texture, and aroma favored by traditional varieties, limiting their acceptance.

(iv) **Low Adoption Rates:** Adoption in crops like wheat, pigeon pea, and mustard is negligible, largely due to socio-economic and agronomic constraints.

(v) **Fragmented Sector:** The hybrid seed market is fragmented, with the top 10 companies holding only 40% of the market share.

Opportunities for Growth

(i) **Climate-Resilient Hybrids:** Developing hybrids that withstand abiotic stresses such as drought, heat, and salinity can address the challenges posed by climate change.

(ii) **Biofortification:** Enhancing nutritional quality in hybrids can combat malnutrition. For example, hybrid varieties with higher zinc and iron content are gaining importance.

(iii) **Policy Support:** Initiatives like subsidies for hybrid rice seed production under the National Food Security Mission (NFSM) and support for seed infrastructure under RKVY, SMSP are pivotal.

(iv) **Technological Innovations:** Leveraging tools like CRISPR-Cas9 for gene editing, marker-assisted selection, and RNA interference can accelerate hybrid development.

(v) **Public-Private Partnerships (PPPs):** Collaborative models can enhance hybrid seed availability and affordability, combining public research with private marketing expertise.

Strategies for Accelerated Hybrid Adoption

(i) **Enhancing R&D Capabilities:** A renewed focus on R&D is essential for developing high-performing hybrids tailored to diverse agro-climatic conditions. Special attention should be given to less explored crops like pulses, millets, and oilseeds. For example, ICAR's program in the late 1990s facilitated the release of hybrids in sorghum, pearl millet, and vegetables, setting a precedent for future initiatives.

(ii) **Optimizing Seed Production Systems:** Standardizing isolation distances, synchronizing parental lines, and using molecular markers for genetic purity testing can enhance hybrid seed quality. Establishing seed production clusters can address regional imbalances and reduce costs.

(iii) **Leveraging Digital Platforms:** Digital tools powered by AI and big data can predict seed demand, optimize supply chains, and streamline marketing.

(iv) **Promoting Awareness Among Farmers:** Farmer-centric programs focusing on the benefits of hybrids, backed by demonstrations and training, can improve adoption rates. Seed minikits under NFSM and extension programs have shown success in this regard.

(v) **Policy Interventions:** Uniform licensing and commercialization policies are crucial for scaling public sector hybrids. Additionally, subsidies for hybrid seed production and distribution should be streamlined to encourage private participation.

Impact of Hybrid Seeds

(i) **Higher Yields**: Hybrids have consistently shown a 20-30% yield advantage over open-pollinated varieties (OPVs).

(ii) **Employment Generation**: Hybrid seed production, especially in vegetables, provides significant rural employment opportunities. For example, the benefit-cost ratio (B:C) for hybrid vegetable seed production is 2.77:1.

(iii) **Export Potential**: India is the fifth-largest global seed economy, with a compound annual growth rate (CAGR) of 9.6%. This positions the country as a key player in the global seed trade.

(iv) **Seed Replacement Rates (SRR)**: Enhanced SRRs reflect the growing use of quality seeds. Government policies promoting newer varieties have driven this trend.

Future Outlook

The hybrid seed sector in India holds immense promise. Key focus areas include: expanding hybrid adoption in staples like paddy, mustard, and pulses, strengthening collaborations between public institutions and private players, investing in advanced breeding technologies to develop high-yielding, climate-resilient hybrids. Hybrid seeds are central to India's agricultural growth and food security. Addressing the challenges of high costs, climate change, and fragmented markets requires strategic interventions and collaborative efforts. With increased R&D investments, policy support, and farmer-centric initiatives, India can harness the full potential of hybrid technology to ensure sustainable agricultural development.

TS-VI-IP-02

Hybrid breeding and maintenance of parental lines

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Hybrid breeding is a scientific approach based on the exploitation of heterosis for crop production and maintenance of parental lines are crucial steps in producing high-quality hybrid seeds. In commercial breeding organizations hybrid breeding programs and product development goals are designed keeping the key stakeholders' (Organization, farmers, consumers) needs in mind. Success of a breeding organization depends how effectively they deliver genetic gain to their customers, while improving internal efficiencies. Time, cost and precision are the key levers to drive an efficient hybrid breeding program. To improve efficiency many enabling technologies, and tools are available in marketplace but one need to choose what is most relevant and cost effective.

Cycle time reduction in the inbred development process has been always the key focus to speed up the product deliver timeline. Though pedigree breeding is still most common method for inbred development through conventional breeding but due to progress in high throughput speed breeding and molecular tools, single seed descent method is also getting popular to speed up inbred development process. Many organizations have started routinely using DH also in crops like corn, mustard, wheat etc. for the inbred development.

Due to advancements in Genetics, breeding methods have evolved over time from traditional phenotypic selection to a combination of molecular breeding, and predictive breeding approaches. Genomic selection (GS) is a great tool for the selection of individuals with traits of interest even for quantitative traits by using various types of the whole genome-scanning markers, which was a limitation in marker-assisted selection (MAS). Also, CRISPR's ability to make precise genetic changes holds great promise for the future.

It is also important to keep track of diversity in the program. Germplasm enhancement is the most important step for sustainable genetic gain. It is always advisable to thoroughly evaluate general combining ability, target traits in new germplasm before using in breeding crosses. Breeders need to keep focus on traits of interest during generation advancement. Too many truncation traits at breeding start will have high implication on diversity and high selection intensity will reduce diversity.

Over the years significant progress has been made in hybrid development technologies, incorporating both traditional and modern techniques to enhance crop productivity and resilience. Key methods used for hybrid development are hand emasculation and pollination, Cytoplasmic Male Sterility (CMS), Genetic Male Sterility (GMS), TGMS etc. In a CMS based model female and male pools are maintained and enhanced separately, and breeding population development occurs within female and male groups. Value of individual inbreds (GCA & SCA) is judged based on their performance in hybrids rather than per se performance. Breeders use inbred GEBV, PEBV and genetic distance data while designing new breeding crosses. To keep inbred development program balanced and efficient, breeders follow breeding and testing matrix based approach. Testing matrix is a general guideline. However, testing and advancement decisions depend on strategic priorities and resources. To improve efficiency in product testing it is advised to raise the bar and reject more when genetic gain is higher. Most breeding organizations follow a 3-4 year hybrid testing system followed by 1-2 years agronomic evaluation in target geographies. When potential hybrids are advanced to pre-commercial stage, parental line multiplication process begins, and this process is called maintenance breeding.

Maintenance breeding is the key to ensure inbred and hybrid purity for a robust seed production program. The basic purpose of maintenance breeding is not to improve the inbred/variety, but only to keep the genetic constitution unchanged (Peng et al. 2010). Zeven (2002) defined maintenance breeding as 'all breeding measures taken to conserve the genetic composition of a variety/inbred'.

During multiplication process of parental lines and hybrid seed production, seed should meet the recommended quality standards in terms of physical, physiological, genetic purity and seed health. In India and other SAARC countries, a three-generation system of seed multiplication is followed (Huda and Saiyed, 2011).

TS-VI-IP-03

Development of hybrid seed production technology and management of male sterile line

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It is well recognized that use of quality seeds of improved crop varieties and hybrids substantially contribute in agricultural production by increasing productivity up to 15-

20%. Efficacy and accuracy in seed production technology are vital in ensuring sufficient quantities of improved quality seed, including those of hybrids, at affordable cost to enhance crop productivity and resilience. Hybrid technology, harnessing the advantage of heterosis between two diverse genotypes to achieve maximum hybrid vigour, is widely recognized and commercially used for crop variety improvement both in field and vegetable crops. Hybrids can be developed using appropriate technology, irrespective of the mating and pollination system in the plant species. Production of hybrid seed depends on plant, pollinator and environment factors, each of which influences it individually or in interactive ways. Hence an understanding of these is important to undertake hybrid seed production of a given crop species. The basic requirements for hybrid seed production at a commercial scale are a) unisexual flower or a bisexual flower with sterile pollen in anther or self-incompatible flower/ plant; or pistillateness; or large conspicuous bisexual flowers for easy emasculation of flowers in plants to be used as the female parent and b) synchrony/matching in anthesis in the seed and pollen parent lines; abundant pollen production, dispersal and its easy transfer from the male parent to the female parent for satisfactory seed setting. These are dependent on floral biology, flower features, mode of pollination and reproduction of the crop species. Agronomic crop management with scientific insights is equally important for successful hybrid seed production. Considering the constraints in and sex expression in the seed parent line innovations have been made to improve plant reproductive systems in crop species. Marker-assisted selection, genomic prediction, genetic engineering, transcriptomics, epigenetics, and bioinformatics revolutionized breeding strategies, facilitating trait manipulation, parent selection, for heterosis exploitation. These multidisciplinary approaches not only streamline production processes, but also drive innovation improving crop performance in the face of contemporary agricultural challenges. By integrating genetic insights with precision technologies, hybrid seed production would revolutionize global agriculture, ensuring sustainable food production for future generations.

TS-VI-IP-04

Agribiotech start-up ecosystem - present status *vis-a-vis* hybrid development

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The Startup India initiative launched in 2016 has witnessed remarkable success through the recognition of 131,211 startups by the Department for Promotion of

Industry and Internal Trade (DPIIT) by May 2024. The Government of India’s purpose of promoting startups in agriculture is mainly focused on creating digital infrastructure to support solutions to farmers and technological innovation to reinforce farm diversification. Accordingly, the Ministry of Agriculture & Farmers welfare, has stated the key focus areas, as per its policy on “Promoting Startups in Agriculture”. These include, Big data, Farming as a service (FASS), Market Linkage models (both for input and output), Finetech for Farmers and IOT for farmers.

The GOI has provided support to agricultural start-ups through policies and programs such as Start-up India, the Atal Innovation Mission, RKVY – RAFTAAR scheme, NIDHI (National Initiative for Developing and Harnessing Innovations), the Venture Capital Finance Assistance (VCA) Scheme, NewGenIEDC (New Generation Innovation and Entrepreneurship Development Centre) and the ASPIRE scheme. It also established more than 120 incubators and five knowledge partners to support the agritech start-up ecosystem.

This ecosystem promoted setting up of more than 5000 agritech startups., and most of them are in the areas of Big Data Analytics, Supply Chain /Market linked model, FaaS and IOT-enabled Innovations. (ICRIER, 2023). The market size of agritech, In India, is expected to more than double from 2022 to 2027, rising from US$ 4 billion to a whopping US$ 34 billion (Avendus, 2023). The global agritech industry, between 2020 and 2027, is expected to grow at a compound annual growth rate (CAGR) of 12.1% (Ernst & Young, 2024). Presently these agri-startups in India are mostly founded by young professionals with engineering and management backgrounds (NAAS, 2022).

The startups evolve through several stages, ideation, validation and scaling stage, before reaching the stage of a full- fledged scalable business. However not all startups reach the stage of scaling. Premature scaling and running out of cash are some of the key reasons for the failure (Cantamessa *et al*., 2018; KPMG, 2018).

However, agriculture, is facing unprecedented challenges, including resource scarcity, climate change, and growing demand for food. India's farm yield is 30-50% lower than that of developed nations. The challenge is seeking affordable, accessible, easy-to-use technologies, products or services to enhance agricultural productivity in India. Genetics is a key issue that cannot be left out of the toolbox to face future challenges (Norero, 2024). As the pressure to adopt more sustainable practices intensifies, the focus on biotechnology becomes even more relevant. Agri biotech startups have the potential to develop new solutions to these problems. Startups need to move beyond the ‘obvious’ innovations and explore crop-specific innovations that add value to farm produce. The shift to biotechnology is not simply an alternative but a necessary evolution in the seed sector and agriculture in general. Gene editing, in addition to other tools of biotechnological support tools for genetic enhancement of crops allows us to do things, we could already do, but in a much faster, more accurate and cheaper way and hence is a great opportunity. With the potential to export both products and technologies, India is poised to offer valuable solutions for global agriculture. Agricultural biotechnology sector's revenues are projected to grow from $56 billion in 2022 to $170 billion in 2040 in the lower range of scenarios and to $230 billion in 2040 in the higher range of scenarios, a CAGR of 6 to 8 percent (McKinsey, 2024)

India having approximately 75 agricultural universities producing over 45,000 students annually (NAAS, 2022). Most of these students are from genetics and/or biotechnology background but are left out of the present agri-tech start up ecosystem. As stated elsewhere, the GOI's focus is on development of digital infrastructure and diversification of the use of the agricultural produce and not necessarily on enhancing the productivity of the agricultural crops. Even the Agriculture Grand Challenge, launched on December 15, 2017, which has listed 12 "Problem statements" in support of agritech ecosystem, has none related to Agribiotech.

The issues and challenges that Agribiotech startups face include, demand for agricultural products, high capital investment and regulatory hurdles. The demand for agricultural products is intrinsically related to productivity and income at each stage of value chain. In the seed sector, the value chain includes, Seed Production farmer, Seed company, Seed trade, farmer who grows the crop, processors and traders and finally the consumers. Each one of them alone or in combination, based on individuals requirements, determines the choice of a crop variety.

Agriculture is known as a slow-growing, long-gestation and is filled with a lot of uncertainties. Hence there is a lot of investor apathy and attracts less attention of the private investors, who are primarily interested in multiplying their investment quickly. Infact, globally biotech has recently encountered investment headwinds: in 2023, industrial and consumer biotech start-ups raised $2.1 billion, down from $4.9 billion in 2022. Ag Funder, a venture capital firm based in California's Silicon Valley, reported a 35% drop in investments across all venture markets, but a 50% drop in the agritech sector, what is generally termed as "agtech capital drought". McKinsey and Company (2024) estimated that approximately USD $6 billion that had been invested in 30 top agritech start-up companies had been lost in 2023 due to turn around or distress situations. In their first year of operations, two out of 10 U.S.-based startups will go under, despite the U.S. offering an enabling environment. Financing agri-startups is one of the significant challenges in India. Agri biotech startups coming from humble background need funding support at initial stage to validate their ideas and develop minimum viable product (MVP). Small and fixed ticket-size grant opportunities, presently offered by government agencies, are of very limited use for many of the agribiotech startups.

Most of agri-biotechnologies need a certain level of 'de-risking' to be done, proof-of-concept demonstrated, prototype built and tested before an enterprise can be built on them. As this 'de-risking' of the technology might take 2–3 years, there is an urgent need of a dedicated, catalytic fund to promote promising business ideas to avoid the death, as an agri-startup, before their birth and for the growth of agribiotech-startups. Hence startups need long term support. Investors need to be here for the long term and be supportive for startups for the whole journey of the investments. One of the major reasons for rejection of funding for agri start-ups have been the business models. The existing systems are too rigid that it is difficult to break and scale up.

The market access for an agribiotech product is often dictated by the regulatory frameworks in place. Seed being a highly regulated commodity world over- from accession of germplasm, deployment of improved cultivars, benefit sharing, IPR, export and import, cross-border collaborations, limiting the scope and scale at which agribiotech startups can operate.

The startups are facing severe challenge in accession of germplasm to initiate the innovations, as DSIR recognition, which in turn has the stipulation of minimum of three years of existence, has been made a mandatory for not only for accessing germplasm through ICAR-NBPGR and also testing minimum value product (MVP) in ICAR/university system. As startups are considered along with an established seed company, the charges for accession as well as testing are beyond the reach of most startups. Further commercialisation of the MVP, is on B2B licensing model, validation normally takes multi year, multilocation testing. Further, for the innovated crop hybrids, producibility validation has to be accompanied by a different set of seed production research data. These regulatory compliances, not only are expensive but also need 3-4 years for compliance. Therefore, the burden of compliance costs cannot be understated.

Startups, especially in their nascent stages, may find the high costs of complying with various regulatory stipulations to be onerous. These costs can divert crucial resources away from core activities such as research (validate their ideas) and development of MVP and market expansion, thereby hindering the growth of these startups. These restriction stifles the growth of individual startups.

State contributions are key to finance innovation, especially in the early stages, when investors and venture capitalists are reluctant to invest in high-risk R&D to develop cutting-edge technologies. Presently, the Government of India's support to agri-biotech startups, through various schemes - Rs 5 lakh at the idea stage and up to Rs 25 lakh at the seed stage for a maximum period of 12-18 months, is very insufficient both in terms of value but also the funding duration, for the reasons briefed above.

Therefore, the following are the suggestions for making an agribiotech startup as an viable venture.

(i) Agribiotech startups to be given a special status in terms of funding and regulatory compliances and not to be treated as private companies.

(ii) Technologies developed by different research organizations should be made available on a shared public platform in an easily discoverable well-categorized format. The validation of the technologies should be within reasonable terms and conditions

(iii) Delinking DSIR recognition for GOI recognised Agribiotech startups for accession of germplasm and also in tastings to validate MVP.

(iv) The charges for accession of germplasm and also testing of MVPs by start ups to be rationalised, both in terms of cost and timeline.

(v) GOI to treat agribiotech startups differently from other startups/Agri startups in terms of funding, both in terms of support as well as duration of the support. ICAR/DBT to establish funding scheme like AgriSure((Agri Fund for Startups & Rural Enterprises), for long term funding for generation and validation of MVPs and also for a period of 5 years to comply with all regulatory/licensing requirements.

Technical Session VI

Strategies for Hybrid Seed Production and Management

- **Abstracts of Rapid Oral Presentations**

TS-VI-OP-01

Standardisation of seed production technology of parthenocarpic gynoecious cucumber; Pusa gynoecious parthenocarpic cucumber hybrid–1 under nethouse conditions

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Cultivation of parthenocarpic and gynoecious hybrids have gained importance for their yield potential and high market demand over monoecious hybrids. ICAR-Indian Agricultural Research Institute, New Delhi has released gynoecious and parthenocarpic hybrid; Pusa Gynoecious Parthenocarpic Cucumber Hybrid – 1 for commercial cultivation. The commercial success of the hybrid, calls for standardization of quality seed production technology. The study was undertaken with the parental lines of the hybrid in the *Kharif* and Spring-Summer season under net house conditions. The flowering pattern, synchronisation behaviour, pollen viability, stigma receptivity, pollination time, fruit setting percentage, fruit load/vine, seed yield and quality were studied for optimization of hybrid seed production technology. The parental lines showed non synchronization of flowering for 10-12 days, thus the late parent (male) should be planted 10 days earlier than the seed parent achieving perfect nicking for hybrid seed production. The stigma receptivity was high upto 4 hrs after anthesis which declined after 12 hrs of anthesis as evident by fruit and seed setting in the vine. The pollen viability was high (above 95%) upto 4 hrs after anthesis which showed steep decline beyond 12 hrs after anthesis. Higher fruit and seed yield could be achieved by undertaking pollination between 6 to 10 am on the day of anthesis. Application of silver thiosulphate @0.03 mM twice at 2-3 leaf stage and 7 days after the first spray induced male flowers in gynoecious lines for their maintenance and seed production. The hybrid seed yield and quality was better in spring-summer season than *kharif* season. A planting ratio of 3:1 (female to male) was found optimum for hybrid seed production. Hybrid fruit load of 3fruits/vine was found optimum for higher seed quality. The study concluded that Spring-summer season was found better for hybrid seed production under north Indian conditions. The seed production technology of Pusa Gynoecious Parthenocarpic Cucumber Hybrid – 1 has been standardized under protected conditions. A hybrid seed yield of 1 to 1.2g /100sqm could be achieved under the nethouse in the Spring-summer season.

TS VI-OP-02

Breaking barriers in maize seed production: The success story of DMRH 1308 & DMRH 1301 hybrids

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Enhancing maize seed production efficiency, quality, and sustainability involves overcoming significant challenges. There is need of proper experimentations before going to commercial seed production. This is for identifying the ideal site, season, sowing time, planting ratio and standardizing flowering synchrony and packages of practices. Availability of technical manpower, isolation, irrigation facilities, productive female and better pollen parent are essential for successful commercial hybrid seeds production in maize. Day-to-day monitoring for maintaining genetic purity and crop health at critical growth stages is extremely important. In the maize seed business, private seed industries are very active and they are mostly targeting assured ecologies. Public sector share is also increasing and it is around 20-25% now. A good amount of breeder seeds demand has been received through DAC for public bred hybrids in the recent past (126 q). Many of them have been commercialized as well. From ICAR-IIMR Ludhiana, DMRH 1308 and DMRH 1301 were released and notified in the year 2018 for Rabi season cultivation in states like Bihar, Odisha, West Bengal, Jharkhand, Western UP, Madhya Pradesh, Gujarat, Rajasthan, and Chhattisgarh. As far as DAC maize breeder seed demand is concerned, DMRH 1308 has held the top position continuously for the last four years with its shares ranging from 20.1-34.9%. Since its release, total 247 q (59 q through DAC and 188 q through non-DAC) parental seeds have been produced and supplied into the seed chain. In the same way, DMRH 1301 is also part of the DAC seed chain since its release. So far nearly 38.40q of its breeder seeds have supplied into the seeds chain. In addition, 21 private seed companies have signed MoUs with IIMR for DMRH 1301 (11) and DMRH 1308 (10). If we want to cover the total 10.7 million hectares (mha) maize area under hybrid maize, we will need nearly 180 q of breeder seeds. By using the minimum seed multiplication parameters for breeder seeds supplied into the chain, so far, the DMRH 1308 have gone into > 6.0 Lakh hectares and DMRH 1301 in > 3.5 Lakh hectares area. Nearly 26175 q of hybrid seed was produced in the last four years for DMRH 1308 (17394

q) and DMRH 1301 (8781 q) in participatory mode involving FPOs, cooperatives, and SMEs in Telangana, Andhra Pradesh and West Bengal. The better female productivity (>2.5 t/ha), good pollen parents, high hybrids yield in the farmers field (6.5 to 10.5 t/ha), responsiveness to the inputs, and wider adaptability of parental and hybrids has contributed significantly to the success of these hybrids. A good public sector hybrid can create impact provided there is strategic efforts on its good seeds production.

TS-VI-OP-03

High yielding CGMS-based safflower hybrid: ISH-402

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Safflower (*Carthamus tinctorius* L.) has a rich historical significance dating back centuries. The area under safflower cultivation globally is declining since the last decade because of its low productivity. High degree of heterosis for seed yield (108-182% over mid parents) has been reported by several researchers. The first CGMS system in safflower in India was developed independently from a cross between *C. oxyacantha* and cultivated species. Considering the high industrial demand for safflower yield, the safflower hybrid, ISH-402 was developed at ICAR-Indian Institute of Oilseeds Research (ICAR-IIOR), Hyderabad, Telangana, India. The Cytoplasmic male sterile line A-133-I was crossed with elite inbred line ISF-855 and F1 was tested in Preliminary hybrid yield trail, F1 designated as ISH-402 and nominated to coordinated trials. Overall pooled performance of ISH-402 for seed yield is 2325 kg/ha with +21% increase over the best variety check, A1 (1932 kg/ha) and +46% increase over the hybrid check, DSH-185 (1667 kg/ha) at national level and it has recorded +35% higher oil yield (723 kg/ha) than A1 (541 kg/ha) and +52% higher oil yield than the hybrid check DSH-185 (509 kg/ha) at the national level. Oil content in ISH-402 was 30.8% whereas it was 27.7 and 30.1% in the variety check, A1, and the hybrid check, respectively at the national level. ISH-402 is a normal duration spiny hybrid; it took 81 days to reach 50% flowering and 129 days to maturity. Seed production of ISH-402 and A- (female parent), B- (maintainer) & R- (male parent) lines have been perfected. ISH 402 is recommended for all safflower cultivating states of India and offers unprecedent opportunities for increasing area under safflower cultivation.

TS-VI-OP-04

Impact of exogenous GA_3 application on morphological traits and flowering synchronization in *Or* gene introgressed in Indian cauliflower

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The orange cauliflower (*Or* mutant) is rich in β-carotene content and has great prospect in challenging vitamin A associated deficiencies in public. But, the *Or* gene causes growth and developmental penalties in cauliflower which limits seed production of homozygous lines and also seriously affect synchronization of parents in hybrid seed production. Thus, the present study investigated the effect of GA_3 application on morphological traits and developmental transitions in *Or* gene introgressed CF_{Or} (PKVA-1_{HM}) and white CF_{WT} (DC 18-19) genotypes of Indian cauliflower during 2021-22 and 2022-23 at Division of Vegetable Science, ICAR-IARI, New Delhi. A factorial randomised block design was employed with 24 treatment combinations comprising four GA_3 concentrations *viz.*, G_o-Control, G_1-250 ppm, G_2-500 ppm and G_3-1000 ppm, two genotypes, CF_{Or} (homozygous orange) and CF_{WT} (white) and three different application stages *viz.*, S_1=Vegetative stage (VS), S_2= VS + Curd initiation stage (CIS) and S_3= VS + CIS + Full curd stage (FCS) with three replications. Observations were recorded for six morphological traits and five developmental transitions. Significant variations were observed for all three factors *viz.*, GA_3 concentration, genotypes and application stages. The application of 500 ppm GA_3 at VS+CIS stage resulted in highest stalk length (69.33cm) in CF_{Or}, however, it was statistically similar to CF_{WT} (69.83cm) with 250 ppm GA_3 spray at VS+CIS stage. Both the levels also resulted in synchronization in flowering time of CF_{Or} (153 days) and CF_{WT} (153.5 days). The findings highlight the role of GA_3 application in CF_{Or} and CF_{WT} genotypes for improving morphological traits, induce satisfactory flowering for production of seeds and also in synchronization of flowering for hybrid seed production of orange cauliflower.

Technical Session VI

Strategies for Hybrid Seed Production and Management

- Abstracts of Poster Presentations

TS-VI-PP-01

Phytohormone-mediated male fertility restoration: A game changer in hybrid seed production

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The three-line system of hybrid seed production, including cytoplasmic male sterility (CMS) and recessive epistatic genic male sterility (GMS), is widely used for large scale production of hybrid seeds. However, this system demands considerable labour, expertise and advanced field management for the effective multiplication of parental lines. To address these challenges, two-line system was introduced such as, thermo-sensitive or photoperiod-sensitive or humidity-sensitive genic male sterility (TGMS/PGMS/HGMS). However, abrupt environmental fluctuations have always posed a serious threat for their wider applications. In the pursuit of innovative strategies for hybrid seed production, it was discovered that male sterility in lines deficient in genes responsible for phytohormone biosynthesis could be restored through exogenous phytohormone application. This approach facilitates the multiplication of parental lines and hybrid seed production. Jasmonic acid (JA) plays a pivotal role in plant reproduction, including male fertility and sex determination. Loss-of-function mutations in the JA biosynthetic pathway have led to complete male sterility. Especially mutation of the genes *defective anther dehiscence 1* in Arabidopsis, *oxophytodienoic acid reductase 3* in Arabidopsis and rapeseed, *oxophytodienoic acid reductase 7* in rice, *allene oxide cyclase* in Arabidopsis, cotton, barley, soybean, tomato caused male sterility. Surprisingly, the application of methyl jasmonate successfully restored male fertility in male-sterile mutants of Arabidopsis, rice, cotton and rapeseed. This represents a significant advancement in hybrid seed production, allowing the use of a two-line system without environmental dependency.

TS-VI-PP-02

Comparative studies on stigma receptivity, pollen viability and seed setting in parental lines of pearl millet as affected by different seasons

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The investigation on Studies on stigma receptivity and pollen viability in parental lines of Aadishakti hybrid of Pearl millet as affected by different seasons was undertaken with following objectives i.e.1.To study duration of stigma receptivity of the seed parent in *kharif* and summer season in pearl millet 2. To study pollen viability of the restorer and maintainer line in *kharif* and summer season in pearl millet. The six treatments for stigma receptivity comprised of six starvation interval period *viz.*, 0-day, 1-day, 2-day, 3-day, 4-day and 5-day interval. The six treatments for pollen viability comprised of six pollination interval period *viz.*, 0-hour, 2-hour, 4-hour, 6-hour, 8-hour and 10-hour interval. The experimental material consists of male sterile line DHLB-8A as female line and maintainer line DHLB-8B, restorer line DHLB-967 as male line. The results presented in Table 1indicated that male sterile line differed significantly for seed setting percentage. On the basis of mean performance over different starvation periods, line DHLB -8A showed significantly higher seed setting in *kharif i.e.* 48.26% as compared to summer i.e. 43.64%. 1 It is also revealed from the results, that stigma of male sterile line remained receptive for two days during *kharif* and summer season. Seed setting was higher in *kharif* season as compared to summer season. This might be due to higher humidity and coupled with average temperature during *kharif* season. As regards pollination periods, significantly higher seed setting was observed when ear heads were pollinated immediately after collection of pollens *i.e.* zero hour. of pollination (T0) (96.20%), which was followed by 2 hr. of pollination (T1) (89.31%). Significant decrease in seed setting was observed at each successive hr. of pollination. Seed setting percentage, number of seeds per ear head, seed weight per ear head and 1000 seed weight were higher in *kharif* season as compared to summer season. On the basis of above results it is concluded that higher viable pollen produced high weight of seeds per ear head than that of low viable pollens a that *kharif* season crop produced high seed yield as compared to summer season.

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