

NATIONAL SEMINAR

ON

Challenges, Opportunities and Strategies of Plant Science for Crop Improvement

at

**BIRSA AGRICULTURAL UNIVERSITY, RANCHI-834006
JHARKHAND (INDIA)**

08-09 NOVEMBER, 2023



ABSTRACTS

Organized by

RANCHI CHAPTER

(Indian Society of Genetics & Plant Breeding, New Delhi)

In Collaboration with

Indian Society of Genetics & Plant Breeding, New Delhi

DEPARTMENT OF GENETICS & PLANT BREEDING

BIRSA AGRICULTURAL UNIVERSITY, RANCHI-834006

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08-09 NOVEMBER, 2023

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C.P. Radhakrishnan



RAJ BHAVAN
RANCHI-834001
JHARKHAND

GOVERNOR OF JHARKHAND

Message

It gives me immense pleasure to know that the Ranchi Chapter of Indian Society of Genetics & Plant Breeding (ISG&PB), New Delhi is organizing National Seminar on 'Challenges, Opportunities and Strategies of Plant Science for Crop Improvement' at Birsa Agricultural University, Ranchi from 8th-9th November, 2023. It is a matter of pleasure that over 100 leading scientists from the country are attending the seminar in hybrid mode.

In the face of rapid urbanization and industrialization, availability of natural resources like land and water for agriculture is shrinking. Crop improvement is solution of this challenge. Future successes on this front will depend critically on researchers' ability to incorporate the knowledge and preferences of technology users.

A number of farmers' participatory research methods that are currently being tested by plant breeding programs throughout the developing world should be linked with centralized global and decentralized local breeding models. Technical, economic, and institutional challenges will have to be overcome to integrate end user-based participatory approaches for crop improvement. The emerging biotechnological approaches, particularly new breeding techniques involving diverse genetic resources should be used widely for rapidly expanding the gene pool for plant improvement. Better collaboration and coordination among research organizations should also be established for desired results.

I extend my greetings to the organizing committee and participants and wish the seminar all success.

(C. P. Radhakrishnan)

बादल

मंत्री

कृषि, पशुपालन एवं सहकारिता विभाग
झारखण्ड सरकार, राँची



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शुभकामना संदेश

मुझे यह जानकर प्रसन्नता हुई कि भारतीय आनुवंशिकी एवं पौधा प्रजनन सोसाइटी, नयी दिल्ली के राँची चैप्टर द्वारा आगामी 8-9 नवम्बर, 2023 को बिरसा कृषि विश्वविद्यालय, राँची में 'फसल सुधार के लिए पौधा विज्ञान की चुनौतियाँ, अवसर एवं रणनीतियाँ' विषय पर एक राष्ट्रीय सेमिनार का आयोजन किया जा रहा है जिसमें देश के विभिन्न भागों से एक सौ से अधिक अग्रणी कृषि वैज्ञानिक भाग लेंगे।

जैव विविधता के मामले में झारखण्ड देश के सबसे समृद्ध राज्यों में से हैं किन्तु यहाँ सिंचाई साधनों की कमी है, इसलिए कम पानी की उपलब्धता में भी बेहतर उपज देनेवाली फसल किस्मों के विकास पर ज्यादा शोध प्रयास करने की आवश्यकता है। किसान और कृषि से जुड़े विषय राज्य सरकार की प्राथमिकता सूची में है और किसानों की स्थिति में बेहतरी लाने के लिए हम कृतसंकल्प हैं।

चूँकि यह आयोजन राँची में हो रहा है इसलिए इसमें झारखण्ड के किसानों की कृषि समस्याओं, जरूरतों, उनकी सामाजिक-आर्थिक परिस्थितियों और प्राथमिकताओं पर विशेष चर्चा होनी चाहिए ताकि सेमिनार में उभरनेवाली अनुशंसाओं के आलोक में यहाँ के वैज्ञानिक, किसान और नीति निर्माणकर्ता आगे कुछ योजना बना सकें।

फसल सुधार जैसे महत्वपूर्ण विषय पर राष्ट्रीय सेमिनार आयोजित करने की पहल के लिए मैं आयोजन समिति से जुड़े लोगों को बधाई देता हूँ तथा आयोजन की सफलता की कामना करता हूँ।

बादल

(बादल)

अबुबक्कर सिद्दीख पी., भा.प्र.से.
सचिव
Aboobacker Siddique P., I.A.S.
Secretary



कृषि, पशुपालन एवं सहकारिता विभाग
झारखण्ड सरकार
Department of Agriculture,
Animal Husbandry and Co-operative
Govt. of Jharkhand



Message

I am glad to note that the Ranchi Chapter of Indian Society of Genetics & Plant Breeding is organizing a National Seminar on 'Challenges, Opportunities and Strategies of Plant Science for Crop Improvement' at Birsa Agricultural University on November 8-9, 2023.

Changes in land quality and climate influence agricultural productivity, especially crop productivity and quality. India's extent of rainfed area, characterized by relatively higher intensity of land degradation, loss of biodiversity, poor soil organic carbon, low moisture holding capacity, and decline in ground water table, is the largest in the world, but its productivity @ 1 ton/ha is one of the lowest. As high as 78 million hectare accounting for 64 per cent of the country's net sown area is rainfed. These areas are home to majority of the nation's farmers and rural population, who encounter multiple risks and uncertainties relating to bio-physical and socio-economic conditions. Problems and expectations of farmers of these regions need to be addressed on priority basis.

Agricultural universities and ICAR research institutes have been regularly developing new crop varieties capable of giving higher yield even under adverse climatic conditions, however, these varieties are not reaching to farmers' fields in desired quantities and manner. Liking, preferences and perspective of end users (farmers) should be better incorporated into the germplasm improvement and varietal development process.

Need of the hour is to develop Climate Smart Agriculture techniques and create a cadre of Climate Risk Managers up to village level by empowering the extension workers with alternate crop strategies to meet the challenges posed by climate change.

I hope, the recommendations emerging out of cross fertilization of ideas of geneticists, plant breeders, biotechnologists and crop physiologists during the two-day deliberations would help prepare an effective roadmap for crop improvement in the country.

I congratulate the organizers of the seminar and wish the event a grand success.


(ABOBACKER SIDDIQUE P.)

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BIRSA AGRICULTURAL UNIVERSITY, RANCHI-834006

Organizing committee

for

National Seminar

on

**Challenges, Opportunities and Strategies of
Plant Science for Crop Improvement**

8th-9th November, 2023

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RANCHI CHAPTER of ISGPB, RANCHI**Secretary's Report**

Indian Society of Genetics & Plant Breeding (ISG&PB) is one of the oldest and prestigious academic societies established in 1941. It is a non-profit organization of scientists and researchers focusing on the promotion of science genetics and related discipline. Ranchi chapter of ISG&PB, which is a satellite unit of this prestigious society, has been trying to increase the interest of researchers and students of all age groups toward the field of genetics and plant breeding by organizing a) painting competition b) essay writing competition c) lectures of eminent scientists, and d) national seminar/symposium on the current research trends in the related field.

Since its inception on 28 August 2012, the Ranchi chapter has organized three national seminars. The first was on “Breeding for Abiotic Stresses: Problems & Prospects”, and was organized on 23–24 February, 2014. The second seminar on “Innovation Breeding Approaches for Agricultural Security” was organized on 13–14 March, 2016. The third seminar on “Crop Breeding for wider Adaptation”, originally scheduled on 21–22 March 2020, was deferred and held in 9th December, 2022.

Since 2020, four guest lectures by different eminent scientists have been organized.

- Guest lecture on “CRISPR-Cas: Next Generation Precision Breeding Tools”, on 28 January, 2021 by Dr. Kutubuddin Ali Molla, Biotechnologist, ICAR-NRRI, Cuttack, Odisha.
- Guest lecture “Molecular Approaches in Hybrid Rice Breeding” by Dr. S.K. Singh, Senior Professor, Dept. of Genetics & Plant Breeding, Banaras Hindu University, Varanasi on the occasion of 200th birth anniversary of G. J. Mendel on 3 September, 2022.
- Guest lecture “New Education Policy-2020 Entrepreneurship through Plant Breeding” by Prof. Jai Prakash Lal, Dept. of Genetics & Plant Breeding, Banaras Hindu University, Varanasi on the occasion of 200th birth anniversary of G. J. Mendel on 3 September, 2022.
- A guest lecture by Prof. A. Pattanayak, Director, IACR-IIAB, Ranchi was organized on 9 December, 2022.

This year the Ranchi chapter took the initiative to involve and sensitize young school students through painting and essay writing competition; the students demonstrated excellent creativity.

The winners of painting and essay competition were:

A. Painting competition:

Topic: Impact of COVID-19 on human life- Class VI-VIII dated: 10.12.2021

- | | | |
|---|---|--------|
| 1 | Ms. Avni Priyal
DAV Public School, Gandhinagar, Ranchi | First |
| 2 | Ms. Barkha Rani Nayak
Anita Girls High School, Kanke, Ranchi | Second |



- | | | |
|---|---|--------|
| 3 | Ms. Astha Kumari
Nirja Sahay DAV, Public School, Kanke, Ranchi | Second |
| 4 | Ms. Neha Lakra
St. Mary's Girls Middle, School, Kanke | Third |

Consolation

- | | |
|---|---|
| 5 | Ms. Komal Kumari
St. Mary's Girls Middle School, Kanke |
| 6 | Mr. Ankit Nayak
St. Joshep's Middle School, Kanke |
| 7 | Mr. Arjun Munda
St. Joseph's High School |

B. Essay Competition

(i) B.Sc. (Agriculture)

Topic: Role of Biodiversity in the natural environment dated: 08.11.2021

- | | | |
|---|---|--------|
| 1 | Ms. Shanya Lal
B. Sc. (Ag.) Student,
RAC, BAU, Kanke | First |
| 2 | Ms. Shreya Singh
B. Sc. (Ag.) Student
RAC, BAU, Kanke | Second |
| 3 | Ms. Aditi Binit
B. Sc. (Ag.) Student
TMAC, Godda | Third |
| 4 | Ms. Sweta
B. Sc. (Ag.) Student
RAC, BAU, Kanke | Third |

M.Sc. (Agriculture)

Topic: Mitigation of inorganic toxins in agricultural crop dated: 08.11.2021

- | | | |
|---|--|--------|
| 1 | Ms. Alice Bara
M. Sc. Student, GPB, BAU, Kanke | First |
| 2 | Mr. Rajni Kant
M. Sc. Student, GPB,
BAU, Kanke | Second |

- | | | |
|---|---|-------|
| 3 | Ms. Nitu Kumari
M. Sc. Student, GPB,
BAU, Kanke | Third |
|---|---|-------|

Ph. D (Agriculture)

Topic: Conversion of C_3 Plants to C_4 plants: A controversial noble concept dated: 08.11.2021

- | | | |
|---|---|--------|
| 1 | Mr. Anjani Kumar
Ph. D. Scholar, GPB,
(Batch 2020-21), BAU, Kanke | First |
| 2 | Ms. Shashina Perween
Ph. D. Scholar, GPB,
(Batch 2020-21), BAU, Kanke | Second |
| 3 | Mr. Surabhi Sinha
Ph. D. Scholar, GPB,
(Batch 2020-21), BAU, Kanke | Third |

As the secretary of the Ranchi chapter, I acknowledge the efforts and am thankful to the judge of the essay writing competition, Dr. Jyotirmoy Ghosh, Principal Scientist, Plant Breeding, ICAR-IINRG, Namkum, Ranchi and to the judges of the painting competition, Shri. Krishna Kumar Prasad of DAV Public School, Gandhinagar, Ranchi and Shri. Tarkeshwar Patel of Nirja Sahay DAV Public School, Goshla Complex, Kanke for their support and unbiased judgment.

(Manigopa Chakraborty)

NATIONAL SEMINAR ON Challenges, Opportunities and strategies of Plant Science for Crop Improvement BIRSA AGRICULTURAL UNIVERSITY, RANCHI CONTENTS

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Key Note Paper



Recent trends in hybrid breeding

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Heterosis remains a biological enigma as it defies genetic, biochemical and physiological explanation. But it has been highly successful commercially and it transformed maize breeding and production to the extent that hybrid breeding has become the exclusive/the most preferred breeding approach in all such crops where commercial scale hybrid seed production is feasible. The maize yields in the United States of America were essentially static so long as the open-pollinated varieties were in cultivation. With the introduction of double cross hybrids, maize yields increased annually at the rate of one bushel per acre, and this rate increased to two bushels per acre after the introduction of single cross hybrids. Although the maize hybrids were developed for higher yields, they were found to be significantly drought tolerant. CIMMYT, Mexico has implemented population selection schemes to successfully develop climate resilient maize populations from which inbred lines have been isolated and used for developing hybrid and synthetic varieties. Hybrid breeding has led to an unprecedented growth of seed industry and the quantum of private investment in the development of hybrid technology has witnessed a phenomenal rise. This has resulted in consistent and remarkable increases in maize yields, which has prompted the spread of this technology to other crops, including self-pollinated crops, including rice and wheat where pureline varieties have dominated the scene.

The emphasis of hybrid breeding has promoted both basic and applied research for gaining an insight into this perplexing phenomenon so that heterosis could be utilized more efficiently and economically. Initially, two genetic theories, *viz.*, dominance and overdominance were proposed to explain heterosis but with time epistasis, additive gene action and even epigenetic mechanisms were invoked. Despite the huge amount of experimental data accumulated over time, we do not have a universally applicable genetic and molecular mechanisms underlying heterosis. But the research efforts for developing alternative mechanisms for pollination control to facilitate hybrid seed production have been more successful and several biotechnology-based male sterility systems have been developed. In addition, a couple of transgenic systems for the maintenance of nontransgenic genic male sterile lines have been devised. For example, the SPT maintainer is a transgenic line which is crossed with the genic male sterile line to produce progeny comprising exclusively nontransgenic male sterile plants. The SPT system thus takes care of the nagging problem of timely roguing of the male fertile plants present in the genic male sterile lines. In addition, inducible and repressible transgenic male sterility systems have been developed that enable the implementation of two-line hybrid breeding in such crops where usable TGMS and/or PGMS systems are not available.

Hybrid breeding is a resource intensive technology, and the breeding cycle is much longer than that in the case of line or pureline breeding. This is because improvement of hybrid varieties is indirect and it involves the improvement of inbred parents of hybrid varieties by either improving the source populations or recycling the existing inbred lines. Both the isolation and evaluation of inbred lines are time consuming procedures, and they involve considerable investment of resources.



The time required for inbred isolation has been drastically reduced by the development of DH technology. Initially, *mtl* inducer strains were available for *in vivo* haploid induction, but other inducer systems, such as *cenH3* and *igl* inducers are being developed for haploid production. In addition, the genomic prediction tools have been extended to make inbred evaluation procedures faster by eliminating the need for topcross test and more efficient by enabling evaluation of a very large number of inbred lines at much lower costs and enabling the identification of such potential inbred parents that would have been missed by the conventional hybrid breeding procedure.

One of the main concerns related to hybrid breeding has been the economic burden placed on farmers due to its inherent requirement for fresh hybrid seed for planting of the commercial hybrid crops every year. Scientists have been trying to develop technologies for circumventing this limitation and a promising development in this context is the creation of synthetic apomixis in rice by simultaneous editing of three genes involved in meiosis and egg cell-specific expression of the *BBMI* transgene. In addition, hybrid mimic lines comparable or even superior to the heterotic parental hybrids have been developed in *Arabidopsis* and some other self-pollinated species and breeding schemes have been proposed for developing such lines by accumulating heterosis loci in homozygous lines.

KP 02

Plant science in relation to crop improvement for food and nutritional security in India

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Introduction

Plant science, also known as botany, is a multidisciplinary field of scientific study that focuses on understanding various aspects of plants, ranging from their structure, function, growth, and reproduction to their interactions with the environment and other organisms. It plays a crucial role in advancing our knowledge of the plant kingdom, which is fundamental to sustaining life on Earth. Plant scientists explore the intricate mechanisms that govern plant life, contributing to various areas such as agriculture, environmental conservation, medicine, and even technological innovation.

Crop improvement, also known as plant breeding, is the process of developing new and improved plant varieties with desirable traits to increase yield, quality, resistance to pests and diseases, tolerance to environmental stress, and other characteristics important for agriculture and food production. It's a combination of scientific methods and traditional practices aimed at enhancing the genetic makeup of crops.

Challenges of plant science for crop improvement

Plant science faces several challenges when it comes to crop improvement. These challenges are complex and multifaceted, often requiring interdisciplinary approaches and innovative solutions. Some of the key challenges include:

1. **Climate change resilience:** Climate change poses a significant threat to global agriculture, with shifts in temperature, precipitation patterns, and the increased frequency of extreme weather events affecting crop growth and yield. Developing crops that are resilient to these changing conditions, through traits such as drought tolerance, heat resistance, and flood tolerance, is crucial.
2. **Pest and disease management:** Pests and diseases can devastate crop yields. Developing crops with enhanced resistance to a wide range of pests and pathogens, while also minimizing the need for chemical pesticides, is a continuous challenge.
3. **Nutritional enhancement:** Many staple crops lack essential nutrients, leading to malnutrition in many parts of the world. Bio-fortification involves increasing the nutrient content of crops, such as adding more vitamins and minerals, to address these nutritional deficiencies.
4. **Sustainable agriculture:** Balancing increased crop production with environmental sustainability is a challenge. Developing cropping systems that reduce soil erosion, improve soil health, and minimize water and nutrient usage is crucial for long-term agricultural viability.
5. **Genetic diversity and erosion:** Modern agriculture often relies on a narrow range of crop varieties, leading to a loss of genetic diversity. This makes crops more susceptible to diseases and changing environmental conditions. Conserving and utilizing genetic diversity is essential for crop resilience.
6. **Post-harvest losses:** A significant portion of global food production is lost after harvest due to improper storage, transportation, and processing. Developing technologies and strategies to reduce post-harvest losses can increase food security.
7. **Crop wild relatives:** Wild relatives of cultivated crops often carry valuable traits that can be introduced through breeding. However, accessing and utilizing these traits while maintaining genetic integrity is a challenge.
8. **Regulatory hurdles:** The development and deployment of genetically modified (GM) crops often face regulatory challenges due to concerns about safety and environmental impacts. Navigating these regulatory frameworks is crucial for the adoption of advanced breeding techniques.
9. **Data-driven agriculture:** Integrating big data, remote sensing, and precision agriculture techniques for monitoring and managing crops requires significant technical advancements and data management strategies.
10. **Ethical and societal considerations:** As technology advances, ethical concerns related to genetic modification, gene editing, and intellectual property rights become more complex.



Ensuring that advancements in crop improvement are aligned with societal values and benefit all stakeholders is a challenge.

11. **Labor-intensive processes:** Traditional breeding methods can be time-consuming and labor-intensive. Developing more efficient and rapid breeding techniques, such as marker-assisted selection and gene editing, is essential to accelerate crop improvement efforts.

Addressing these challenges requires collaboration between plant scientists, agronomists, geneticists, biotechnologists, ecologists, policymakers, and other stakeholders. It also demands a holistic approach that considers not only crop yield but also sustainability, nutritional content, environmental impact, and social implications.

Opportunities of plant science for crop improvement

Plant science offers a wide range of opportunities for crop improvement, encompassing various disciplines and technologies. These opportunities have the potential to enhance crop yield, quality, resistance to pests and diseases, and adaptation to changing environmental conditions. Some key areas of opportunity include:

1. **Genetic improvement:** Advances in genetics and genomics have opened up opportunities to manipulate plant genomes for desired traits. This includes traditional breeding methods as well as modern techniques like genetic modification and gene editing (CRISPR-Cas9), allowing for precise modification of specific genes to achieve desired traits such as disease resistance, increased yield, and improved nutritional content.
2. **Disease and pest resistance:** Plant scientists can develop crops that are more resistant to diseases and pests, reducing the need for chemical pesticides. This can involve identifying and introducing resistance genes, enhancing natural defense mechanisms, or using biocontrol methods that involve beneficial microorganisms to suppress harmful pathogens.
3. **Abiotic stress tolerance:** With climate change affecting growing conditions, there's a need to develop crops that can withstand various stresses such as drought, heat, cold, and salinity. Plant scientists can work on identifying genes and pathways that confer tolerance to these stresses and introduce these traits into crop plants.
4. **Nutritional enhancement:** Bio-fortification involves enhancing the nutritional content of crops to address malnutrition and dietary deficiencies. For instance, researchers can develop crops with higher levels of essential vitamins, minerals, and proteins to improve human health, especially in regions with limited access to diverse diets.
5. **Yield improvement:** Increasing crop yield is a constant goal in agriculture. Plant scientists can explore ways to enhance photosynthesis, improve nutrient uptake, and optimize plant architecture for higher productivity. This might involve altering plant hormone pathways, optimizing nutrient utilization, and designing crops that are better suited for high-density planting.
6. **Sustainable agriculture:** Developing crops that require fewer inputs (such as water, fertilizers, and pesticides) while maintaining high yields are crucial for sustainable agriculture. Plant scientists can work on creating plants that have efficient nutrient utilization, reduced water requirements, and built-in resistance to common pests and diseases.



7. **Crop adaptation to changing climates:** As climate patterns shift, plant scientists can focus on developing crops that can thrive under new environmental conditions. This might involve selecting or engineering plants with shorter growing cycles, improved temperature tolerance, and other traits that enable them to adapt to changing climates.
8. **Post-harvest quality and shelf life:** Improving the post-harvest quality and shelf life of crops can reduce food waste and increase the availability of fresh produce. Plant scientists can work on delaying fruit ripening, reducing spoilage, and maintaining nutritional quality during storage and transportation.
9. **Innovative breeding techniques:** Beyond traditional breeding, techniques like marker-assisted selection, genomic selection, and genome-wide association studies can help identify valuable traits and accelerate the breeding process by targeting specific regions of the genome associated with desired outcomes.
10. **Data-driven agriculture:** The integration of big data, remote sensing, and precision agriculture technologies can optimize resource use, predict disease outbreaks, and enable targeted interventions for maximum crop productivity.
11. **Synthetic biology:** Plant scientists can use synthetic biology to engineer novel metabolic pathways, leading to the production of valuable compounds such as bio-fuels, pharmaceuticals, and specialty chemicals in crops.
12. **Wild crop:** Exploring and utilizing genetic diversity in wild relatives of crops can provide valuable traits for crop improvement, such as drought tolerance, disease resistance, and unique flavors.

These opportunities in plant science for crop improvement highlight the potential to address some of the most pressing challenges in global agriculture, including food security, sustainability, and resilience in the face of a changing climate. However, it's important to approach these advancements with careful consideration of ethical, environmental, and regulatory implications.

Strategies of plant science for crop improvement:

Plant science employs various strategies for crop improvement to enhance yield, nutritional content, resistance to pests and diseases, and adaptability to changing environmental conditions. Mile stones in molecular biology is well displayed in fig 1. Some of the key strategies under conventional and non conventional methods are given in table 1 and fig. 2 and explained as below:

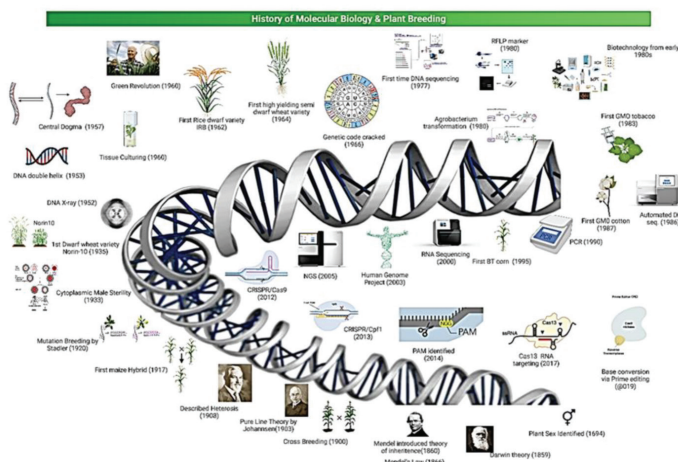


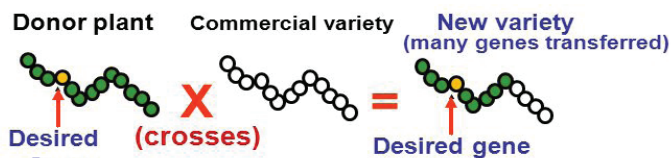
Fig 1. Milestone in molecular biology & Plant breeding

Table 1: Strategies of plant science for crop improvement

Conventional methods	Non-conventional method
Selection	Marker assisted selection (MAS)
Hybridization	Mutation breeding
Mass selection	Polyploidy method
Pure line selection	Biotechnological approach like tissue culture & genetic engineering.
Pedigree method	QTLs mapping
Back cross methods	Omics technology i.e. Genomics, Proteomics, Metagenomics.
Single seed decent method	Genome editing (CRISPR/Cas9, TALEN & ZFN), RNAi technology
Bulk breeding method	
Speed breeding	
Shuttle breeding	

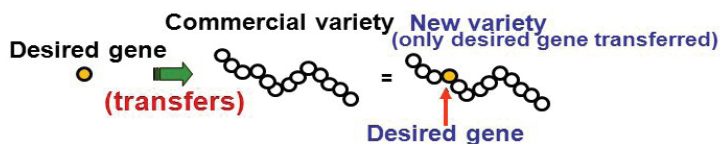
Traditional Breeding

DNA is a strand of genes, much like a strand of pearls. Traditional plant breeding combines many genes at once.



Plant Biotechnology

Using plant biotechnology, a single gene may be added to the strand.



However, cloned DNA does not have to be from same species

Fig: 2 Conventional breeding methods vs. Non-conventional breeding methods

1. **Traditional breeding:** Conventional breeding methods involve crossing plants with desirable traits to create offspring with improved characteristics. This technique has been

used for centuries and is still widely used today. Selective breeding helps accumulate desirable traits over generations.

2. **Hybridization:** Hybrid crops are created by crossing two genetically distinct parent plants. This can lead to hybrid vigor, where the resulting plants exhibit superior traits compared to the parents. Hybridization is often used to achieve higher yield, better disease resistance, and improved quality.
3. **Genetic modification (GM):** Genetic engineering involves introducing specific genes into plants to confer desired traits. This can include traits like insect resistance, herbicide tolerance, increased nutritional content, and longer shelf life. GM crops have generated both excitement and controversy due to their potential benefits and ethical considerations.
4. **Marker-assisted selection (MAS):** This technique involves identifying and selecting plants with desired traits based on genetic markers linked to those traits. Fig 3 MAS accelerate the breeding process by allowing breeders to screen and select plants with the desired characteristics more efficiently.

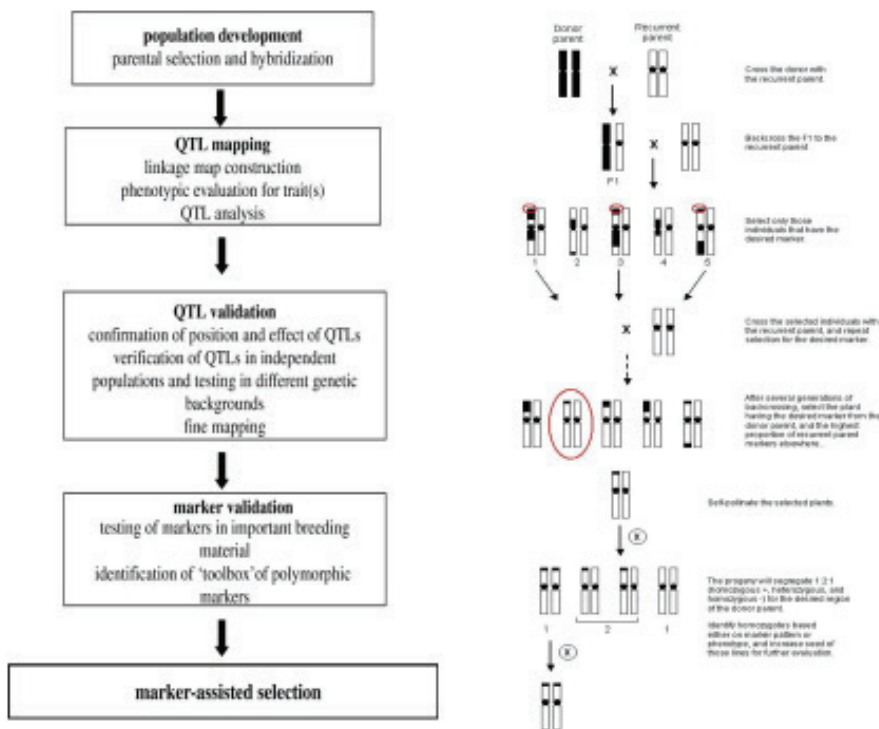


Fig 3: Marker Assisted selection (MAS)

5. **Genome editing:** Tools like CRISPR-Cas9 allow scientists to make precise modifications to a plant's genome, without introducing foreign genes. This technique can be used to edit existing genes or introduce beneficial mutations, leading to traits such as disease resistance or enhanced nutrient uptake.

6. **Transgenic plants:** These are plants that have been genetically modified by adding genes from other organisms. For example, adding a bacterial gene for producing a toxin can make plants resistant to certain pests. However, public concerns about the potential ecological and health impacts of transgenic plants have led to regulatory scrutiny.
7. **Mutagenesis:** Mutagenesis involves inducing mutations in plant DNA (Fig 4) through various methods, such as chemical treatments or radiation. Some mutations can result in desirable traits, like improved yield or disease resistance. However, this method is less precise than genome editing.

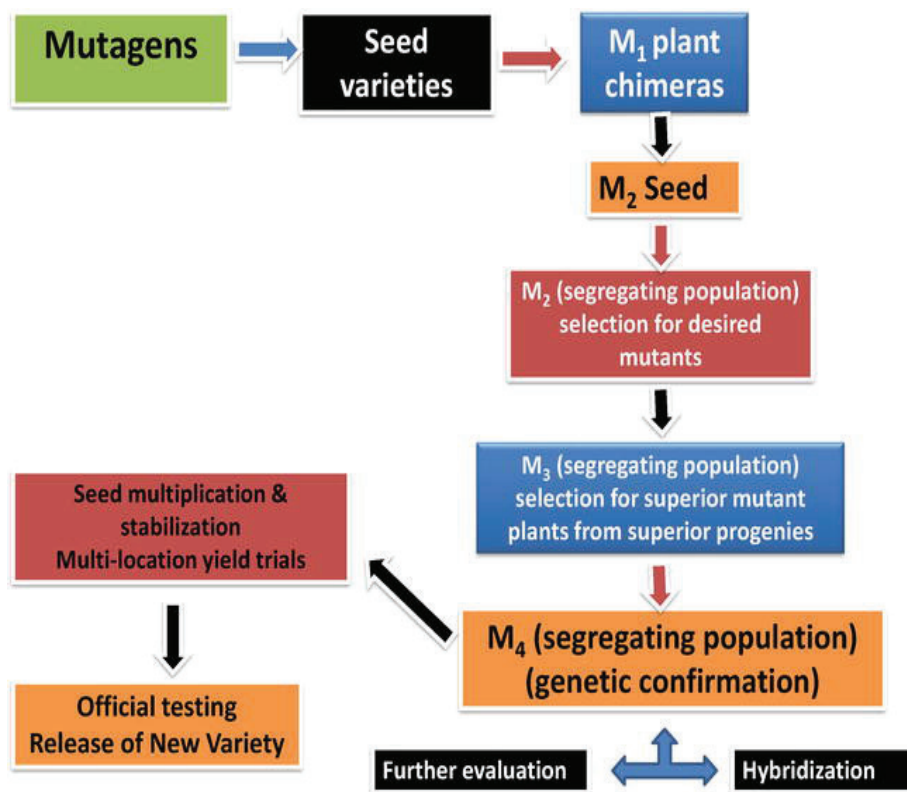


Fig: 4 Mutation breeding or mutagenesis

8. **Phenotypic selection:** This involves selecting plants based on observable traits (phenotypes) rather than specific genes. It's a classic approach that's been used for centuries and is still valuable, especially when breeding for complex traits that are controlled by multiple genes.
9. **Tissue culture and cloning:** Tissue culture allows for the propagation of plants from small pieces of tissue, which can be used to rapidly multiply desirable plants. Cloning can preserve the genetic characteristics of elite plants, ensuring their traits are maintained in future generations.

10. **Bioinformatics and data analysis:** Modern plant science leverages computational tools to analyze large datasets, including genomic information. This helps in identifying candidate genes associated with desirable traits and predicting the effects of genetic changes.
11. **Phytoremediation:** Some plants have the ability to absorb and accumulate pollutants from the environment. This strategy can be used to clean up contaminated soils or water bodies.
12. **Intercropping and polyculture:** Mixing different crops in a single field can promote biodiversity, reduce the spread of pests and diseases, and improve overall yield stability.

These strategies are often used in combination, depending on the specific goals, challenges, and ethical considerations in crop improvement projects.

Conclusions:

The field of plant science offers a myriad of challenges, opportunities, and strategies for crop improvement that are vital for addressing global food security, environmental sustainability, and economic prosperity. Challenges of climate change, population growth, and biotic stresses require innovative solutions from the plant science community. Leveraging genetic diversity, advanced technologies, and strategic approaches like precision agriculture and synthetic biology will drive crop improvement. By embracing collaboration, ethical considerations, and a holistic view of sustainability, plant science can contribute significantly to ensuring food security and environmental stability for generations to come.

Suggested readings

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Genomics-assisted breeding for enhancing genetic gain in rainfed rice

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The genetic gain achieved in rice is very low during the last few decades. However, marker-assisted breeding has been very successful in developing improved versions of superior varieties. Genomic (or genome-wide) selection is a method that has promise over marker assisted selection & other methods. Genomic assisted selection is to determine the genetic potential of an individual instead of identifying the specific QTL. Low costs of genotyping using high-density single nucleotide polymorphism (SNP)-arrays and development of statistical methods to accurately predict marker effects have led to the breakthrough of GS. To capture the total genetic variance, the effect of each marker in the whole marker-set is estimated in GS regardless of the significance threshold, assuming that markers are in linkage disequilibrium (LD) with the QTLs.

Marker effects are estimated using individuals with both genotypic and phenotypic information. The estimated marker effects are combined with marker information of an individual to give the genomic-estimated-breeding-value (GEBV). Marker effects are estimated using individuals with both genotypic and phenotypic information. The predictive ability of the model is calculated based on a cross-validation (CV) system using a training- and a test-population to optimize the model. Highest prediction accuracies are achieved when training data represented the whole population and had a strong relationship to the test data. The estimated marker effects are combined with marker information of an individual to give the genomic-estimated-breeding-value. Cost, population size, relatedness determines the marker density.

Genetic gains are linearly related to standardized selection differential, but not selection intensity. Selection of suitable elite parents in a training population is very important for achieving the desired gain through genomic selection. Prediction accuracy increases with increase in marker density. The pedigree-based BLUP serves as the basis of one of the most-popular practical approaches to estimate GEBV by using “genomic BLUP” (GBLUP). While predicting close relatives and target traits are affected by many genes of small effect, the differences between the methods are small, and methods like (G)BLUP and ridge regression are effective and robust. However, when traits have some larger QTL or when considering prediction of distant relatives, improvements in prediction accuracy can be obtained from Bayesian and machine learning methods, where in particular BayesB and BayesC(π) are popular. Genomic best linear unbiased predictor performs a genomic-estimated relationship matrix, it assigns equal variance to all markers, and also assumes that they are equally contributing to the trait of interest. Ridge-regression best linear unbiased predictor (RRBLUP) predicts based on that all markers have common variance but allows that markers have unequal effects. However, it shrinks all the marker effects equally towards zero, regardless of the size of their effect, which can possibly lead to over shrinking of large-effect loci. While the Bayesian alphabet models (BayesA, BayesB, BayesC, BayesC(π)) works on different types of prior distribution to marker effects, thus having a more realistic assumption of marker effects. LASSO (Least absolute shrinkage and selector operator) and Bayesian LASSO

(BL) models take both variable selection and shrinkage methods, with the difference that BL additionally applies prior exponential distribution on marker variances. Elastic net (EN) uses two penalty methods—the LASSO and ridge regression, which results in averaging markers that are highly correlated and then using the averaged gene for the model. Random forest (RF) and support vector Machine (SVM) in averaging markers that are highly correlated and then using the averaged gene for the model.

For achieving genetic gain of upland rice, Include Parent materials carrying drought yield QTLs viz., *qDTY12.1*, *qDTY2.2*, *qDTY3.1*, *qDTY4.1*, *qDTY6.1* and *qDTY9.1* are to be in the parent pool. Parents with high water use efficiency in the parent pool need to be present. Use parents for weed competitiveness & seedling vigour traits in the parents pool. Include Parent materials carrying Dro, Pup & NUE QTLs for root angel, better phosphorus and nitrogen uptake. Biotic stresses like diseases (rice blast, brown spot, sheath rot) and insects (yellow stem borer, leaf folder, gundhi bug and termite).

For Shallow lowlands, traits viz., high grain yield, strong culm, Submergence & drought tolerance, anaerobic germination, photoperiod-sensitive & thermo-insensitive, heavy panicle weight type & seed dormancy, insect pests tolerance (SB,BPH,GM) and disease tolerance (BB, false smut, ShB, RTV). Therefore, Include parents for high yielding varieties with Sub1 + qDTYs+ AG+ strong culm+ BB+ BPH for shallow lowland ecology.

The need for semi-deep water ecology, plant height (115-130cm), drought tolerance at seedling stage, submergence tolerance with less elongation, moderate water logging tolerance, anaerobic germination, stiff culm, erect leaves & moderate tillering ability, high N-use efficiency at low N level, early seedling vigour, photoperiod-sensitive & thermo-insensitive, heavy panicle & strong seed dormancy, insect pests tolerance (SB,LF) and disease tolerance (BB, ShB, sh.rot, RTV). Thus, parents for high yielding varieties with moderate water logging tolerance + qDTYs+ Sub1 + AG + strong culm + BB +SBR are needed for semi-deep water ecology.

For deep water ecology, plant height (130-160cm), stiff culm & erect leaves, water logging tolerance, kneeling ability, anaerobic germination, low tillering ability, high N- use efficiency at low N level, early seedling vigour & drought tolerance at seedling stage, submergence tolerance with leaf sheath and culm elongation, photoperiod-sensitive & thermo-insensitive, heavy panicle & strong seed dormancy, insect pests tolerance (SB, LF) and disease tolerance (BB, ShB, Sh.rot, RTV). Hence, include parents for high yielding varieties with water logging tolerance + qDTYs + kneeling ability + AG+ BB+SBR in the initial shortlisted population.

Suitable prediction models need to be used for optimization and estimation of breeding values.



MILLETS – NUTRI-CEREALS

Onkar Nath Singh

Millets are favoured due to its productivity and short growing season under dry, high temperature conditions owing to which these are considered as climate resilient crops. India is the largest producer of millet as of 2021, with a total share of 41%, followed by Niger (~12%) and China (~8%). India also ranks 12th among those countries that produce high yields of millet. Millets have been an integral part of our diet for centuries. They offer a plethora of health benefits and are also good for the environment with low water & input requirements for production. With the aim to create awareness and increase production & consumption of millets, the United Nations, at the request of the Government of India, declared 2023 as the '*International Year of the Millet*'. The estimated millet yield in India has more than doubled since 1966. India's average yield in Millet farming (2021-22) is 1208 kgs per hectare. The production of millets has also increased by 7% (1966-2022) despite the area for millet cultivation in India decreasing consistently since 1971-72. A major drop in the area for millet cultivation occurred between 2006-2016. The consistent improvement in yield estimates over the years indicates the adoption of better farming practices in India in the past few decades.

In Jharkhand context the climate is very suitable for the cultivation of millets and 20 -30 years ago farmers cultivate millets in their 50-60% of total agriculture land. Various types of millet have been cultivated in Jharkhand like Finger millet (*Eleusine coracana*) commonly known as Ragi or Maduwa, Little millet commonly known as Gundali, Kodo millet (*Paspalum scrobiculatum*) commonly known as Kodo, Sorghum (*Sorghum bicolor*) commonly known as Jowar or Tilai Gangai and Pearl millet (*Pennisetum glaucum*) commonly known as Bajra,. There are 32 tribes having their habitat in Jharkhand state and mainly those people were cultivated millet in entire Jharkhand and millets were in the list of their staple food. But that trend is going to end. There are some told and untold reason bears the responsibility to decrease millet cultivation in huge way in spite of having more nutritional value than rice or wheat. In the case of decreasing area production of millets, the main cause in the sowing and transplanting time of millet is same with the paddy so labour scarcity hold the major reason followed by the lack of facilities for primary processing of various millet are the limiting factors for decline in the areas under these crops .

Challenges and Future Prospects in Millet Sector:

In today's context, the millet sector has been facing a lot of challenges pertaining to the production of millets, processing, value addition, marketing, and consumption. At the same time, there are a lot of opportunities for entrepreneurs in the millet sector. The challenges can be mitigated by taking extra efforts in solving the problems faced in the value chain of millets. The challenges are not only faced in India but also throughout the world. Let us first understand what are the challenges faced in the millet sector and then we can dive into the opportunities in the millet sector and how the millet entrepreneurs can take advantage of the opportunities created around millets.

Challenges in Millets Production:

1. Low productivity of millets:

When we compare the productivity of millets with other crops like wheat, rice, and maize, it is very low. As you know millets are grown in marginal land with low fertility and most of them are rainfed which results in low productivity. Apart from these, there are many limiting factors responsible for low production of millet among which the major constraints are weeds and most of the farmers cultivate millets in a traditional way. They simply broadcast the seeds on the onset of monsoon and harvest the crop after 75-90 days. The yield gap of millets can be minimized if a proper package of practices will be followed. It is found that for the farmers who practiced good practices like the System of Millet Intensification (SMI) in Finger Millet, the yield has doubled as compared to the traditional methods. When millet farmers were asked about the factors that were to be followed to increase the yield of millets, the foremost response was sowing/transplanting on time, followed by weeding on time, proper nutrient management, and using improved varieties.

2. Area under Millet is Declining:

It has been found that the area under millet is declining drastically in India. If we compare the area under millets during the 1960s to the present scenario, it has reduced by more than 50%. If the fallow and wastelands are brought under millet cultivation, then the production can be increased to a great extent. Along with this, the millet farmers need to be incentivized to encourage them to grow millets.

3. Resistance to Pests and Diseases:

As you know millets are hardy crops and very less infestation happens due to pests and diseases. But some pests and diseases often cause significant loss in major millets like Sorghum, Pearl Millet, and Finger Millet. If more cultivars with significant resistance to pests and diseases are made available to the farmers, this problem could be solved up to some extent.

4. Millet Seed Production:

Even today farmers are facing problems in getting quality seeds of millets. Although there are no issues in Sorghum and Pearl Millet as private players have entered into this segment and made it available to the farmers in India. There are opportunities to bring quality seeds of minor millets and this can be done by establishing **seed hubs** for breeding and producing seeds. This seed production needs to be demand-driven and all the stakeholders need to join hands together to improve the seed value chain. There are many traditional millet varieties that are performing well in the farmer's field and these varieties need to be brought in the seed chain through Farmer Producers Organization. This intervention will help the farmers to get the right quality seeds and that too in time.

5. Challenges in Millet Processing:

The millet processing machines available in India have a low recovery of 70-80% of grains and this becomes a challenge for the millet processors. Due to less efficiency, the output has more un-hulled and broken grains. Dehulling efficiency of millets is affected by the impeller speed. As you know millet grains differ in size, shape, and husk content, so it becomes difficult to handle. Depending upon one dehuller for dehusking all types of millets is not suitable rather it requires



two types of dehuller. As Kodo and Barnyard Millet contain multiple seed coats, it requires a double-stage dehuller to remove the husk.

Separation of the husk of millets and its collection is quite difficult as it causes spillage all over the processing unit and often gets mixed with the final product. Even many millet processors are facing difficulty in handling and disposing of the husk of the millets. If the husk of millets could be used in making value-added products, then the issue could be solved. Millets being 100% gluten-free, it becomes very difficult to make some products with all total millet ingredients. Still, more research and development are needed for enhancing the availability of nutrients and decrease the anti-nutritional contents.

Still, progress is continuing on improving the shelf life of processed millet grains. In today's scenario, the shelf life of millets is enhanced to 4-6 months. But to cater to the international market and exports from India, the shelf life of millets is to be enhanced to a minimum of 12 months. To overcome all the challenges in the millet sector, there is a need for constant efforts from all the stakeholders and institutions toward mainstreaming millet. It is not only addressing the challenges discussed above but also building forward and backward linkages by creating a better millet ecosystem. No doubt, the Government has taken a lot of initiatives in this sector last decade to bring millets to the plate of all and has taken vital steps to promote millets in India and also abroad.

6. Low Investment in Research and Development:

Research and development activities play a crucial role in generating knowledge and disseminating it to farmers, processors, and other stakeholders in the millet sector. Low investment in R&D results in a lack of updated and accessible information on millet cultivation techniques, processing technologies, and market trends. This limits the adoption of best practices and hinders the overall growth and sustainability of the millet sector.

Future Prospects

Opportunities in Millet Sector:

The millet sector offers several opportunities, driven by increasing consumer demand for nutritious and sustainable food options. Millets are small-seeded grains that are highly nutritious, gluten-free, and have a low glycemic index. They are rich in fiber, protein, minerals, and antioxidants, making them a valuable component of a healthy diet. Here are some opportunities in the millet sector.

Food Processing:

Millets can be processed into various food products, including flour, flakes, porridge, and snacks. There is a rising trend of using millet-based products as a substitute for wheat and rice due to their nutritional benefits. Entrepreneurs can set up millet processing units to manufacture these value-added products and cater to the increasing demand. Department of Community Science, BAU, Ranchi has developed more than thirty value added products of millets including Ragi Laddu, Barfi, Pasta, Macaroni, Sewai, Cookies, Biscuits, Ragi Flacks, Cakes, Multigrain flour and also recipes for various local products like Dhuska, Idali, Dosa, Pitha etc.



Retail and Distribution:

Establishing retail and distribution networks for millet products can be a lucrative opportunity. This can include setting up dedicated millet stores, partnering with grocery chains to stock millet products, or developing an online presence for e-commerce sales. Creating awareness about the health benefits of millets and promoting its usage can help to drive consumer demand.

Govt. of India has planned to include the millets based value added products in PDS system, Mid day Mill programme for the Schools, Angan bari yojana and all the ICDS programm. Railways and Tourism Ministry, Govt. of India has also planned to make it compulsory to include millet based food in all the Rajdhani Exp., Shatabdi and Vande Bharat Exp. Trains as well as all the Big Hotels through Ministry of Tourism. It will increase huge demand of value added products of Millets and creates lots of opportunities for the farming communities.

Export Opportunities:

Millets have gained popularity globally as a sustainable and healthy food option. Exporting millet products to countries where there is a growing interest in alternative grains can be a profitable opportunity. Understanding international trade regulations and building strong distribution channels is crucial for success in the export market. To know the potential of the export of millets from India, APEDA has also came forward to boost up the promotion of Millet's cultivation and export of Millet and millet's products.

Millet-based Hotel Business:

Focusing on a millet-based hotel business can be a unique and exciting opportunity that aligns with the growing demand for healthy and sustainable food options. Here are some key considerations and potential opportunities for a millet-based hotel business:

1. Menu Development:

Designing a menu that showcases millets as a core ingredient can be a distinguishing factor for many STAR Rated Hotels. Develop a variety of millet-based dishes, including breakfast items, salads, main courses, and desserts. Experiment with different millet types such as pearl millet, finger millet, or foxtail millet, and incorporate them into traditional and innovative recipes to cater to a wide range of tastes. Now a days we could find a QR Code placed on the dining table. It was interesting to find the different types of millet recipes.

2. Millet-Based Events and Festivals:

Organize events or festivals that celebrate millets and their culinary significance. This could include themed dinners, food tastings, or even partnering with local millet festivals or organizations. Such events can attract food enthusiasts, create buzz around the hotels, and position it as a destination for millet-based cuisine. On 18th May 2023, Michael's Kitchen, Bhubaneswar, Odisha conducted a Millet Food Festival in collaboration with Odisha Millets Mission, where Home Cooks & Housewives were invited to the Millet Cooking Competition, and the winners were awarded. Awesome and yummy millet recipes were displayed and this attracted many people to this restaurant.



3. Millet-Based Catering Services:

Extension of millet-based offerings beyond the hotel premises by providing millet-focused catering services for events, conferences, and weddings. Highlight the unique aspect of catering services with a diverse selection of millet dishes that cater to different dietary preferences and requirements. In the recent years, Ahmedabad, Gujarat where got the opportunity to taste the Millet Lunch offered by the Self-Help Groups of SEWA NGO. Really the food was very tasty and yummy and anyone can enjoy it. Hope this type of initiative will definitely support the SHGs.

4. Collaboration with Wellness and Health Retreats:

Partner with wellness retreats or health-conscious establishments to offer millet-focused experiences. This could involve creating customized menus, hosting wellness retreats that include millet-based meals, or providing catering services for wellness events. Collaborating with like-minded businesses can expand your reach and tap into a niche market.

Conclusion:

Today, Considering unpredicted environments and changes in the Global climatic condition as well as nutritional profile of millets, a lot of opportunities for farmers and entrepreneurs is growing up, as India is taking the lead in the celebration of the International Year of Millets-2023. This celebration around the globe is creating awareness among the people. Awareness of the nutritional, ecological, health, and economic benefits of millet is pushing people to start their millet journey. Nowadays, people are bringing back forgotten foods to their plates and believe that these foods can bring a positive impact on their health. I think this change in India, is opening up opportunities for entrepreneurs and investors to invest in Millets.



Lead Paper



Targeting induced local lesions in genomes ‘TILLING’, an alternative to pre-breeding programme for crop improvement

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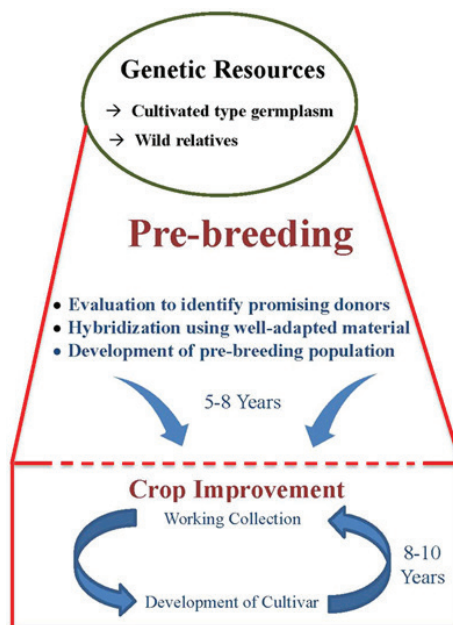
Abstract

TILLING is one of the important methods in functional genomics and crop improvement. This allows researchers to examine the effects of specific mutations on gene function. It can be used to develop new plant varieties with desired traits. Additionally, TILLING can be applied to animal models for genetic research and disease modeling. This technology is particularly useful for studying non-model organisms where genetic tools such as CRISPR/Cas9 may not be readily available.

Key word: Pre breeding, CRISPR/Cas9, TILLING

Pre-breeding is an important aspect of plant breeding for crop improvement that prepares and diversifies the genetic resources available to breeders for the development of improved crop varieties. The primary purpose of pre-breeding is to enhance the genetic potential and growing ability of crops, making them more adaptable to changing environmental conditions, pests and diseases. Here are some key steps and considerations in pre-breeding for crop improvement. Pre-breeding begins with the identification and collection of genetic resources, which may include ancestral relatives, landraces, or other non-adapted or underutilized plant varieties related to the cultivated crop. These genetic resources contain valuable traits that can be incorporated into improved crop varieties. Breeders identify specific traits in need, such as disease resistance, tolerance to abiotic stresses (e.g., drought, salinity), improved nutritional content, or other agriculturally important traits. The traits selected should be in line with the needs and preferences of farmers and consumers. Controlled crosses are made between a cultivated crop and genetic resources to transfer desired traits. It involves selecting parent plants with desired traits and making crosses to produce hybrid offspring. To retrieve the genetic background of a cultivated crop while retaining the desired trait, backcrossing is done. The process involves making repeated crosses between a hybrid and a cultivated crop and selecting offspring with the target trait in each generation. Molecular markers and DNA sequencing are often used during the backcrossing process to track and confirm the presence of the desired trait. This helps breeders to efficiently select plants with required traits. Selected materials are evaluated in field trials to assess their performance in real-world conditions. This step helps determine the effectiveness of trait transfer and identify any potential negative traits that may have inadvertently been passed on. Depending on the crop and region, there may be regulatory and biosecurity considerations when working with genetic resources from wild relatives or non-adapted sources. Pre-breeding often involves collaboration between researchers, institutions and plant breeders. Sharing knowledge, resources and expertise is critical to success in this complex process. Thus, pre-breeding provides plant breeders with a broad genetic base and useful genetic traits that can be incorporated into breeding programs, ultimately leading to the development of improved crop varieties. These improved

varieties are better equipped to meet environmental challenges and contribute to food security and agricultural sustainability.

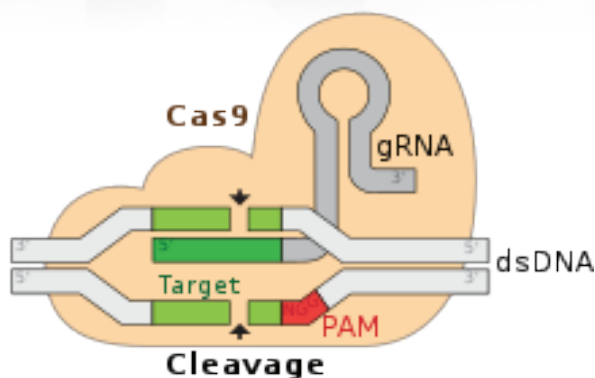


Courtesy, Sharma et al 2013

CRISPR-Cas9 is a unique technology that enables geneticists to edit parts of the genome by removing, adding or altering sections of the DNA sequence. It is currently the simplest, most versatile and precise method of genetic manipulation and is therefore causing a buzz in the science world. The system consists of two key molecules that introduce a change (mutation) into the DNA. These are:

- An enzyme called Cas9. This acts as a pair of ‘molecular scissors’ that can cut the two strands of DNA at a specific location in the genome so that bits of DNA can then be added or removed.
- A piece of RNA called guide RNA (gRNA). This consists of a small piece of pre-designed RNA sequence (about 20 bases long) located within a longer RNA scaffold. The scaffold part binds to DNA and the pre-designed sequence ‘guides’ Cas9 to the right part of the genome. This makes sure that the Cas9 enzyme cuts at the right point in the genome.

The guide RNA is designed to find and bind to a specific sequence in the DNA. The guide RNA has RNA bases that are complementary to those of the target DNA sequence in the genome. This means that, at least in theory, the guide RNA will only bind to the target sequence and no other regions of the genome. The Cas9 follows the guide RNA to the same location in the DNA sequence and makes a cut across both strands of the DNA. At this stage the cell recognizes that the DNA is damaged and tries to repair it. Scientists can use the DNA repair machinery to introduce changes to one or more genes in the genome of a cell of interest.



Courtesy: https://en.wikipedia.org/wiki/CRISPR_gene_editing

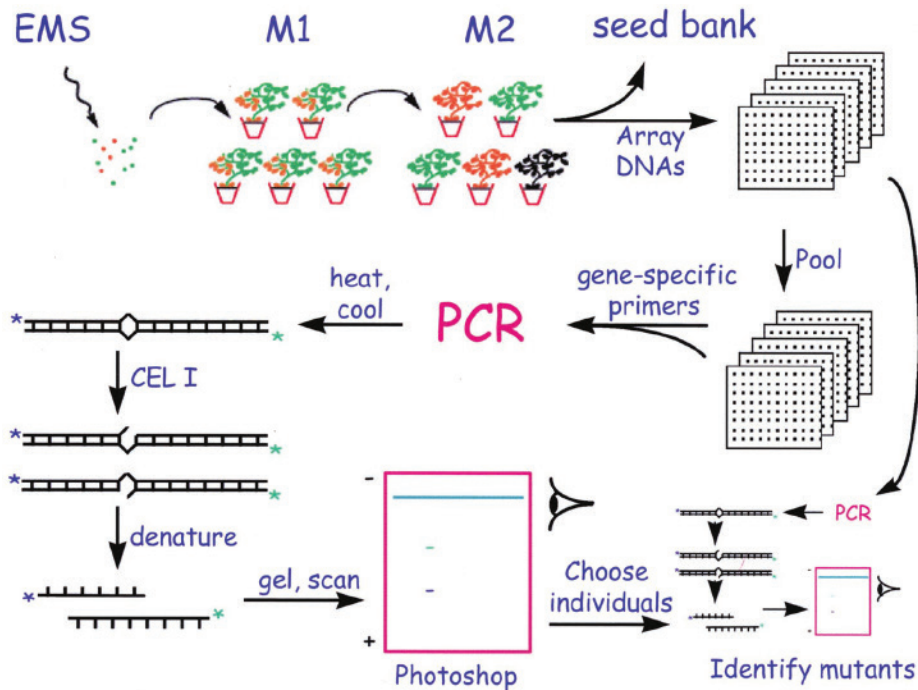
On the other hand “targeting induced local lesions in the genome” (TILLING) is a powerful technique used for functional analysis of genes (functional genomics) and genetics research. It is a method of identifying and characterizing mutations in specific genes by creating a library of mutant genes, which can be used to study the function of those genes and their role in various biological processes. It is used for functional analysis of genes that combine deleterious mutations and rapid high-throughput identification of mutations within the gene of interest. It is used to identify desirable alleles of interest for crop improvement, an alternative to the transgenic method.

TILLING is not a pre-breeding program itself, but rather a method within the broader context of plant breeding and genetic research. TILLING is a valuable tool for identifying and characterizing mutations in specific genes of interest. These mutations can then be used in breeding programs to develop new plant varieties with desirable traits, such as disease resistance or improved crop yield. TILLING helps researchers and breeders identify and select plants with the desired genetic changes, which can be further incorporated into breeding programs to develop new cultivars. Utility of TILLING in many crops viz, maize (Till et al., 2004), rice (Till et al., 2007; Suzuki et al., 2008), sorghum (Xin et al., 2008), wheat Chen et al., 2012), legumes, oilseeds (Dalmais et al., 2008), sunflower, soyabean (Kumar et al., 2013), rapeseed (Gilchrist et al., 2013), tomato Piron et al., 2010; Okabe et al., 2011), pumpkin (Vicente-Dólera et al., 2014), cucumber (Fraenkel et al., 2014), radish (Kohzuma et al., 2017), cotton (Aslam et al., 2016), flax (Chantreau et al., 2013), banana (Jankowicz-Cieslak et al., 2012) etc was well proved for development of new population with induced desirable traits.

Here's how TILLING works:

High yielding leading variety deficit for a trait is being used. Many techniques are available for mutation; the simpler one is uses of standard chemicals or physical mutagen treatment. Modern technique like CRISPER/Cas9 based system which facilitates mutation within a specific target gene. In TILLING, mutagenic agents, such as Ethyl Methanesulfonate (EMS), N Methyl-N-Nitrosourea (NMU) and Sodium Azide (NaN₃) are used to randomly induce mutations in the genome of an organism. These mutations are typically point mutations, meaning changes in single nucleotides (A, T, C, G) within the DNA.

Maximum numbers of seeds are treated with specific chemicals. Germination affected due to effect of mutagen which depends on doses and duration of mutagen treated. Seeds are harvested from each M1 plant. One plant from each M1 plant is raised in M2. DNA isolation and phenotypic traits are taken in over 11000 plants. In M3, progenies were sown in neighboring rows and phenotyped at different developmental stages. Traits like presence of chlorophyll in seedlings, shape and colour of rosettes, morphology of leaves and spike, time of flowering, height of plants etc. All data collected from M1 to M3 are stored in data bank. Each individual in this library carries different random mutations. DNA isolation and Pooling Samples are to be done from M2 generation. The CTAB method using solid phase extraction avoids phenol and chloroform and is best used for assays where smaller DNA fragment sizes are acceptable. DNA quantity and quality is measured by NanoDrop ND-100 UV vis spectrometer. The is a high-energy laser that measures the concentration of DNA, RNA, or protein in the UV/visible light range. It can measure absorbance spectra or single wavelengths of these macromolecules in solution. DAN pooling is done from 8 different M2 plant. Eight fold serve as a template for PCR reaction. The specific genes of interest are amplified using PCR (polymerase chain reaction) from the DNA of each pool. This results in a collection of DNA fragments representing the genes of interest from each pool. The DNA fragments from each pool are then compared to the corresponding DNA from the wild-type (non-mutant) organism. By looking for differences in the DNA sequences, researchers can identify which pools contain mutants with changes in the target genes. Once a pool with potential mutants is identified, individual mutants within that pool are further screened to identify and characterize the specific mutations in the target gene. This can be done through DNA sequencing or other molecular biology techniques.



Courtesy: Colbert et al 2001

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Breeding strategies for abiotic stress tolerance in maize

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Introduction

Maize (*Zea mays* L.) one of the most widely cultivated crops globally, serving purposes ranging from food and animal feed to biofuel production (Rani et al., 2016 and Sah et al., 2016). However, the productivity of maize is intricately linked to the climatic and soil conditions. Abiotic stresses, including drought, salinity, high temperatures, and cold, are formidable factors that pose significant limitations on maize yield and productivity (Farooqi et al., 2022). Drought, in particular, emerges as a substantial threat contingent upon its severity and duration. Maize is vulnerable to drought throughout its growth cycle, from flowering to grain filling and directly impacts photosynthesis rates within chloroplasts. In response to drought, the concentration of abscisic acid (ABA) in leaves is disturbed, triggering the elevation of various antioxidant enzymes, including GR (glutathione reductase), APX (ascorbate peroxidase), CAT (catalase), and SOD (superoxide dismutase) (Mehla et al., 2017 and Sah et al., 2020). Salinity affects a significant portion of irrigated (50%) and all cultivated (20%) lands (Wang et al., 2017). Maize growth and development are influenced by salinity, with plant responses varying based on the degree of salinity and the crop growth stage. Short-term exposure to salt stress induces osmotic stress, affecting maize growth. In saline soils, the accumulation of sodium and chloride ions in the rhizosphere disrupts the balance of essential mineral elements, resulting in severe nutritional imbalances in maize. Heat stress is another challenge that reduces crop growth and productivity. Under combined drought and heat stress a disrupt in cell metabolic activity and physiological networks has been observed, which adversely impacting processes such as pollen dehiscence, stigma and silk emergence, seed set, and grain filling, thereby reducing maize grain yield (Sah et al., 2020 and Barnabás et al., 2007). Furthermore, maize exhibits sensitivity to low temperatures (<15°C), when combined with excessive light, chilling temperatures (10°C) impede CO₂ assimilation, leading to irreversible inhibition of photosynthesis and cellular damage (Farooqi et al., 2016).

To navigate these abiotic stresses, plants possess adaptive mechanisms that come into play under challenging conditions, encompassing molecular, cellular, metabolic, and physiological responses (Farooqi et al., 2022). Maize, for instance, exhibits phenotypic adaptations such as altered leaf angles, increased leaf wax, compacted tassels, and reduced anther evaporation rates, which are crucial for preventing anther dehiscence (Shah et al., 2011 and Sah et al., 2020). Genetic and metabolic networks are also modulated in response to abiotic stresses. The advances in genetics and molecular biology have ushered in the era of high-throughput sequencing technology, enabling plant scientists to pinpoint genes and genetic regions associated with traits of interest. Over the years, these genetic insights have been harnessed for crop improvement, encompassing yield, biotic stress resistance, and abiotic stress tolerance. Multi-omics approaches, including genomics and metabolomics, have played a pivotal role in unraveling the complexities of maize crop growth, senescence, yield, and responses to both biotic and abiotic stresses.



Morphological and Physiology changes under abiotic stress in maize

Maize exhibits various morphological changes and physiological responses when exposed to abiotic stresses. These stresses, including high temperatures, salinity, and drought, lead to alterations in several physiological traits such as membrane permeability, net photosynthesis, osmolyte accumulation, respiration, osmotic potential, and mineral uptake in maize. Research has shown that specific processes like photorespiration and raffinose metabolism play crucial roles in drought tolerance. In addition, changes in metabolic profiles within maize cells occur during stress conditions, affecting processes such as cell wall remodeling, metabolic stability, and signaling mechanisms, all of which contribute to the plant's ability to tolerate multiple stressors.

Reactive oxygen species (ROS) levels within maize are influenced by factors like catalase (CAT), glutathione reductase (GR) activities, chlorophyll content, and membrane stability. Under stress conditions, maize seedlings exhibit increased levels of osmoprotectants, which are essential for salt stress tolerance. Furthermore, temperature stress activates various responses within maize, involving heat shock proteins, kinases, phosphatases, and metabolic networks that collectively enhance the plant's heat tolerance. Adjusting planting times to avoid extreme temperature periods during crucial growth stages can reduce the negative impacts of temperature fluctuations, resulting in reduced yield losses. Maize exhibits specific morphological changes in response to stress. For instance, exposure to high temperatures during the flowering stage can lead to pollen desiccation, which delays the silking interval and negatively impacts maize productivity. Stresses can initially inhibit cell proliferation, and prolonged exposure may prevent cell expansion, accelerate vegetative growth, and result in the completion of the maize life cycle before the onset of temperature stress. Roots also play a crucial role in maintaining effective water uptake during drought stress, and adjustments to the hydraulic root architectural system, soil, and water management, as well as transpiration activities, contribute to maize's ability to endure heat and drought stresses (Farooqi et al., 2022 and Sah et al., 2020).

Approaches for improving abiotic stress tolerance

Utilization of wild relative for abiotic stress tolerance

Maize, wild species known as teosintes, are native to Mexico and Central America. Modern maize is believed to have evolved from annual teosinte, particularly *Zea Mexicana*. These wild ancestors share plant architecture and growth traits with maize but possess higher chromosome numbers, making hybridization challenging. Orthologous genes in maize and *Tripsacum* revealed distinct genes with frequent non-synonymous substitutions in *Tripsacum*. These substitutions played a role when adapting domestic maize to temperate regions through artificial selection. *Tripsacum*'s unique metabolic pathways, such as phospholipid metabolism, were associated with cold and freezing tolerance. Special anatomical features, like aerenchyma tissue in roots, contribute to drought resistance. Root penetration and increased biomass in *Tripsacum* have also shown drought resistance. *Tripsacum* introgression lines exhibit superior root systems, deep soil penetration, and higher grain yields compared to modern maize cultivars. Hybrid plantlets of maize and *Tripsacum* demonstrated improved salt tolerance, retaining sodium in their leaves and maintaining turgor pressure, essential for vegetative development. Utilizing the genetic potential of wild relatives is crucial for creating new genetic resources to develop maize lines with enhanced abiotic stress tolerance (Farooqi et al., 2022).



Utilization of speed breeding and genomic selection

Traditional maize breeding involves time-consuming steps, including developing parental lines and producing hybrids. Speed breeding methods have been introduced to shorten the breeding cycle. These methods include off-season nurseries, double haploid (DH) technology, and in vitro nurseries. Off-season nurseries grow crops in locations suitable for their photoperiod, but they require additional permissions, transportation time, and may introduce new pests and diseases. DH technology reduces the breeding cycle by producing homozygous lines in two generations, but it may have low success rates. In vitro nurseries combine DH technology and off-season nurseries to produce homozygous and homogenous lines. Genomic selection is a valuable tool for improving polygenic traits like grain yield in maize. It estimates breeding values using molecular markers covering the entire genome, allowing the prediction of the genetic value of candidates. In the quest to identify maize lines and hybrids with superior yield potential in specific environments, evaluations are carried out under controlled stress conditions. Unfortunately, many parent lines, hybrids, and crosses are often discarded due to their underperformance in the field. This can be attributed to the limited genetic value of the selected parents used for these crosses. To maximize the accumulation of desirable alleles for important traits in their offspring, it is crucial to employ parents with high Genetically Estimated Breeding Values (GEBV) in the breeding process. Genomic selection has been shown to improve stover and grain yield in maize populations. Combining genomic selection with marker-assisted selection (GSMAS) has advantages over the QTL-MAS approach for drought-stressed growth characteristics. Maize is susceptible to abiotic stresses, particularly drought and waterlogging, which create genotype-environment interaction in breeding programs. Furthermore, it's important to note that genetic gain is constrained when dealing with abiotic stresses and significant environmental variations. Therefore, the integration of genomic selection and speed breeding techniques for enhancing abiotic stress tolerance can significantly improve parent selection accuracy, *leading* to increased genetic gain and improved abiotic stress resilience in maize breeding programs (Trachsel et al., 2019 and Farooqi et al., 2022).

Genome editing

Genome editing tools represent a significant milestone in molecular biology, providing a precise and efficient means to alter a genome. The CRISPR/Cas system has rapidly gained popularity as a versatile genome editing technology, particularly in plants. This is due to its high efficiency, ease of use, cost-effectiveness, and its ability to target multiple genes simultaneously. Several studies have focused on enhancing abiotic stress tolerance in plants, including maize, using CRISPR/Cas technology. For instance, researchers have successfully introduced drought-resistant traits in maize through the precise insertion and substitution of genes using CRISPR/Cas9.

In one study, CRISPR-Cas was employed to create novel variants of the ARGOS8 gene, which is associated with drought tolerance. By modifying the ARGOS8 gene's expression, researchers were able to enhance drought tolerance in maize. Field evaluations demonstrated that these genetically modified maize lines produced five additional bushels of grain per acre under drought conditions compared to the wild type. This illustrates the potential of CRISPR-Cas9 technology to generate new genetic diversity in crops, ultimately leading to the development of drought-tolerant varieties. In another study, CRISPR/Cas9 was utilized to investigate the ZmWRKY40 gene, which encodes a transcription factor associated with drought tolerance. By enhancing the



expression of this gene, researchers were able to confer drought tolerance to maize plants. Genome editing techniques hold tremendous promise for crop improvement. By carefully selecting the appropriate genome editing tool, designing target sequences, and delivering them using suitable vectors, researchers can introduce desired genetic changes. This process involves modifying the target sequence, regenerating edited calli, and producing edited plants.

Conclusion

Maize productivity is significantly affected by various abiotic stresses. These stresses can disrupt the growth and development of maize plants, leading to reduced yield and quality of the crop. Maize has developed various adaptive mechanisms, including changes in morphology and physiological responses, to cope with these challenges. Advancements in genetics and molecular biology have provided valuable tools and insights for improving maize's ability to withstand abiotic stresses. The use of wild relatives, such as teosintes, offers genetic diversity that can be harnessed to develop maize lines with enhanced abiotic stress tolerance. Additionally, speed breeding and genomic selection techniques expedite the breeding process and enable the selection of maize lines with high genetic potential for stress tolerance. Genome editing, particularly the CRISPR/Cas system, represents a cutting-edge technology that allows for precise modifications of maize genes to enhance its tolerance to abiotic stresses. In this era of rapid technological advancement, the integration of these strategies and approaches, along with traditional breeding methods, holds great promise for developing maize varieties that can thrive under challenging environmental conditions. By leveraging the genetic potential of wild relatives, expediting the breeding process, and using genome editing tools, we can contribute to ensuring food security and sustainable agriculture in the face of changing climate patterns and abiotic stress.

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LP 03

Identification of novel donors and underlying QTLs for P use efficiency and transfer of *pup1* into mega varieties for improving low soil P tolerance in rice

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In last seven decades, India has witnessed more than 6 fold increase in food grain production from 50.58 million tons in 1950-51 to 329.68 million tons in 2022-23. Credit of this increase goes to release and wide scale adoption of high yielding varieties of rice and wheat and better management practices including fertilizer applications. On the other hand, there has been a dramatic increase worldwide in fertilizer applications in the last 60 years, and this has particularly been the case in India. Imbalanced and indiscriminate use of chemical fertilizers has not only greatly deteriorated the soil health but also resulted in widespread water eutrophication. In addition, high cost of fertilizers reduces the economic return and placed a heavy economic burden on the farmers. Eventually, ever increasing fertilizer cost is rendering the agriculture non-remunerative. So far,



breeders have been developing varieties that respond to heavy doses of fertilizers and nutrient use efficiency or tolerance to low nutrient status in soil has never attracted the attention of the breeders. As a result, the high yielding varieties could not become popular among the poor farmers. To sustain agriculture in future, to preserve environment and soil health there is an immediate need for reduction in soil nutrient input (Vinod, 2014). Therefore, developing crop varieties that use applied nutrient efficiently and perform well even under low input situation is essential for sustainability and profitability. Adequate availability of phosphorus (P) is a major production constraint in India and as far as the soils are considered as they are low (49.3% of soils) to medium (48.8% of soils) in terms of actual or available P content. Tolerance to low soil P has polygenic inheritance in rice and so far only one major QTL, *Pup1* has been identified and characterized to be associated with low soil P tolerance and utilized in breeding programs across the world (Chin et al. 2011). Keeping these points in view, this study focused on identification of novel, non-*Pup1* type donors for tolerance to low soil P, low phytic acid, molecular mapping of the genomic regions associated with tolerance and deployment *Pup1* into elite rice varieties.

METHODOLOGY:

A total of 152 diverse set of rice germplasm including collections from north-eastern region and rice varieties along with the tolerant checks- Swarna, Kasalath and susceptible (i.e. sensitive) checks Improved Samba Mahsuri (ISM) and MTU1010 were screened in the low soil P plot (available P < 2 kg ha⁻¹) at ICAR-IIRR, Hyderabad, India for tolerance associated phenotypic traits in order to identify tolerance rice lines. They were then screened with a set of PCR based markers, specific for *Pup1* to identify novel sources of tolerance (Mahadevaswamy et al 2019; Kale et al, 2020). Similarly, 80 rice germplasm including 5 checks of diverse origin was screened for phytic acid (PA) content in grains at ICAR-IIAB, Ranchi (Kothapelly, 2023). Two RIL populations were developed from two such novel non-*Pup1* donor lines namely, Rasi and Wuzuhophek by crossing them with Improved Samba Mahsuri. The RILs were screened in the low soil P plot of ICAR-IIRR and molecular mapping was performed with the help of SSR markers (Kale et al, 2021). In order to transfer *Pup1* into elite rice varieties, Swarna was used as donor for *Pup1*, crossed with Improved Samba Mahsuri and MTU1010 (which are sensitive to low soil P conditions) and marker-assisted backcross breeding approach was adopted to develop NILs (Anila et al. 2018; Mahadevaswamy et al, 2020). The developed NILs were subjected for testing in the low soil P plot of ICAR-IIRR and also in low phosphorus tolerance trials of AICRIP. Marker assisted *Pup1* introgression was further carried out in IR64 Dtr1 (Teja, 2022).

RESULTS

Evaluation of 152 rice germplasm lines under both low P as well as normal P conditions and further screening for presence of *Pup1* QTL with the help of associated molecular markers (K46-1, K46-2, K46-K1, K452 and K46CG-1) it was found that Rasi, Wuzuhophek, IC216831 and IC216903 exhibited tolerance to low P conditions even though devoid of *Pup1* indicating novel genetic control in these four lines with respect to low soil P tolerance. These lines showed high value for stress tolerance index (STI), yield stability index (YSI) and yield index (YI), and the lowest value for tolerance index (TOL), stress susceptibility index (SSI) and percent yield reduction (PYR).



Phenotypic evaluation of recombinant inbred line (RIL) mapping population consisting of 330 lines derived from the cross Wazuhophek x Improved Samba Mahsuri in a plot with low soil P for tolerance associated traits and molecular mapping with SSR markers revealed a total of 16 QTLs (seven major and nine minor QTLs), which are associated with low soil P tolerance related traits. Interestingly, a QTL hotspot, harbouring 10 out of 16 QTLs was identified on the short arm of chromosome 8 (flanked by the makers RM22554 and RM80005). Five major QTLs explaining phenotypic variance to an extent of 15.28%, 17.25%, 21.84%, 20.23%, and 18.50%, associated with the traits viz., plant height, shoot length, the number of productive tillers, panicle length and yield, respectively, were located in the hotspot. Two major QTLs located on chromosome 1, associated with the traits namely, total biomass and root to shoot ratio explaining 15.44% and 15.44% phenotypic variance, respectively were also identified.

Screening of 80 rice germplasm lines for phytic acid content in grains revealed wide variation, which ranged from 1.11mg/g (BAU21802) to 3.33 mg/g (GSR IR1-DQ186-Y2-D1). BAU21802 is an elite breeding line which offers opportunity for development of low phytic acid varieties without compromising on performance.

With an objective to improve the performance under low soil P conditions of the mega rice varieties - Improved Samba Mahsuri (ISM) and MTU1010 by targeted introgression of the major QTL, *Pup1* from Swanra (possessing *Pup1*) marker assisted backcross breeding was taken up. Promising, low P tolerant NILs of ISM and MTU1010 of BC₂F₆ generation possessing *Pup1* were identified (which were > 95% similar to the recurrent parents) and validated in low soil P plot of ICAR-IIRR. Two best lines each from ISM and MTU1010 were tested at multilocations in AICRIP. Based on their superior performance under low P conditions as well as normal conditions one line each in ISM and MTU 1010 backgrounds were released as DRR Dhan 60 and DRR Dhan 66 respectively as low P tolerant version of mega varieties. Analysis of F₂ population segregating for *Pup1* revealed that presence of *Pup1* invariably enhanced effective tiller numbers under upland rainfed conditions.

CONCLUSION:

Identification of novel sources and their utilization for development of low P tolerant varieties helps in reducing the application of P fertilizers, import burdens, and environmental contaminations due to fertilizer run-offs and for getting sustainable yields, thus enhancing the income of farmers. Four novel non-*Pup1* type donors and one low phytic acid donor have been identified through the present study. Major and minor QTLs associated with novel low soil P tolerance have been identified from Wazuhophek. Breeding lines of the elite rice varieties, ISM and MTU1010 possessing *Pup1* and showing excellent tolerance to low soil P levels have been developed through MABB approach. The present study highlights the effective use of modern molecular tools in rapid identification of novel sources of low soil P tolerance and also in improving low soil P tolerance of elite rice varieties through MABB approach.

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LP 04

Genetic analysis of quality and yield traits in aromatic rice (*Oryza sativa* L.)

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Introduction

Rice, the world's most important food crop is cooked and consumed mainly as a whole grain, so quality considerations are of paramount significance. Grain dimension is a key determinant of quality, and can improve optimal appearance and hence fetch higher market value. Grain dimension is a complex quantitative trait controlled by polygenes (Huang et al., 2013). Hence, mapping and cloning novel QTL for grain size is essential to have a thorough understanding of how grain size is regulated and could give useful gene resources for assisting in grain size and

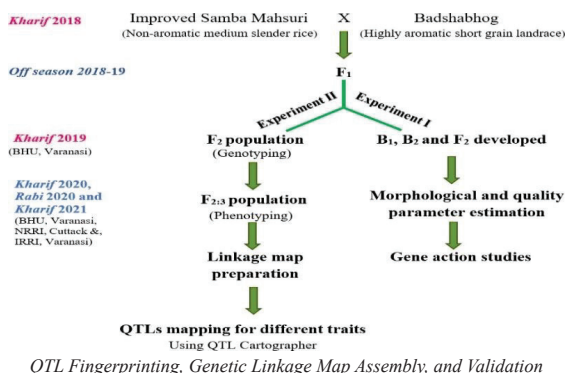
yield improvement in rice (Jiang et al., 2022). So, in the present investigation traits linked to grain shape i.e., grain length (GL), grain breadth (GB), kernel length (KL), kernel breadth (KB), kernel length breadth ratio (KLBR), kernel breadth after cooking (KBAC), elongation ratio (ER), elongation index (EI) were studied in detail and their QTLs were mapped.

Materials and Methods

Plant Materials and Field Experiments

Experiment I (Kharif 2019): Study of gene action and components of genetic variations using six populations i.e. P1, P2, F1, F2, B1, and B2 of the cross Improved Samba/ Badshabhog for grain quality and yield traits.

Experiment II (Kharif 2018, Rabi 2019-20, Kharif 2020, Rabi 2020-21): Validation of the parents for different grain quality traits, genotyping, and phenotyping of F2 and F_{2:3} populations respectively for identification and mapping of QTLs for grain quality and yield traits.



In the present study randomly selected SSR markers and some gene-specific markers related to the aroma, cooking and eating quality, grain dimension, and yield- related traits were used for genotyping of F₂ population, linkage analysis, and mapping QTLs for grain quality and yield traits. The markers were selected in such a way that they cover the entire length of each of the 12 rice chromosomes. The details about all the markers were obtained from the Gramene markers database (www.gramene.org). For those markers whose details were not available on the Gramene database, they were searched on RAP-DB (Rice Annotation Project Data Base) by using its BLAST tool and submitting query sequences (forward and reverse) in FASTA format to run the search against the DNA database (blastn) (<https://rapdb.dna.affrc.go.jp/>). GGT 2.0 software was used to study the distribution pattern of markers across the length of 12 rice chromosomes (Van Berloo, 2007; Van Berloo, 2008). GGT is a graphical representation software that visualizes the distribution pattern of markers according to their physical positions (Mb) on a genetic map.

QTL nomenclature was followed as per (McCouch *et al.*, 1997) where the initial small letter q is followed by two to three letters in abbreviated form of the corresponding trait for which QTL is identified followed by the chromosome number indicating the location of QTL and at the end a terminal suffix, separated by a period, which provides a unique identifier to distinguish multiple QTL on a single chromosome.

Results and Discussion

Results revealed a near-continuous distribution for all the traits indicating their governance by polygenes. The highest heritability was observed for traits GL followed by EI at BHU, whereas GL and GB after cooking at NRRI. It was observed that PCV was higher than GCV for all the traits studied, suggesting considerable effects of the environment at both locations. GMA studies showed the prevalence of duplicate epistasis in all the traits except KL and EI. The parents were screened for polymorphism with 576 SSR markers, of which 96 showed polymorphism. A linkage map constructed from 304 F₂ plants revealed 11 QTLs, of them *qGL5.1* for GL, *qGB3.1* and *qGB12.1* for GB, *qLBR4.1* for KLBR, *qBAC4.1* and *qBAC5.1* for KBAC, *qKER3.1* for ER and *qKE14.1* for EI were found to be common at both the locations. A maximum of five QTLs were common for the trait aroma, followed by three QTLs for grain yield per plant, two QTLs each for the traits grain breadth, kernel breadth after cooking and days to maturity while, one QTL each for the traits grain length, kernel length breadth ratio, elongation ratio, elongation index, days to 50 percent flowering and 1000 grain weight (Dwivedi *et al.*, 2021). Out of these five QTLs viz., *qARO8.1*, *qARO8.2*, *qARO8.3*, *qBAC4.1*, and *qBAC5.1* were major QTLs. (Table1). These findings provide valuable information for improving rice grain quality using marker-assisted selection.

Table 1. QTLs identified for different quality and yield related traits in F_{2:3} population derived from Improved Samba Mahsuri × Badshabhog at BHU and NRRI

S.No.	Trait	Chr n	QTL Nam	Loca- tion	Flanking Marker interval	Position of flanking (cM)	Composite Interval mapping				Al- lelic effect
							Position (cM)	LOD	Addi- tive	PVE %	
1.	Aroma	8	<i>qARO8.1</i>	BHU	RM42-nksbad2	178.4 - 182.8	180.71	83.80	1.73	40.55	BB
				NRRI	RM42-nksbad2	178.2 – 182.1	180.71	74.31	1.71	38.88	BB
		8	<i>qARO8.2</i>	BHU	nksbad2-BADEX7_5	187.5 – 191.1	188.91	71.87	1.75	39.16	BB
				NRRI	nksbad2-BADEX7_5	184.4 – 187.2	185.91	62.84	1.68	38.73	BB
		8	<i>qARO8.3</i>	BHU	BADEX7_5-RM404	194.6 – 198.7	197.21	38.95	1.50	23.33	BB
				NRRI	BADEX7_5-RM404	194.3 – 197.5	196.21	35.56	1.43	22.86	BB
		8	<i>qARO8.4</i>	BHU	RM80-RM42	147.1 – 158.2	153.01	5.24	-0.50	32.19	IS
				NRRI	RM80-RM42	145.4 – 155.8	151.01	6.23	-0.71	0.001	IS
		8	<i>qARO8.5</i>	BHU	RM404-RM547	201.2 – 213.3	207.41	4.24	0.001	1.74	BB
		4	<i>qARO4.1</i>	BHU	RM6748-RM317	241.2 - 256.8	246.81	3.64	-0.21	3.21	IS
				NRRI	RM6748-RM1113 and RM1113-RM317	243.6 – 252.2	246.81	2.56	-0.24	2.90	IS
2.	GL	5	<i>qGL5.1</i>	BHU	RM122-RM3616	205.2 – 223.2	213.31	2.57	0.26	1.22	BB
				NRRI	RM122-RM3616	203.8 – 224.7	214.31	3.94	0.23	2.72	BB

S.No.	Trait	Chr n	QTL Nam	Loca- tion	Flanking Marker interval	Position of flanking (cM)	Composite Interval mapping				Al- lelic effect
							Position (cM)	LOD	Addi- tive	PVE %	
3.	GB	1	<i>qGB1.1</i>	BHU	RM9-RM562 and RM562-RM220	32.0 – 72.6	54.41	2.62	0.04	3.12	BB
		3	<i>qGB3.1</i>	BHU	RM16-CHR3_20	105.9 – 137.3	120.81	5.45	0.07	9.10	BB
				NRRI	RM16-CHR3_20	108.9 – 139.0	124.81	4.23	0.06	6.64	BB
		5	<i>qGB5.1</i>	NRRI	RM548-RM13	92.5 – 105.7	100.21	3.06	-0.02	0.19	IS
		12	<i>qGB12.1</i>	BHU	RM1337-RM17	0.0 – 13.8	0.01	2.68	-0.04	4.99	IS
				NRRI	RM1337-RM17	0.0 – 15.0	0.01	2.91	-0.04	5.33	IS
4.	KB	3	<i>qKB3.1</i>	BHU	RM16-CHR3_20 and CHR3_20-RM3513	106.8 – 141.8	124.81	2.95	0.04	3.03	BB
				NRRI	NONE						
5.	KLBR	4	<i>qLBR4.1</i>	BHU	RM335-RM261	0.0 – 15.6	2.01	2.68	0.00	1.91	IS
				NRRI	RM335-RM261	0.0 - 14.8	2.01	2.93	0.00	2.18	IS
6.	KBAC	4	<i>qBAC4.1</i>	BHU	RM280-RM6748	186.3 – 213.8	201.51	3.46	0.11	10.12	BB
				NRRI	RM280-RM6748	186.5 – 214.7	202.51	3.93	0.12	91.74	BB
		5	<i>qBAC5.1</i>	BHU	RM163-RM289 and RM289-	23.7 – 68.2	57.21	3.31	0.07	10.49	BB
7.	ER	3	<i>qKER3.1</i>	BHU	RM514-CHR3_14	0.0 – 5.7	0.01	2.56	0.02	0.003	BB
				NRRI	RM514-CHR3_14	0.0 – 5.8	0.01	2.69	0.02	0.005	BB
		3	<i>qKER3.2</i>	NRRI	CHR3_20-RM3513 and RM3513-RM4796	142.6 - 155.8	148.11	2.76	-0.04	4.25	IS
8.	EI	4	<i>qKEI4.1</i>	BHU	RM335-RM261	0.0 - 12.3	0.01	2.66	0.00	1.53	BB
				NRRI	RM335-RM261	0.0 – 12.8	0.01	2.90	0.00	1.89	BB

Conclusion

Transgressive segregants were detected in the F2:3 population in almost all of the traits except grain length at both locations, which are heritable and adds further genetic gains to the next generations. A near-continuous distribution was observed for all traits across the locations, suggesting the presence of significant variation and their governance by polygenes. Kernel length and elongation index showed complementary epistasis. 13 QTLs for the seven traits were detected, of them 7 are robust QTLs i.e., found to be common at both locations, among them qBAC4.1 and qBAC5.1 were major QTLs. The detected QTLs would be useful for accelerating marker-assisted breeding for grain quality traits

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LP 05

Accelerating hybrid rice breeding through molecular approach

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The increase in population coupled with climate change, reduced natural resource mainly land and water possess challenges for food security worldwide. As such, increasing rice production is essential to sustain and improve people's livelihood, national economy, and even national food security. Rice is grown worldwide including most of the tropical countries and globally it occupies 164.19 mh areas and produces 756.74 mt (507.95 mt milled rice). India ranks second after China in rice production of 129.40 mt grown in 43.78mh during 2021-22. To meet the world's rice demand in 2030 we have to produce 820 mt (550 mt milled rice) from present production of 756.74mt (507.95 mt milled rice). To meet the Indian rice demand by 2030 we have to produce 186.87mt from present production of 129.40 mt (2021-22). In the last two decades India has steadily increased its export potential and now gained the position of world no.1 Exporter of rice by exporting total 17.72 mt rice with total worth of 8815 million USD(Rs.65298 Crore) during 2020-21(Source: DGCIS report, Govt. of India). The other major rice exporting countries are Thailand, Vietnam, Pakistan, Burma, China USA, Cambodia, Brazil and Uruguay. This year India is taking all care to keep the inflation under control. Hence, India is putting different types of restrictions on rice Export. As per print media, Dr. Pierre-Olivier Gourinchas, Chief Economist of the International Monetary Fund, Washington had said that if India continues restrictions on rice Export it may create problem of global inflation. Hence, India's rice production is playing a crucial role in global food and nutritional security and in balancing the inflation.

Hybrid rice (*Oryza sativa* L.) has provided a fundamental guarantee for food supply all over the world (Cheng *et al.* 2007). The commercial hybrids in rice is estimated to outperform conventional inbred rice by >20% in grain yield. In China, it has contributed 65% of the total rice production accounting for 57% of the total rice planting area (Yuan, 2014). Compared with the three-line hybrid rice, the two-line hybrid rice has played an increasingly significant role in rice production

due to the avoidance of negative effects by sterility-inducing cytoplasm and its independence on the restorer genes. In the past decade, breeders have paid more attention to super two-line hybrid rice for increasing yields (Yuan, 2017).

But, in India only three-line system of hybrid seed production is being used. However, probably India has also entered into commercial exploitation of two line system by releasing 1st two line hybrid rice in 2022 developed by IARI New Delhi and JNKVV Jabalpur in collaboration. The hybrid rice area in India is about 3.0 mha, which is still even less than 10% of the total rice cultivated area in India. More than 80% of the total hybrid rice area is in eastern Indian states like Uttar Pradesh (1.0 mha), Jharkhand, Bihar, Chhattisgarh, with some little area in states like Madhya Pradesh, Assam, Punjab and Haryana (ICAR-IIRR, Progress Report-2017). But 70-80% of hybrid seeds are being produced by private sectors in South-Indian states particularly in Andhra Pradesh, Telangana, Karnataka, Maharashtra and Tamil Nadu. As rice is a key source of livelihood in India, considerable increase in yield through hybrid rice technology will have a major impact on food and nutritional security. Till 2018 **India has released 101 hybrids for commercial cultivation**. Due to the quantitative nature of yield attributing traits, many genetic mechanisms are regulating the heterosis; therefore, it is probable that no single genetic mechanism can adequately explain all aspects of the heterosis phenomenon (Birchler *et al.*, 2010).

Molecular breeding with the help of Marker-Assisted Selection (MAS), used to infer phenotypic or genotypic data for breeding material have great potential to improve the efficiency and precision of conventional Plant Breeding. It will ultimately lead to accelerate the release of new crop varieties. The potential advantages of Molecular Breeding demonstrated by numerous examples of MAS in rice (e.g- Improved Pusa Basmati with *xa13*, *Xa21*, Improved Samba Mahsuri with *xa5*, *xa13*, *Xa21*, Swarna-Sub1 with Submergence tolerance, Swarna-Sub1+Drought with *qDTY_{1.1}*, *qDTY_{2.1}*, *qDTY_{3.1}*) and in other crops for identification and introgression of major genes and QTLs for biotic and abiotic stresses and quality traits. In the past twenty years, genetic mapping of the loci controlling heterosis in rice using molecular markers has been performed. The accuracy of early genetic mapping suffered from the use of low-density markers; for example, the mapping resolution was low and did not allow differentiation between **over-dominance and pseudo-overdominance**. Most of these studies used parental materials derived from bi-parental mapping populations, and the genetic diversity among these parental materials was very low. Therefore, the genetic mechanisms derived from studies of these populations might be of little relevance to actual hybrid rice production. So population based mapping approaches like **Genome-wide association study (GWAS)**, **genome sequencing** using high-density genetic markers has been widely used to dissect the genetic mechanisms underlying quantitative traits in crop species (Huang and Han, 2014). In rice, GWAS has proven to be a useful tool for identifying important genes related to agronomic traits. These studies indicate that genetic mapping in a multi-parental population using high-density markers could be utilized to discover the genetic basis of heterosis. The molecular approach has made it easy to identify the restorer and maintainer lines which is necessary for moving forward for developing hybrid rice. Now molecular approaches are helping hybrid rice breeding in many ways.



Towards healthier rice: harnessing genetic diversity for low phytic acid in grain

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Phytic acid, also known as inositol hexaphosphate, is a naturally occurring compound found in many plant-based foods, including rice. It is the primary storage form of phosphorus in seeds and grains and plays a crucial role in plant growth and development. While phytic acid is essential for plants, its presence in the human diet has raised concerns due to its impact on mineral bioavailability. Phytic acid possesses the unique ability to bind to minerals such as iron, zinc, and calcium, forming complexes known as phytates. These complexes are relatively insoluble and indigestible for humans, and this property gives phytic acid its reputation as an anti-nutrient. When consumed, phytic acid can inhibit the absorption of essential minerals in the human digestive system, potentially leading to mineral deficiencies in individuals whose diets are high in phytic acid-rich foods. Approximately 85% of the phosphate (P) found in rice grains and other plants exists in the form of phytic acid (PA), a compound known as myo-inositol-1,2,3,4,5,6-hexakisphosphate. PA plays a role in binding cations and inhibiting it releases of minerals for absorption during digestion process. Consequently, the presence of PA reduces the bioavailability of crucial minerals like iron, zinc, potassium, calcium, and magnesium in food. While ruminants possess the phytase enzyme to break down PA during digestion, monogastric animals, including humans, have limited phytase activity during digestion, resulting in only about 10% of PA breakdown, with over 90% being excreted, causing eutrophication. Rice is a primary staple food in many underdeveloped regions, particularly in South Asia. Moderate to high levels of PA, making it an inadequate source of essential micronutrients for nearly 3 billion people who rely on rice for their daily caloric intake. Enhancing the mineral content of rice grains, specifically calcium, magnesium, iron, and zinc, requires reducing PA content to an optimal level. The approach to reducing phytic acid content in rice typically involves harnessing genetic diversity and employing breeding techniques. Scientists study different rice varieties and their genetic characteristics to identify specific genes or traits that influence phytic acid levels. Through selective breeding and genetic modification, they aim to develop rice cultivars with lower phytic acid content while preserving other desirable traits, such as yield and disease resistance. Thus, developing low PA rice cultivars offers a sustainable, cost-effective, and environmentally friendly approach to provide nutrient-rich rice to global consumers (Azharudheen et al., 2023). Developing rice varieties with lower phytic acid content has the potential to address nutritional challenges and improve the overall health of populations that heavily rely on rice as a dietary staple. Lower phytic acid levels can enhance the bioavailability of essential minerals in rice, making it a more nutritious source of sustenance.

Through mutagenesis, researchers have developed low-PA mutants with significantly reduced grain PA content. These mutants exhibited a 45-95% decrease in PA compared to wild-type seeds. Knockout mutants of the SULTR-like phosphorus distribution transporter (SPDT) that modify phosphorus distribution led to a 30% reduction in grain PA content. However, these induced mutations resulted in a 12.5-25.6% reduction in grain yield and a 7.8-26.3% decrease in seed



viability. Due to the non-targeted mutagenesis used, the agronomic performance of these mutants was notably inferior to conventionally bred cultivars. Alternatively, limited genomic resources are available for identifying naturally occurring genetic variants related to grain PA. Recent research reported a single nucleotide substitution in the SPDT gene associated with low PA and increased mineral bioavailability in the Khira rice variety. Similarly, natural low-PA variants of rice lines have shown enhanced zinc bioavailability. Quantitative inheritance of PA content, influenced by environmental factors, poses challenges in its genetic understanding. An improved comprehension of genetic and environmental factors affecting grain PA content, along with genomic resources for selecting low PA genotypes, holds promise for rice breeders. To date, only two QTLs for grain PA content have been reported based on natural variation. Few QTLs and several candidate genes for low PA have been identified from mutant genetic stocks. The candidate genes associated with low PA in rice can be categorized into catalytic enzymes directly involved in PA biosynthesis and transporter genes related to phosphorous homeostasis, transport, and allocation (Larson et al., 2000; Frank et al., 2009; Raboy et al., 2000; Zhao et al., 2008).

Mapping and Development of functional marker

Marker-assisted selection (MAS) utilizing DNA markers is a valuable tool for enhancing the efficiency of breeding, particularly for complex traits like grain phytic acid (PA) content, which are challenging to phenotype and influenced by multiple genes. However, molecular marker resources for grain PA content in rice are currently limited. To develop genic or functional markers, it is necessary to identify candidate genes associated with the trait and mine alleles in natural populations. Understanding the allelic diversity in candidate genes associated with low PA and their effects is crucial for genetic enhancement aimed at reducing PA content in rice. Previous research has revealed that a T-C mutation in the fifth exon of the SPDT gene leads to spontaneous variation in grain PA content and enhanced mineral nutrient bioavailability in rice. However, a single SNP in the SPDT gene may not account for the entire diversity in grain PA levels across rice germplasm. Therefore, it is essential to investigate the impact of polymorphic loci in other potential genes linked to grain PA content.

Marker alleles derived from two potential transporter genes, SPDT and OsPT8, were significantly linked to variations in grain PA content within the panel. Specifically, a 201 bp allele located in the 3' untranslated region (UTR) of the SPDT gene exhibited a negative association with grain PA content, explaining 7.84% of the observed phenotypic variation. Additionally, a rare allele within the coding sequence of the OsPT8 gene was positively associated with grain PA content, accounting for 18.49% of the phenotypic variation. These findings shed light on the genetic basis of grain PA content in rice and provide valuable insights for future breeding efforts aimed at developing low-PA rice varieties (Azharudheen et al., 2022). In the case of the OsPT8 gene, a rare allele within its coding sequence was positively linked to grain PA content. This allele explained a significant portion of the phenotypic variation, amounting to 18.49%. These findings underscore the role of these alleles from SPDT and OsPT8 genes in influencing grain phytic acid content in rice. One of these markers from the OsMIK gene, which is known to be directly involved in the regulation of grain phytic acid (Zhao et al., 2013). Some other genes like ILI5, SPIKE, OsAAP11D, and Sdr4, also associated with grain PA respectively. These genes have documented roles in various aspects of grain development, such as grain enlargement (Shi et al., 2019), grains per panicle (Zhang et al., 2019), amino acid uptake and grain development (Ji et al., 2020), and seed dormancy (Chen et al., 2021) (Unpublished data).



Natural variation for PA content in rice

The inheritance of grain phytic acid (PA) content in rice is indeed a complex process influenced by a combination of genetic and environmental factors. Genotype-environment interactions play a significant role in determining the levels of PA in rice grains, which means that both the specific genetic makeup of rice varieties and the growing conditions can impact the variation in grain PA content. Research, has shown that there is a significant interaction between the genotype (genetic factors) and the environment (non-genetic factors) (Sanghamitra et al., 2018 and Azharudheen et al., 2022). This interaction implies that both genetic and non-genetic factors contribute to the observed variations in grain PA content among different rice genotypes.

Despite the impact of environmental factors, high heritability and a small difference between the genetic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) suggest that genetic factors have a more substantial influence on the variation in grain PA content. High heritability implies that a significant portion of the observed variability is due to genetic differences rather than environmental factors. When GCV and PCV are close in value, it suggests that the observed variation is primarily due to genetic factors. This information is promising for breeding programs aiming to develop rice varieties with lower PA content. It suggests that selecting low-PA genotypes under appropriate growing conditions can lead to the identification of rice varieties with reduced PA content. Moreover, the relatively high genetic advance indicates that breeding efforts have the potential to successfully improve grain PA content in rice, making it a feasible goal for crop improvement programs.

A recent study involving a panel of 96 rice genotypes showcased the significant variation in grain PA content. This variation ranged from as low as 0.3 percent in the Khira cultivar to as high as 2.98 percent in the Manipuri black cultivar (Azharudheen et al., 2022). Such studies provide critical insights into the genetic diversity of rice and offer opportunities for breeding programs to develop rice varieties with lower phytic acid content while still maintaining other desirable characteristics like seed viability, grain weight, and yield.

Conclusion

Research focused on reducing phytic acid in rice grain is a critical step towards promoting healthier diets and addressing nutritional deficiencies in regions where rice is a primary food source. By harnessing the genetic diversity within rice varieties and employing advanced breeding techniques, scientists are working towards making rice a more nutritionally valuable crop, thereby contributing to global food security and improved public health.

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LP 07

Time to capitalise androgenic based doubled haploid technique in *indica* rice

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Doubled Haploid (DH) technique is able to accelerate development and facilitates fast delivery of 100% homozygous lines within 1-2 years as compared to the conventional approach that takes ~5 to 6 years, thus saving time, labour and financial resources. Besides, the technology is also applicable to biotechnological strategies such as MAS (Marker assisted selection), GS (Genomic selection), gene/QTL mapping for biotic and abiotic stresses, transgenics and genome editing. Though anther culture has been exploited to develop several varieties and improved breeding lines, mostly in japonica cultivars, this technique has poor implications in indica rice cultivars owing to poor-androgenic response. Early anther necrosis, genotype dependency, poor-callus proliferation, and albino-plant regeneration are some of the major problems encountered in the case of indica rice androgenesis, which needed vast improvement; these problems encouraged ICAR-NRRI to find the solution for indica rice. As a result, many years of hard work at ICAR-NRRI led to the establishment of an excellent genotype independent androgenic protocol for indica rice that has enabled high frequency generation of DHs from a number of commercial and experimental hybrids which has steered in releasing of five DH varieties named Satyakrishna, Phalguni, CR Dhan 323, CR Dhan 324 (high protein, and moderate zinc) and CR Dhan 911 (aromatic). Surprisingly, without the use of any anti-mitotic agents, DHs were produced with the spontaneous doubling of 92-95%. Additionally, extensive research to mitigate the recalcitrance nature of indica rice to anther culture led to the grant of an Indian patent (401679 dated 20.07.2022) for an androgenic albino free protocol in indica rice. Further, a mapping population was developed for the identification of QTL for salinity and drought tolerance using intervarietal crosses of Savitri x Pokkali and IR 20 x Mahulata, respectively. Application of the DH technique showed its potentiality in introgression of QTLs and genes of various traits related to climate



change in indica rice through which a number of DH lines were generated; this could cope with the climate changing scenarios.

Several trainings were conducted for the skill development of faculties/senior rice researchers and students along with commercialization of the patent through an MoU with a private company, which generated significant financial resources for the institute. Since ICAR-NRRI showed its significant achievements in the production of DHs, now there is a need to capitalize this experience for which NRRI can be recognised as an advanced centre.

LP 08

Plant genetic resources in chhotanagpur plateau region and adjoining areas: status, challenge and prospects

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Chhotanagpur plateau region is the land of rich traditions where farmers known to grow diverse crop crops and horticultural plants. Among field crops landraces of Paddy, Finger millet, Pigeon pea, Horsegram, Niger etc helped to meet nutritional requirements of the natives farmers since ages. Often the yield capacity of such traditional varieties/landraces found limited but well compensated by other intrinsic properties like high nutritional value, good cooking qualities including pleasurable aroma, and sufficient volume of cooked meal with less quantity of raw grain, etc. As a result, these land races valued enormously as a remedy to overcome otherwise chronic dietary deficiencies like iron and zinc in the country without investing in developing cost intensive transgenic crops. Nevertheless, undulated landscape and climatic diversity naturalised wide range of tropical fruits in the region including Jackfruit, Bael, Tamarind, Jamun, Chironjee etc. These tropical fruits are underutilised resources often harvested as non timber products from forest area, but play a very critical role in sustaining human life and livelihood particularly during difficult time. ICAR-National Bureau of Plant Genetic Resources, Regional Station Ranchi in collaboration with various research institutes and agricultural universities collected about 13000 accessions of these crops and their wild relatives. For instance, significantly high number of paddy landraces collected from the Central and North-Eastern Plateau (CNEP) sub-zone. Landraces from iron- and aluminium (West and East Singhbhum) and mica (Giridih and Koderma) rich regions are a potential source of extraordinary mineral tolerance and bioaccumulations. These ecologically stressful habitats owing to limitations in soil pH, soil texture, and other factors are considered potential sites for the evolution of unique traditional varieties. However, the resource base was critically genetically eroded from 2005 to 2021, particularly in Ranchi, Hazaribagh, Ramgarh, Chatra, Bokaro, Dhanbad, Koderma, Deoghar, and Palamu. The CNEP sub-zone witnessed the most genetic erosion of landraces. At the same time, the continued cultivation of landraces in the steeper landscape of both the Western Plateau and South Eastern Plateau sub-zones underscored their value in risk aversion under challenging environmental conditions.

Selection criteria analysis of continued paddy landraces demonstrated farmers' preference for functional traits that influence livelihood security in the local context. These traits are vital for mainstreaming registered landraces into the production chain under changed climatic conditions.

On other hand, a total of 240 accessions of Jackfruit collected and conserved in Field Gene Bank of ICAR-NBPGR Regional Station Ranchi. These resources representing wide functional diversity as revealed during morphological and EST-SSR based characterisation. Accessions namely IC 24369, IC 542360, IC 438858, IC 24351 & IC 24345, IC 542353 and IC 542353 with unique traits viz. extra early bearing, prolonged bearing, maximum number of fruits/tree, dwarf canopy, very low inter-ovular sterile tissues in fruit and incomplete septa in fruit, respectively are of immense academic as well as commercial prospects. This diversity georeferenced to prioritised conservation sites. Palamu and Khunti districts of Jharkhand found promising for fruit yield attributing traits. While, Gaya district of Bihar, Latehar district of Jharkhand and Sundergarh district of Odisha emerged as a relevant niches for seed weight. In addition, quantitative trait-based clustering indicated dominance of vegetable purpose accessions in the collection. Both South Eastern Population of Jharkhand and Western Plateau Population of Jharkhand subpopulation of Jackfruit found accumulated rare morphological traits and genic SSR private alleles. These accessions represent unique evolutionary products that could provide the species with numerous industrial and adoptive properties, including resilience to changing climate. Their biochemical profiling and marker trait association helped to identify trait specific source plant and underlying markers enabling accelerated improvement programme in the fruit. Our result demonstrated efficacy of using morphological and genic-SSR markers together to explain complex biological diversity, particularly in perennial cross pollinated fruit trees like Jackfruit. These endeavours hold promise for improving livelihood security of farmers and forest dwellers of the region on sustainable basis.

However, to realise the potential, establishing community driven seed management system in the state is of utmost importance. Presently, there is no existing seed bank in the state. However, native farmers are endowed with rich traditional wisdom to manage and store farm saved seed. The heritage are being well utilized for establishing community seed bank. Further, ICAR - NBPGR organizing training and awareness campaigns on regular basis in these areas to highlight the significance of local crop diversity and the necessity to conserve the diversity for posterity. These endeavours acting as a launching pad for establishing Community Seed Bank and accordingly three model CSBs are being established in Garhwa, Godda and Saraikela Kharsewan districts of Jharkhand to cater the need of farmers in all three agro-climatic zones. The seed banks will provide unique opportunity and impetus towards conservation building efforts of the local tribal farmers and their indigenous knowledge



New dimensions of grain and nutritional quality improvement in wheat

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Wheat (*Triticum species*) is a vital staple crop that feeds millions of people across the globe. It is one of the universal cereals of old world agriculture and the world's foremost crop plant, which represents a large part of the history of agriculture itself besides its ancestry. Presently, wheat makes up a significant part of the world's diet and provides about one-fifth of the calories and proteins used by humans, making it the second-most important staple, after rice. India produced 112.74 million tons of wheat from 31.8 m ha area during 2022-23 and contributed about 34% to the total food grain production in India. The major wheat-growing states in India are Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, and Bihar which contribute approximately 91.5% of India's wheat produce. Wheat cultivation in India is unique as all the three major cultivated species namely bread wheat, durum (kathia) wheat and dicoccum (khopli) wheat are being cultivated. Approximately 95% of wheat cultivated is hexaploid with the remaining 5% being durum wheat (*T. turgidum* L.) and few other less important types. The wheat is widely adopted by mankind owing to its high environmental adaptability because of its allopolyploid nature and, thereby, genomic plasticity in addition to its excellent food/feed qualities regarding carbohydrates, proteins, vitamin content, and unique elastic property of its gluten, which make it suitable for more diverse use of its flour.

Indian wheat germplasm has always been recognized for their better product specific quality traits. Early bread wheat germplasm lines like Sharbati, Dara, Chandausi, Hard Red Calcutta, Mondhya 417, Muzaffar Nagar White, Buxar White, NP4, NP6, NP12, NP22, NP52, NP783, NP824, Niphad4, K 65, K 68, C306, etc. earned international recognition due to their excellent grain appearance and are still considered valuable genetic resource. The durum wheat evolved in India viz., Bansi, Kathia, Malvi, Amrut, N 59, NP 404, etc. are mostly used as chapati or dalia due to their unique quality characteristics.

The continuous increase in the urban population, mainly in developing countries, comes with increasing demands of industrially processed wheat-based foods. With the growth of industrialisation and increasing demand for bread, pizza, and pasta, there is now a need for specific varieties tailored for each end-use product. Increasing wheat production based on improved grain yield has been the breeding priority in developing countries and emerging economies. Therefore, the specific quality attributes required by the processing industry may not be found domestically. Till now, there are more than 500 varieties released in India for commercial cultivation leading to ensured food security in India and region. After attaining, self-sufficiency in wheat

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production, emphasis has been laid on improvement for quality traits especially for product development and nutritional security. Breeding for wheat quality is now gaining importance. Wheat holds significant value as a commodity in the realm of international trade. Its potential to be exported in adherence to quality standards serves as a driving force behind economic growth. It is imperative to conduct a thorough analysis of the stress-resistant, high-yielding crop varieties to determine their end-use and nutritional attributes.

There is multiple utilization of the wheat in the form of various bread, biscuit and chapatti products which have different quality requirements. A number of physical and biochemical parameters are associated in defining the quality of wheat for various products. Targeting the surplus wheat, export potentials and wheat consumption pattern in changing socio-economic scenario and expected high demand for value added wheat products, the quality parameters have been standardized and special emphasis was given in varietal evaluation procedure for release to identify specific varieties to *chapatti*, bread, biscuit and pasta products. Now a days high yielding and better quality varieties are available in bread, durum and dicoccum wheats. Improving wheat quality is highly complex and involves various factors such as genetics, environment, and agronomic practices. In the current era of molecular breeding, an array of genomic techniques is being employed to expedite the process of quality enhancement.

Due to its high nutritional value and variety of dietary elements, wheat is vital for human health. Nearly 55% of carbohydrates intake and 20% of food calories consumed in the world are attributed to wheat. Wheat grain contains 60–80% carbohydrates mainly as starch, 8–15% proteins, 1.5–2.0% fats, 2–3% crude fibres, 1.5–2.0% minerals, and traces of vitamins with 11% water and provides about 340 calories of energy. Nutrients that are vital to human nutrition can be found in abundance in wheat kernels. White flour comes from the endosperm, which makes up around 83% of the weight of the kernel. Most of the protein, carbohydrates, iron, and various B-complex vitamins, including thiamine, niacin, and riboflavin, are found in the endosperm of the entire kernel. Approximately 14.5% of the kernel's weight is composed of bran containing small amounts of protein. Whole wheat contains large amounts of the B-complex vitamins, trace minerals, and indigestible cellulose fiber known as dietary fiber. Wheat germ is the embryo of a wheat kernel that contain high levels of protein, lipids, and several B vitamins. The efficiency of the separation process between the germ, bran, and endosperm of the wheat grain is determined by the milling process which affects the nutritional value of food products made from wheat. It is well recognized that the form, size, texture, density, and chemical composition of wheat grains all have an impact on the milling process. To mill wheat, various techniques are used, including stone milling, roller milling, jet milling, ultrafine milling, and hammer milling. The refined wheat flour obtained from this process is utilized to make baked goods and other food items that appeal to consumers because of their flavor, texture, and appearance.

The term wheat quality is distinctly acknowledged from farmers to the consumers including millers, bakers. Wheat grain components such as proteins, carbohydrates, vitamins and minerals are linked to and influence the technical wheat quality for different products. The main traits that can be focused to understand wheat quality are grain hardness, hectoliter mass, falling number, grain color, protein, amylose, Fe and Zn contents. Grain protein content varies from 7% to 18% with gluten as main component. Gluten is comprised of gliadins contributing mainly to extensibility, viscosity and high molecular weight (HMW-Gs) and low molecular weight glutenins (LMW-Gs).



Weak, medium and strong gluten give different strengths to dough and therefore end-use product is accordingly determined as high level of strong gluten is suitable for pasta making while weak gluten is used for cookies and cakes. The end-use quality of wheat is also characterized by dough rheological properties namely, water absorption, dough stability, dough development time, dough extensibility, resistance to deformation, and flour viscosity, which can be well estimated using available instruments such as- farinograph, alveograph, extensograph, rapid visco analyzer.

Enhancing the quality of wheat grain is a paramount objective, as it directly impacts the nutritional value, milling, and baking characteristics. Quality improvement depends on understanding genetic control & diversity associated with quality traits, effects of G x E interactions on the expression of quality traits, improving specific genotypic quality traits (hardness, gluten strength and extensibility, etc.) and intensified use of marker-assisted selection (MAS) to screen for genes or alleles affecting quality traits. The genomic approaches including Genome Sequencing, Genome-wide Association Studies (GWAS), Quantitative Trait Loci (QTL) Mapping, Marker-Assisted Selection (MAS), Marker-assisted recurrent selection (MARS), Genomic Selection, omics technology, and Genomic Databases provide valuable tools for crop scientists and breeders to enhance not just produce but also crop quality and resilience to environmental challenges. The two main characteristics that impact wheat's economic worth are its grain protein content and yield. Nonetheless, the majority of research points to a negative correlation between these two characteristics in most cereals, including wheat. Finding independent QTL for these two traits and incorporating them into breeding programs through MAS should be one method to concurrently increase GPC and grain yield without substantially reducing grain production. Recent genomic efforts using data from hexaploid wheat like Chinese Spring (CS) have unveiled crucial insights on glutenin and gliadin genes. Total of 106 QTLs for 13 quality traits including grain protein content (GPC), sedimentation value (SV), farinograph parameters (WA, DT, ST), falling number (FN), and starch pasting properties (PV, TV, FV, BD, SB, PTi, PTe) were mapped across the 21 chromosomes.

Insufficient diversity in daily food intake has been identified as a key factor contributing to the rise of malnutrition and hidden hunger, particularly in developing countries. To proactively tackle this concern, it is recommended to enhance the micronutrient levels in staple crops such as wheat through fortification. This approach can potentially contribute to a more sustainable solution for improving the nutritional value of our food supply. With tremendous human resource and emerging food processing technologies, India has a large scope to develop instant food industries, thus, the Indian wheat programme has to strengthen a systematic breeding programme to improve nutritional and industrial quality to meet requirements of domestic and international market. Efforts are in progress to improve nutritional traits beta-carotene, protein content, iron and zinc content and health safe wheat. Food processing industries can take maximum benefit from superior varieties of wheat if procurement and processing of grains at market level is attended with special care. Small-scale industries for wheat-based value added products also needs to be encouraged in the rural sector to improve livelihood of farmers especially of rural woman.



Invited Paper



Pre-breeding approaches for munificent utilization of the wild and related species for the diversification of traits in rapeseed mustard

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Indian Mustard (*Brassica juncea*, $2n=36$, AABB) is an important oilseed crop in India. It is an amphidiploid in nature and is naturally derived from the diploid progenitor species *B. rapa* and *B. nigra*. *Brassica juncea* covers more than 90% of the cultivated oilseed Brassica species. India ranks second in acreage (19.81%) and fourth in rapeseed-mustard production (10.37%). Rapeseed-mustard's total area and productivity from 2019-20 were 35.95 MHA and 1990 kg/ha, respectively and oilseed production was 33.21 Mt. India is now self-sufficient in food grain production, but we still depend on imported vegetable oil. Statistics for the year 2020-21 reveal that India imported approx. 13.53 million tonnes of vegetable oil worth Rs. 1.17 lakh crore.

There is a need to develop high-yielding varieties by utilizing diverse germplasm lines to give us more chances to identify and select better parents in the breeding program. The occurrence of wide genetic diversity in the germplasm of a crop guarantees its further improvement and development for desired traits. However, the curve of Brassica improvement regarding the economic yield is in a flattening phase, and it is due to the lack of genetic diversity in the primary gene pool of cultivated amphidiploid species. A low genetic base in the germplasm pool is limiting the scope of further improvement and exclusively retarding the potentiality of yield enhancement. It imposes genetic sealing to improve agronomically important traits. *Brassica juncea* (Indian mustard) is the predominant crop in the Indian oilseed sector. Still, most of the present improved cultivars of Indian mustard are derived from one or few common parents and its derivatives and so have a very narrow genetic base. Therefore, broadening its genetic base for sustainable and successful oilseed breeding programmes in India is imperative. Therefore, there is an urgent need to broaden the genetic base of Indian mustard to develop new cultivars with enhanced yield and stress tolerance.

Pre-breeding encompasses activities that transfer desirable genes and traits from non-adapted materials, which cannot be directly used in breeding programs, to an intermediate set of materials that breeders can employ to develop new varieties for farmers. The primary goal of pre-breeding is to isolate valuable genetic characteristics, such as disease resistance, from unadapted sources like crop wild relatives (CWR) and utilize diverse germplasms to introduce these traits into breeding lines that can be readily crossed with modern elite varieties. At the same time, the diploid species have a vast diversity that can be further harvested to enhance the diversity of the Brassica amphidiploid species and further utilize this in improving these crops. For this, the resynthesis



of these amphidiploid species is a unique tool for utilizing the parental diploid species genetic diversity by wide hybridization and amphidiploidization. Wide hybridization is used to broaden genetic diversity by either producing new species or can be used for introgressing specific traits between species. Usually, hybridization between distant relatives in natural conditions rarely occurs, which justifies conducting such hybridizations under controlled conditions.

In addition to potential challenges in producing hybrids, introducing desired genetic material from wild relatives into the crop can also be complex. Introgression, or “introgressive hybridization,” involves incorporating alleles from one species into the gene pool of another, usually through hybridization and backcrossing. Creating introgression lines is a multi-step process. Initially, a cross is made between the cultivated species and the desired wild relative. After obtaining true F_1 hybrids, multiple backcross generations with the recurrent parent are carried out, with selection for the desired trait and possibly for agronomic traits. The number of backcross generations needed depends on factors like the frequency of recombination between the wild relative and the crop genome, the ease of eliminating excess wild relative chromosomes, and the fertility of the resulting progeny.

Furthermore, researchers focus on increasing Brassica's productivity by generating genetic diversity through traditional and modern techniques. One such technique is mutation breeding, which involves inducing mutations in plant DNA through methods like chemical treatments or radiation. These induced mutations can lead to the development of new traits and characteristics, ultimately enhancing the genetic diversity of Brassica crops. This approach also allows researchers to explore and select desirable traits that can improve crop yield, disease resistance, or nutritional value.

ICAR-NIPB has been working on developing genetic stocks since the institute's inception. We utilized CWRs to develop Synthetic amphidiploids species and total of few synthetic amphidiploids have been developed at ICAR-NIPB, Delhi, utilizing *Diplotaxis eruroides*, *Brassica oxyrhina*, *Diplotaxis muralis*, *Erucastrum gallicum*, *Erucastrum canariense*, *Erucastrum lyratus*. These synthetic amphidiploid species will serve as the intermediate transition hybrid for transferring the genes from the diploid wild species to amphidiploid *B. juncea*, which is not possible or very difficult directly. These lines are being used to develop introgression lines in *B. juncea*. One introgression population of *B. juncea* has been developed for *Alternaria* resistance from wild species *Diplotaxis eruroides*, which is in an advanced stage of BC_2F_{12} generations and exhibiting a high genetic diversity along with the *Alternaria* blight resistance. During the past decade, we have developed and characterized 92 advanced and 27 early-generation resynthesized *Brassica juncea* lines using its progenitor species, viz., *B. rapa* and *B. nigra*. We have also conducted a study to evaluate the radio sensitivity of *Brassica* wild species, diploid, amphidiploid, and synthetic amphihaploid seeds for gamma irradiations to determine the growth reduction dose (GR_{50}). The seeds were exposed to different doses of gamma irradiation and the effect of induced mutagenesis was seen on seedling length, germination, and survival percentage, which were further analyzed for variance for determining GR_{50} . This established dose can be utilized in large-scale mutagenesis programs to create genetic variability in mustard. In addition, we crossed the diploid progenitor species of *B. juncea* viz. *B. rapa* ($2n=20$) and *B. nigra* ($2n=16$) to obtain the amphihaploid hybrid seeds with AB, $n=18$ chromosomes. These amphihaploid F_1 seeds were subjected to gamma irradiation at 900 Gy dose followed by the colchicine treatment for



chromosomal doubling. This created enormous genetic variability clearly visible in amphidiploid (S_1M_2) plants. The material generated is utilized in various abiotic and biotic stress tolerance programs. So, the pre-breeding will be very effective for the creating the huge diversity and it can be utilised for the developement of the improved varieties after proper charaterization.

Keywords: Indian mustard, synthetic *B. juncea*, introgression, induced mutagenesis, climate resilience.

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IP 02

Characterization of local landraces of rice of Bihar using morphological descriptors and SSR molecular markers

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Introduction

Rice is the world's single most important food crop and a primary food for more than a third of the world's population. There are three subspecies of *Oryza sativa*, namely: *indica*, *japonica* and *javanica*. It is grown under diverse ecologies over wide geographical range. Globally, it is grown over an area of 161 million hectares with an annual production of 678 million tons. In India, rice is grown on nearly 43.97 million hectares with the production of 112.91 tonnes and productivity of 2.57 tones/ha. In India, rice is grown in almost all the states like, Andhra Pradesh, Bihar, U.P.,



M.P. and West-Bengal. In Bihar total land under rice cultivation is nearly 3.31 million hectares with production of 8.09 million tonnes with an average productivity of 2.45 tonnes per hectare. Asian farmers have selected and maintained a vast array of rice landraces. Landraces, plays a very important role in the local food security and sustainable development of agriculture, in addition to their significance as genetic resource for rice genetic improvement. Landraces and wild species possess immense potential of most valuable genes which can be effectively utilized in the present day breeding programmes. In this respect, the present study was designed with 23 Rice genotypes using Agro- morphological traits and Molecular markers for characterization.

Material and methods

The present investigation was carried out with the objective of Distinctiveness, Uniformity and Stability (DUS) characterization of Rice landraces of Bihar by morphological descriptors and molecular markers. The field experiment was carried out with twenty- three landraces of Bihar using thirty-three agro-morphological traits, during kharif 2021 in Randomised Block Design with three replications.

Morphological Characterization

For morphological characterization of genotypes plants were recorded at different growth stages as per DUS test guidelines on Rice issued by IIRR. Besides, observations on agro-economic metric traits were recorded on 5 randomly selected plants from middle row of each plot.

Molecular Characterization

For molecular characterization five-gram seed from each of the entry was germinated and then sown in earthen pots for growth and subsequent DNA extraction. The genomic DNA was extracted for molecular characterization studies using the CTAB method of **Doyle and Doyle (1990)** with some modifications and quantified (separation and purification) using gel electrophoresis. The fragments were amplified in PCR using SSR primers. Molecular size (bp) of amplified DNA fragment was determined by the DNA ladder marker. Polymorphism information content (PIC) of the SSR markers was obtained by calculating the value according to the formula as described by Anderson *et al.* (1993).

Statistical Analysis

The morphological traits (31) investigated in this study were assessed visually and no statistical method was used for the interpretation of visually assessed characteristics and their different states of expression were directly used to assess distinctiveness. The measurable traits (17) were interpreted by statistical methods to deduce information on variability estimates.

Results and Discussion

The present investigation was undertaken with the objective of Distinctiveness, Uniformity and Stability (DUS) characterization of twenty- three Rice landraces of Bihar using thirty-three agro-morphological descriptors and fifteen SSR primers. The mean performance of genotype showed a wide range of variation for most of characters amongst genotypes. Amongst the visually assessed characteristics, 6 were found to be monomorphic, 6 were dimorphic and rest 20 were found to be



polymorphic. Two measurable characters 1000 grain weight and length of leaf blade showed high polymorphic nature. The amplification of genomic DNA using fifteen SSR primer pairs exhibited different levels of polymorphism among the twenty-three rice genotypes under evaluation, which allowed unique genotyping of twenty-three entries included in the analysis. Microsatellite marker based analysis revealed unique or variety specific allele which could be useful as DNA fingerprints in the identification and characterization of these landraces of rice.

IP 03

Dissecting genetic variability for salt tolerance in pigeonpea

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Pigeonpea (*Cajanus cajan* L.) is a highly consumed (split pulse), nutritious (dietary protein), ethnobotanical (Qasim et al. 2014), and medicinal (Upadhyay et al. 2010; Varshney et al. 2012) legume that is consumed widely in about 80 tropical and subtropical nations. The crop is mostly rainfed and grows in diverse agro-climatic settings. As such, it is susceptible to various edaphic pressures, particularly those linked to moisture and salinity over its life cycle, which can negatively impact crop performance and output. According to Qadir et al. (2014), salinity in soil or water severely threatens crop productivity and yield, resulting in yearly losses of US \$27.3 billion globally. The primary causes of this severe stress include nutritional imbalances, ion toxicity, and physiological drought ((Hasegawa et al. 2000, Murphy et al. 2003, Islam et al. 2008). Because of the fluctuation of salt concentration in the field (Richards 1983; Shannon and Noble 1995; Daniels et al. 2001) and its interaction with other environmental factors such as temperature, soil fertility, availability and kind of irrigation water, light intensity, and transpiration losses, evaluating field performance under saline conditions is practically complex.

However, the best approach would be to screen first in hydroponics and then later in field circumstances to identify tolerant genotypes of salt. The developmental stage, amount, and length of salt exposure all influence a plant's response to salinity. It was discovered that plants are more sensitive to saltwater during the seedling stage, and 80 mM was the threshold level that distinguished between the genotypes of pigeonpeas that were salt tolerant (Joshi et al. 2022). The intricacy of the salt tolerance mechanism and the extensive range in genotype performance make it difficult to choose a plant efficiently based on a single trait's response or using basic statistics. Thus, it is essential to consider physiological and biochemical parameters for genotype and how it reacts to salt stress. (Ahmad Muhammad, 2004)

Screening as many lines as is practically feasible and choosing salt-tolerant genotypes are required to help plant breeders understand the morphological response and physiological mechanisms underlying plant salinity tolerance and to aid in developing cultivars tolerant to salt stress. Various characteristics have been used to assess salt, including seedling survivability, salt reaction score, fresh weight, dry weight, Na⁺, K⁺ levels, hydrogen peroxide production, and antioxidant activities. Therefore, a set of one hundred and fifty-one distinct pigeonpea genotypes were tested at the seedling stage based on 15 morphological and physiological traits, along with anatomical dissection to identify salt tolerant genotypes. Multiple statistical techniques were



employed to obtain more reliable selection parameters for identifying the more relevant traits and salt-tolerant lines. Five groups of genotypes have been identified based on visual observations: the salinity reactivity score and the percentage of seedling survivability. With over 80% seedling survivability and an average salinity reaction score ranging from 1 to 1.33, seven genotypes—BDN-708, JKM-189, ICP 14104, BDN-716, Phule Rajeshwary, ICP 15873, and TV-1—have shown strong salt tolerance among these geno. Salt stress resulted in only slight reductions in traits including FW, DW, SL, and RL for these specific genotypes.

On the other hand, sixty-three genotypes—such as HY3C, ICP 15667, ICPL 87091, ICP 6973, Sel. ICP 10509, ICP 13193, and others—lie in the very salt-sensitive group and exhibit over 90% mortality and an average SR score of greater than 4. Furthermore, fresh weight, dry weight, shoot length and root length were all significantly decreased due to salt stress.

IP 04

Evaluation of sesame (*Sesamum indicum* L.) genotype for determinate and semi - determinate character

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Sesame (*Sesamum indicum* L.) is one of the most important oilseed crop and also the oldest crop known to humanity. It is a short duration crop grown throughout the year. Because of high presence of antioxidants, sesame seeds are known as “seed of immortality”. Sesame crop is indeterminate in nature and its after effect is non-synchronous maturity and shattering effect. With the view of above character of this crop we proceed for the study of determinate and semi-determinate sesame genotypes. Experiment of Sesame (*Sesamum indicum* L.) was conducted at Bihar Agricultural University, Sabour, Bihar in the year 2022 and 2023 during summer season. Trial was conducted with 24 genotypes including two national checks (GT-10, TKG-22). The trial was conducted in randomized block design in three replications. The data were recorded for flowering period (days to end of flowering – days to beginning of flowering), maturity period (days to maturity- days to terminal flowering), days to physiological maturity, seed per capsule, test weight, thickness of mesocarp and yield per hectare. Genotypes has been categorised on the basis of flowering duration, maturity period and thickness of mesocarp. On the basis of above data lowest flowering period was observed for RT-54, RT-103, RT-125 and Sabour til-1 whereas maturity period after terminal flowering recorded less than 10 days for RT-54, RT-103, Sabour til-1, BRT-08, BRT-09, and BRT-10-1. Mesocarp thickness was classified as per DUS guidelines; thin and thick. Thin mesocarp was observed in Sabour Til-1, BRT-08, BRT-09, BRT-10-1 and Subhra. Physiological maturity range was in between 77 to 108 days. Seeds per capsule were also found significantly superior to checks. Data of other characters recorded and statistical analysed. Genotype which shows less flowering duration and maturity duration have significant positive effect in synchronised maturity which leads to minimise shattering effect and thin mesocarp reduces the maturity period was observed.

Key Words : determinate, maturity period, flowering period and semi-determinate

Employing QTL-meta-analysis for improving abiotic stress tolerance in rice

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A 2.4% yearly increase in agricultural productivity is required to meet the world's projected food demand. Growing enough food to feed a world population that is constantly expanding on less land, while contending with increased competition for labor, energy, and water due to growing demands from non-agricultural sectors, fast urbanization, and climate-related challenges, has been a major worldwide concern in recent times. Almost half of the world's population depends on rice as a staple diet, and for nearly one-fifth of those who cultivate, it provides a secure source of income. 20% of the calories consumed by over >4.5 billion individuals in Asia, Africa, and Latin America come from rice. According to the International Food Policy Research Institute (IFPRI), climate change would cause a 12–14% drop in world rice production by the year 2050 when compared to 2000. Furthermore, it is anticipated that between 2010 and 2035, rice consumption in Asia will rise from 388 to 465 million tonnes. In the upcoming ten years, an additional 8–10 million tons of rice must be produced each year to close the gap between supply and demand (Khedwal et al. 2023).

Growing concern is there over the sustainability of rice production in the puddled transplanted state, which accounts for more than 70% of rice production in Asia. Direct-seeded rice has the potential to become a sustainable method of producing rice that addresses the efficient use of all resources, including land, labor, water, energy, and chemicals, along with shorter crop duration, resolving edaphic conflicts, a smaller environmental footprint, and resilience building. In direct seeded rice (DSR), the pre-germinated seed is sown either wet (in puddles on the soil's surface), dry (on a prepared seedbed), or in standing water (in water seeding). Several Southeast Asian nations have switched from cultivating TPR to DSR in recent years). Although there are several benefits to DSR over PTR that have led to this paradigm shift, some major drawbacks include poor crop establishment, high weed infestation, crop lodging because of insufficient root anchorage, micronutrient deficiencies, high seed rate, and increased susceptibility to diseases and soil-borne pathogens, salinity and drought situations during cropping. There is the non-availability of specific varieties purposely limits the adaptability and yield potential vis-à-vis an ideal plant type for realizing maximum genotypic potential under direct seeded rice conditions. The lack of systematic understanding regarding ideal plant types under DSR ecology caused this. The current TPR cultivars don't seem well suited for seedling growth in a microenvironment that is initially oxygen-depleted, i.e., under anaerobic conditions. The widespread adaptation of direct seeded rice is therefore severely limited, leading farmers to frequently turn to the expensive technique of raising the seeding rate for DSR by two or three times.



The world is currently dealing with climate anomalies that it has never seen before. According to Prakash et al. (2020), soil salinity is one of the most enduring issues that is becoming worse due to human activity, excessive use of contaminated water, abuse of pesticides and fertilizers, flooding of seawater, irregular rainfall patterns, etc. About 21.5 million hectares (saline = 12 million ha and alkaline/sodic = 9.5 million ha) of soil are damaged by salt in Asia alone (CSSRI Vision Document – 2050; <https://cssri.res.in/vision-2050/>), where rice is most adaptable. Rice can be produced anywhere from below sea level to around 2,500 meters above mean sea level. An estimate states that the area affected by soil salinity will rise from 12 million hectares to 16.2 million hectares in India alone (CSSRI Vision Document - 2050). This has made it harder to grow rice and made all problematic soils unsuitable for agricultural production. Several agromorphological and physiological phenomena, including decreased plant height, root growth, unstable ionic balance in cells, high salt accumulation, decreased metabolic activity, ionic toxicity, and decreased nutrient uptake, are all impacted by soil salinity and have an impact on rice yield. The primary factor affecting plant growth is the physiological drought situation caused by soil ions that affect osmosis, nitrogen exchange, and water uptake. While rice plants are vulnerable to salinity throughout their whole life cycle, salinity is thought to be extremely harmful during the seedling and reproductive phases. The growth and development of rice seedlings are impeded by soil and water salinity during the seedling stage, which consequently affects the overall plant output. Salinity during the reproductive stage reduces pollen viability, spikelet fertility, and photosynthetic ability, and creates ionic toxicity, all of which lead to a decrease in output. The degree of variety in saline tolerance exhibited by various rice genotypes, which include landraces, cultivars, and variations, is evident in the seedling and reproductive stages of rice growth. It is astounding to see how different rice genotypes respond to salinity at different growth stages in diverse ways. It has been discovered that several rice landraces can withstand elevated saline levels, which makes them useful for enhancing contemporary rice cultivators. Pokkali, Kasalath, Sadri, Tampha, Nona Bokra, Bengal, Jiucuiqing, Kolajoha, and other rice landraces are included in this. It may be possible to trace and analyze the genetics of rice's salinity resistance using these landraces (Snehi et al., 2022).

Breeders are now better able to navigate the obstacles of modern crop breeding, thanks to the assistance of genomics in plant breeding. Plant breeding today has benefited from the ease with which complicated traits like salt tolerance and anaerobic germination may be dissected thanks to robust and consistent genotyping and phenotyping. Many main and minor QTLs have been identified as a result of numerous genetic research that was carried out to determine the genes/QTLs controlling rice's ability to withstand salinity and germination stage oxygen deficiency. A salinity-tolerant landrace named Pokkali provided the salinity tolerance QTL known as *SALTOL* (chromosome 1) at the seedling stage. This QTL has been utilized to create salinity-tolerant cultivars by marker-assisted backcross breeding in the recent past. It has a gene named *SKCI* that controls potassium homeostasis in rice plants under salt stress. A number of significant and minor QTLs for several attributes in rice have been identified utilizing biparental population and association panels through QTL mapping research conducted in recent years (Ganie et al. 2019). Similarly, to date only two major QTLs *qAG9-2* (*OsTPP7*) in “Khao Hlan On” and *qAG7.1* in “Kharsu80A” have been used in the breeding program, thus there is an urgent need to mine and utilize robust QTLs for precision breeding.



Monitoring a large-effect QTL in genomics-assisted breeding is a pretty simple process. The application of these QTLs in breeding programs may be restricted by the very broad confidence interval that has been anticipated in a number of QTL mapping investigations. However, cloning and the identification of the underlying gene linked to the characteristic present in that QTL interval are also being delayed by a huge confidence interval. As a result, we need to use a methodology to find a consensus region across multiple research that influences a certain characteristic, lowering the QTL's confidence interval and identifying a Meta-QTL. There have been numerous QTL mapping experiments conducted on rice that control salt tolerance during the seedling and reproductive stages. In breeding programs controlling salinity tolerance at the seedling stage of rice, breeders have so far been successful in using *SALTOL* QTL. There is not much detailed research on the meta-QTL analysis influencing rice's ability to withstand salinity as well as anaerobic germination. In order to identify genomic regions harboring consensus QTLs governing salinity tolerance and for anaerobic germination, studies were carried out by our team. Our study has focused on the prediction and validation of Meta-QTLs governing salinity tolerance along with anaerobic germination in rice. A group of characteristics influencing or regulating these traits have been taken into consideration for examination. Meta-QTL (MQTL) analysis is a statistical method that combines the examination of many QTLs associated with target traits to identify consensus genomic regions. For predicting meta-QTLs for anaerobic germination in rice, the consensus rice genetic map was projected with 240 reported QTLs associated with anaerobic germination from 26 research. 46 Meta-QTLs, spread across all chromosomes but not on chromosome 12, were predicted by the study. 67% and 72% of MQTL had high weightage (>0.1) and low confidence interval ($<4\text{cM}$), respectively. The predicted MQTL ranged in weight from 0.06 to 0.46 and in confidence interval from 0.01 to 16.41. Moreover, gene ontology (GO) analysis was carried out after extracting all of the annotated genes found in MQTL regions from the IRGSP site. Significant results were obtained for a number of GO keywords, including protein serine/threonine kinase activity (GO:0004674) and lipid transport (GO:0006869). Afterward, a whole-transcriptomic expression dataset from NCBI for AG susceptible (IR42 and IR64) and tolerant (MR, KHO, Kharsu 80A, and Nanhi) genotypes was obtained, and 56 differentially expressed common genes (Tolerant vs. Susceptible) related to 21 MQTLs were found. The research will offer new perspectives on the genetic factors influencing rice's ability to withstand anaerobic germination. The MQTLs found in this study could be used to generate functional markers and use marker-assisted breeding to help rice acquire tolerance to anaerobic germination.

For predicting meta-QTLs for salt tolerance in rice, 34 QTL mapping studies with 696 unique QTLs on rice salinity tolerance at the seedling stage and 11 research with 219 unique QTLs on rice salinity tolerance at the reproductive stage are included. A total of 915 QTLs were selected in order to forecast, validate, and investigate the consensus genomic areas governing component traits. All twelve rice chromosomes had a total of 65 projected Meta-QTLs for the seedling stage and 49 for the reproductive stage. For validation, a set of 36 extremely important Meta-QTLs for the seedling stage and 25 for the reproductive stage were chosen, and microsatellite markers were employed to link them. Eight extreme genotypes were chosen out of thirty-two genotypes that were assessed for salinity tolerance at the seedling stage in hydroponics ($\text{EC} = 10.0 \text{ dSm}^{-1}$). Validation was performed on the seedling stage Meta-QTL MSQTL4.2 ($\sim 295.43\text{kb}$), which is located on chromosome 4 (Chr4:20680856-20986280) close to marker "RM5635." Based on functional annotation and previously published expression data, the candidate gene analysis has suggested that it is a protein that binds to the FAD binding domain of monooxygenase (*Os04g0423100*). It



is anticipated that this gene plays a role in the synthesis and conversion of ubiquinone, coenzyme transport metabolism, and energy. This Meta-QTL's underlying characteristics included leaf chlorophyll content, the concentration of sodium and potassium in roots and shoots, etc. The genetic area that has been found and confirmed is very important for rice breeding that tolerates salinity.

The consensus genomic regions identified by our studies are very robust and have the potential to be utilized for breeding programs through marker-assisted selection, genomic selection, and haplotype-based targeted breeding. The narrowed consensus regions can be targeted to dissect functional genes of component traits governing salinity tolerance and anaerobic germination.

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IP 06

Genome-wide analysis (GWAS) and haplotype gene analysis for vegetative stage drought tolerance in rice

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Abstract

In the rainfed rice agro-ecosystem, the most important limiting factor of rice yield is drought stress. Droughts are expected to become more frequent and severe as a result of climate change, putting more burden on rice production around the world. Even a transient drought stress can result in a considerable yield drop in rice. The vegetative stage drought stress is also regarded as significant for its effect on rice production and productivity because it inhibits leaf formation and

tillering, which affects ultimately the yield. Therefore, this research work has been carried out in order to better understand the genetics of vegetative stage drought tolerance and to identify QTL(s)/gene(s) associated with it in rice. The phenotyping of vegetative stage drought stress was carried out in 329 genotypes (320 genotypes and 6 checks of 3k panel along with Mahulata, CR143-2-2 and IR20) in summer 2023 using augmented RCB (randomized complete block design) at two different locations; drought experimental field of ICAR-NRRI, Cuttack and research cum experimental farm, IGKV, Raipur (under rain out shelter condition). All the parameters related to vegetative stage drought were recorded like plant height, number of tillers, number of leaves, leaf area, leaf rolling score, leaf tip drying score, chlorophyll content index and relative water content. Genome-Wide Association Studies (GWAS) analysis identified 12 major QTLs for six different traits such as leaf rolling, relative water content, plant height, leaf area, tiller number and leaf number. Further, haplotype gene analysis was also carried and identified six genes related to leaf rolling, relative water content, plant height, tiller number, leaf number and a gene responsible for nucleotide-binding. The two *indica* genotypes; TSAO SHENG LI 1 and PODIWEI were considered superior based on their representation in the superior haplotypes of the studied traits. These tolerant genotypes can be utilized in the breeding programs for the development of ideal varieties with vegetative stage drought tolerance. Furthermore, haplotypes breeding strategy can be implemented for the introgression of the superior haplotypes of the genes identified to be responsive to vegetative stage drought tolerance.

Key words: Candidate gene, GWAS, haplotype analysis, vegetative stage drought

METHODOLOGY

In summer-2023, 329 rice genotypes (320 genotypes of 3k panel and 6 checks along with Mahulata, CR143-2-2 and IR20) were phenotyped for vegetative stage drought stress at two locations; drought experimental field of ICAR-NRRI, Cuttack and research cum experimental farm, IGKV, Raipur (under rain out shelter condition). The following parameters related to vegetative stage drought stress were recorded like; plant height, number of tillers, number of leaves, leaf area, leaf rolling score, leaf tip drying score, chlorophyll content index and relative water content. The data were statistically analyzed to calculate genetic parameters and correlation among the traits. For GWAS analysis, genotype data were retrieved from SNP seek database (<https://snp-seek.irri.org/>). Further, identification of QTLs was performed in GAPIT using four different models; BLINK, FarmCPU, MLM and MLM.

The candidate genes were searched within the 200kb window (200kb upstream and 200kb downstream) of the detected significant SNPs using the Rice Annotation Project Database (RAPDB). The genes with annotations such as “hypothetical” and “non-protein coding transcript” were excluded from the identification of candidate gene analysis. Additionally, all the available research reports and other online resources were searched exhaustively for any information regarding the genes within the 200kb window. Then based on gene function and expression analysis data of RNA-sequencing, candidate genes were selected. Haplotypes between the significant associated loci in the candidate genes were manually identified and analyzed for their phenotypic mean significant difference using single factor ANOVA.



RESULTS

Analysis of variance of 329 rice genotypes of 3k- rice panel (including checks) showed significant variation among genotypes for all the traits under study for vegetative stage drought tolerance at both locations indicating presence of high genetic variability. High heritability coupled with high genetic advance as % of mean was observed in all the traits studied except number of tillers indicating that these traits were less influenced by environmental fluctuations and governed by additive gene action. Therefore, selection based on these traits will be rewarding under vegetative stage drought stress. The association of plant height was significant and positive with tiller number, leaf number and leaf area and number of tillers exhibited significant positive association with leaf number at both the locations. Likewise, at both locations, RWC is negatively correlated with both leaf tip drying and leaf rolling score, whereas, both leaf rolling and leaf tip drying score were positively associated with each other. The result of ANOVA showed significant variation among genotypes for all the traits studied at both locations indicating the presence of high genetic variability, which will be beneficial for the selection of breeding material. This finding was like the findings of Subedi *et al.* (2019) for plant height, leaf area and chlorophyll content. Kadam *et al.* (2018) reported the variation in grain yield, its components, and other related traits differ significantly between genotypes, treatments (non-stress and water-deficit stress conditions) and years.

GWAS analysis identified 12 major QTLs for six different traits such as leaf rolling, relative water content, plant height, leaf area, number of tillers per plant and leaf numbers per plant across multiple models (BLINK, FarmCPU, MLM and MLM). However, five QTLs were significantly associated with different vegetative stage drought parameters across multiple models with the highest PVE value were selected for the identification of candidate genes. These QTLs were distributed across chromosomes, one in chromosome 1 for leaf rolling (SNP_ 23715622), two in chromosome 2 for plant height (SNP_ 48944363) and relative water content (SNP_ 55632102), one in chromosome 3 for tiller number (SNP_ 102509308), and one in chromosome 8 for leaf number (SNP_ 263283231).

Based on gene function and expression analysis data from RNA sequencing, six candidate genes namely; Cytochrome P450 72A32 (*OsCYP72A32*) for leaf rolling, Sodium (Na⁺)/calcium (Ca²⁺) exchanger 5 (*OsNCX5.2*) for relative water content, SPX (SYG/PHO81/XPR1) domain gene 2 (*OsSPX2*) for plant height, a gene similar to ASL1 (*OsSTA104*) for tiller number, and two genes for leaf number *i.e.* RING-type E3 ubiquitin ligase 313 (*OsRING313*) and a gene responsible for nucleotide-binding, alpha-beta plait domain-containing protein coding (*Os08g0436000*) were identified which were involved in responsive to vegetative stage drought stress in rice. Further, based on their representation in the superior haplotypes of the studied traits, the two *indica* genotypes; TSAO SHENG and PODIWEE were considered superior and can be useful for future studies to design ideal plants with drought tolerance at the vegetative stage.

CONCLUSION

- GWAS analysis identified 12 major QTLs for six different traits related to vegetative stage drought stress such as leaf rolling, relative water content, plant height, leaf area, number of tillers per plant and leaf numbers per plant across multiple models. However, five QTLs with the highest PVE value were selected for the identification of candidate genes.

- Based on haplotypes analysis two *indica* genotypes; TSAO SHENG and PODIWEE were considered superior for future studies to design ideal varieties with drought tolerance at vegetative stage.
- Haplotypes breeding strategy can be implemented for the introgression of the superior haplotypes of the genes identified to be responsive to vegetative stage drought tolerance.

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IP 07

Deploying molecular tools for trait-specific improvement of pulses

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The availability of genome sequences in a wide range of crop plants over the past one and a half decades have opened up a plethora of knowledge-based new possibilities towards combining the strengths of phenotyping with genotyping. Integrating computer based powerful statistical tools and state-of-art analytical methods with robust experimental designs and breeding management systems have further made it easy to develop superior and climate resilient varieties of crop plants in addition to identifying the underlying genes controlling complex traits. The so called “orphan crops” such as pulses have been the most advantageous in this era which saw a boom of information with numerous varieties developed through direct or indirect deployment of molecular tools in their improvement. The introduction of DNA sequencing in the early 1980s, followed by development of polymerase chain reaction (PCR)-based methods for marker-assisted selection and subsequently the development and deployment of next-generation sequencing tools led to tremendous improvements in food legumes. Interestingly, the last decade witnessed the narrowing down of a diverse set of molecular markers techniques developed over the past 4 decades to a few most preferred and practically applicable DNA marker based techniques. Consequently, the emphasis is now more on deploying these techniques towards their cost-effective and result oriented deployment towards development of improved varieties of crop plants. There has been an exponential increase in availability of genomic resources and their effective deployment in trait



discovery and breeding. The availability of a wide array of molecular markers facilitated dissecting complex and polygenic traits hampering crop production using QTL mapping and genome wide association mapping approaches in crops like chickpea, urdbean, pigeonpea, common bean and soybean. Genomics-assisted breeding was deployed to its full might improving several traits in food legumes such as resistance to Fusarium wilt and ascochyta blight, and tolerance to drought in chickpea; Striga resistance and improved seed size in cowpea; resistance to rust, soybean mosaic virus, and low phytate in soybean; pyramiding of genes for resistance to ascochyta blight and anthracnose in lentil; introgression of powdery mildew resistance, lodging resistance, frost tolerance, and Aphanomyces root rot resistance in pea and resistance to common bacterial blight disease, rust, anthracnose, and angular leaf spot in common bean. Among the complex traits, QTL hotspot from ICC4958 was introgressed into Pusa 372 and JG 16 varieties of chickpea using the MABC approach. Likewise, the gene/QTL pyramiding efforts are also at an advanced stage in several legume crops such as in chickpea (fusarium wilt resistance + ascochyta blight resistance + drought tolerance), and cowpea (resistance to Striga + aphid + macrophomina root rot). Genomic prediction is now also increasingly being used in plant breeding. Nevertheless, this seems to be a start rather than the end and many more revolutions are in offing besides the marker assisted breeding technology. The only caution that needs to be adopted is that the technical advancements have to be put only to the welfare of the living beings and ultimately, the mankind is to be benefitted.

IP 08

Molecular and biochemical characterization of double low genotypes of indian mustard (*Brassica juncea* L.)

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ABSTRACT

Indian mustard (*Brassica juncea* L.) is the most important source of oilseed in India among other cultivated Oleiferous Brassicas like *B. rapa* and *B. napus*. Development of genotypes with improved nutritional qualities like low erucic acid (<2 %), high oleic acid (>40%), reduced linolenic acid (<12%), a ratio of 2:1 for ω -6 to ω -3 in the oil and <30 micromoles glucosinolate per gram of defatted seed meal with high antioxidants are highly desirable in Indian mustard. A set of forty-four advanced breeding lines of Indian mustard with double low (<2 % erucic acid in oil and < 30 micromole glucosinolate in seed meal) trait derived from cross [EC564648×(Rajat×NUD-HYJ3)], [NRCHB101×NUDHYJ5], [EC552573×(Varuna×NUDHYJ3)] and [NRCDR02×NUD-HYJ5] as well as quality check (PDZ1) and non-quality check (NRCHB101) were undergo genotyping for low erucic acid in oil and low glucosinolate content in seed meal using linked

molecular markers. The same set of genotypes were also characterized biochemically for oil and seed meal nutritional parameters (oil content, percentage fatty acids including erucic acid, beta carotene, antioxidants, flavonoid and glucosinolate content). Genotyping for low erucic acid using linked CAPS markers (CAPS591 and CAPS1265) for the gene *FAE1.1* revealed that digestion of PCR amplified product of CAPS591 marker with *Hpy99I* restriction enzyme resulted in one undigested fragment (432 bp) and two digested fragments (224 bp and 198 bp) for NRCHB101, whereas, a single undigested fragment of 432 bp for PDZ-1 and all the double low genotypes under study and digestion of PCR amplified product of CAPS1265 marker with *BglII* restriction enzyme resulted in one undigested fragment (427 bp) and two digested fragments (209bp and 198 bp) for PDZ-1 and all double low genotypes whereas, a single undigested fragment of 427 bp for NRCHB101; The PCR-based promoter marker for allele *FAE 1.2* resulted fragment of 534bp for high erucic acid check i.e. NRCHB101, while 399bp in low erucic acid check i.e. PDZ-1 and all double low genotypes under study. The result confirmed presence of low erucic acid linked gene *FAE1.1* and *FAE 1.2* in all the 44 genotypes. Genotyping for low glucosinolate content using two trait linked markers i.e., GER1 (*QTL-J2GsII*; Linkage group-A2) and GER-5 (*QTL-J3GsII*; Linkage group-A3) revealed that the marker GER-1 amplified allele of the size of 650 bp in PDZ-1 and in all double low genotypes, whereas, an allele of the size of 950 bp was observed in NRCHB101; Allele amplified by GER-5 marker was of the size of 310 bp in PDZ-1 and all double low genotypes, whereas, 350 bp in NRCHB101. The result confirmed presence of low glucosinolate linked QTLs in all the 44 genotypes. The same set of genotypes and checks were undergone nutritional profiling for oil and seed meal. The double zero genotypes, viz. DRMRQ4-7-23 (high oleic acid), DRMRQ1-11-32 (moderate linoleic acid with high oleic/linoleic ratio), DRMRQ4-5-25 (low linolenic acid with high ω -6/ ω -3 ratio), DRMRQ4-1-58 (high β -carotene content), DRMRQ 2-3-17 (high flavonoid content) and DRMRQ1-16-27 (high antioxidant) were reported to be nutritionally improved. The genetic parameter study revealed that flavonoid content exhibited highest GCV (34.74%) and oil content exhibited the lowest (0.83%) one. Traits like oleic acid, linoleic acid, linolenic acid, oleic/linoleic ratio, ω -6/ ω -3 ratio, antioxidant and β -carotene exhibited more than 90 percent heritability. These nutritionally enriched double zero genotypes have been deposited in NBPGR, New Delhi for further exploitation as important genetic resources for quality breeding in Indian mustard.

Key words: Double low, Linked molecular markers, Nutritional enrichment, Genetic parameters



Biofortification of rice for high iron and zinc contents in Jharkhand conditions

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Rice is one of the most important global staple food crop. On average, the grain comprises 80% starch, 7.5% protein, 0.5% ash, and 12% water. Though rice is the predominant source of energy, protein and micronutrients for more than 50% of the world population, it does not provide enough essential mineral nutrients to match human requirements. One third of the world population is at risk due to low dietary intake of Zn. Zinc and iron deficiency are recognized as major nutrient disorders in humans and its effects are more profound in children. Therefore, Zn and Fe deficiency is a chronic problem among human populations that have rice based diets. Raza Q. *et al.* (2020). Identification of the amount of genetic variability for Fe and Zn concentration in the germplasm is the initial step, then improving rice Fe and Zn concentration. Seventy entries were planted in three replications in Alpha lattice in GXE interaction trial at BAU, Research Farm under biofortified rice through Harvest Plus Challenge Programme under the collaboration of BAU and IRRI for developing high zinc and high iron rice varieties suitable for Eastern India including Jharkhand during *kharif* 2014. Micronutrient estimations were carried out using the XRF technology and cross checked with AAS/ICP in selected entries especially those that are highs for iron/zinc facilitated by Harvest Plus-ICRISAT. The entry no. 22 (SAPONYO), Fe 7.7 ppm and Zinc 20.7 ppm recorded maximum yield (38.14 q/ha) followed by entry no. 20 (PORA MEUNYA) Fe 7.7 ppm and zinc 22.7 ppm which yielded 33.45 q/ha. Consequently, new genetic and management strategies need to be developed to minimize Iron and Zn deficiency for people whose staple diet is rice and emphasis should be being given to nutritional aspects since micronutrient deficiency, especially of Zn and Fe, has become a global issue.

Keywords: Rice, Iron, Zinc, Biofortification, contents

Introduction:

Rice is most dominant crop of Jharkhand and it is grown in all agro- ecological conditions existing in 24 districts of the State. The total geographical area of state is 79.71 lakh ha which is 46% of undivided Bihar. The cultivation of different crops are restricted to only 25.0 lakh ha and out of which rice alone is cultivated in 18.20 lakh hectare during the wet season. This clearly speaks the importance of rice cultivation in socio-economic condition of Jharkhand. Moreover, it occupies more than 70% of total cultivated area as it is grown from Tanr-I, Tanr-II, Tanr-III, Don-III, Don-II and Don-I. The area of each category may be summarized as.

Sl.No.	Category	Sub Category	Area in lakh/ha.
1	Upland	Tanr-I to Tanr-III	5.0
2	Medium Land	Don-III & Don-II	9.0
3	Lowland	Don-I	4.0

Out of total cultivated area (18.0 lakh ha) under rice, only 2.0 lakh ha are direct seeded or broadcasted and remaining 16.0 lakh hectare are transplanted. The average rainfall of the State is 1380 mm in a year. But more than 83.5% of total rainfall is received in monsoon months starting from 15th June to 30th September but due to global warming and climate change not only the total amount of rainfall has been reduced but its distribution has also gone very erratic and uneven. In the month of July and August when more water is required for transplanting of rice, comparatively less rainfall is received which are effecting transplanting of rice in a very negative manner and when less water is required in the month of September and October, more rainfall is received. It means production of rice and other crops totally depend on rain received during monsoon months. Drought has become regular feature of the State and it is witnessed once in every three years. Area under assured irrigation is 12% and remaining 88% is total rainfed meaning thereby rainfed agriculture is the main feature of Jharkhand State. In such a situation, drought tolerant varieties of rice at least for upland and medium land and resistance to blast having many good agronomic traits are very much required so that farmers can harvest better yield even in drought like situation.

Micronutrient malnutrition, or hidden hunger, afflicts billions of people. It is caused by a lack of micronutrients in the diet. Fruits, vegetables, and animal products are rich in micronutrients, but these foods are often not available to the poor. Their daily diet consists mostly of a few inexpensive staple foods, such as rice, wheat, maize, etc, which have few micronutrients. The consequences, in terms of malnutrition and health, are devastating and can result in blindness, stunting, disease, and even death. Biofortification is an additional tool to current interventions, it complements other strategies such as supplementation, fortification and dietary diversity to reduce micronutrient malnutrition. Biofortification is a plant breeding technique used to increase the levels of micronutrients in staple food crops. In Harvest Plus we use plant breeding to enhance the levels of 3 micronutrients that are most limiting: vitamin A, iron and zinc to measurable impact on nutritional status at the public health level.

Further rice is the main crop which is in a food habit of State of Jharkhand. The varieties/hybrid of rice which are grown by farmers of State lacks in desired quantities of zinc and iron. Most of the varieties which are popular and grown are having zinc availability of 14.0 ppm/gm and 5.0-6.0 ppm/gm in iron. Similar result was given by Kappara S and *et al.* (2018). This is resulting to poor percentage of hemoglobin especially in ladies and problem of diaroohea in children. It has also been observed that less percentage of zinc available in cultivated varieties of rice is responsible for diaroohea and less availability of iron leads to problem of hemoglobin. Khan JA, *et al.* (2019) and Yoneyama T. *et al.* (2015). Considering the importance of rice in social economic condition and food habit in natives of State, the International Centre of Tropical Agricultural (CIAT) and International Food Policy Research Institute (IFPRI) had initiated a programme of biofortified rice through Harvest Plus Challenge with BAU and IRRI of following objectives:



- Zinc content in adapted cultivars and available breeding lines to be validated and justifies further development of biofortified rice with target enhanced expression of zinc. Positive correlation between iron and zinc content in rice grain allows simultaneous improvement.
- Transfer of high zinc density traits into high yielding adapted cultivars and/or generation of micronutrient density via exploiting transgressive segregation, maternal effects etc.
- Crosses directed to target agro-ecologies combining zinc density with traits relevant for variety adoption with particular environments will be conducted and early breeding populations developed.
- Best early and intermediate products are advanced towards final products following intensive selection and testing for attributes relevant for variety adoption in target agro-ecologies and micronutrient density.

Breeding strategy:

- High zinc content among the advanced breeding lines will be explored from locally developed and introduce sources and proceed for varietal release system.
- Existing widely grown mega-varieties will be converted into zinc dense versions
- New zinc-dense rice varieties will be developed through cross-breeding followed by trait directed selection

Materials and Methods:

Harvest Plus Challenge Programme was sanctioned by CIAT and IFPRI to BAU and IRRI in July 2013 for developing high zinc and high iron rice varieties suitable for Eastern India including Jharkhand. The IRRI had provided 62 lines of biofortified rice. The nursery was raised on 27.08.2013. The phenotypically superior genotypes were selected and identified at the time of flowering and all the required data on agronomical traits were recorded. Phenotypically superior selected/ identified genotypes were earmarked and number of crosses were made with the most popular or adapted variety like IR-64. The large number of crosses were made from a single cross so that sufficient quantities of F_1 's seed were produced. The seed of phenotypically superior genotypes, cross seed (F_1 s) were sent to Hyderabad for analysis of Zinc and Iron. Seventy entries were planted in three replications with plot size Plot Size : 4 x 0.8 m², Fertilizer: 80:60:40 NPK Kg/ha, Spacing : 15 x 20 cm in Alpha lattice. The Date of sowing was 11/7/2014 and date of transplanting: 12/8/2014.

Estimation of zinc and iron contents in rice grains:

Zinc (Zn) and Iron (Fe) contents of rice grain samples are determined by using Atomic Absorption Spectrophotometer (AAS). In this process the samples are digested by the application of di-acid mixture which includes nitric acid (HNO₃): and perchloric acid (HClO₄) in 2:1 ratio. Zinc and iron contents are estimated in the aliquot of seed extract by using Atomic Absorption Spectrophotometer (AAS) at 213.9 nm and 248.33nm respectively.

Results and Discussion:

The varietal differences were not significant. The entry no. 22 (SAPONYO), recorded maximum yield (38.14 q/ha). The iron content of the entry was 7.7 ppm and Zinc content was 20.7 ppm followed by entry no. 20 (PORA MEUNYA) where the iron content was 7.7 ppm and zinc content was 22.7 ppm which yielded 33.45 q/ha. Similar findings were suggested by Shilpa M Naik *et. al.* (2020) and Wang Y, *et al.* (2020).

Table:

Entry No.	Entry Name	Yield (q/ha)	DTF	Plant height	Fe (ppm)	Zinc (ppm)
20	PORA MEUNYA	33.45	96	83	7.7	22.7
37	TAKER AM	30.13	93	98	7.8	21.0
23	ROSHO	27.95	96	95	11.2	24.8
52	IR 82475-110-2-2-1-2	26.19	101	70	7.1	20.4
64	RP Bio 5477-NH 686	25.59	100	113	8.9	21.2
65	Swarna	14.57	99	67	5.9	16.4
68	IR 64	14.74	79	76	7.2	20.3
66	Sambha Mahsuri	9.47	105	73	6.2	22.7
67	MTU1010	16.15	96	104	7.0	15.6
70	Local check 2 (Naveen)	16.32	88	92	7.8	21.0
69	Local check 1 (Lalat)	16.52	110	102	5.0	17.6
CD		NS				
CV %		27.96				

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IP 10

CRISPR-Cas9 in yield improvement in rice

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The *Ideal plant architecture 1 (IPA1)* gene is found to be responsible for increased spikelet number and panicle length in rice (*Oryza sativa*) making it a suitable target for the development high-yielding rice varieties through genome editing. A *miR156* target site in the *IPA1* gene functions as negative regulator of yield related traits. Therefore, gRNA primers targeting *miR156* binding site in *IPA1* gene were designed and used for the development of IPA1-Cas9 construct through golden gate assay. Using *Agrobacterium* transformation, IPA1-Cas9 construct was transferred to the calli of popular *indica* rice variety – Swarna. The number of spikelets per panicle in the edited lines was found to be higher than the wild type. The edited lines showed highest increased number of spikelets per panicle (~223 nos). Similarly, mean number of panicle branches per plant was also more in edited lines than WT. This increase in spikelets number and panicle branches in edited lines resulted in the gain in the mean single panicle weight as well as single plant yield by at least 23 percent. Further, sequence analysis of the T2 plants also showed heterozygous/bi-allelic mutation in the plants. However, most of the editing was found to be substitution type rather than in/dels. Besides, one of the lines also showed chimeric mutations. As of the many plant related other traits, panicle architecture in edited lines was significantly improved. This includes improved in panicle length and number of panicle branches. The mean number of panicle branches and spikelet number per panicle were higher in all edited lines. This resulted in increased average single plant yield of ~23% in all edited lines compared to Swarna variety. Apart from yield characters, it is reported that *IPA1* gene also has role in regulating biotic and abiotic stress tolerance in rice. We performed the preliminary screening for sheath blight and bacterial blight pathogen. The actively growing plants of edited lines along with Swarna were artificially inoculated with the fungal pathogen and observed for symptoms, especially lesion length. Based on the symptom area, edited lines were showing some enhanced resistance to the pathogen than Swarna. Moreover, grain traits particularly grain length and width was found to be slightly different in the edited lines as compared to the parent variety Swarna. Therefore, this analysis showed IPA1 edited lines in Swarna not only improved yield but also biotic stress tolerance.

Prospects of early pigeonpea varieties in Jharkhand

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Introduction-

Pigeonpea occupies a prominent place in the Jharkhand agriculture. The total area of Pigeonpea in Jharkhand is 2.3 lakh hectares, and production is 240.0 thousand tons. The productivity of Pigeonpea in the state is (1049kg ha⁻¹). Mostly Late and medium duration varieties are preferred by the farmers. However, it causes grazing problem as it is only standing crop in the field. Although, early maturing (125-140 days) varieties are grown in various inter cropping systems along with cereals, millets and oilseed..

The productivity of Pigeonpea in Jharkhand has remained stagnant since last few decades. This is mainly due to lack of high yielding varieties grown in the regions and other major constraints including poor adaptability of the exiting varieties to different agro-ecological zones, erratic rainfall, non availability of quality seeds of the improved varieties and biotic stresses such as Fusarium wilt and sterility mosaic diseases, insect pests such as *Helicoverpa* pod borer, and *Maruca*. Drought is also a major bottleneck in Pigeonpea production. The trends of area, production and productivity fluctuates regularly in Jharkhand and it will remain fluctuating in Jharkhand due to higher and erratic rainfall, use of poor quality seed, non- adaptation of improved technologies and non-practicing of adequate plant protection measures by the poor farmers of the region. The research is conducted for early maturing genotypes to escape the high rain fall during flowering and pod initiation stage.

Results-

The several trials were carried out from 2016-2017 to till date where several early maturing genotypes were subjected to testing for yield and yield parameters including biotic factors (Wilt, Mosaic and Pod borer). In each year observation were recorded for grain yield, days to maturity, wilt percentage, pod borer percent and sterility mosaic. These observation for 2016-17 were found in the ranged of [yield(9.37 q – 13.43 q /ha), maturity (132-152 days), Wilt Incidence (5.0-21.6 %) , Mosaic (0.8-2.1 %) , for 2017-2018 [yield (5.55 q – 12.36 q/ha), maturity (117-143 days), Wilt incidence (1.0-3.1%),Mosaic (1.0-3.5%)],for 2018-19, yield (2.58-9.83 q/ha), maturity (105-122 days), wilt (2.5-18.5%) pod borer (2.1-7.7%) mosaic (2.5-18.5%), for 2019-20 [yield (4.65 q – 7.12 q/ha), maturity (112-163 days), Wilt (0.0-4.5%), pod borer (7.5-19.6%) ,Mosaic (2.2-20.8%)], for 2020-21, [yield (6.29-24.29 q/ha), maturity (161-196 days), wilt (6.8-56.9 %), pod borer (1.4-2.9%)],for 2021-22, [yield (4.61-14.98 q/ha), maturity (154-161 days), wilt (0.4-17.3%) ,pod borer (3.7-6.4 %) mosaic (0.3-1.1 %)].



Conclusion-

It was concluded in 6 year trials that yield varied between 2.58 to 24.29 q/ha, maturity 105-196 days. This suggests that wide variation in yield and days to maturity was due to several abiotic (Rainfall, Climate, soil condition) and biotic factors (Pest such as *Helicoverpa* pod borer, and *Maruca*, and diseases such as Fusarium wilt and sterility mosaic). This wide variation can be exploited in breeding for early maturing varieties of Pigeonpea with resistance to biotic and abiotic stress as early maturing varieties can increase the cropping intensity and land will be made available for Rabi crop as well which will further enhance the economy of farmers.

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Soybean in Jharkhand under farmers perspective

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Soybean (*Glycine max* L. (Merrill)), popularly known as golden bean, is one of the leading oilseed crops grown worldwide in terms of production and foreign trade. It is mainly produced for oil and protein, which is used as edible oil, protein source and livestock feed. Soybean is native to East Asia, probably North and Central part of Asia and it has been in cultivation in China since, 4000 years (Hymowitz, 1970). Later it had spread to Korea and Japan about 2000 years back. Yellow seeded soybean was introduced into India during early seventies of the 20th century and has been growing as an annual crop propagated through seed. Soybean belongs to Genus *Glycine*, which is a member of the family Leguminosae, sub family Papilionaceae and tribe Phaseoleae. Soybean is divided into two subgenera, *Glycine* (perennials) and *Soja* (annuals). In India, Soybean has emerged as one of the major oilseeds and revolutionized rural economy and lifted the socio-economic status of soybean farmers. The total area under soybean worldwide is 129.52 million hectares with production of about 370.24 million metric tonnes while in global scenario of soybean production, India's rank fifth and in acreage fourth, occupying 11.40 million hectares area with production of 12.41 million tonnes and productivity 1084 kg/ha. (Ministry of Agriculture & Farmers Welfare, New Delhi 2021-22).

This gap has however been narrowing down in recent years with the efforts of the agricultural scientist. Still much more is to be done for bringing the productivity of soybean in India to level of world average or even more to meet the protein requirement of predominantly vegetarian population to protect the rapidly increasing population from malnutritional diseases. It is said that Chinese infants using soybean milk in place of cow's milk are practically free from rickets. Recent studies indicate that consumption of soybean reduces cancer, blood serum cholesterol, osteoporosis and heart disease (Birt et al., 2004). Soybean has termed as wonder bean because it contains 40 % good quality protein rich in Lysine and 20% oil high in essential fatty acids omega-6 and Omega-3. Additionally, Soybean is very good source of vitamin B complex and minerals. It also contains phytochemicals known as isoflavones which protect human body against chronic diseases such as cancer, diabetes, osteoporosis, blood pressure, coronary heart disease etc. In India it is mainly grown in Madhya Pradesh, Maharashtra and Gujarat state.

Jharkhand is largely inhabited by tribal population. The whole region is socio-economically backward, quite a large section of tribal population is still practicing primitive type of agriculture. Among tribals and poor farmers of the state the nutritional security is an important issue which has to be met through low cost and high quality foods. In view of the high nutritional advantage of soybean through value addition such as soymilk, tofu, soy-flour etc, there is a vast scope to supplement to nutritional demand in rural as well as urban household diet and contribute to alleviation of malnutrition of majority, particularly child malnutrition. Increased production and consumption of Soybean is one of the best way to overcome protein malnutrition among poor tribal farmers of Jharkhand. Besides it can be a potent candidate crop for diversification in the rice cultivation area during kharif season in the state.

In Jharkhand, till date soybean occupies only 1043 ha area with production of 604 tonnes and productivity 579 kg/ha though the soil and climatic condition of Jharkhand is very much suitable for this crop. The productivity level of soybean in Jharkhand is very low. The major concern today is the low productivity of soybean in the state which is around 0.6 t / ha. One of the major causes of low productivity is limited availability of soybean varieties suitable for the state. Soybean has the potential to address the food and nutritional security concerns of the farmers of state provided development of varieties suitable for agro-ecological condition of Jharkhand and appropriate scientific management are put in place in a mission mode.

As per PPV & FR Act. a new variety should be distinct from other varieties; stable genetically as well as there must be uniformity in the characteristics. So, development of high yielding promising varieties of soybean is the utmost need for the farmers of the state which could perform well in all the agro-climatic condition Jharkhand and show consistency in yield as well as quality traits.

Considering the importance of development of high yielding improved varieties of Soybean for Jharkhand, Scientists of Birsa Agricultural University, Ranchi working on Soybean have developed a high yielding variety of Soybean, namely, Birsa Soybean-3 (BAUS-40) in the year 2021 after extensive testing in different co-ordinated trials, station trial, multilocation trials over the years and locations. It is a cross of Bragg and JS 71-05 and has been developed by pedigree method. Its performance was also evaluated in front line demonstration. The variety, Birsa Soybean-3 has yield potential of 25-30 q/ha. It is found superior to the existing varieties Birsa soybean -1, Birsa



safed soybean-2, RKS-18 and JS 97-52 in yield. It matures in 115-120 days. It has 38.80 per cent protein and 19.50 per cent oil content. For the character seed yield, 100 seed weight and pod per plant, it performed the best with plant population 0.4 m/ha and 45 cm row spacing. It performed well under severe stress condition during two consecutive years and found tolerant to drought condition. It is found tolerant to major disease viz., Rhizoctonia Aerial Web Blight, Frogeye Leaf Spot and Cercospora Leaf Spot. It is also tolerant to major pest prevailing in state viz., Bihar hairy caterpillar and Leaf roller in Jharkhand. In farmer field Birsa Soybean-3 showed 10-38% increase in yield over farmer's variety over the year 2018-2020. Increased production and consumption of Soybean is one of the best way to overcome protein malnutrition among poor tribal farmers of Jharkhand. Besides it can be a potent candidate crop for diversification in the rice cultivation area during kharif season in the state.

Key words: Soybean, low productivity, malnutrition, upliftment of socio-economic condition of farmers, Birsa Soybean-3 : a new variety .

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Millets – smart food for future: constraints, opportunities and strategies to increase production and consumption

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Millets are a group of highly variable small seeded grasses, widely grown around the world as cereal crop or grain for fodder and human food. Millets may have been consumed by humans for 7000 years. The crop is favoured due to its productivity and short growing season under dry, high temperature conditions. India is the largest producer of millet as of 2021, with a total share of 41%, followed by Nigeria (~12%) and China (~8%). India also ranks 12th among those countries that produce high yields of millet. Millets have been an integral part of our diet for centuries. They offer a plethora of health benefits and are also good for the environment with low water & input requirements for production. With the aim to create awareness and increase production & consumption of millets, the United Nations, at the behest of the Government of India, declared 2023 as the 'International Year of the Millet'. The estimated millet yield in India has more than doubled since 1966. India's average yield in Millet farming (2021-22) is 1208 kgs per hectare. The production of millets has also increased by 7% (1966-2022) despite the area for millet cultivation in India decreasing consistently since 1971-72. A major drop in the area for millet cultivation occurred between 2006-2016. The consistent improvement in yield estimates over the years indicates the adoption of better farming practices in India in the past few decades.

In Jharkhand context, the climate is very suitable for the cultivation of millets and 20 -30 years ago farmers cultivate millets in their 50-60% of total agriculture land and various types of millet like Sorghum (*Sorghum bicolor*) commonly known as Jowar or Tilai Gangai in Jharkhand, Pearl millet (*Pennisetum glaucum*) commonly known as Bajra, Finger millet (*Eleusine coracana*) commonly known as Ragi or Maduwa. Kodo millet (*Paspalum scrobiculatum*) commonly known

as Kodo. There are 32 tribes having their habitat in Jharkhand state and mainly those people were cultivated millet in entire Jharkhand and millets were in the list of their staple food. But that trend is going to end. There are some told and untold reason bears the responsibility to decrease millet cultivation in huge way in spite of having more nutritional value than rice or wheat. In the case of decreasing area production of millet the main cause in the sowing and transplanting time of millet is same with the paddy so labour scarcity occurs then primary processing of various millet is laborious work.

Challenges and Opportunities in Millet Sector:

In today's context, the millet sector has been facing a lot of challenges pertaining to the production of millets, processing, value addition, marketing, and consumption. At the same time, there are a lot of opportunities for entrepreneurs in the millet sector. The challenges can be mitigated by taking extra efforts in solving the problems faced in the value chain of millets. The challenges are not only faced in India but also throughout the world. Let us first understand what are the challenges faced in the millet sector and then we can dive into the opportunities in the millet sector and how the millet entrepreneurs can take advantage of the opportunities created around millet.

Challenges in Millet Production:

1. Low productivity of millets:

When we compare the productivity of millets with other crops like wheat, rice, and maize, it is very low. As you know millets are grown in marginal land with low fertility and most of them are rainfed which results in low productivity. Apart from these, there are many limiting factors responsible for low production of millet among which the major constraints are weeds and most of the farmers cultivate millets in a traditional way. They simply broadcast the seeds on the onset of monsoon and harvest the crop after 75-90 days. The yield gap of millets can be minimized if a proper package of practices is followed. It is found that for the farmers who practiced good practices like the System of Millet Intensification (SMI) in Finger Millet, the yield has doubled as compared to the traditional methods. When millet farmers were asked about the factors that were to be followed to increase the yield of millets, the foremost response was sowing/transplanting on time, followed by weeding on time, proper nutrient management, and using improved varieties.

2. Area under Millet is Declining:

It has been found that the area under millet is declining drastically in India. If we compare the area under millets during the 1960s to the present scenario, it has reduced by more than 50%. If the fallow and wastelands are brought under millet cultivation, then the production can increase to much extent. Along with this, the millet farmers need to be incentivized to encourage them to grow millets.

3. Resistance to Pests and Diseases:

As you know millets are hardy crops and very less infestation happens due to pests and diseases. But some pests and diseases often cause significant loss in major millets like Sorghum, Pearl Millet, and Finger Millet. If more cultivars with significant resistance to pests and diseases are made available to the farmers, this problem could be solved up to some extent.



4. Millet Seed Production:

Even today farmers are facing problems in getting quality millet seeds. Although there are no issues in Sorghum and Pearl Millet as private players have entered into this segment and made it available to the farmers in India. There are opportunities to bring quality seeds of minor millets and this can be done by establishing seed hubs for breeding and producing seeds. This seed production needs to be demand-driven and all the stakeholders need to join hands together to improve the seed value chain. There are many traditional millet varieties that are performing well in the farmer's field and these varieties need to be bought in the seed chain through Farmer Producers Organization. This intervention will help the farmers to get the right quality seeds and that too in time.

5. Challenges in Millet Processing:

The millet processing machines available in India have a low recovery of 70-80% of grains and this becomes a challenge for the millet processors. Due to less efficiency, the output has more un-hulled and broken grains. Dehulling efficiency of millets is affected by the impeller speed. As you know millet grains differ in size, shape, and husk content, so it becomes difficult to handle. Depending upon one dehuller for dehulling all types of millets is not suitable rather it requires two types of dehuller. As Kodo and Barnyard Millet contain multiple seed coats, it requires a double-stage dehuller to remove the husk.

Separation of the husk of millets and its collection is quite difficult as it causes spillage all over the processing unit and often gets mixed with the final product. Even many millet processors are facing difficulty in handling and disposing of the husk of the millets. If the husk of millets could be used in making value-added products, then the issue could be solved. Millets being 100% gluten-free, it becomes very difficult to make some products with all total millet ingredients. Still, more research and development are needed for enhancing the availability of nutrients and decrease the anti-nutritional contents.

Still, progress is continuing on improving the shelf life of processed millet grains. In today's scenario, the shelf life of millets is enhanced to 4-6 months. But to cater to the international market and exports from India, the shelf life of millets is to be enhanced to a minimum of 12 months. To overcome all the challenges in the millet sector, there is a need for constant efforts from all the stakeholders and institutions toward mainstreaming millet. It is not only addressing the challenges discussed above but also building forward and backward linkages by creating a better millet ecosystem. No doubt, the Government has taken a lot of initiatives in this last decade to bring millets to the plate of all and has taken vital steps to promote millets in India and also abroad.

6. Low Investment in Research and Development:

Research and development activities play a crucial role in generating knowledge and disseminating it to farmers, processors, and other stakeholders in the millet sector. Low investment in R&D results in a lack of updated and accessible information on millet cultivation techniques, processing technologies, and market trends. This limits the adoption of best practices and hinders the overall growth and sustainability of the millet sector.



Now, its time to look at the opportunities in Millet Sector

Opportunities in Millet Sector:

The millet sector offers several opportunities, driven by increasing consumer demand for nutritious and sustainable food options. Millets are small-seeded grains that are highly nutritious, gluten-free, and have a low glycemic index. They are rich in fiber, protein, minerals, and antioxidants, making them a valuable component of a healthy diet. Here are some opportunities in the millet sector.

Food Processing:

Millets can be processed into various food products, including flour, flakes, porridge, and snacks. There is a rising trend of using millet-based products as a substitute for wheat and rice due to their nutritional benefits. Entrepreneurs can set up millet processing units to manufacture these value-added products and cater to the increasing demand.

Retail and Distribution:

Establishing retail and distribution networks for millet products can be a lucrative opportunity. This can include setting up dedicated millet stores, partnering with grocery chains to stock millet products, or developing an online presence for e-commerce sales. Creating awareness about the health benefits of millets and promoting its usage can help drive consumer demand.

Inclusion in MDM, PDS, ICDS, Railways and Tourism Department:

Govt. of India has planned to include the millets based value added products in PDS system, Mid day Mill programme for the Schools, Angan bari yojana and all the ICDS programm. Railways and Tourism Ministry, Govt. of India has also planned to make it compulsory to include millet based food in all the Rajdhani Exp., Shatabdi and Vande Bharat Exp. Trains as well as all the Big Hotels and tourism Department. It will increase huge demand of Millets and creates lots of opportunities for the farming communities.

Export Opportunities:

Millets have gained popularity globally as a sustainable and healthy food option. Exporting millet products to countries where there is a growing interest in alternative grains can be a profitable opportunity. Understanding international trade regulations and building strong distribution channels is crucial for success in the export market. To know the potential of the export of millets from India, I have written a blog "Millet Export from India is creating opportunities for new entrepreneurs".

Millet-based Hotel Business:

Focusing on a millet-based hotel business can be a unique and exciting opportunity that aligns with the growing demand for healthy and sustainable food options. Here are some key considerations and potential opportunities for a millet-based hotel business:



1. Menu Development:

Designing a menu that showcases millets as a core ingredient can be a distinguishing factor for your hotel. Develop a variety of millet-based dishes, including breakfast items, salads, main courses, and desserts. Experiment with different millet types such as pearl millet, finger millet, or foxtail millet, and incorporate them into traditional and innovative recipes to cater to a wide range of tastes. Now a days we could find a QR Code placed on the dining table. It was interesting to find the different types of millet recipes.

2. Millet-Based Events and Festivals:

Organize events or festivals that celebrate millets and their culinary significance. This could include themed dinners, food tastings, or even partnering with local millet festivals or organizations. Such events can attract food enthusiasts, create buzz around your hotel, and position it as a destination for millet-based cuisine. On 18th May 2023, Michael's Kitchen, Bhubaneswar, Odisha conducted a Millet Food Festival in collaboration with Odisha Millets Mission, where Home Cooks & Housewives were invited to the Millet Cooking Competition, and the winners were awarded. Awesome and yummy millet recipes were displayed and this attracted many people to this restaurant.

3. Millet-Based Catering Services:

Extend your millet-based offerings beyond the hotel premises by providing millet-focused catering services for events, conferences, and weddings. Highlight the unique aspect of your catering services with a diverse selection of millet dishes that cater to different dietary preferences and requirements. In the recent years, Ahmedabad, Gujarat where got the opportunity to taste the Millet Lunch offered by the Self-Help Groups of SEWA NGO. Really the food was tasty and yummy and anyone can enjoy it. Hope this type of initiative will definitely support the SHGs.

4. Collaboration with Wellness and Health Retreats:

Partner with wellness retreats or health-conscious establishments to offer millet-focused experiences. This could involve creating customized menus, hosting wellness retreats that include millet-based meals, or providing catering services for wellness events. Collaborating with like-minded businesses can expand your reach and tap into a niche market.

Conclusion:

Today, Considering unpredicted environments and changes in the Global climatic condition as well as nutritional profile of the millets, a lot of opportunities for farmers and entrepreneurs is growing up, as India is taking the lead in the celebration of the International Year of Millets-2023. This celebration around the globe is creating awareness among the people. Awareness of the nutritional, ecological, health, and economic benefits of millet is pushing people to start their millet journey. Nowadays, people are bringing back forgotten foods to their plates and believe that these foods can bring a positive impact on their health. I think this change in India, is opening up opportunities for entrepreneurs and investors to invest in Millets.



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IP 14

Soft Wheat: A potential crop for import substitution in baked and protruded bakery products industry

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Wheat is one of the oldest and most important strategic cereal crops globally as well as in India. It is one of the top three most produced crops, along with corn and rice, because of its very nutritious and valuable grain. About two billion people consume it as their primary source of nutrition (36 percent of the world population). Wheat species, both hexaploid (*Triticum aestivum* L.) and tetraploid (*Triticum durum* and *T. dicoccum*) are staple foods for 30% of the world's population (Eversole *et al.*, 2014). Grain hardness is a grading factor that is used to determine the type of wheat (Morris, 2002). It is an important factor in wheat classification and end-product quality (Campbell *et al.*, 1999). Grain hardness is important in the flour industry because it influences water absorption capacity, milling, baking, and wheat quality (Bettge *et al.*, 1995). The gene for grain hardness (Ha) is located on the short arm of 5D chromosome which distinguishes between the two main market classes of wheat (*Triticum aestivum* L.): “soft” and “hard.” Puroindoline a and b (commonly called as PinA and PinB respectively) are the two proteins that make up friabilin, a marker protein for grain softness. The Indian milling and baking industries have grown quickly as a result of the rising demand. The majority of bakery items consumed by the Indian population are bread and biscuits. The bread and bakery items are responsible for around US\$3,358 million in sales in 2019. According to estimates, the market will grow by 6.2 percent per year (Sharma *et al.*, 2016). Soft wheat has a smoother endosperm texture, takes less energy to mill, and tends to produce smaller particles with less starch damage when milled than hard wheat. Hard wheat is used to make bread and other yeast-leavened foods, whereas soft wheat is used to make cakes, cookies, pastries, and some types of noodles (Morris and Rose, 1996). Wheat is used for different purposes and hence quality requirements vary on its end use. Hard wheat (*T.aestivum*) with strong gluten and > 12.0 per cent protein has been found suitable for



bread making, for biscuits soft wheat with less gluten and < 11.0 protein is best suited. India had imported 3,108 tonnes of soft wheat at a cost of 4,226/quintal in 2021-22 against 2,147 tonnes at ₹3,797/quintal in 2020-21. The Indian Agriculture Research Institute has developed a few varieties of this kind. Recently one viz., HD 3443 has been registered with the PPVFRA. This has opened door for import substitution and a new crop opportunity of Indian farmers. Soft varieties come with a yield penalty and are susceptible to insect damage in storage. So, it raises a need to develop a sound package of practices to ensure safe storage and also ensure a premium pricing regime to compensate for the compromised yield levels.





Theme -I

Pre Breeding & Plant Genetic Resource Management



O-I 1

Studies on assessment of heterosis for fruit yield and attributing characters in okra [*Abelmoschus esculentus* (L.) Moench]

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In the present investigation twenty one F₁ hybrid were generated from ten parent (7 lines and 3 testers) using line × tester mating design, these F₁ hybrids along with 10 parents and 1 commercial check (GJOH-4) were sown in a randomized block design with three replication during *kharif*-2022 were evaluated to study the magnitude of heterosis. The mean sum of squares due to genotypes were highly significant for all the traits except fruit girth under investigation. The combination VRO-6 × Arka Abhay recorded the highest and significant heterosis over better parent (20.80%) and standard hybrid check (11.96%) for fruit yield per plant. The crosses combination VRO-6 × Arka Abhay, NOC-1808 × Arka Abhay, NOC-1808 × GAO-5, NOC-1808 × Punjab Suhavani, JOL-11-12 × Arka Abhay were found promising based on significant heterosis over mid parent heterosis, heterobeltiosis and standard heterosis over check GJOH-4 for fruit yield per plant.

O-I 2

Identification of tolerant genotype for bakanae disease resistance in rice

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Bakanae disease, instigated by the fungus *Fusarium fujikuroi*, remains one of the paramount threats to rice production, leading to significant yield losses globally. The disease, characterized by the elongation of seedlings, has led to substantial yield losses in affected areas. Due to the disease's rapid proliferation and the environmental concerns associated with chemical control measures, there is a growing emphasis on breeding rice genotypes resistant to Bakanae. With an escalating demand for rice as a staple food, the identification of tolerant genotypes is of the essence for ensuring sustainable rice production. This study aimed to identify rice genotypes that exhibit inherent tolerance against Bakanae disease.

A diverse set of 150 rice genotypes including landrace, breeding lines and released varieties of diverse ecologies (upland, aerobic, irrigated, shallow lowland, medium to deep water, and coastal salinity) was screened under controlled conditions where they were exposed to *Fusarium fujikuroi* inoculum. Disease severity was assessed based on elongation of seedlings, chlorosis and the overall vigor of the plants after a duration of 12 days of sowing.

Preliminary results indicated the presence of several 100 genotypes exhibiting varying levels of tolerance to Bakanae. Furthermore, a set of 61 genotypes showcased strong resistance, making them ideal candidates for further breeding programs. Molecular analyses provided insights into potential genetic markers associated with the resistance, which can be instrumental in future marker-assisted breeding endeavours.

In conclusion, this study successfully identified rice genotypes with inherent tolerance to Bakanae disease, offering promising avenues for developing Bakanae-resistant rice cultivars. The findings also underscore the potential of combining phenotypic observations with molecular tools to expedite the breeding of disease-resistant crops.

Keywords: Rice, *Bakanae* Disease, resistance genotypes

O-I 3

Genetic evaluation and diversity studies for growth attributing traits among different populations of *Shorea robusta* Gaertn. f in Jharkhand

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Shorea robusta Gaertn. is a tropical tree species that belongs to the family Dipterocarpaceae. It is one of the most important timber species in India, which accounts for more than 10 percent of the total tree stand in the country. The species is one of the major sources of livelihood in tribally dominated states like Jharkhand and is designated as the state tree of these states. The biotic and abiotic factors like low and irregular rainfall, fluctuating temperature, soil degradation, forest fires, elicited felling, overexploitation of NTFPS, etc. place the species under threat. To preserve the genetic diversity of the species and devise conservation strategies, it was important to study the population genetic diversity present across the range of its distribution in the state of Jharkhand. Under the present study, to carry out the vegetation sampling, a grid-based approach (5 km x 5km) was followed as per the Forest Survey of India. Out of 23721 km² of forested area in Jharkhand, sampling and study were done in 4744 km² (20% of the total forested area). During the study, 190 sample grids were covered using map numbering systems as per the Survey of India (SoI). From these layers, 15 populations of sal were identified, and data on growth-contributing morphological traits were recorded and studied. According to the study, the Saranda population had the highest mean value (2 m³) for the trait individual tree volume, whereas the Khunti population had the lowest mean value (0.61 m³) for the same trait, with a grand mean value of 1.21 m³. Similarly, the Saranda population had the highest mean value for the trait (dbh) diameter at breast height (0.45 m), and the Khunti population had the lowest mean value for dbh (0.25 m), with a grand mean value of 0.36 m. For the trait plant height, the Saranda population had the highest mean value (21.73 m), but the Latehar population had the lowest mean plant height (16.61 m), with a grand mean value of 18.89 m. Genotypic selection for volume and growth improvement will be effective only when the relationship between the volume and

growth-contributing traits is well established. At a significance level of 0.1%, but at a significance level of 5%, the trait volume was also found to be significantly positively correlated with tree height. However, with regard to crown length and clear bole length, the trait volume was not significant. The trait D.B.H was significantly positively correlated with GBH and basal girth at 0.1% and 1% significance, respectively. At 5% significance, it was discovered that the trait tree height was significantly positively linked with the length of the clear bole and the length of the crown, but not with the GBH or the basal girth. According to the study, the population of Saranda is the most promising, whilst the population of Khunti is the least effective. In addition, traits like diameter at breast height (dbh) and plant height were found to be substantially positively correlated with the economical trait tree volume.

Keywords: *Shorea robusta*, genetic diversity, traits correlation, conservation

O-I 4

Assessing nutritional quality and green forage yield of cowpea genotypes under coastal plain zone of Odisha

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The lack of sufficient quantity of quality green fodder throughout the year seems to be a major constraint for maintaining proper growth of animal husbandry in India. The livestock rearing plays a significant role in the economy of Odisha, yet forage cultivation has remained almost neglected. The major part of livestock forage resources in the state is met either from by product (rice straw/ crop residues) or from the less nutritious grasses leading to low production and productivity of livestock. Therefore, there is a need to boost the green and dry fodder yield from the available resources. Cowpea (*Vigna unguiculata* L. Walp.) has emerged out as a potential legume crop for meeting the requirement of high-quality fodder to fast expanding cattle population. This goal can only be achieved by developing high yielding varieties with better nutritional quality. Therefore, the present investigation was under taken to study variation in nutritional quality and green forage yield (GFY) of fodder cowpea genotypes for selection of genotypes with high yield and better nutritional quality. Twenty two pre breeding lines along with two national check varieties were evaluated in a randomised block design with three replications at AICRP on forage crops and utilisation, OUAT, Bhubaneswar during kharif, 2022. Observations were recorded on GFY, dry matter %, crude protein%, ash %, and other micro and macro nutrient content. GFY of the genotypes ranged from 112g/plant (GETC-2) to 1158 g/plant (GETC-19). The national check variety Sweta and UPC 625 recorded 325 and 300 q/ha and the pre breeding line GETC-24 recorded the maximum GFY of 514.20 q/ha. Days to 50 % flowering ranged from 35 days in GETC-12 to 95 days in case of GETC-34. Pre breeding line GETC-31 recorded the maximum crude protein (22.89%) followed by GETC-36 (20.14 %). Dry matter content was the maximum in GETC-19 (26.55 %). Ash % of the genotypes ranged from 4.91 to 11.41 %. Crude fat % ranged from 0.42 to 3.78. The maximum iron content was recorded in GETC-42 (10.456 mg/L). The



maximum potassium content was recorded in GETC-42 (162.5 mg/L). This variability study will help in selecting superior fodder cowpea lines.

O-15

Title: Response of packaging materials and different storage duration for determining different physiological and quality parameters on Rapeseed and Mustard genotypes during seed storage

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For early growth and establishment of crop as well as proper seed development, proper knowledge of rapeseed-mustard genotypes, their management through seed priming treatments is essential. Seed priming is a pre-sowing-controlled hydration process which brings certain biochemical and physiological changes within the seeds for germination without allowing them to emerge. For Rapeseed and Mustard, observations regarding details of physiological and biochemical changes help in understanding the pattern of changes in developing seeds at various stages of seed storage. Thus, the present research work entitled, '**Response of packaging materials, seed priming treatments and different storage duration for determining different physiological and quality parameters on Rapeseed and Mustard genotypes during seed storage**'

The investigation comprised both field and laboratory components. The field experiment was conducted at A-B block farm, B.C.K.V., Kalyani, Nadia, West Bengal during *rabi* season of 2017-18 and 2018-19 in split plot design comprising 6 rapeseed-mustard genotypes (Anushka, Sanchita, TBM-143, TBM-204, Kranti and Pusa Bold) and different packaging materials (Aluminium foil, Plastic Packet, Brown Paper Packet and Cloth bag) with different storage durations (0 month, 2 months, 4 months, 6 months and 8 months). The laboratory experiment on various seed quality, biochemical parameters and enzymatic activities was conducted in the Department of Seed Science and Technology, B.C.K.V., Mohanpur, Nadia, West Bengal. Observations on storage potential of produced seeds in different containers (aluminium foil, plastic packet, brown paper packet and cloth bag) were recorded at 2 months interval up to 8 months of storage. Better results expected up to 6 months storage under aluminium foil for all genotypes.

Keynote: Seed priming, seed storage, packaging container, storage duration, genotypes



Theme -II

Crop Improvement for Climate Resilience



O-II 1

Evaluation of brinjal genotypes during winter season for the plateau region of Jharkhand

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Brinjal ($2n=2x=24$) botanically *Solanum melongena* L., is an important vegetable crop of the Solanaceae family, popularly known as eggplant in USA and Canada, *aubergine* in France and England and *baigan* in North India. It is commercially cultivated all-round the year in the most parts of India and abroad. Shape, size and colour of marketable fruits are important characteristics for its commercial cultivation. Its choice among the people varies with one region to another. Keeping these views in mind an experiment was carried out during *rabi* seasons of 2021-22 and 2022-23 at Vegetable Experimental Area of the Department of Horticulture, BAU, Ranchi to find out the most suitable genotype of brinjal for the plateau region of Jharkhand. Seven promising genotypes were evaluated against three checks *viz.*, Swarna Pratibha (Local Check), Pusa Kranti (National Check) and Green Round (Pvt. Check). Field trial was laid out in the randomized block designed with three replications. Observations on nine quantitative characters were recorded and mean data was subjected to suitable statistical analysis. Analysed data revealed that almost all characters showed significant effect for both the years except, days to first flowering during 2021-22. RCBR-22 gave significantly highest yield during both the years with the yield of 417.36 q/ha and 473.36 q/ha during *rabi* 2021-22 and 2022-23, respectively. It was followed by CB-41(409.09 q/ha), CB-27(399.89 q/ha), CB-1(393.07 q/ha) and Lal Gulab Sel-1(377.58 q/ha) during *rabi* 2021-22, whereas CB-1(454.11 q/ha), CB-27(443.35 q/ha) and CB-41(432.42 q/ha) during *rabi* 2022-23. The result revealed that the genotypes RCBR-22 and CB-1(Birsa Chianki Baigan-1) both having purple fruits were found most suitable brinjal genotypes for its commercial cultivation in the plateau region of Jharkhand as well as adjoining areas of similar agro-climatic conditions.

Keywords: Brinjal, eggplant, promising, genotypes, evaluation, plateau region, Jharkhand.

O-II 2

Selection of superior parental inbred lines based on combining ability effects on different growth and yield parameters in quality protein maize

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Abstract: In order to choose the parents for hybrid breeding projects and to assess the kind and degree of genotypic variation, combining ability experiments are routinely performed. In

the creation of hybrids and composites, it was estimated that the general combining abilities of the parents had a fundamental importance. In order to select superior parents for different hybridization program in quality protein, eight Quality Protein Maize (QPM) inbred lines were chosen and crossed in half-diallel mating, producing in twenty-eight hybrid combinations. The experiment was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar, under the AICRP on Maize during *kharif*-2020 in a randomized block design with three replications for ten yield and component characters. All the observations recorded were statistically analyzed and found to be highly significant. It was observed from the study that parent inbred lines Q1-DQL 2261, Q2-DQL 2099, Q3-DQL 2159, and Q4-DQL 2221-1-1 had high GCA effects for most of the characters, while parent Q5-70160 had medium GCA effects, and parents Q6-71266, Q7-72154, and Q8-72242 had pretty low GCA effects. The inbred lines Q4-DQL 2221-1-1(833.792), Q2-DQL 2099 (517.658) and Q3- DQL 2159 (350.325) were identified as good general combiners for yield. They also matured earlier compared to other parents. Twelve of the twenty-eight crosses showed significant positive sca effect on grain yield. The best experimental crosses for grain yield based on per se performance and sca effects were Q2 x Q8 (2106.748), Q1 x Q6 (2053.048), Q3 x Q7 (2027.082), and Q3 x Q6 (1719.884). The parents with significantly high GCA effects had high heritability with less environment effects and their selection for different hybridization program will be more effective.

Keywords: general combining ability, hybridization, quality protein maize, Inbred lines, specific combining ability

O-II 3

Morphological variation study among different root characters and yield in new generation rice

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Rice, (*Oryza sativa* L.), holds a paramount position as the primary dietary staple for over half of the world's population. However, there is an urgent necessity to enhance rice cultivation, particularly in regions prone to drought, by improving its ability to efficiently capture and utilize water resources. Addressing this challenge has given rise to the concept of New Generation Rice (NGR), a ground breaking approach designed to surpass current yield limitations under favorable management conditions. NGR is built upon the idea of an "ideotype," which essentially involves creating a specific plant type with enhanced quantitative and physiological traits. One of the primary focuses within NGR is to enhance the root system of rice plants, achieved through both breeding techniques and improved soil management practices. To achieve this goal effectively, it is critical to understand the relative impact of genetic factors (genotypic) and environmental conditions on root development, as well as their interaction, under varying soil conditions and agricultural management practices.

In a recent study, an in-depth analysis of the phenotypic variation in seven distinct root traits and yield across 43 elite rice genotypes. The aim was to uncover correlations among these traits and gain insights into their complex relationships. Notably, the study revealed significant correlations between several root characteristics, such as root tips and root weight. Furthermore, yield exhibited a strong positive correlation with root surface area, closely followed by root tips and root average diameter. These correlation analyses offer valuable insights, indicating that a range of root indexes is closely linked to actual crop yield at various growth stages. This suggests that by focusing on these root traits, breeders can identify rice genotypes with superior ideotype characteristics, thereby harnessing their potential for high grain yield alongside robust root traits. Additionally, it lays the groundwork for identifying potential recombinants that have the potential to significantly boost grain yield in rice, offering a promising avenue toward ensuring food security in regions heavily reliant on this critical crop.

Key words: Ideotype, New Generation Rice, Correlation, root characteristics

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Genetic analysis for yield and attributing traits in mungbean (*Vigna radiata* L. Wilczek)

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Mungbean having a predominately self pollinated pulse crop mainly grown during kharif & summer season in northern India, lacking in desired genetic variation. Genetic analysis of quantitative traits is of prime importance in self-pollinated crops like mungbean to exploit existing genetic variations by recombination and shuffling of genes through hybridization creating new genetic variations. Considering the importance in our daily diet and low productivity of the crop, there is an urgent need to enhance the genetic base through extensive crossing programme with diverse genotypes. In the present study, 7x7 half diallel crosses mating design was carried out following Griffing (1956) numerical approach (Method 2) to estimate general combining ability (gca), specific combining ability (sca), heritability in narrow sense and various genetic parameters which can explain the quantitative genetic variation for seven different quantitative traits.

Both *gca* and *sca* effects were significant for three traits viz., days to 50% flowering, days to maturity and seed yield (kg/ha), which indicated that both additive and dominance components of variances were important for governing these quantitative traits. Whereas, for the trait plant height (cm) only SCA effect was significant indicating importance of dominant component of variance. Pods per plant was significant for GCA only. The values of mean degree of dominance were significant and greater than one for all the traits indicative of over dominance. Higher proportions of dominant genes were found for all the traits except number of primary branches per plant and seeds per plant. Significance of the variance component due to dominance deviation (H_1) and variance due to dominance effects corrected for genes distribution (H_2) clearly showed the possible changes in the genes governing these traits.

Key words: Combining ability, heritability, half diallel, Griffing Method 2, *Vigna radiata* L.

Investigation of G×E interaction in brinjal (*Solanum melongena* L.)

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A line x tester design involving 5 females and 6 males parents and their thirty resultant F_1 s with two standard checks were tested for eleven traits under the three growing season. The linear component was found important in building up total G x E interactions. None of the parents and hybrids was found average stable for all the traits studied across environments. Among parents NSRP 1, IIHR-534, GAOB 2, GJB 2 and IC-111066-2 were observed to be stable genotypes for fruit yield and its attributes. The utilization of these stable parents in hybridization programme resulted five hybrids viz., IC IIHR-587 x NSR-1, IC-0742241 x GAOB-2, IC-0742241 x GJB-2, IC-0742241 x GAOB-2, IIHR-534 x GAOB-1, IC-111066-2x NSRP-1 and IIHR-534 x GJB-2 which were identified to be stable for fruit yield and some of its component traits along with high fruit yield per plant and could be utilized for yield improvement in brinjal.

Study on genetic variability, character association and diversity analysis among soybean [*Glycine max* (L.) Merrill] Genotypes

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Soybean [*Glycine max* (L.) Merrill] is a major oil seed crop in the world with versatile nutritional qualities having 20 percent oil content and 38 to 45 percent protein content, and is also rich in amino acids like lysine and tryptophan. The crop presently concentrated in the country's Central zone has a high potential to be extended to the extreme parts of the country by identifying potential varieties and improving existing ones. In the current study, 40 genotypes of soybean were evaluated in a randomized block design with 3 replications in the ICR experimental farm, AAU, Jorhat, Assam. The present investigation incorporated the assessment of the genetic variability parameters, the causal relationship between yield and its components and the pattern of genetic diversity among the soybean genotypes. Analysis of variance for yield and its components showed the presence of significant differences among all the genotypes for all the 11 quantitative characters under study. In order to assess the extent of variability of seed yield and yield attributing characters among the 40 soybean genotypes, various genetic variability parameters like the genotypic coefficient of

variation (GCV), phenotypic coefficient of variation (PCV), heritability in a broad sense (h^2 bs) and genetic advance as per cent of mean (GAM) were calculated. The associations of yield and its components were analysed by correlation coefficient and further subjected to path coefficient analysis to estimate the direct and indirect effects of each character on seed yield per plant. The seed yield per plant was positively and significantly correlated with 100 seed weight, number of pods per plant, oil content, number of primary branches per plant, harvest index and number of seeds per pod, while it was negatively correlated with plant height, protein content, days to 50% flowering and days to maturity. Using Mahalanobis D^2 statistics and Principal Component analysis, the pattern of genetic diversity among 40 genotypes of soybean was evaluated based on 11 quantitative characters. All 40 genotypes were grouped into four clusters using Tocher's clustering pattern. It was observed that the most contrasting clusters were Cluster II and Cluster IV with a maximum inter-cluster distance between them of 2572.391. The maximum contribution to the genetic divergence was made by 100 seed weight, followed by seed yield per plant and protein content. The principal component analysis showed that PC1 and PC2 had Eigen values higher than unity and explained 74.931% of the total variability among the soybean genotypes. This study outlined the potential for further in-depth research to improve soybean genotypes in terms of its major qualitative and quantitative traits.

Keywords: soybean, variability, correlation analysis, path analysis, diversity

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Combining ability and heterosis in maize (*Zea mays* L.) inbred lines

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The present study was framed to determine the combining ability and the extent of heterosis in maize using line \times tester design at maize section, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India. Crosses were made involving ten lines and three testers in *rabi*, 2019-20 for the study. 30 Crosses along with 13 parents and 2 checks were evaluated in randomized block design with two replications during *kharif*, 2020. The hybrids DHM 117 and SHM 1 were used as checks. Data were recorded on 13 morphological traits. The contribution of lines is found to be greater than that of the testers for most of the characters studied. On the basis of GCA effects, the lines VL109476, VL109475, VL1010848, VL109479 and tester VP15295 were identified as good combiners for grain yield, whereas the line VL1017524 and the tester SML-1 were also identified as good combiner in terms of earliness. These can be used as parents in multiple hybridization programme. On the basis of SCA effects, the crosses VL109476 \times V P15295, VL1010763 \times VP15295, VL1018419 \times VP15295 and VL109475 \times SML-1 were identified as



good specific combiners for grain yield, whereas on the basis of standard heterosis VL109476 x V P15295, VL1010763 x VP15295, VL109475 x SML-1 and VL109479 x SML-1 were superior to the better check (DHM 117) in grain yield. The good general combiner for yield observed in the study, may be used in hybridization programmes for greater yield. The best cross combinations for greater yield in the study, may be forwarded for multi-location testing and large scale testing in farmers' field and finally may be released as commercial hybrid.

Keywords:- Combining ability, Heterosis, GCA, SCA

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Genetic analysis of quantitative traits and selection of transgressive segregants in crosses of sesame (*Sesamum indicum* L.)

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Sesame is an important oil seed crop having lots of health benefits. Low productivity of sesame as compared to other oilseed crop is less which is a major drawback of its worldwide cultivation. Combining ability and hybridization plays a vital role in improvement of sesame. Keeping it in view the experiment was conducted in EB II research station, OUAT, Bhubaneswar. The experimental materials comprising of nineteen genotypes were sown during *Pre rabi* 2018 in Randomized Block Design with three replications and evaluated for eight quantitative characters for the diversity analysis. In *Summer* 2019, seven genotypes (OSM-22, Nirmala, Prachi, Amrit, VRI-1, Rama and PKDS-11) were selected and crossed in half diallel fashion to develop 21 F_{1s} . In *Pre rabi* 2020, 21 F_1 along with their 7 parents were evaluated in RBD design for study of gene action involved in inheritance of quantitative traits and the magnitude of heterosis expressed by the crosses. Four crosses *viz.* OSM22×Rama, OSM22×VRI-1, Nirmala×Prachi, Prachi×VRI-1 were selected on the basis of *sca* effect and carried forward to F_2 in *Kharif* 2021 to study the transgressive segregants. The crosses like OSM-22 × Rama, OSM-22 × VRI-1, Nirmala × Prachi and Prachi × VRI-1 exhibited significant *sca* effect and good amount of heterosis for plant height, no. of capsules per plant and seed yield per plant. Out of the four selected crosses OSM-22 x Rama showed high transgressive segregants in F_2 for seed yield and its component traits, indicating its further advancement in segregating generations to select good genotypes, to be developed as a variety.

Studies on genetic variability and divergence analysis in advanced generation mutagenized population of sesame (*Sesamum indicum* L.)

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Sesame (*Sesamum indicum* L.; $2n=26$), the “Queen of oilseed”, is the most ancient oilseed crop with high nutritional value, although its productivity gets hampered due to production challenges. Consequently, to produce novel varieties, the present work entails the utilization of gamma rays induced mutation, which is in continuation of previous project work wherein 22 advanced putative mutant lines of Rama and Tilottoma (used as control) were characterized for both morphological as well as quantitative characters.

The experiment was grown during pre-kharif in 2022 in Randomised Block Design (RBD) with three replications at agriculture farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati. Genetic variability, heritability, genetic advance, correlation and path analysis between yield and its contributing traits, and genetic divergence were evaluated. The analysis of variance revealed highly significant differences among the genotypes in respect of all the traits, thereby indicating presence of wide genetic diversity. Higher values of GCV, PCV, heritability and genetic advance as percent of mean for seed yield per plant, number of capsules per plant, and number of branches reflect preponderance of additive genetic factors and less influence of environment. Seed yield per plant inferred significant positive association with number of capsules per plant and the number of primary branches per plant at both genotypic and phenotypic levels. Path coefficient analysis suggested the considerable positive direct effect on seed yield which was exerted mainly by three of the traits viz. number of capsules per plant, number of seeds per capsule, and plant height. Based on diversity the mutant lines were grouped into 6 clusters and highest inter-cluster distance was observed between Clusters IV and VI, followed by Clusters III and IV, Clusters I and IV, Clusters V and VI. Among the traits studied days to 80% maturity followed by the number of capsules per plant, seed yield per plant contributed maximum while evaluating divergence. Hybridization involving mutant lines of cluster III, IV, V and VI may result in deploying maximum heterosis to produce desirable transgressive segregants for crop advancement.



Studies of combining ability and gene action in sesame (*Sesamum indicum* L.) for yield and its attributing characters

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Sesame (*Sesamum indicum* L.) is an important *kharif* oilseed crop of Jharkhand mostly grown under rainfed condition. The state observed on and off drought or drought like situation in alternate year. Sesame seeds contain about 50-60% oil and it is considered as the queen of high quality vegetable oils. It harbours wide array of phytochemicals (in seed) with antioxidant, antifungal, hypolipidaemic and hypoglycemic properties. The aim of the study was to estimate gene action, identify and select superior parents and best hybrid combinations on the basis of estimates of general and specific combining abilities for yield, its related traits in sesame. Twenty eight offspring were synthesized by crossing of eight diverse parents in a diallel fashion excluding reciprocals during *Kharif* 2018-19. These 21 crosses along with eight parents were sown in *Kharif* 2019-20 in randomized block design with three replication at Zonal Research Station, Chianki, Palamu. The differences among genotypes were highly significant for all the characters studied. Estimates of variance due to general combining ability (gca) and specific combining ability (sca) and their ratio revealed that both additive and non-additive gene effects were important for different characters studied. The estimates of gca effects as a whole suggested that if most of the traits are to be improved through hybridization and selection, then priority should be given to parents PKVNT-11 and Kanke White. The estimates of specific combining ability revealed that the crosses JTS-8 x Shekhar, PKV-NT-11 x Kanke White and JLT-408 x Shekhar were the best specific combiner for seed yield per plant. The above cross combinations may be useful for genetic improvement of seed yield of the crop.

Key Words: Sesame, gene action, general combining ability, specific combining ability

Genetic variability correlation and path analysis in Niger (*Guizotia abyssinica* L.) Genotypes

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In present study genetic variability and associations among yield components and their direct and indirect influence on the grain yield of niger were investigated. For this purpose, twenty one

Niger genotypes were tested using randomized block design in experimental field of BAU, Ranchi during kharif 2019-20. Significant difference was observed among all the genotypes was observed for the characters under study. The estimate of genotypic coefficient of variation was found high for almost all the characters. High heritability in broad sense coupled with high genetic advance observed for the characters days to 50 % flowering , number of capsule per plant ,number of of seed per capsule, 1000 seed weight (g) and grain yield (q/ha) indicating the scope of genetic improvement for these characters. A strong and positive significant association observed for the characters plant height,no of primary branches, no of secondary branches, days to maturity, no of capsule per plant, no of seed per capsule with grain yield plot. Phenotypic path analysis revealed that no of secondary branches, days to maturity, no of capsule per plant, no of seed per capsule to exert positive direct effects on grain yield. Therefore it may be considered that these yield attributing characters are important for improving the yield of Niger. The entries NRS1804,NRS1805,ONS181 and Birsa Niger 3 found significant superior for grain yield(q/ha).

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Screening of *Stemphylium* blight resistant genotypes in lentil under controlled conditions

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Lentil (*Lens culinaris* sub sp. *culinaris*) is an important pulse crop due to nutritious food having high protein content ranging 22 to 26%, vitamins, and minerals such as iron, and calcium. Several biotic and abiotic stresses affect the production and productivity of lentil. In the past few years, stemphylium blight caused by *Stemphylium* spp. Wallr. teleomorph *Pleospora tarda* Simmons has emerged as a devastating disease of lentil in the north-eastern part of India. Breeding resistant cultivars is an important way to minimize the yield losses caused by this disease. For this, in the present investigation, the procedure of preparing the pure culture of *Stemphylium* spores from infected diseased samples was established for screening the *Stemphylium* blight disease under controlled conditions. Testing of four different media (LDA, PDA, Rose Bengal, V5) for growing and development of the *Stemphylium* fungus resulted in the identification of the PDA media for this purpose. The pure culture of *Stemphylium* spores was prepared from spore suspension of 30 days old culture to test the pathogenicity under controlled conditions in a growth chamber. The fungus was re-isolated from leaves having disease symptoms after inoculation and confirmed the presence of *Stemphylium* fungus through microscopy. After confirmation, the same pure culture of *Stemphylium* spores was used to inoculate the 20 lentil genotypes at (i) 20-25 days after sowing (DAS), (ii) 35- 45 DAS, and (iii) 55- 65 DAS for screening the resistant genotypes against *Stemphylium* disease in poly house. This resulted in the identification of five resistant genotypes namely IPL-220, IPL-225, IPL-315, IPL-316, and IPL-321 having disease severity <2 % for *Stemphylium* blight under controlled conditions that will be further revalidated under natural conditions in hotspot regions.

Gamma radiation-induced mutations improve drought tolerance in wheat: genotype-specific responses to peg-induced stress at the seedling stage

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This study conducted a comprehensive assessment of drought tolerance in ten wheat genotypes, including the widely cultivated HD2967 and its gamma-mutagenized progenies, at the seedling stage by inducing drought stress using polyethylene glycol (PEG 8000). The research revealed distinct genotype-specific responses to drought stress, with TAW95 and TAW98 emerging as standout performers, displaying remarkable drought tolerance. These genotypes exhibited higher chlorophyll content, shoot length, root length, and fresh shoot and root weight under stress conditions, indicating their superior stress resilience. In the face of escalating climate change-induced heat and drought challenges, such findings hold significant implications for global food security, as wheat is a dominant staple crop. The use of gamma rays for mutagenesis proved instrumental in expanding the genetic diversity of wheat, potentially paving the way for the development of more resilient cultivars. Moreover, the employment of PEG 8000 as a drought-inducing agent allowed for controlled assessments of drought tolerance at the crucial seedling stage. This research underscores the importance of genotype-specific responses in drought tolerance and identifies TAW95 and TAW98 as promising candidates for breeding programs aimed at enhancing wheat's resilience to drought stress, thereby contributing to the establishment of sustainable and resilient agroecosystems. As climate change continues to pose increasing challenges to global agriculture, identifying and developing drought-tolerant wheat varieties becomes paramount. The study's focus on early seedling-stage screening offers a cost-effective and efficient approach to identifying promising genotypes for further breeding efforts. Overall, this research not only contributes valuable insights into enhancing wheat's drought resilience but also highlights the importance of innovative genetic techniques and controlled stress-inducing methods in crop improvement strategies, ultimately contributing to food security in the face of a changing climate.

Keywords: Gamma radiation, drought tolerance, PEG-induced stress, seedling stage, physiological, stress tolerance index, genetic diversity.

Identification of fodder cowpea genotypes by leveraging GGE biplot under multi-environment

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Cowpea (*Vigna Ungriculata*) has the immense potential to be used as an important fodder crop under future climate scenarios due to its adaptability. Hence, it necessary to study on different fodder cowpea genotypes x environment interaction. In this context, an experiment was carried out with thirty fodder cowpea genotypes (G) containing check Bundel Lobia-1 at Pusa farm of Dr. RPCAU, Pusa, Samastipur, Bihar during *kharif* season of 2019 and 2020. Randomized Block Design was used with three replications and spacing 45 x 10 cm. The environment combinations were E1 [Date of sowing (DOS) 15th July 2019 in irrigated open field condition], E2 (DOS- 26th July 2019 in irrigated open field condition), E3 (DOS- 15th July 2019 in rain out shelter for drought condition), E4 (DOS- 15th July 2020 in irrigated open field condition), E5 (DOS- 26th July 2020 in irrigated open field condition) and E6 (DOS- 15th July 2020 in rain out shelter for drought condition). Ideal genotypes on the basis of GGE biplot “genotype view” was genotype G3 for highest production efficiency (gm/m²/day) and G29 for highest green fodder yield (gm/plant). “What – Won – Where” GGE biplot results showed existence of two mega environment, where genotype G3 was winner in both E3 and E6 environment for production efficiency; whereas for green fodder yield also two mega environments were existed where G3 was winner in E6 and G29 in E4. The environment E5 was found as best for identifying cowpea genotype adapted for the region for production efficiency and E4 was best for green fodder yield.

Keyword: Fodder cowpea, GGE Biplot, Green fodder yield and Production efficiency.



Neglected underutilized crops: a key to climate smart farming.

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The two existing issues in the agrarian community is to I) bridge the yield gap, a 30 per cent increase in overall yield is demanded to feed the all 9 billion population projected by the year 2050 and II) bridge the nutrition gap for a balanced diet, though traditional crop spp. Satisfy hunger index, may not always provide all the nutrients required. World wide food habits reveal a poor diversity in consumption patterns, encompassing high cereal intake accompanied with less fruits and vegetables leading to nutrition gap. This paved the path to understand and utilize the *hidden treasures* – Neglected and Underutilized Species. As of available, 30,000 spp. meant for edible purposes, only 106 are being brought to plate encompassing 90% of human diet, and only three viz., rice, wheat and maize contribute to 60% diet, emphasizing the fact that majority of the plants spp. are “Under-utilized”. NUS have a high nutritional value and can be a good source of vitamins, protein, energy, and fibre, all of which help with food and nutrition security. Aside from their exceptional nutritional properties, many of these crops do not require significant inputs, can be cultivated on marginal soils, and are readily intercropped or cycled with staple crops. They also fit well into integrated practises such as agro-ecology. NUS may make agricultural systems more sustainable and climate resilient owing to their evolution in marginal circumstances and many have the unique capacity to resist or endure fluctuations. Millets, one such potential NUS, which are grown in over 130 countries, have long been regarded an essential part of the nutrition of nearly half a billion people in Asia and Africa. Millets are climate resilient; they require nearly two-third water lesser compared with conventional crops like rice, wheat and sugarcane. They also demand relatively lesser inputs comparatively and can perform exceptionally well under arid and semi-arid regions. Though in the past few decades, the global carbon dioxide levels are alarmingly rising, millets were left unaffected as they are typical C₄ plants.

Key words: Neglected underutilized species, Climate resilience agriculture, Sustainable agriculture, Millet, Nutrition, Future smart foods.

Environmental factors promoting blast disease in non-basmati aromatic rice

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Northern part of West Bengal is a repository of traditional aromatic rice cultivars. Non-basmati aromatic rice cultivar Kalonuniya is very unique to this region. In addition to aroma, these

cultivars are rich source of antioxidants and of higher nutritive value. Despite higher value and demand its cultivation is not substantial due to rice blast disease. Rice blast is recurring and devastating disease caused by a fungal pathogen *Magnaporthe oryzae*. Occurrence of neck blast is more severe in both Kharif and Boro season as the grain development stage coincides with hot and humid weather condition of this region. Occurrence of leaf blast is more in kharif season than boro season. Phenotypic screening of Kalonuniya and its cross with rice blast resistant genotypes (PB-1637, PB-1509 and UBKVR-124) for F₄, F₅ and F₆ suggests a correlation between area under disease progress curve value (AUDPC) with Soil plant analysis development (SPAD), Normalised difference vegetation index (NDVI), Canopy temperature (CT) values. SPAD and NDVI at boot and grain filling, canopy temperature at grain filling and milky stage was recorded. Higher SPAD value indicates good chlorophyll content and NDVI suggest better plant health, lower CT value is related to altered microclimatic conditions avoiding progress of rice blast disease which can be used for screening of resistant and tolerant lines, the result is also supported by molecular screening under this study. F₄ generations of Kalonuniya X Pusa Basmati 1637 were screened for the presence of pi9 genes and positive events were selected for the next generation.

Key words: non-basmati aromatic rice, Phenotyping, AUDPC, Rice blast

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Stability analysis for identification of high-yielding stable pigeonpea genotypes for different agro-climatic zones of Jharkhand

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Pigeonpea is one of the major protein sources among grain legumes. However, major constraints like climate uncertainties are resulting in an increase in the yield gap of Pigeonpea in Jharkhand. The assessment of GXE's impact on the Pigeonpea genotypes can aid in overcoming the influence of the environment. The objective of the study was to identify the stable and high-yield Pigeonpea genotypes for various agro-climatic zones of Jharkhand. Twelve Pigeonpea genotypes were evaluated for high yield and stability at four locations in Jharkhand using randomized block design with 3 replications. Data collected was subjected to AMMI and GGE biplot analysis. The combined ANOVA revealed the existence of significant differences in environment, genotype and GXE. The first two principal components of Yield per plot accounted for 54.4% and 26.3% respectively. The which won where polygon of the GGE biplot analysis identified that genotypes BAUPP 18-10 in Darisai and Dumka, whereas BAUPP 15-21 and BDN-2 are identified as superior performers in both Chianki and Ranchi environments. The Ranchi environment has



been identified as the most discriminative and representative and the most ideal environment. All the environments were positively correlated with each other. Based on the genotype ranking plot, the order of ideal genotypes follows as BA-1, BAUPP 19-10 and BAUPP 19-11 respectively. The genotypes BAUPP 18-10, ICP8863, JKM 189, BDN-2, ICPL 87119 and BDN716 are high-yielding and among these ICP8863 was the most stable. The utilization of identified high-yielding and stable genotypes can bridge the existing yield gap in Pigeonpea.

Key Words: Climate uncertainties, Agro-climatic zones and Principal components.

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Evaluation of chickpea (*Cicer arietinum* L.) genotypes for yield and yield attributing traits under limited water condition

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The present research work was conducted on 28 genotypes of chickpea (*Cicer arietinum* L.) including three checks during rabi season, 2021-2022 at research farm of Birsa Agricultural University, Ranchi, Jharkhand to evaluate the performance of the genotypes under normal condition and rainout shelter for morphological, biochemical and physiological traits. The experiment was designed in a randomized block design with three replications. The study unveiled significant findings regarding genetic variability and the influence of different physiological and biochemical traits on yield. Genotypic variance was particularly high for yield per plot and specific leaf area, highlighting substantial genetic diversity among the genotypes. Several traits, including proline content, chlorophyll content, protein content, specific leaf area, the number of pods per plant, and specific leaf weight, exhibited considerable genetic variation. Heritability estimates ranged from low to high, for the traits specific leaf area, specific leaf weight, and proline content displaying high heritability, emphasizing the genetic control of these traits. Path coefficient analysis indicated that several traits directly affected yield per plant, with implications for breeding programmes aimed at enhancing chickpea productivity. Positive correlations were found between yield per plant and traits like the number of secondary branches, number of primary branches, proline content, protein content, and relative water content, underscoring the significance of these traits in yield improvement. Results also revealed a stronger genetic correlation compared to phenotypic correlations, indicating limited environmental influence in the transmission of these traits. Notably, a negative correlation was observed between yield per plant and specific leaf weight, suggesting a trade-off between these traits. These findings provide valuable insights for chickpea breeders, offering a basis for developing chickpea varieties with improved yield and resilience to limited water conditions.

Keywords: Genetic variability, Correlation, Path coefficient, Variance

Enhancing the tolerance of plants to combined stress factors: a strategy for the development of climate-resilient crops

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The phenomenon of global warming and climate change has been identified as a significant driver behind the notable rise in both the frequency and intensity of various abiotic stresses, including but not limited to droughts, heat waves, cold snaps, and flooding. These adverse environmental conditions have had detrimental effects on crop yields, leading to a shortage in food supply. Climate change is exerting a significant influence on the makeup and behaviour of various insect and disease populations, hence contributing to global reductions in crop yields. Agriculture faces additional limitations due to the escalating levels of contaminants generated by human activities, with the detrimental effects of climate change on soil microbiomes. While laboratory settings often focus on studying the effects of individual stress conditions on plants, it is important to note that in natural environments, plants are often subjected to several stressors such as pollutants, pests, and various other factors. Consequently, plants may experience combinations of stress situations in the field. Due to the anticipated impact of climate change on the occurrence and severity of stress combination events, such as the convergence of heat waves with drought, flooding, abiotic stresses, pollutants, and infections, it is imperative to undertake a focused investigation into the effects of stress combination on agricultural crops. The urgency of this requirement is of utmost importance, given that numerous studies have demonstrated the distinct and unpredictable response of plants to combined stress conditions, which cannot be deduced solely by examining individual stressors within the combination. Therefore, the implementation of strategies aimed at improving crop tolerance to a certain stress may not necessarily result in enhanced tolerance to this stress when combined with other factors. In this paper, we undertake a comprehensive examination of recent research on the effects of stress combinations in various plant species. Additionally, we put forth novel strategies and pathways to enhance the cultivation of stress combination- and climate change-resistant crops. The present discourse centres around the topics of climate change and global warming, specifically in relation to the impacts they have on crop plants. These impacts manifest in the form of abiotic stress, such as temperature extremes and water scarcity, as well as biotic stress caused by pests and diseases. Furthermore, the combination of these stressors, known as multifactorial stress combination, poses additional challenges for crop plants. In response to these challenges, crop plants have developed acclimation techniques to mitigate the negative effects of stress and maintain optimal output.

Keywords: globalwarming, stres tolerance, breeding, acclimitization, sustainability



Genetic variability, heritability and genetic advance in black gram (*Vigna mungo* L. Hepper)

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The present study was conducted using a population of 50 diverse genotypes of Black gram (*Vigna mungo* L. Hepper) in the department of genetics and plant breeding, Birsa Agricultural University, Ranchi. The experiment was carried out at the agriculture research farm, Birsa Agricultural University, Ranchi during the kharif season of the year 2021-22. The experimental design used was randomized block design (RBD) with three replications. The thirteen yield attributing characters, disease and pest, related trait were taken under the study. The analysis of variance has revealed the existence of significant differences for all the characters under consideration. It was observed phenotypic variability was higher than the genotypic variability, indicating that environment has impact on characters under investigation. It was observed that phenotypic coefficient of variation was higher than the genotypic coefficient of variation. Higher values of Phenotypic and genotypic coefficient of variation are recorded for traits like number of effective pods per plant, seed yield per plant, number of pods per plant, number of seeds per pod, number of primary branches per plant and number of pods per cluster are having high values of phenotypic coefficient of variation. High heritability with high genetic advance as % of mean was recorded for the plant height, number of primary branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, number of effective pods per plant, number of seeds per pod, seed yield per plant and biological yield. Correlation analysis revealed that the trait days to maturity, number of clusters per plant, number of pods per cluster, number of pods per plant, number of effective pods per plant, biological yield, and harvest index recorded a substantial positive association with seed yield per plant. The path coefficient analysis found that several traits had a positive direct effect on seed yield per plant like days to 50% flowering, number of cluster per plant, number of pods per cluster, number of effective pods per plant, number of seeds per pod, 1000 seed weight, and harvest index Therefore it may be considered that these yield attributing characters are important for improving the yield of black gram and use as further breeding programme.

Key word: Phenotypic and Genotypic coefficient of variation, Heritability, Genetic advance, correlation and Path path coefficient coefficient analysis

Character association studies and path coefficient analysis in F_7 generation of a Rice (*Oryza sativa* L.) cross

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Rice is considered as one of the major staple food crops for more than 3.5 billion people who rely on this crop for almost 20% of their regular calorie intake and thereby considered as a lifeline for food and nutritional security. The present investigation was conducted at the experimental plot of Birsa Agricultural University, Kanke under the rainfed conditions of Jharkhand, India during kharif 2020 and 2021 in the F_6 and F_7 generation seeds of the cross Pusa-1176 x BPT-5204 respectively. The F_6 generation plants were particularly examined for the trait spikelet sterility and plants to be grown in F_7 generation were selected based on sterility percentage. Then, selected plants were sown as panicle to progeny rows at two different dates as set I and set II with the interval of 15 days in order to study the influence of environment on the traits under study. The objective was to establish the nature of association between grain yield and yield components by partitioning the correlation coefficients between grain yield and its components into direct and indirect effects by using simple correlation and path analysis in each set for comparative studies among the segregants. The correlation coefficient analysis showed that the characters such as number of tillers, plant height, panicle length, number of panicles, number of filled spikelet, number of unfilled spikelet, spikelet fertility, grain width, L/B ratio and 100 seed weight showed highly significant positive correlation with seed yield per plant in both the sets. But path analysis revealed that number of panicles and number of filled spikelet exhibited the highest positive direct effect on seed yield per plant in both the sets among all other characters under study indicating it to be used directly as selection criteria for effective improvement in grain yield.

Mitigate climate change through carbon sequestration

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Global warming and an increase in the atmospheric concentration of carbon dioxide (CO_2) are related to climate change. But compared to the preindustrial level of 280 ppm, the atmospheric CO_2 level today is approximately 397 ppm, a considerable rise. Global warming is caused by the trapping of heat in the earth's atmosphere, which is increased greenhouse gas (GHG) emissions. Due to its massive emissions of greenhouse gases such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O), the agriculture industry is largely responsible for climate change. In order to minimize global warming, carbon dioxide emissions must be decreased. Scooping up and storing atmospheric carbon dioxide for a long time is known as carbon sequestration. In addition to lowering emissions and increasing removals, the agriculture sector also contributes significantly to sequestering carbon dioxide by avoiding or shifting emissions as mitigation



strategies are implemented. According to Smith et al. (2007), the agricultural sector has the potential to mitigate carbon emissions globally by 2030 by around 5.5 to 6.0 Gt year, with soil sequestration accounting for 89% of this amount. Carbon sequestration via means of conservation Agroforestry, crop diversification, conservation tillage, residue management, agroforestry, and the use of biochar as bio amendments are a few examples of climate savvy agricultural practices. These methods enable sustainable resource usage, boost food production, and have a strong chance of sequestering soil organic carbon (SOC). Emissions are reduced by 30 to 35 kg C per ha per season when conventional till farming is switched to no-till farming. One crucial measure of soil health is SOC. The SOC rose to 0.39% with zero tillage (ZT) after a 4-year research, compared to 0.26% under conventional tillage (CT) (Shekhawat et al., 2018). The zero tillage (ZT) condition produced the highest carbon sequestration potential rate (CSPR). Because a significant amount of C in biochar does not break down, it remains bound for a long time, resisting global warming. Fixation of C in soil as biochar can improve soil fertility at low cost. Through slow pyrolysis and amended soil, increased soil organic carbon and organic matter content in an eggplant field, corn husk and rice husks were converted to biochar (Mohan et al., 2018). Agroforestry systems are important both as a source and sink of C and in linking food production with environmental services. They also improve the system's resilience to the adverse effects of climate change by conserving SOM through above- and below-ground litter and residues. The potential average carbon supply of agroforestry systems is 9, 21, 50 and 63 Mg C ha⁻¹ in semi-arid, sub-humid, humid and temperate climates, respectively.

Soil C sequestration is a strategy to achieve food security by improving soil quality. This is a by-product of the inevitable need to adopt Recommended Management Practices (RMP) to improve yields. By slowing the rate of atmospheric carbon dioxide enrichment, soil C sequestration improves and maintains biomass/agricultural productivity and can offset fossil fuel emissions by 0.4-1.2 Gt C per year, or 5-15% of global emissions. Soil C sequestration can mitigate climate change by reducing atmospheric CO₂ levels and increasing SOC through sustainable agriculture (reducing tillage, retention and crop diversification to include legumes in the rotation), agroforestry and using biochar as bioremediation.

Key Words - Carbon Sequestration, Soil Organic Carbon(SOC), Zer-tillage, Conventional tillage(CT),Biochar, Agroforestry, Crop diversification

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Anatomical, physiological and agro-morphological responses of rice genotypes under multi-stage and stage-specific drought conditions in eastern indo-gangetic plain

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With the changing climate, drought stress has become one of the most important limiting factor to sustainable crop productivity. Drought can occur at any stage of the rice crop in a year with

varying duration causing significant yield loss in rainfed as well as water limited irrigated areas. Most of the current high-yielding rice varieties grown in the drought-prone areas of eastern Indo-Gangetic Plain (EIGP) are highly susceptible to drought. Keeping in view, present study was conducted to identify extreme drought tolerant rice genotypes and explore the effect of stage specific and multi-stage drought (MSD) effect on rice genotypes sown in the field condition. Twenty four rice genotypes were evaluated under individual (seedling stage drought; SSD, vegetative stage drought; VSD, reproductive stage drought; RSD) as well as the multiple growth stages (multi-stage drought; MSD) for two consecutive rice growing seasons (2019–2020). Moderate to severe drought stress during both years leading to average grain yield reduction of 43.5%, 28.9%, 59.3%, and 69.9% under SSD, VSD, RSD, and MSD conditions, respectively. Average grain yield for the 24 genotypes during non-stress, SSD, VSD, RSD, and MSD ranged within, 4.17–5.68, 1.94–3.46, 2.65–4.36, 0.99–2.86, and 0.37–2.39 t ha⁻¹, respectively. Further, stage-specific as well as cumulative (MSD) drought caused reduction in plant height, flag-leaf length, biological yield, test weight, tillers m⁻², grains panicle⁻¹. Identified promising rice genotypes, IR83929-B-B-291-2-1-1-2, IR93827-29-1-1-2 and IR84899-B-183-20-1-1-1 showed extreme drought tolerance and better maintained photosynthetic rate, stomatal conductance, relative water content, (RWC) membrane stability index (MSI), and total chlorophyll content under drought conditions irrespective of growth stages. The present study also validated that the identified promising genotypes critically maintained their pollen viability and spikelet fertility under drought stress, and thus have better grain yield. Identified promising rice genotypes could be good substitutes for the existing drought tolerant varieties under rainfed and water limited irrigated ecosystems. Overall, this study provided a comprehensive understanding of stage specific and MSD tolerance in rice, and identified drought tolerant rice genotypes which may ensure the food security in drought-prone areas of eastern Indo- Gangetic Plains.

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Performance of sweet pea (*Lathyrus odoratus* L.) genotypes under Ranchi condition

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An experiment was conducted under RBD with seven genotypes of sweet pea (*Lathyrus odoratus* L.) viz. PAU-1, PAU-2, PAU-3, PAU-4, Ranchi Local-1, Ranchi Local-2 and Pantnagar Local-1 during the year 2018-19 to assess performance of sweet pea genotypes under Ranchi condition. Maximum plant height of 75.33 cm was observed in the genotype PAU-3 however, it was statistically on par with PAU-1 (73.00 cm), PAU-2 (70.00 cm) and PAU-4 (68.33 cm). Days to first bloom was recorded minimum with Pantnagar Local-1 (100 days) which was statistically at par with Ranchi Local-1 (102.66 days) for this character. Number of flowering stalks per plant was also recorded maximum (25.00) with the genotype Pantnagar Local-1 however, it was again statistically at par with Ranchi Local-1 (24.33). Flowering duration which is also an important character, was found longest with Ranchi Local-1 (57.66 days) which was statistically at par and numerically very close to Pantnagar Local-1 (57.00 days). Length of pods was found maximum (5.67 cm) in PAU-4 however, it was statistically on par with rest four genotypes except Pantnagar Local-1 for the character length of pod. Number of seeds per pod was found maximum (6.00) with



Ranchi Local-1 which is also a remarkable parameter for seed production and this character was statistically at par with only one entry PAU-2 (5.00). Similarly, number of pods per plant was also recorded maximum (29.33) with the genotype Ranchi Local-1 which was statistically at par with Pantnagar Local-1 (28.33). On the basis of observations recorded, it can be preliminarily inferred that Ranchi Local-1 was superior to other genotypes regarding flowering duration, number of seeds per pod and number of pods per plant however, it was at par with Pantnagar Local-1 for days to first bloom and number of flowering stalks per plant.

Key Words: *sweet pea, flowering duration, days to first bloom*

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Heat and drought tolerance in wheat crop – a review

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Wheat (*Triticum aestivum*) is one of the world's most important cereal crops, providing a staple food source for a significant portion of the global population. It is a source of basic calories and protein. However, increasing temperatures and changing climate patterns have led to an escalation in heat waves and prolonged droughts, severely affecting wheat productivity and quality. Heat and drought stress pose significant challenges to wheat crop production, impacting global food security. The climate is drastically changing day by day and with the increasing population we are in need of new technologies with higher rate of production. Drought and heat stresses are major component that effects the yield. Moreover, it also reduces reduces grain number, photosynthetic activity and chlorophyll content and starch synthesis in the endosperm. Reactive oxygen species accumulated under heat stress cause severe oxidative damage to the crop. Plant rapidly produces heat shock proteins to minimize the effect of heat stress. Several traits such as stay green, chlorophyll fluorescence and canopy temperature play significant role in heat tolerance. In order to develop new crop varieties that can cope with future climate, knowledge of heat stress effect and tolerance at physiological, biochemical and morphological level is highly important. This review article aims to provide an overview of the current understanding of heat and drought tolerance and the morphological, physiological and biochemical responses of heat and drought stress in wheat. It states the conventional and advanced breeding for heat and drought tolerance. The article highlights the importance of breeding methods for enhancing heat and drought tolerance in wheat. Genetic Basis of Heat and Drought Tolerance in Wheat Advancements in molecular biology and genomics has allowed for the identification of genes and genetic factors associated with heat and drought tolerance in wheat. It also highlights the potential for genetic engineering and breeding strategies to develop heat and drought-tolerant wheat varieties. Combining different methods and analysis will be the best option for development of such tolerant genotypes/varieties. Understanding the genotypes and the interactions of environment and under stress some integrated system can be used wheat stability of yield.

Keywords: Wheat, heat stress, drought stress, reactive oxygen, photosynthetic activity, morphological responses, physiological responses, biochemical responses, conventional breeding, advanced breeding, genomics.

A sustainable approach of biofertilizers to fruit crops

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Biofertilizers are basically microbial preparations comprising living cells of diverse microorganisms which have the capability to mobilize plant nutrients in soil from unusable to usable form through biological process. They are environment friendly and play significant role in crop production. Perilously it was primarily used for field crops but now a days it is used for fruit crops also. Biofertilizers are able to fix 20-200 kg N/ha/year, solubilize P in the range of 30-50 kg P₂O₅/ha/year and mobilizes P, Zn, Fe, Mo to varying extent. Biofertilizers are used in live formulation of beneficial microorganism which on application to seed, root or soil, mobilize the availability of nutrients particularly by their biological activity and help to build up the lost microflora and in turn improve the soil health sustainable in general. Nitrogen fixing biofertilizers mainly Azospirillum and Azotobacter can able to fix 20-40 kg N/ha and produce growth promoting substances like IAA. Use of microbial inoculants is not only a low-cost technology but also it takes adequate care of soil health and environmental safety. Thus, the use of biofertilizer is increasing day by day due to rise in the price of chemical fertilizers, its beneficial effect on soil health and increase in production of crop.

Keywords: Azospirillum, Azotobacter, Microorganisms, Sustainable

Stability and Genetic diversity in faba bean under terminal heat

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Faba bean (*Vicia faba* L.) is an important potential pulse crop in India. It contains 22-28% protein in seed and can fix about 219-63 Kg N/ha. Genotype and Environment (GE) interaction and genetic diversity analysis are important in it's in a breeding program. Total 35 genotypes of faba bean (*Vicia faba* L.) were sown in Randomized block design in three sowing environments in 'Rabi 2021-2022. Stability parameter based on the Eberhart and Russell model and D² analysis based on Mahalanobis cluster were study for the 15 quantitative characters. It was evident from the pooled analysis that, the mean sum square among the genotypes were highly significant for days to flower initiation, plant height, number of primary branches per plants, number of pods per plants, number of seeds per plants, seed yield per plant and 100-seeds weight indicating the considerable amount of genetic variability in the for these following characters. The optimum temperature



for flowering of faba bean is 22–23 C. Temperature above the 27 during pod development stage tends to reduce the seed weight. Based on high mean, unit regression ($b_i=1.0$ i.e., $b_i=S E m_1$) and least deviation from regression coefficient $S^2 d_i=0$ genotypes Hanma-2 was most stable under three different environments. Based on the mean values of D^2 analysis of 35 genotypes of faba bean (*Vicia faba* L.) under present investigation revealed the existence of considerable genetic diversity among them. In environment I hybridization between the genotypes RFB-14 (cluster x) with ET226414 (cluster xiv), ET226415 genotype (cluster xii) with ET226414 (cluster xiv), HFB-1 (cluster xii) with ET226414 (cluster xiv), In environment II hybridization between the any one genotypes of cluster I with Rebaya-40 (cluster III) and In environment 3 hybridization between the genotypes ET226430 (cluster X) with ET226426 (cluster XII), ET226417 genotype (cluster VIII) with ET226430 (cluster X) may be exploited for development of varieties for higher yield. These genotypes in the most divergent clusters may be able to take advantage of the maximum heterosis under different environment.

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Differential responses of indica rice (*Oryza sativa* L.) landraces towards germination and early seedling growth under hypoxic conditions

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In Odisha most of the rice grown area is under rainfed conditions which is stretched through upland, medium and lowland. Medium and lowland areas are situated at lower elevation so during heavy rainfall receive most of the runoff from uplands and are mostly flood fed with low drainage leading to water logging conditions. Flooding at seedling establishment stage in paddy causes maximum yield reduction. The landraces grown here mostly belong to the *aus* group of *indica* sub-species which has evolved in these hilly terrains are tolerant to many biotic and abiotic stresses.

Screening of rice genotypes grown in Jeypore tract and neighbouring areas was conducted to identify their capacity to germinate and grow under low oxygen conditions for this a total of 110 rice genotypes including traditional varieties, landraces, basmati types and released varieties of Odisha, were used from the germplasm maintained at Regional Research and Technology Transfer Station (OUAT), Bhawanipatna, Kalahandi, Odisha during 2020-2021.

Ten seeds each of the 110 genotypes were allowed to germinate in test tubes with a standing water height of 10 cm for 3 weeks. Only 16.36 % (18 genotypes) showed over 40% germination rate in the initial screening. These eighteen genotypes were taken up for direct dry seeding in earthen pots with soil inside plastic grow bags. Dry seeds (25 No.) of each line were sown at 5.0 cm soil depth and submerged with a water depth of 10 cm and seedling emergence rate was determined based on the number of seedlings that reached the surface of the water.

Only four landraces (Parbatjeera, Dhobaluchi, Kalikati and Deulabhog) were found to have more than 70 % seedling emergence rate when sown in submerged conditions (pots). From these experiments it was observed that the landraces have the capacity to germinate and survive under hypoxic conditions. These landraces directly or by using them for breeding cultivars with tolerance to flooding during germination and early seedling establishment will help in improving production from these ecosystems.

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Genetic diversity study in wheat

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Plant Breeder's prime goal is to develop new plant variety in a systemic and ongoing method. Novel crop varieties, which will survive in more severe, changing and uncertain environmental condition, can only mitigate the effects of climate change on crop productivity and food security. For this very purpose, genetic variation among individuals within a plant species is studied with respect to desired traits and introgress to produce new improved varieties. Acknowledging the same, an experiment was carried out at Western section of Research Farm, BAU, Kanke, Ranchi during *Rabi* season 2022-23. A total of 105 genotypes of Wheat were evaluated against four check varieties viz., DBW 187, DDW 48, HD 2967 and Sonalika, to study genetic diversity present among them. Experiment was laid down in Augmented Block design within seven blocks, each having fifteen genotypes and the checks were replicated in each block. The Analysis of Variance revealed that all the genotypes were highly significant for almost all the traits at 0.05% probability level. Genetic diversity analysis revealed formation of three clusters accommodating all the genotypes. Cluster-I has maximum number (85) of genotypes with average intra-cluster distance of 3.084. Maximum average inter-cluster distance was recorded between Cluster-II and Cluster-III, whereas, maximum intra-cluster distance was observed by Cluster-II. This result indicates that the genotypes present in these clusters are genetically more diverse among the others. Furthermore, based on the cluster mean, Cluster-III has been identified for selecting parents for incorporating traits like early maturity, plant height, tillers per square meter and spike length; whereas, cluster II for number of grains per spike, total grain weight and Grain yield per plot.

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Variability in dark response of tomato leaves under ex-vivo condition for identification of low light tolerant genotypes

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Unpredictable weather condition in our day to day live creates huge loss in crop production. Development of climate resilient crop is the need of the time to achieve success. Leaf



senescence is an important agricultural trait and is influenced by environmental conditions such as temperature, poor light (dark), restricted nutrient supply and pathogen attack. Dark affects chloroplast development and causes etiolation. Dark-induced senescence has immense importance in the field of agriculture, as it can be used as a potential tool in breeding for optimization of senescence pattern (Saulescu *et al.*, 1998). Exposure of tomato plants to dark period promotes leaf senescence, which takes place at different speed in young, mature and old leaves of intact plants. The objective of the present research work is to reveal variability in dark response of tomato leaves under ex-vivo condition for identification of low light tolerant tomato genotypes for climate resilience. Yield performance of 45 tomato genotypes were evaluated in a randomised block design with two replications at OUAT, Bhubaneswar. At 40 days after transplanting, five numbers of fully expanded and healthy leaves were detached from 5th node (from the top to bottom of the plant) and exposed to dark treatment for 7 days and chlorophyll content was indirectly measured by using Minolta SPAD-502 meter. Based on eye observation, the leaves were scored as 0, 1 and 2 for green, partially yellow and fully yellow leaflets of each compound leaf on 7th day of dark treatment to calculate senescence index. Analysis of variance revealed significant variation among the genotypes in respect of chlorophyll content of dark treated leaves. At 3rd day of dark treatment the SPAD value ranged from 5.16 to 26.60 with a mean of 16.15; At 5th day of dark treatment the SPAD value ranged from 4.17 to 21.33 with a mean of 12.06 and At 7th day of dark treatment the SPAD value ranged from 3.32 to 14.33 with a mean of 8.03. The SPAD value was found to decrease with the increase of dark treatment duration. Fruit yield of the genotypes varied from 1.203 to 3.142 kg/plant with a mean of 2.330 kg/plant. Correlation analysis showed a significant positive association (0.399) between chlorophyll content and fruit yield on 3rd, 5th and 7th day of dark treatment (0.399, 0.445 & 0.315). Senescence index value of the genotypes ranged from 0.07 to 0.81 with a mean of 0.41. Senescence index of the genotypes exhibited a negative correlation with fruit yield (-0.203). Some genotypes showed consistency in their dark tolerance and some showed inconsistency performance. The national check variety Arka Vikash showed tolerance on 5th day only, whereas OUAT released variety Utkal Deepti (BT 2) having the highest yield showed tolerance to dark treatment on 3rd, 5th and 7th day. The genotypes showing high SPAD value on 3rd, 5th and 7th day and low senescence such as BT 2, BT 18, BT 218, BT17-2, BT442-2, BT 12-3-2, BT 224-3-1, BT 413-1-2, BT 429-2-2, BT 433-1-2, BT 19-1-1-1, 11/TOBW-3 & BT 17-2-5X1 were identified as low light tolerant genotypes and could be utilised in crossing programme in future for developing climate resilient crop. This approach for selection of dark tolerant genotypes is simple, rapid and inexpensive.

Key words: Tomato, dark treatment, climate resilience, senescence

Effect of male gametocides on pollen fertility in castor (*Ricinus communis* L.)

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An experiment were conducted to understand the effect of chemically induced male sterility in castor. Degree of pollen sterility varied with nature of chemical, concentration and genotype of castor. Ethrel @ 0.3 % sprayed three time at initiation of flower inflorescence before the anthesis, which resulted in highest pollen sterility (61.91 %) with genotype SKI 215 followed by ethrel @ 0.2 % (53.89 %) with genotype JI-96 and Ethrel @ 0.1 % (52.81 %) with genotype SH-72 sprayed at same stage. Pollen sterility increased with increasing concentration and depends on genotype. The plant height increased significantly due to GA₃ and decrease with ethrel and EMS. All chemicals increased the number of branches significantly. However, number of branches decreased with increase the concentration of chemical and also along with different genotype of plant. Higher concentration of all gametocides resulted in reduction in number of capsule per primary raceme per plant and number of seed per primary plant by causing the ovular sterility. The effective dose EMS @ 40 mM with genotype GEETA caused 77.78 per cent ovular sterility thrice time before the anthesis in the plant. The lowest ovular sterility per cent was recorded in GA₃ @ 1000 ppm with SKI-215 caused 1.53 per cent thrice time before the anthesis in the plant. Anther development studies revealed that shriveling of anther, anther locule, microspores, degeneration of anther wall, clumping of meiocytes and early degeneration of tapetum in ethrel induced pollen sterility whereas, all these were normal in control plants

Survey and evaluation of genotypes of linseed (*Linum usitatissimum* L.) against alternaria blight disease

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Linseed (*Linum usitatissimum* L.) is one of the most important winter oilseed crop and stands next to rapeseed-mustard in area and production. It has an important position in Indian economy due to its wide industrial utility. There are different varieties of linseed meant for dual purposes. Oilseed-type plants are generally shorter, have more branches and produce more seeds, while fiber flax types are usually taller, have few branches. It is mostly grown under conserved moisture and limited nutrient conditions with poor management practices. Diseases are one of the major hurdles that limit the productivity of linseed. Extensive surveys were carried out in major linseed growing areas of Jharkhand and the result revealed that the Alternaria blight disease was

prevalent in all surveyed districts of Jharkhand. The incidence of disease ranged from 6.3% to 54.4% in different surveyed villages with maximum severity in Kanke and Chanhoh Block. The incitant *Alternaria lini* is predominant necrotrophic pathogen that cause destruction of host tissue through the reduction of photosynthetic area by inciting spots and blights during all the growth stages of plants. The pathogen is genetically diverse showing variability in respect of cultural and morphological characters. Use of resistant cultivar is a reasonable and easy method for disease management. Therefore, the present investigation was carried out to evaluate 96 genetically diverse genotypes against *Alternaria* blight of linseed under natural epiphytotic conditions. The result revealed that out of 96 entries, none of the genotypes recorded disease free (F), 9 entries (Divya, Priyam, Rashmi, RLC-92, LC-54, F8-2, BAU13-01, BAU-13-08, BAU-15-06) recorded resistant reaction (upto 10% severity), 37 as moderately resistant (upto 25% severity), 40 as moderately susceptible (upto 50% severity) and 10 entries recorded susceptible (F5-7, BAU 14-04, BAU 13-06, Pusa 2 (R552), F1-15, PKDL-NL-260, F8-6, Sival, Kota-Barani-Alsi-4, Rashmi×Meera) reaction (upto 75% severity) to the disease. However none of the entries showed highly susceptible (HS) reaction.

Keywords: Linseed, *Alternaria* blight, survey, screening

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Genetic variability studies in advanced mutant lines of soybean (*Glycine max* L. Merrill)

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262 mutants (M5 and M6) of soybean genotype BSS-2 and 254 mutant (M5 and M6) of soybean genotype RKS-18 were used as experimental material in the year 2019-20. A set of both genotypes were irradiated with five doses [50Gy, 100 Gy, 150 Gy, 200 Gy and 400 Gy] of Gamma rays in Kharif 2014 as well as in Kharif- 2015 under BRNS-BARc Project of Soybean in Deptt. of Genetics and Plant Breeding. The experiment was conducted in Birsa Agricultural University research farm, Ranchi. Non-replicated plant to progeny rows of all the 262 M5 & M6 mutant plants of BSS-2 and 254 M5 & M6 mutant plants of RKS-18 were grown along with parent genotypes. Observations for quantitative characters were recorded in random ten plants of each mutant progenies of both the genotype to assess the polygenic variations in the M6 and M7 generation of both BSS-2 and RKS-18 for traits such as plant height, number of pods per plant, 100-seed weight, and yield per plant. Genetic parameters, including genetic variability, heritability, and genetic advance. Qualitatively, both genotypes exhibited distinct responses to different gamma ray doses. BSS-2 showed consistent trait variation across different plant populations, while RKS-18 displayed significant differences, particularly in the number of pods per plant in the M6 generation. Traits like plant height, number of pods per plant, 100-seed weight, and yield per plant exhibited low genetic and phenotypic coefficients of variation, suggesting minimal environmental influence on their expression.

Screening of greengram [*Vigna radiata*] genotypes for salinity tolerance

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Green gram [*Vigna radiata*] is one of the most important pulse crop of India one of the major producers. Green gram is a self-pollinated, low input-requiring crop with short duration (65–90 days) and wider adaptability. Raising salinity will have irresistible global effects, It may result in 50% yield losses by 2050. Salinity tolerance genotypes is needed to withstand the soil conditions of the coastal soils. A total of 22 green gram genotypes viz. SM-22-79, SM-22-80, SM-22-83, SM-22-84, SM-22-85, SM-22-90, SM-22-94, SM-22-95, SM-22-96, SM-22-98, SM-22-99, SM-22-100, SM-22-101, SM-22-102, SM-22-103, SM-22-106, SM-22-107, SM-22-108, VBN-5, CO-6, CO-7, CO-8 were collected from Department of PGB, AC&RI Madurai. Genotype CO-8 was used as a check. The treatments in the experiment were laid out in CRBD under in-vitro conditions with three replications in 4 different EC levels – control, Ec4 dS/m, Ec8 dS/m, Ec12 dS/m. The mean germination percentage was higher (90%) in SM-22-95 and had the highest shoot length in all three stress levels followed by SM-22-84(16.75), SM-22-94(15.26). The SM-22-99 recorded highest root length of 14.74 cm followed by SM-22-100(14.48), SM-22-84(14.36), at 12ds/m. SM-22-84 recorded the highest Vigour index at both the highest and lowest salinity levels of 4183.61 and 1454.84 respectively. Simple linear correlation analysis showed that dry matter had a positive correlation with radicle length (0.4458) at control followed by radicle length (0.5660) at 8 EC, positive non-significant correlation was noticed in root length (0.3539) at 12EC, plumule length (0.2187) at control, (0.2471) at 8Ec, (0.3595) at 12Ec. The coefficient of variation varied among data from different characters and the maximum for dry weight (56.18) was followed by root length (18.58) and the minimum coefficient of variation was recorded in germination percentage. A positive correlation between germination and radicle length at higher levels of salt concentration is a possible selection criterion for salt tolerance in green gram. Studying the variation among cultivated varieties and advanced cultures may help us to identify the suitable genotypes for saline soils and they can be deployed as a donor for the development of saline-tolerant varieties.

KEYWORDS: Vigour index, salinity tolerant, germination percentage, dry matter.



Identification of imazethyper resistance families for high yielding and early maturity in rice (*Oryza sativa* L)

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Rice (*Oryza sativa* L.) is a monocot plant ($2n=24$) belonging to family gramineae and is a self-pollinated crop. It is most important cereal food crop of India and is the major source of calories for more than half of global population. It contains 6-12% protein, 70- 80% carbohydrate, 1.2-2.0% minerals and significant content of fat and vitamins. Rice is the staple food of Asia and part of the Pacific region, where more than 56 percent of the world's population live, adds 51 million more rice consumers annually. To feed growing population the demand of increasing production of rice faces many constraints. Weeds are identified as a major biological constraint that hinders attainment of optimal rice productivity in major rice producing ecology. So, successful method for controlling weeds is the rational application of herbicides. Herbicide-resistant rice genotypes combined with the appropriate herbicides can be used to efficiently eradicate weeds in rice farming. As a result, rice that resists herbicides has drawn increasing interest and significance. The experiment was conducted during kharif 2023 in Alpha lattice design with two replications at Rice Research farm of Birsa Agriculture University, Ranchi. Study material consists of 120-M4F4 families tolerant to Imazethapyr herbicide, received from Rice Research Scheme, Birsa Agricultural University. The herbicide tolerant segregants was developed by application of Sodium Azide on commercial hybrid (27P28). The hybrids are segregating for different agronomical traits in later generation, however plant families are fixed for Imazethapyr tolerance. On the ongoing research days to 50% flowering is observed and families are identified as short duration, medium duration and long duration comprising on an average 82, 33 and 5 families respectively. The study can further be conducted on selection for agronomically superior families in future generation. Identified families can also be selected as donor parent with a suitable recurrent parent for development of high yielding herbicide resistant lines as per need of different agro climatic zone or different selection factors along with duration of maturity can be studies in further generation as we are observing drought like condition prevailing in Jharkhand where DSR and short duration crops can be utilized efficiently.

Keywords: Imazethyper Resistant lines, Early maturity, Rice

Effect of biofertilizer consortia and their application mode on growth and yield of lentil (*Lens culinaris* L.)

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Pulses are the powerful super food because they are known as important and cheaper source of dietary protein and fat, low glycemic index & fat content, zero cholesterol, gluten free, high content of Iron & Zinc as well as rich in minerals & B-Vitamins. Among commonly grown pulses in India, Lentil (*Lens culinaris* L.) grows as an important *Rabi* (winter) pulse crop. In general, India's output of pulse crops is insufficient to supply the country's expanding population and meet the recommended consumption of pulse per day per person. There is still scope for technology advancements and refinement to achieve significant gains in productivity, which is now below the genetic potential of recently released and available varieties of lentil. Among many new emerging technologies, application of biofertilizer consortia by varying mode of application is considered an efficient tool for enhancing yield. Apart from this yield benefits, consortia biofertilizer also improves physico-chemical including the biological properties of the soils, where they are being applied, thereby restore fertility as well as overall soil health parameters. The current experimental entitled "Effect of Biofertilizer Consortia and their Application Mode on Growth and Yield of Lentil (*Lens culinaris* L.)" was carried out at the Research Farm of Tirhut College of Agriculture, Dholi (Muzaffarpur) with the main focus on study the impact of biofertilizer consortia and their mode of application on the growth, yield, nutrient content in grain & straw, economic feasibility and nutrient balance sheet in soil of lentil. The fourteen treatments were repeated three times, and the variety used was IPL-220. The experiment was conducted with Randomized Block Design (RBD). Treatments included: T₁-Absolute control (No fertilizer, No biofertilizer), T₂-100% Recommended Dose Fertilizer (RDF), T₃-*Rhizobium* (local best), T₄-Seed treatment with consortium biofertilizer inoculant (Pantnagar), T₅-Seed treatment with consortium biofertilizer inoculant (Ludhiana), T₆-Soil application of consortium biofertilizer inoculant (Pantnagar) incubated with FYM, T₇-Soil application of consortium biofertilizer inoculant (Ludhiana) incubated with FYM, T₈-Seed treatment with consortium biofertilizer inoculant (Pantnagar) + FYM, T₉-Seed treatment with consortium biofertilizer inoculant (Ludhiana) + FYM, T₁₀-Soil application of consortium biofertilizer inoculant (Pantnagar) incubated with vermicompost, T₁₁-Soil application of consortium biofertilizer inoculant (Ludhiana) incubated with vermicompost, T₁₂-50% of N, 50% P₂O₅ & 100% K₂O of RDF + Seed treatment with consortium biofertilizer inoculant (Pantnagar), T₁₃-50% of N, 50% P₂O₅ & 100% K₂O of RDF + Seed treatment with consortium biofertilizer inoculant (Ludhiana), T₁₄-50% of N, 50% P₂O₅ & 100% K₂O of RDF + *Rhizobium* (Local) + PSB (Local). The soil of experimental site was categorized under alluvial class, having a texture of sandy loam and a pH of 8.3 and Electrical conductivity 0.36 ds m⁻¹. The



soil fertility status was low in organic carbon, available nitrogen, phosphorous, and potassium content i.e., 0.43%, 191.7 kg/ha, 21.6 kg/ha, and 125.8 kg/ha, respectively.

The growth and yields of the lentil crop, as well as NPK and protein content in plant,

were significantly influenced by all experimental variables over control treatment. Among

different treatments, application of 50% of N, 50% P_2O_5 & 100% K_2O of RDF + Seed treatment with consortium biofertilizer inoculant (Pantnagar) recorded highest plant elongation (height), dry matter accumulation, leaf area index, number and weight of nodules per plant, number of primary and secondary branches, number of pods per plant, test weight, grain yield, straw yield, B:C Ratio, Protein content and Nutrient Uptake (N, P and K). Administration of 50% of N, 50% P_2O_5 & 100% K_2O of RDF + Seed treatment with consortium biofertilizer inoculant (Pantnagar)-treatment also showed marked monetary advantages as compared to rest treatments under study. This treatment produced highest gross returns (89505 ₹ ha⁻¹), net returns (52322 ₹ ha⁻¹) and B:C Ratio (1.41) over the rest treatments.

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Screening of germplasm against major diseases of linseed under rainfed ecosystem of Jharkhand

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Linseed is an important oilseed and flax crop grown in India. Among constraints in the production of linseed diseases are the most important limiting factors which restrict the cultivation and decrease the productivity of linseed. Keeping in view, cultivation of varieties resistant to diseases is a better option for its management, therefore, one hundred twenty eight promising entries were screened against wilt, *Alternaria* blight and Rust under artificial condition of inoculation during Rabi, 2021-22 with a row length of three meter each and checks were repeated after every ten entries. Among 128 entries, ten entries viz., RLC 109, BAU 09-08, SLS 68, LCK 9313, LMS 149, RRN 7, BAU 14-08, JLJ 2000, BAU 15-05 and Nagarkot were recorded as multiple disease resistance reaction i.e., against wilt, *Alternaria* blight and rust diseases. Fifteen entries viz., RLC 143, LC 14, RLC 143, SLS 58, LMS 2007-1, Kiran X OLC 10, Meera X Subra, Garima X LMS 149, BAU 16-08, JANKI, JLT-98 X SHEKHAR, Rashmi, RLC 85, Himalsi X SLS 61, SLS 108 were found to be resistant reaction against wilt whereas, twenty entries of linseed viz., BAU-14-09, Binwa, RL 270-33, RLC 109, SLS 29, BAU 06-07, RLC 45, SLS 85, SLS 85, NDL 2004-5, PKDL 62, LMS 149-04, Shekhar X SLS61, BAU 2015-05, BAU 15-06, NL 124, PKDL 65, MUKTA X BAU13-1, NAGARKOTA x Pusa -2, PADMINI X PUSA 3 showed resistant reaction against *Alternaria* blight disease and fifty four entries viz., Binwa, Kota Brani Alsi- 4, NL259, RJK 37, R 1017, SLS 40, RLC 116, RL 270-33, RL 260-28, LCK 1-1009, , RKD 18, LC 2279-4, RLC 129, Padmini, RLC 168, RLC 165, PKDL 165, RL 27004, PCL 1-06, OL 08-2-7, RLC 109, SLS 68, LCK 1404, BAU 06-07, SLS 85, PKDL 21, PKDL 62, RRN-7, BAU 13-01,

Shekhar X SLS61, NDL 2004-5, Sweta x T397, LMS 149, Mukta X BAU 13-01, Janki, Neelum X Sweta, Neelum X Shekhar, BAU 14-04, BAU13-01, Kota Brani Als1 3, RLC 92, RLC 100X T 397, Jeevan x Shekhar, SLS 86, BAU 15-05, SLS 86, RLC 85, LC 54, NDL 5, SLS 38, NL 124, Rashmi x Meera, Nagarkota, RLC 155, JLI 2000, PKDL 65, LMS 230, MUKTA X BAU13-1, Himalsi X SLS 61, Subra x LMS 427, PADMINI X PUSA 3, SLS 108, RLC 178 were recorded as resistant reaction against rust of linseed.

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Effect of sodium azide treatment on seed germination, seedling survival and seedling growth parameters in pomegranate (*Punica granatum* L.)

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An experiment in pomegranate to study the effect of sodium Azide (SA) mutagen on the seed germination(%), seedling survival(%), plant height(cm), number of primary branches/plant and number of secondary branches/plant and to determine its optimum dose which can be used in pomegranate mutation breeding programs was carried out at ICAR-NRCP, Solapur. Wherein, freshly harvested seeds of “Bhagawa” cultivar was treated with 10 different concentrations of SA i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 mM for 1hr, 2hrs., 3hrs. and were evaluated by comparing with the untreated Control seeds. The experiment was conducted in Completely Randomized Design with three replications consisting of 25 seeds per replication. Analysis of Variance showed the significant differences among treatments and timings for the evaluated parameters except for number of primary branches/plant. Increase in SA concentration upto 6mM caused a remarkable decrease in the percentage of seed germination and seedling survival for 1 hr. treatment; while upto 5 mM and 4 mM treatments in case of 2hrs and 3 hrs duration treatments. SA treatment upto 3mM, 8 mM and 4 mM for 1hr., 2 hrs., and 3 hrs. showed significant increase in plant height(cm) in comparison to control plants. Among various concentrations, 1mM for 1 hr. (31.90cm), 2mM for 2 hrs (35.90cm) and 2mM for 3hrs (19.90cm) treatments showed maximum plant height in comparison to control plants (29.70cm, 26.70cm, 16.70 cm) respectively. For number of primary branches, 1 hr SA treatment has only showed slight increment upto 4 mM doses (maximum 7.30) in comparison to control plants (6.1). While, SA treatment of 8 mM–1hr (35.3), 1 mM–2hrs (38.4), 8 mM–3hrs. (38.5) showed maximum number of secondary branches per plant in comparison to control plants (28.70, 37.30, 23.50). Among different duration treatments, 2 hrs treatment of SA has exhibited maximum Coefficient of Variation(%) for seed germination (16.36%); seedling survival (20.78%) and plant height (29.38%) characters in comparison to others. Accordingly, 5 mM for 2 hrs is identified as the LD₅₀ dose of SA mutagen which can be applied for inducing genetic variability in pomegranate.

Key words: Sodium Azide; Pomegranate; Seed germination; Seedling survival; growth parameters; LD₅₀

Combining Ability analysis for yield and yield attributing traits in maize under soil with low pH

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Combining ability study of the 25 inbred lines with three testers BML 6, UMI 1200 and LM 13 were made at ICAR-IARI, Jharkhand. The resulting 75 crosses along with 28 parents and check (BIO 9544) were evaluated during kharif 2022 in the soils with low pH (5.6) in randomized block design in two replications. ANOVA for combining ability revealed significant mean squares for GCA and SCA for all the traits studied which indicated the presence of both additive and non-additive gene action in the inheritance of these traits. The parent Z21 followed by Z6 and Z14 were identified as best combiner for grain yield under low pH condition. Out of the 25 lines, nine showed the positive significant GCA for grain yield which can be utilized for development of medium maturity hybrid varieties suitable for regions having soil with low pH. In terms of grain yield, the four cross combinations were superior over check BIO-9544. The same four crosses were also performing better than the standard commercial check under soil with normal pH too. The crosses (Z21×LM 13, Z14×LM 13 and Z6×LM 13) having grain yield higher than standard commercial check also showed positive significant SCA. These promising cross combinations identified in this study could be utilized for future breeding programme.

Crop residue management: challenges and opportunity

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Crop residue is the vegetative crop material that remains on the field after a crop has been harvested, pruned, or processed. Approximately 35%, 10%, and 80% of the total N, P, and K that the crop absorbs are found in the straw of most cereal crops (Barnard and Kristitoferson, 1985). Crop output is reduced when crop wastes are removed because it reduces soil fertility. The major negative consequences of burning crop residues are the release of greenhouse gases (GHGs) that aggravate global warming, elevated concentrations of particulate matter (PM) and smog which cause health risks, a decline in soil fertility, and a loss of biodiversity on agricultural lands. Burning crop residue greatly raises the amount of air pollutants, including CO₂, CO, NH₃, NO_x, SO_x, and non-methane hydrocarbons (NMHC), volatile organic compounds (VOCs), semi volatile organic compounds (SVOCs) and PM. Undoubtedly, improper handling of an abundance of crop residue has a negative impact on the ecosystem, soil, and public health. According to the study, 24% of the agricultural residue (116 Mt) was burned in 2017, which resulted in the yearly emission of GHGs (211 Tg), OC (239 Gg), and PM₁₀ (812 Gg). The burning of crop residue will result in a 45% rise in atmospheric emissions in 2050 when compared to the base level in 2017.

Burning agricultural fields has posed a threat to soil fertility and released harmful gasses like CO₂, CO, SO₂, PM_{2.5}, and PM₁₀, among other environmental issues. Consequently, a variety of alternative approaches should be considered as substitutes for open field burning, e.g., in-situ incorporation, mulching, composting, happy seeder machines and bio energy uses.

Crop residue management enhances the physiochemical characteristics of soil because it results in higher percentages of organic carbon (0.75%), available N (154 kg/h), available P (45 kg/ha), and available K (85 kg/ha) when integrated rather than burned in the rice-wheat cropping system of the Northwestern Indo Gangetic Plain. Sharma et al. (2020) working at PAU, Ludhiana reported that N 120 kg/ha followed by rice straw 7.5 t/ha is a viable management method for improving micronutrient transformation and crop yield of sandy loam soil. According to experimental results, when crop residues were added to the field, wheat grain output increases from 42.60 q/ha to 63.50 q/ha. To obtain higher yield and benefits from wheat on a sustainable basis, rice residue incorporation with 25% additional N or rice residue retention with 25% additional N + recommended NPK or surface rice residue retention + Sesbania - wheat with recommended NPK fertilizer under rice-wheat cropping system (Ali et al., 2016). Conservation agriculture establishes principles for sustainable production systems, which must be implemented according to site-specific needs. By providing compost and manure for the crops, the decomposer increases the fertility and productivity of the soil, reducing the need for future fertilizer applications. Soil microbial biomass was enhanced by consistent ZT application along with the retention of previous crop leftovers. N-fertilization had no effect on soil microbial activity during the first cropping cycle, but when 100% RDN was administered instead of 125% RDN during the second cropping cycle, there was an improvement (Rathore et al., 2016). This method of putting an end to stubble burning is practical, affordable, efficient, and effective. This technology is both environmentally beneficial and eco-friendly, and it will help to achieve the Swachh Bharat mission.

Key Words: Crop residue, Greenhouse gases (GHGs), Volatile and semi volatile organic compounds (VOCs & SVOCs), Conservation agriculture, Zero-tillage, Fertility, and productivity, Eco-friendly

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Study of combining ability and heterosis for some chemomorphological characters in grasspea (*Lathyrus sativus* L.)

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The present investigation was conducted to isolate good general combiner and specific crosses of grasspea based on their combining ability and to understand heterotic behaviour of various characters including β -ODAP content in seed and protein content. Five parental lines viz. BK-1, Nirmal, Ratan (Biol-212), Prateek and Mahateora were crossed during *Rabi* season of 2017-18 in half diallel fashion and their crosses along with the parents were evaluated in Randomised



Complete Block Design in subsequent *Rabi* season at the AB Block Seed Farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia. Wide range of genetic variability was observed for most of the characters. Important characters exhibiting high heritability were no. of pods per plant, protein content of seed, β -ODAP content in seed and seed yield per plant. The parents BK-1, Mahateora, Ratan and Nirmal appeared to be good general combiners for different desirable traits. The cross BK-1 x Ratan proved to be the best specific combiner for days to 50% flowering (early flowering), days to maturity (early maturity), protein content of seed, β -ODAP content of seed and seed yield per plant whereas, the crosses BK-1 x Pratik and Mahateora x Pratik proves to be the better specific combiners for seed β -ODAP content and protein content. Interestingly, seed yield and most of the yield contributing characters showed considerable heterosis. The selected crosses from this study can be used to raise segregating generations for obtaining transgressive segregants for yield and low β -ODAP content in seeds which can be used as donor parents in breeding for developing high yielding low neurotoxin grasspea.

Keywords: Grasspea, lathyrus, β -ODAP, nutritional quality, combining ability



Theme -III

**Allele mining and gene discovery for
improving food and vegetable crop**



O-III 1

Population genetic structure and marker-trait association studies for *cercospora* leaf spot (CLS) resistance in mung bean (*Vigna radiata* (L.) Wilczek)

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Mung bean production is significantly lowered by the biotic stress caused by *Cercospora* leaf spot (CLS) in various parts of the globe. The most effective way to increase mung beans' resilience towards this stress is to map the gene(s)/QTL that regulate it and then transfer that gene(s)/QTL to high-yielding mung bean cultivars. A panel population of 90 genotypes was created for the purpose of association mapping to identify the candidate gene(s)/QTL. Classification of the population was accomplished using GenAlEx 6.51b2, TASSEL 5.0 and STRU CTU RE V.2.3.4 software, using 66 SSR markers. The stress resistance of the panel population's genotypes showed a great deal of variance, and linkage disequilibrium was also observed. Two distinct genetic clusters were identified within the population. A significant connection of CLS resistance with markers CEDG006 and CEDG071 was found in marker-trait association study using both the generalized linear model (GLM) and the mixed linear model (MLM). Two novel QTLs controlling CLS resistance were detected and designated as *qCls_2* and *qCls_8*. Furthermore, novel QTLs were also identified for some of the quantitative traits, such as for plant height (*qPh_8*), for number of clusters (*qNcl_6* and *qNcl_10*), for hundred seed weight (*qHsw_3* and *qHsw_11*) and for yield (*qYld_2*, *qYld_7* and *qYld_8*) under CLS stress. The novel QTLs obtained from the present investigation could be further validated in diversified mung bean germplasms to understand the stability of the QTLs and then could be introgressed to elite mung bean varieties to develop CLS resistance lines. This study will help the breeding process towards CLS resistance in mung beans using genomic tools.

Keywords : *Cercospora* leaf spot resistance, Marker-trait association, Mung bean, SSR, QTL

O-III 2

Genome-wide characterization of leaf rust responsive NAC transcription factors in wheat

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Transcription factors (TFs) are proteins that regulate the physiological and biochemical processes in plants, respond to the environment by regulating the gene expression. Genomic studies in wheat have identified genes, hormones and processes that are important in controlling plant

response to multiple abiotic or biotic stresses and provide targets for improving stress tolerance. NAC are plant-specific TF families having important roles in pathogen defense, abiotic cues and phytohormone signaling, yet little is known about their roles and molecular mechanism of function in response to wheat rust diseases. In this study we have identified and characterised leaf rust responsive NAC transcription factors in wheat. Phylogenetic study provided valuable insights into the evolutionary aspects of *TaNAC* genes. Protein structure determination will provide valuable insights for improving the properties of crop. Protein-protein interaction study will help in understanding the gene function. Hence, these candidate genes will be used in molecular breeding programs to improve biotic stress tolerance in wheat.

Keywords: Wheat, Transcription factors; leaf rust; NAC

O-III 3

Differential defense responses among *Alternaria* resistant *Sinapis alba* and susceptible *Brassica rapa*

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Every year, the production of rapeseed and mustard suffers significant losses due to *Alternaria* blight disease caused by *Alternaria brassicicola*. Due to a paucity of adequate resistant parent germplasms of cultivated *Brassica* spp., traditional breeding to develop disease-resistant cultivars has so far proved ineffective. The management of diseases would be greatly aided by a complete understanding of the genetic basis of resistance and the discovery of defense-related genes involved in resistance responses in wild crop relatives. In order to identify differentially expressed genes (DEGs) specifically modulated in response to infection by *A. brassicicola*, the defense transcriptome of resistant *Sinapis alba*, a close wild relative of Brassicas, was investigated and compared with that of the highly susceptible *Brassica rapa*, in the present investigation. The results revealed that, a total of 3396 genes were upregulated and 23239 were downregulated after 48 hours of inoculation with the pathogen, and 4023 genes were upregulated while 21116 were downregulated after 72 hours. The DEGs were found to be involved with different biological pathways and processes such as, cellular metabolism, signal transduction, cell wall modification, antioxidation, transcription regulation, etc. Moreover, a significant number of genes linked to resistance or defense responses have been found to be uniquely altered by *Alternaria* infection in the resistant cultivar, which demonstrates that *S. alba* activates a stronger defense response reaction against the disease. The expression patterns of eight defense-related DEGs were examined using qRT-PCR to validate the transcriptome data, and the results showed that *S. alba* had much larger fold change in gene expression than *B. rapa*, upon infection. Most of the chosen genes were significantly activated at all the time points, but in the resistant germplasm, expression increased noticeably at the later time point of 72 hpi. Overall, the investigation offers new insights into the defense mechanism of *S. alba* against *Alternaria* infection which will help in formulating plans for breeding and generating disease resistant oilseed Brassicas.

An integrative Meta-QTL and candidate genes analysis for anaerobic germination tolerance in rice (*Oryza sativa* L.)

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Direct-seeded rice (DSR) has of late gained popularity among the rice-growing nations of Asia owing to rising labour and water crisis and increasing cost of cultivation. However, rice is extremely sensitive to oxygen-depleted microenvironment during germination and early seedling growth. Hence, tailoring rice varieties tolerant to anaerobic germination (AG) will be a key determinant in the adaptation of direct seeding in rice. Albeit, numerous AG tolerance QTLs have been reported in the last decade but none of the major and stable QTLs has been utilized in the breeding program. Meta-QTL (MQTL) analysis is a powerful statistical approach aimed at compiling QTLs from diverse independent studies for a given trait and providing a target genomic region with a small confidence interval (CI), thus aiding in precision breeding. In this study, 240 reported QTLs from 26 studies related to anaerobic germination tolerance were subjected to meta-QTL analysis. The study predicted 46 MQTLs distributed across all chromosomes except chromosome 12. The weight of predicted MQTL ranged from 0.06 to 0.46 while the confidence interval ranged from 0.01 to 16.41. 67% and 72% of MQTL had high weightage (>0.1) and low confidence interval (<4cM) respectively. Moreover, gene ontology (GO) analysis was performed for all the annotated genes present in MQTL regions extracted from the IRGSP portal. Several GO terms such as lipid transport (GO:0006869) and protein serine/threonine kinase activity (GO:0004674) were found significant. Later, whole-transcriptomic expression dataset of AG tolerant (MR, KHO, Kharsu 80A, and Nanhi) and susceptible (IR42 and IR64) genotypes were retrieved from NCBI and 56 differentially expressed common genes (Tolerant vs Susceptible) pertaining to 21 MQTLs were identified. Hence, identifying consensus genomic regions and identification of candidate genes is a credible, simple, and low-cost solution to provide novel insight into understanding the genetic determinants of the anaerobic germination tolerance of rice. MQTLs reported here may be used for functional marker development and marker-assisted breeding for anaerobic germination tolerance in rice.

Keywords: Anaerobic germination tolerance, MQTL, direct seeded rice, gene ontology



Mapping of genomic regions associated with vegetative stage drought tolerance in rice

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Drought stress is one of the predominant causes of rice yield reduction and production stability in rainfed and poorly irrigated rice ecosystems. Many QTLs have been mapped and identified for drought tolerance at the reproductive stage in rice. However, very few numbers of QTLs/genes have been reported to date for vegetative stage drought tolerance in rice. Therefore, this experiment was undertaken to identify QTLs for traits related to drought tolerance at the vegetative stage. Doubled haploids (DHS) were generated from the cross of two indica genotypes, IR20 x Mahulata, at ICAR-NRRI, India. The population was phenotyped under stress conditions and genotyped with STMS and SNP markers. Thirteen QTLs have been identified for eight traits, and eleven QTLs have been identified for six traits for drought tolerance at the net house and rainout shelter, respectively. Of these, 8 QTLs were newly identified. In chromosome number 2, a single minor QTL named *qRWC-2.1* for RWC was placed in the interval of SNP marker chr02_35818319 & chr02_21060669 and STMS marker RM475 & RM207, under net house and rain out shelter conditions, respectively. These QTLs can be helpful in the enhancement of vegetative stage drought tolerance in popular rice varieties through a marker-assisted breeding approach.

Genome-wide association study to identify QTNs for agro-physiological traits in bread wheat grown under contrasting tillage regimes

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Wheat (*Triticum aestivum* L. em. Thell) is the second most important global cereal crop, grown in diverse agro-climatic conditions. To sustainably increase wheat yield to meet the growing world population's food demand in the face of climate change, Conservation Agriculture (CA) is a promising approach. Agronomic understanding of CA is well reported, however, genetic basis of crop adaptation to CA is still in infancy. To dissect the genetic architecture of 19 morpho-physiological traits that could be involved in the enhanced adaptation and performance

of genotypes under CA, we performed genome wide association studies (GWAS) to identify quantitative trait nucleotides (QTNs) under four contrasting production regimes viz., conventional tillage timely sown (CT-TS), conservation agriculture timely sown (CA-TS), conventional tillage late sown (CT-LS) and conservation agriculture late sown (CA-LS) using an association panel comprising of 183 advanced wheat breeding lines along with 5 checks. The genotyping of the association panel was done using 35K Breeders' Axiom array and 9,771 highly informative SNPs were utilised for analyses. The population structure and kinship analyses identified two sub-populations in the association panel. Furthermore, LD decay rate was observed to be fastest for A sub-genome (4.63Mb) followed by D sub-genome (5.40Mb) and B sub-genome (7.41Mb). GWAS using the BLINK model discovered 80 MTAs for 19 morpho-physiological traits across the four production environments. CT-TS had the most significant MTAs (35), followed by CA-LS (25), CA-TS (11), and CT-LS (9). The phenotypic variation explained by these QTNs ranged from 2.15 to 40.22%. Gene annotation provided highly informative SNPs that associated with Phi2, NPQ, PS1 and RC which were linked with genes that play crucial roles in the physiological adaptation under both CA and CT. A highly significant SNP **AX94651261** (9.43% PVE) was identified to be associated with Phi2, while two SNP markers **AX94730536** (30.90% PVE) and **AX94683305** (16.99% PVE) were associated with NPQ. Also, SNPs **AX94476007** (19.45% PVE), **AX94658713** (22.87%PVE) and **AX94525104** (31.33% PVE) linked with stress tolerance were identified for DTH, DTM and GL, respectively. In addition, highly significant and informative SNPs were identified for most of the traits. The findings of the study revealed traits that are responsible for adaptation of genotypes to CA.

Keywords: Conservation agriculture (CA), Fluorescence (ϕ II, ϕ NPQ), GWAS, Linkage disequilibrium, QTNs, SNP





Theme -IV

Molecular Breeding for Crop Improvement



Mapping the genetic determinants for *bakanae* disease resistance in Indicarice genome

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An emerging rice disease known as *bakanae*, or foot rot, which is caused by the fungus *Fusarium fujikuroi* (teleomorph: *Gibberella fujikuroi*, Sawada, Wollenweber), has turned into a major food security concern in Asia. Rapid germplasm screening targeted at locating resistance sources, mapping QTLs/genes, and developing resistant rice cultivars are a few simple and reliable approaches for combating disease losses. Disease resistance is a complicated trait that is controlled by several genes, either directly or indirectly. Using QTL mapping and candidate gene identification, we can find QTLs or genes that influence these variables, which can help us reduce the yield loss in rice. In the current investigation, artificial screening of the bi-parental rice population through soaking rice seeds for 24 hours at room temperature in a suspension solution of fungal spores and the growth of inoculated seedlings in the greenhouse. The mapping population (RIL) was developed using the resistant (Thavalakkannan) and susceptible (Pooja) genotypes as parents and QTLs/genes imparting resistance to the *bakanae* disease were identified. The disease screening was repeated three times in three replications each time under artificial screening conditions. A set of 400 SSR markers includes 260 random SSR markers and 140 candidate gene sequence-derived SSRs were initially screened for finding polymorphic markers between parents. A total of 103 polymorphic markers between parents were assayed on 149 RILs derived from the parents. The marker information and percent disease incidence data were used as inputs to detect the QTL for *bakanae* disease resistance. The significant QTL found through analysis was defined by the logarithm of odds (LOD) of 3. One QTL, qBK5.1, was found with the flanking markers RM249 (Left) and RM289 (Right) on chromosome 5. Seven genes putative candidate genes in the flanking region were found to show an association with biotic stress resistance in rice. By applying marker-assisted selection and recurrent selection breeding, this novel QTL can likely be used to boost *bakanae* disease resistance in non-basmati rice plants after it has undergone additional validation.

Keywords: Rice, Allele mining, *Bakanae*, Candidate gene, *Fusarium fujikuroi*, QTL mapping.



Hormonal regulation of defense gene expression in *Brassica rapa*

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The key modulators to a plant's defense response are signalling molecules like jasmonic acid (JA) and salicylic acid (SA), which have been found to have a major role in initiating host responses to stresses through signal transduction and subsequent activation of defense-related genes. Elucidating hormonal regulation of defense gene induction and associated pathways would not only contribute towards understanding plant response to various stresses, but also aid in the development of stress tolerant cultivars. With this rationale, we carried out expression profiling of selected defense related genes namely, chitinase, β -1,3-glucanase, PR5, β -glucosidase, NB-LRR and LRR-RK, in *Brassica rapa* in response to exogenous methyl jasmonate (MeJA) treatment, in order to investigate how expression of the genes are modulated upon the treatment. Quantitative RT-PCR analysis was carried out using *B. rapa* cDNA prepared from total RNA extracted from leaf tissues (treated with MeJA and water treated control) collected after 24 and 48 hours of the treatment. The expression analysis revealed that, application of MeJA results in fast induction of chitinase and β -glucosidase in *B. rapa*, within 24 hours. Interestingly, the transcript levels of PR5 and NB-LRR were observed to be decreased after the treatment. Moreover, no significant changes in expression were seen in case of β -1,3-glucanase and LRR-RK genes. Hence, it can be concluded that, while JA has a major role to play in regulating the activation of chitinase and β -glucosidase, it may not be involved in the activation of β -1,3-glucanase and LRR-RK. Furthermore, significantly reduced levels of PR5 and NB-LRR immediately after MeJA treatment indicate a possible involvement of cross-talk with other endogenous signaling pathways in the host plant.

Introgression and confirmation of everbearing trait in strawberry (*Fragaria x ananassa* Duch.)

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The present investigation was targeted towards highly desirable overbearing trait in strawberry (*Fragaria x ananassa* Duch.) via marker assisted selection while seeing its worldwide commercial applicability through extended harvest season. The crosses were made between everbearing and june-bearing cultivars to raise the F₁ individuals. Morphological characters (plant, floral and fruit) were assessed that showed significant differences among the strawberry cultivars. Molecular

characterization was carried out between everbearing and non-everbearing cultivars using RAPD and SSR markers. For phenotyping, a chi-square test was performed and revealed that out of all four cross combinations, the best fitted cross found to be in Mendelian segregation ratio (1:1) was 'Confectura' × 'Torrey' with χ^2 -value 1.58. Further, the identified polymorphic markers were assessed across the F_1 individuals of cross 'Confectura' × 'Torrey' for its genotyping. It could be revealed that the targeted everbearing trait is governed by dominant gene(s) in the subjected strawberry genotypes. Further, the identified polymorphic markers would be successfully employed in DNA fingerprinting of strawberry under various crop improvement programmes.

O-IV 4

Study on defense gene induction in *Sinapis alba* in response to alternaria blight in *Brassica rapa*

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Alternaria blight disease is one of the most prevalent and devastating diseases of oilseed Brassicas caused by the necrotrophic fungi *Alternaria brassicicola* and *A. brassicae*. Traditional breeding strategies to develop resistant cultivars has not been successful due to unavailability of resistant cultivated germplasms. However, non-host resistance against Alternaria blight has been reported in the wild and close relatives of Brassica species such as *Sinapis alba*. Understanding the molecular basis of plant-pathogen interactionis needed to unravel novel features of plant defense, in order to design newer control strategies. With this rationale, the present investigation was carried out to study the changes in expression patterns of defense related genes in response to infection by *A. brassicicola* in the non-host *S. alba* in comparison to that in the highly susceptible cultivated host *Brassica rapa*. Firstly, *A. brassicicola* was isolated and purified, and pathogenicity test was performed in both *B. rapa* and *S. alba*. *In vitro* detached leaf assay and *in planta* inoculation experiments revealed distinct differences in symptom development in the two cultivars. The level of infection was found to be severe in case of *B. rapa* but in case of *S. alba* it was negligible. Subsequently, a quantitative PCR (qPCR) analysis was performed to assess the differential expression patterns of 12 defense related genes selected from a previous transcriptome study, across different time points. The selected genes are PR4, PR5, beta-1,3-glucanase, chitinase, disease resistance (DR) gene, LRR-NB, LRR-RK, MKK4, cytochrome P450, F-box, bZIP, and WRKY. The study demonstrates that most of the defense related genes are induced immediately upon infection by the pathogen. Moreover, their transcript levels were elevated across all the time points under study with significantly high expression towards the later time point in *S. alba* compared to *B. rapa*. These genes could serve as potential candidates for developing Alternaria resistant varieties of Brassica in future.



Expression profiling of pathogenesis related (PR) genes in response to *Pseudocercospora eumusae* infection in banana (*Musa spp.*)

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Pseudocercospora eumusae causing Eumusae leaf spot is an economically important disease of banana (*Musa spp.*). The disease has a major impact in India's key banana growing regions, including the North-Eastern region. The disease causes significant yield loss mainly in the Cavendish subgroup of cultivars. In the present study, a differential expression profiling of PR genes was conducted between banana cultivars resistant and susceptible to the pathogen, in order to deduce the expression patterns of important PR genes against this serious disease. Pathogenicity assays were conducted using pure culture of *P. eumusae* through artificial inoculation of the plants. In the susceptible cultivar Sapor Jahaji, the intensity of infection was severe and the disease progression was very fast. On the other hand, in the tolerant cultivar Simolu Monuhar, symptom development was much slower and less intense. For semi-quantitative RT-PCR based expression analysis, leaf samples were collected from the plants inoculated with *P. eumusae* as well as from the uninoculated plants (water treated control) at 48 and 96 hpi (hours post inoculation) for RNA extraction and subsequently, cDNA synthesis. Five PR genes namely PR1, Chitinase, PR4, Germin-like protein and Thaumatin-like protein were selected for differential expression profiling among the resistant and susceptible cultivars. The expression analysis revealed that, all the PR genes were highly upregulated after infection in Simolu Monuhar in which, the expression levels remained high across both the time points as compared to those in controls. On the other hand, in Sapor Jahaji, the expression levels of the genes were very low as compared to those in case of Simolu Monuhar, even after infection by the pathogen. Thus, all the PR genes clearly have potential roles in generating active defense responses against the pathogen in the tolerant cultivar.

Allelic diversity and population structure in rice varieties release in last 55 years using gene-based yield related markers

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Genetic diversity of a crop is the major source of variability in every crop improvement initiative. Allele mining is used to discover superior alleles that affect critical agronomic and qualitative characteristics. Genetic improvement aimed to increase yield, improve quality, and biotic and abiotic stresses, as well as the selection of better parental lines for hybridization. We need a thorough grasp of genetic diversity and relationships across genotypes to selected the best allelic combination for the targeted traits. Grain yield is complex trait governed by many indirect traits thus, diversity in grain yield at molecular level needs to be explored appropriately. Plant genetic (G) constitution, environmental (E) variations, and their interactions (GxE) influence the overall phenotype magnitude of the plant. To understand real variation, existing rice germplasm must first be evaluated and characterized at the molecular level. Molecular markers can distinguish genotypes that are difficult to distinguish based on morphology. Keeping this in view, an experiment was conducted with the objective to investigate genetic variation and population structure among 128 rice varieties release in last 55 years using 39 gene-based yield related markers. A total of 396 alleles were identified, with a mean PIC value of 0.22. Using the UPGMA cluster analysis based on genetic dissimilarity and the neighbour-joining approach, the 128 rice varieties were categorized into three distinct groups. The varieties fall into three separate subgroups even after the population structure analysis utilizing model-based and distance-based methods. Using the software Past 4.03 PCA was conducted which show the result similar to cluster analysis and structure analysis. Three separate PCA plots were generated to visualize the distribution of genotypes based on released year (decadal), maturity duration (62-170 days), and growing ecologies (6 ecologies). The cluster formed by population structure and PCA were used to estimate molecular variance analysis and F-statistic. AMOVA accounted for 4% of population variation and 96% of individual variation, which is quite higher side. We observed F_{st} , F_{it} , and F_{is} values of 0.069, -0.127, and -0.049, respectively. This study reveals a broad genetic base among the 128 varieties on the basis on yield related markers used.

Keywords: Rice, Grain yield, Genetic diversity, Cluster analysis, Population structure



Integrating GWAS results improves the prediction accuracy of genomic selection in rice breeding

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The precision of genomic selection for quantitative traits may be improved by using genome-wide genic markers. This idea was investigated by analyzing rice thousand grain weight trait using a panel of gene-based markers. To evaluate the value of these novel genic markers for gene discovery, a thorough Genome-Wide Association Study (GWAS) was performed employing a wide range of models. A single-locus mixed linear model (MLM) was used, along with two multi-locus models (FarmCPU and mrMLM), in this experiment. A total of 28 significant associations between markers and the thousand-grain weight character were discovered by these models. There were pleiotropic effects seen in several of the genes linked to changes in grain weight. The YD91 marker, which is designed from the *OsAAP3* gene on chromosome 1, was found to have a significant effect on grain weight. To optimize the genomic selection model with these genic markers, a leave-one-out five-fold cross-validation approach was employed, encompassing nine distinct genomic selection strategies. These strategies included both regression-based and machine learning-based models. Among them, the Kernel Hilbert Space Regression (RKHS) emerged as the most effective regression-based model, while Random Forest Regression (RFR) outperformed other machine learning-based models. To evaluate the significance of these markers, genomic prediction accuracy was compared in the presence and absence of GWAS-significant markers. The results indicated a substantial decline in prediction accuracy when these markers were excluded, underscoring the importance of these unique genic markers in genomic selection. Furthermore, it was demonstrated that gene-based markers, as utilized in this study, offered superior precision compared to other marker types in genomic selection programs.

Keywords: Genomic selection, multi-model approach, GWAS, Genic markers, Machine learning models



Theme -V

Breeding for Grain and nutritional quality of crop plants



Cluster analysis in fodder oats (*Avena sativa* L.)

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Oats is an important crop used globally for food and fodder, holding significant economic value. In the context of livestock farming, fodder oats (*Avena sativa* L.) is an important crop during winter season. A comprehensive analysis of thirty oat genotypes was conducted at The Regional Agricultural Research Station at Ambalavayal in Wayanadan Eastern Plateaux of Kerala to identify superior genotypes that could increase forage production and improve nutritional quality during the Rabi season of 2022-23. A cluster analysis using Mahalanobis D² statistics was performed employing the Tocher method within the Indostat software, involving eleven morphological and six nutritional traits. The thirty genotypes were categorized into seven clusters based on their D² values using the Euclidean method. Cluster I consisted of 14 genotypes (OL-1942, OL-1944, OL-1980, OL-15, OL-212, OL-11, OL-1952, OL-1874-1, OL-1975-2, OL-1976-1, OL-12, OL-1967, AVT-1, OL-13), followed by Cluster II with 8 genotypes (OL-10, OL-2000, OL-1977, OL-1964, OL-1988, OL-1896, OL-1802, OL-1974). Cluster IV comprised 3 genotypes (OL-1937, OL-1963, OL-125), Cluster III included two genotypes (OL-9, JHO-822), and Cluster V (OL-1931-1), VI (OL-1969), and VII (OL-1949) each had one genotype. The inter-cluster D² values were found to be higher than the intra-cluster D² values implying that there is a substantial amount of diversity among the genotypes under study with respect to the considered characters. The highest intra-cluster distance was observed in Cluster IV (42.81), followed by Cluster II, Cluster I, and Cluster III. The maximum inter-cluster D² values were observed between Clusters IV and VII (102.31), and the minimum was observed between Clusters II and V (45.44). Based on the cluster mean, Cluster III was observed to be a significant contributor of days to first and 50% flowering, days to maturity, crude fibre content, total phenolic and antioxidant content. Cluster IV was a potential contributor to green fodder yield, dry matter yield, leaf and stem dry weight, plant height, and phytate content. Cluster V was associated with the number of tillers and crude protein content. Cluster VI was related to the number of leaves and condensed tannin content. Cluster VII was pertaining to the leaf-stem ratio.

Genetic variability study of grain quality traits of diverse rice (*Oryza sativa* L.) Germplasm in Irrigated Ecology

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A field experiment was conducted during kharif 2021 at research field of Crop Improvement Division of National Rice Research Institute, Cuttack, Odisha to find out the genetic variability present in different 150 rice (*Oryza sativa* L.) genotypes on fourteen grain quality traits such

as hulling percent, milling percent, head rice recovery percent, moisture content, kernel length, kernel breadth, kernel length to breadth ratio, alkali spreading value, water uptake, volume expansion ratio, kernel length after cooking, linear kernel elongation ratio, amylose content and gel consistency. The variance study revealed that there was enormous existence of variance among the germplasm trait wise that indicated there is scope for selection of desirable traits in rice grain quality. There was minimum influence of environment on the expression of traits except alkali spreading value, volume expansion ratio and amylose content. All the traits exhibited high heritability (h^2 , broad sense) and high to moderate genetic advance in percent of mean. There was considerable influence of genetic factors for all the traits with high heritability and moderate genetic advance. The study revealed that head rice recovery percentage, kernel length before cooking, kernel length after cooking and gel consistency have high values of variance, genotypic variance, genotypic coefficient variation, genetic advance by percent of mean and heritability which indicated that the genetic worth of the germplasm could be exploited by selecting these traits.

O-V 3

Estimation of genetic parameters of vegetable pea (*Pisum sativum* L.) genotypes for yield and yield attributing characters

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The experiment was conducted during rabi season of 2021-2022 at the Vegetable Research Farm of Department of Horticulture, Birsa Agricultural University Kanke, Ranchi, Jharkhand. The experiment was laid out in RBD design with three replications, using 21 genotypes of vegetable pea including two checks viz., Arkel and US-10. Observations were recorded under growth, yield attributing characters and qualitative parameters. In addition to this GCV, PCV, Heritability, Genetic advance, Correlation, Direct and indirect effects of different traits on yield were also estimated. Pea has high nutritive value and dietary proteins and is considered as an important vegetable crop. In spite of such an economic importance, production per unit area is still low in the country especially when crop is grown during off-season and the major problems attributed to this are lack of high yielding varieties. Genetic diversity provides desirable variation among parental genotypes to produce new and valuable combinations. Genotypes were found significant for all the characters. The mean performance of the genotypes revealed that the significantly highest yield was recorded in Arkel Mutant-1 followed by Chianki-VP-1, Arkel Mutant-2, CS-8. Phenotypic variance was higher than genotypic variance for all the traits and similar trend was followed for PCV and GCV. Correlation study revealed that positive genotypic significant correlation was observed for green pod yield per plot and TSS % with green pod yield per hectare. High value of heritability in broad sense was estimated for green pod yield per hectare and green pod yield per plant. High genetic advance as percent of mean was estimated for green pod yield per hectare and green pod yield per plot. Positive phenotypic correlation was observed with

plant population at last harvest, survival %, 100 seed weight and number of green pods per plant, number of seed per pod, shelling % and green pod yield per plot showed positive direct effect with green pod yield per hectare.

Keywords: Vegetable pea, Genotypes, Growth, Yield, Quality, Arkel

O-V 4

Identification of elite heterotic combinations in sweet corn for yield and quality

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Sweet corn (*Zea mays* L. *saccharata*) is one of the special types of normal corn (*Zea mays* L.) with high sugar content, originated through natural recessive mutation in the genes controlling sugar to starch conversion inside the corn kernels. Cultivation of sweet corn is gaining momentum due to higher profitability and its suitability for peri-urban cultivation. An investigation was carried out to evaluate fourteen sweet corn inbred lines and their hybrids in line x tester mating design to identify superior heterotic combinations for yield and quality as well as to understand the importance of parental diversity in obtaining elite hybrids. The fourteen parental lines were crossed in line x tester mating design (7 lines and 7 testers) and all the 49 hybrids were evaluated along with a check variety, Sugar 75 to identify superior heterotic combinations for yield and quality. Molecular screening of parental inbreds using 14 SSR markers followed by cluster analysis were conducted to group them into different clusters based on their diversity status. Highly significant positive standard heterosis for green cob yield over the check Sugar 75 was reported by three hybrids $L_4 \times T_6$ (19.09%), $L_5 \times T_6$ (9.27%) and $L_4 \times T_5$ (8.35%). Besides yield, $L_4 \times T_6$ showed significant heterosis for cob length, green cob weight, cob placement height, tassel length, days to 50% silking, number of kernel rows per cob, number of kernels per row, dry cob weight, seed weight per cob, 100 seed weight, total chlorophyll content and zinc content. $L_5 \times T_6$ recorded significant economic heterosis for total sugar content, cob length, cob placement height, cob breadth, dry cob weight, seed weight per cob and days to 50% tasseling. Parental polymorphism study identified four polymorphic markers (umc 1969, umc1142, umc1896, umc 2061) with PIC value range of 0.142(umc 1969) to 0.497(umc 2061). Cluster analysis grouped the 14 parents into six clusters at 0.52 similarity coefficient. Parents of the hybrids $L_4 \times T_6$ and $L_5 \times T_6$ were positioned in diverse clusters, emphasizes the importance of diversity among parental lines to harness heterosis.



Evaluation of genetic diversity among aromatic rice accessions using SSR markers

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The success of any crop improvement program is conditioned in the foundation population by the expanse of existing genetic diversity. Therefore, the present experiment designed to evaluate 48 aromatic rice accessions employing 23 markers of simple sequence repeat (SSR) for genetic assortment and population structure. The study of data relied on the genetic parameters of the population and marker. The mean polymorphism information content stood reported to be 0.72 suggesting that the selected microsatellite marker exhibited high polymorphism among the rice germplasm lines. The Bayesian-based model process and distance based methods for investigation of population structure showed that the rice accessions delineated into 3 and 2 distinct clusters individually. The analysis reflected the presence of important genetic diversity between the selected aromatic rice germplasm. Hence, the selected rice genetic resource which represents a small but economically and culturally important segment will be potentially useful in rice improvement by contributing significantly superior alleles controlling important agronomic, qualitative as well as quantitative traits.

Multi-environment evaluation for selection of stable and ideal wheat genotypes for quality traits using the GGE biplot

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Understanding the impact of genotype, environment and their interaction on the expression of quality attributes aids in the precise selection for quality improvement in the wheat breeding program. In the current investigation, forty-one diverse wheat genotypes grown at three different locations namely, IARI - New Delhi, IARI - Indore, GBPUA&T – Pantnagar, during *rabi* season of 2019-20 were analysed for seven quality traits of grain, refined and whole wheat flour. Analysis of variance of the quality data revealed highly significant differences ($P < 0.01$) among the genotypes and environments. The results of pooled ANOVA exhibited significant differences among genotypes at the three test environments and when locations were combined. Similarly, the G×E interaction was significant for most of the traits, High genotypic mean performance was observed in Delhi and Indore for most of the traits, suggesting the favorable environments for expression of quality traits. The results of GGE biplot analysis showed that genotypes C273, C518, C591 and C306 were the best performing and stable across locations for grain protein content (GPC), falling number (FN), total sugar (TS) and grain hardness (GH). Average-

environment coordination view of GGE biplot analysis showed that genotypes GW322, C518, HD3226 and HD3086 were ideal for damaged starch (DaS). Genotypes HD2982 and CS5 were found to be ideal for test weight (TW) and thousand kernel weight (TKW). Genotypes C273, C518, C591 and C306 were also found to be most ideal and desirable for multiple quality traits related to chapati quality and these genotypes have high value as a parent in the breeding program for simultaneous improvement of multiple quality trait components of *chapati*. The results of multi-environmental trials with the elucidation of G×E interaction using GGE biplot model can thus be of great significance in guiding the selection and recommendation of stable and superior varieties in wheat production zones for quality purpose.

O-V 7

Genetic diversity study for yield and quality parameters in wheat

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Climate change is impacting severe constraints on the present agricultural production. Therefore, Main aim of Plant Breeder is to develop environmentally resilient crop cultivar in order to overcome rapid shifts in cultivation conditions and resources due to climate change. Breeders use genetic diversity to develop new cultivars with improved characteristics such as higher yield, biotic and abiotic stress tolerance and improved nutritional values. Keeping in view, an experiment was carried out to study genetic diversity for grain yield and four quality characters in Bread wheat. Fifty genotypes were evaluated against four nutritionally rich check varieties viz., DBW 187, DBW 222, GW 322 and WB 02 in Augmented Block design. The results revealed that genotypes under study were grouped into six clusters. Maximum numbers of genotypes (21) was grouped into Cluster-VI with the intra-cluster distance of 24.97. The intra-cluster distance was however recorded maximum for cluster-I whereas maximum inter-cluster distance was observed between cluster-I and cluster-II indicating that the genotypes belonging to these clusters are more genetically diverse.

KEYWORDS: Climate change, Wheat, Genetic Diversity.

O-V 8

Quality seed a backbone for food & nutritional security

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Quality seed is essential for healthy crops to enhance the agriculture productions and productivity. At the same time, advances in breeding technology require equivalent advances in seed technology. In order to ensure food security, it is crucial to develop seeds that are high yielding and resistant to drought, heat, cold and insects pests. Seed production requires favourable weather conditions during flowering and reproductive stage and absence of damaging insects. The continued efforts



of plant breeders and genetics to accomplish miracles in the development of more useful crop plants could reserve people worldwide from the fear of hunger. Seed needs to be genetically and physically pure, physiologically viable and free from weeds, insect pest and diseases. To achieve this, trained and skilled personnel have to be included in the production and postharvest activities prior to the seed reaching the end user. Commercial seed production systems are based on crop uniformity. A good packaging and labelling are also important in seed business.

O-V 9

Hydrponic screening of rice genotypes for low phosphorus tolerance

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Phosphorus deficiency in rice significantly affects its growth and yield. A total of 72 upland rice genotypes including three checks, viz. Dular, Kasalath and Gobindobhog, collected from gene bank, ICAR-NRRI, Cuttack were screened for tolerance to low phosphorus. Hydroponics experiment using modified Hoagland solution was conducted with two phosphorus treatments (phosphorus deficient and phosphorus sufficient) and two replications in a completely randomized design. The genotypes were grown in nutrient solution for 21 days and data was recorded on shoot length, root length, shoot-root ratio, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight and chlorophyll content. The genotype, AC 35119 recorded highest shoot length in phosphorus sufficient condition, whereas, Gobindobhog and AC 35000 recorded highest shoot length under phosphorus deficient condition. Kasalath, AC 35100 and AC 35097 recorded highest root length under phosphorus sufficient condition, whereas, Dular, Kasalath and AC 35090 recorded highest root length in phosphorus deficient conditions. Under phosphorus sufficient conditions, AC 35090 showed highest root-shoot ratio whereas, AC 35003 recorded highest root-shoot ratio under phosphorus deficient conditions. Gobindobhog and AC 35173 recorded highest shoot fresh weight under phosphorus sufficient and phosphorus deficient conditions. Under phosphorus sufficient condition, AC 35178 and Kasalath recorded highest shoot dry weight whereas, AC 3498, Dular and Gobindobhog recorded highest shoot dry weight under phosphorus deficient condition. Under phosphorus sufficient conditions, Kasalath, Gobindobhog and AC 34981 recorded highest root fresh weight, whereas, Kasalath, Gobindobhog and AC 35196 recorded highest root fresh weight in phosphorus deficient condition. Under Phosphorus sufficient condition, Kasalath and AC 35196 showed highest root dry weight, whereas, Kasalath, AC 35066, AC 35137, AC 35178 and AC 35090 recorded highest root dry weight under phosphorus deficient condition. Kasalath, AC 35196, AC 34979, AC 35178 and AC 3173 recorded highest total dry weight under phosphorus sufficient conditions, whereas, Dular, AC 35192, AC 35170 and AC 35142 has the highest total dry weight in phosphorus deficient conditions. The genotype AC 35014 showed highest chlorophyll content (SPAD value) under phosphorus sufficient conditions whereas, AC 35044 recorded highest chlorophyll content (SPAD value) under phosphorus deficient conditions. Molecular screening for low phosphorus tolerance was carried out using 20 SSR markers. Therefore, the genotypes, AC 35000, AC 35173, AC 35178, AC 35090, AC 35196, AC 35066, AC 35137 and AC 35044 which performed better under phosphorus deficient condition can be used as donors for improving low phosphorus tolerance in rice.

Understanding genetic diversity and variation in rice (*Oryza sativa*) grain Phytic Acid Content and developing genic markers for associated Genes

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Phosphorus (P) is an important macronutrient that plays a vital role in the initial establishment of seedlings and the promotion of optimal plant growth. However, at the world level, more than 5.7 billion hectares of land are lacking in accessible P that plants use (Ahmad et al. 2020). Mutant resources with grain LPA content have limited breeding potential and are not commonly utilised in rice breeding due to their significant adverse effects, such as reduced grain weight, low seed yield, and decreased seed viability. These mutant stocks also exhibit a visible reduction in grain phytic acid content. Therefore, it is essential to leverage the inherent variability in grain phytic acid content to lower it to a level that does not detrimentally affect the crop's agronomic performance. Furthermore, only the utilization of DNA marker-assisted selection holds promise for effectively modifying natural variations in grain phytic acid content. In this research, we evaluated the PA content of rice varieties with grain dimension and grain weight characteristic, and we evaluated and analysed the components of inheritance and natural genetic variation. A remarkable range (0.54%-2.13%) of significant variation in grain PA content was detected among different rice types, which can be attributed to changes in seed dimension and grain weight ecology. The presence of a significant genotype associated with a particular seed attribute indicates the prospect of polygenic inheritance. The genotypes were found to exhibit a total of 1153 alleles through using a number of novel candidate gene-based markers. The novel CgSSR markers very informative, as seen by their PIC values ranging from 0.46 to 0.79, with an average value of 0.64. Additionally, these markers indicate an in-depth understanding of the whole germplasm. Marker alleles derived from a single putative transporter gene, namely OsLPA1, had a strong association with the variation in grain PA. Grain PA accounts for 7.84% phenotypic observation and 213 base pair allele was observed. The presence of a less common allele within the coding region of the OsLPA1 gene exhibited a positive correlation with the concentration of grain PA. This association accounted for approximately 1.286% of the observed phenotypic variation.



Evaluation of aroma in F₂ population of rice (*Oryza sativa* L.) using KOH method

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An investigation in rice (*Oryza sativa* L.) was undertaken during kharif season, at rice research field, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, to evaluate the aroma in F₂ population of aromatic and nonaromatic parents by using sensory method. The sensory test of leaf aroma using a 1.7% KOH solution for F₂ Populations Sahbhagidhan x Birsamati where Sahbhagidhan is non aromatic and Birsamati is aromatic. The sensory test appeared to be a simple and reliable method for rapid identification of aromatic plants in breeding programmes. One gram of young rice leaves at the flowering stage were weighed by using electronic balance in laboratory and cut into very small pieces and placed in petridishes. After that 5ml of 1.7% of KOH solution was added onto the small pieces of rice leaves, and covered by petridish cap and left for 30 minutes at room temperature. A panel of ten persons smelled the samples one by one. Segregation ratios of nonaromatic : aromatic samples for the evaluation of the mode of inheritance of the aroma trait in leaf tissues by the sensory test using a KOH 1.7% solution were determined by chi square test. Segregation ratios of two F₂ populations (Sahbhagidhan x Birsamati) were 3:1 between the nonaromatic and aromatic samples, indicating the involvement of one single recessive gene for the aroma trait in Sahbhagidhan. This finding confirmed the complexity of the mode of inheritance of the aroma trait in rice. These results confirmed that aroma in rice is a quantitative character and that several genes are involved in the expression of the aroma trait in rice.

Key Words: Aromatic substance, Genetic analysis, Sensory test

Genome-wide association analysis of iron deficiency tolerance in aus rice (*Oryza sativa* L.)

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Resource-poor areas with moisture deficit lands following aerobic and direct seeded rice methods of cultivation face severe problems of iron deficiency. In this study, the Bengal and Assam Aus rice panel was studied under an iron-deprived hydroponic medium at the seedling stage at ICAR-NRRI, Cuttack. They were phenotyped for various shoot and root traits along with the seed iron content before germination. A novel iron deficiency scoring scale (0-9) was used to classify the panel based on their tolerance reaction; with 0 being the most tolerant and 9 being

the most susceptible reaction. GWAS results highlighted six putative candidate genes; OsFLA for the number of leaves and shoot length, OsBIDK1 for root average diameter, root volume, root biomass, root projected area, root surface area, SHR5 for total root length and number of root tips, OsSEC24 for number of crown roots and maximum root length, OsHPL3 for chlorophyll index of the 3rd leaf. AKR2B (XBOS252) was selected as the putative candidate gene for Fe score and found to be involved in maintaining the membrane integrity of chloroplast, which was earlier reported in relation to Xa21. The SNP variations in these gene sequences were used to group them into haplotypes. If the candidate genes can be validated using functional genomics, the SNP polymorphisms reported here can be used as markers to identify tolerant traits, the constructed haplotypes can assist in haplotype assisted breeding programmes, and the superior donors can be used as a source of genetic variant conferring tolerance to Fe deficient soils directed at low input, resource poor aerobic or direct seeded rice cultivation.

Keywords: Aus rice, direct-seeded rice, Fe score, GWAS, Haplotype, Iron deficiency

O-V 13

Studies on genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in bread wheat (*Triticum Aestivum* L.)

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A study was undertaken to analyse the genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in twenty-Eight wheat genotypes grown at BAU Agricultural Farm, Ranchi during Rabi season of 2019-20 in three different dates of sowing with a interval of 15 days which is considered as three environments E1, E2, E3. The Pooled analysis of variance revealed that the treatments were highly significant for all the characters. Wide genetic variation was observed among genotypes for number of grains per spike, plant height, 1000 seed weight, Days to maturity and Flag leaf area. Considering genetic parameters, high genotypic co-efficient of variation (GCV), was observed for 1000 seed weight, no of grains per spike, plant height, flag leaf area, days to 50% flowering, days to maturity, chlorophyll content, biological yield and harvest index whereas, low GCV was observed for Spike length, grain yield plant, no of effective tillers, protein content. In most of the cases, phenotypic variances were higher than the genotypic variances. Environmental variance is much higher in harvest index, days to 50% flowering, low environmental variance was observed in plant height, flag leaf area, days to maturity, no of grains per spike, chlorophyll content and biological yield. High heritability with low genetic advance in per cent of mean was observed for plant height, days to maturity, chlorophyll content & harvest index which indicated the involvement of non-additive gene action for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in per cent of mean was observed for grain yield per plant and no of effective tillers indicating that these traits were under additive gene control and selection for genetic improvement



for these traits would be effective. In the present investigation on correlation studies carried out and pooled analysis of all the three environments (E1, E2, E3) has been done which showed that grain yield has been strongly and significantly correlated with plant height, 1000 seed weight, harvest index, biological yield, no of effective tillers, no of grains per spike and days to maturity. Pooled Path analysis under all three environments timely sown (E1), late sown condition (E2), very late sown condition (E3) has been done which showed genotypic positive direct effect on yield via spike length, flag leaf area, no of grains per spike, no of effective tillers and harvest index however for phenotypic positive direct effect on yield via plant height, spike length, no of effective tillers, chlorophyll content, protein content, biological yield per plant and harvest index.

Keywords- Genetic Variability, GCV, Heritability

O-V 14

Variability, heritability and genetic advance of some Soybean (*Glycine max* L. Merrill) parents and their F1 in different environments

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Forty five genotypes along with ten parents and three checks of Soybean were evaluated for 11 characters in four environments. The analysis of variance revealed significant differences among the genotypes for all the characters. Estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding genotypic coefficient of variation (GCV) for all the characters. High phenotypic coefficient of variation (PCV) was found for clusters per plant followed by pods per cluster, plant height, seed yield per plant, pods per plant and biological yield per plant. A combination of high heritability and high genetic advance as percent of mean was noted for plant height, clusters per plant, pods per cluster, pods per plant, biological yield per plant and seed yield per plant which indicated that additive gene action might be operated predominantly in the inheritance of these characters. Thus the results suggested that significant improvement can be made by individual plant selection in early generations.

O-V 15

Heterosis for yield related attributes in soybean [(*Glycine max* L. Merrill)]

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In the present investigation, heterotic effects were studied over mid parent, better parent and check variety for yield and its components with an experimental materials consisted of 10 diverse parental lines, which were selected on the basis high yield, oil content, resistant to disease and

pests from different parts of India. These lines were, crossed as per diallel mating design (Model-1 Method-II), where crossing programme includes one way crosses and parents. This method is used when reciprocal differences are not significant (**Griffing, 1956**). Crossing programme was taken during Kharif 2009 at BAU, Ranchi and SHIATS Allahabad, which results in 45 F_1 s. These 45 F_1 s along with parent's and checks, viz. Birsa Safed Soybean-2, JS-335 and JS80-21 were evaluated during Kharif 2010 in a randomized block design with three replications under four environments. Considering overall performance, the superior F_1 s were Hybrid $P_9 \times P_{10}$ for oil content and harvest index. Hybrid $P_8 \times P_{10}$ for protein content, hybrid $P_5 \times P_7$, $P_3 \times P_7$ for number of seeds per pod, hybrid $P_2 \times P_3$ for days to maturity, hybrid $P_3 \times P_8$ for 100 seeds weight, hybrid $P_8 \times P_9$, $P_3 \times P_8$, $P_4 \times P_8$ and $P_3 \times P_9$ for yield per plant for economic heterosis over best check "JS-335" in environment E_1 , E_2 , E_3 and E_4 . These hybrids are, therefore, suggested to be utilized for developing high yielding soybean cultivars.

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Evaluation of advance varietal trial of pigeonpea (*Cajanus cajan* [Millsp.])

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(*Cajanus cajan* [Millsp.]), commonly known as pigeonpea, is the designated botanical nomenclature for this plant species. Pigeonpea is classified within the *Cajanus* genus, a member of the Leguminosae family. Advance Varietal Trial (AVT) was constituted by the seven entries (GRG 622, ICPL 87119, PT 11-16, AKTM 1637, BDN 716, GJP 1915, JKM 189) promoted from initial varietal trial on the criteria specified. Morphological characters namely initial plant stand (varied from 108 to 116), final plant stand (varied from 74 to 112), days to 50% flowering (first 50% flower from 86 to 108 days), plant height (196 to 239 cm), number of primary branches per plant (branches varied from 15 to 18), number of secondary branches per plant (branches varied from 11 to 15), number of pods per plant (ranged from 229 to 292), number of pod borer (varied from 229 to 292), Pod Borer% (0.7 to 1.6), wilt % (ranged from 6.0 to 34.2 %), 100 seeds weight (g) (ranged from 8.32 to 10.99), grain yield (g/plot) (varied 2560 to 3540), grain yield (kg/ha) (1185 to 1639) were recorded in AVT. Genetic divergence was also studied among the seven entries. The dendrogram produced from pigeonpea entries show three main cluster (cluster I, cluster II, cluster III).

Keywords: pigeonpea, advance varietal trial, genetic divergence.



Genetic evaluation of Interspecific Hybrids between Pearl Millet *Pennisetum glaucum* (L.) × Napier Grass *Pennisetum purpureum* (K.)

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Pearl millet grains are valued as human food while its dry stover makes important livestock ration in crop–livestock farming system. Its forage has better nutritional quality in terms of crude protein (%) and dry matter digestibility (%) along with good palatability whereas Napier grass (*Pennisetum purpureum* Schumach.) is a perennial, allogamous species commonly known as elephant grass. It has high productive potential, carrying capacity, nutrient quality and low water and nutrient requirements that have highlighted it as the chief tropical forages used for dairy grazing system enhancement. Pearl millet and napier grass were hybridized to produce perennial, vigorous, robust plants. They have the ability to combine the perennial nature, high biomass, winter hardiness, drought tolerance and multicut behaviour of Napier grass with pearl millet which is well adapted to drought and has better nutritional quality coupled with high palatability. Several hybrid progenies were obtained and then examined based on the morphological traits during 2020-21 at RVC, BAU, Ranchi. The F1 seed of each combination was harvested at maturity and the F1 seed was planted on raised nursery bed to remove the bajra like plants. The row to row and plant to plant spacing was 60 cm. All the recommended cultural practices were followed to raise the healthy crop. Thin napier lines were procured from PAU, Ludhiana. Several yield and yield attributing traits were recorded. The highest no. of slips were obtained by LN 3 (24) followed by LN 1 (20). In bajra, 10 forage A lines (male sterile lines) and 18 forage pollinators (OPVs) (recurrent lines) were procured from ICRISAT, Hyderabad. The characters recorded were days to 50% flowering, plant height, no. of tillers/plant, spike length and green fodder yield (q/ha). In case of male sterile line, the highest green fodder yield (q/ha) was recorded by ICMA 00444A4 (545 q/ha) followed by ICMA 07999A5 (430 q/ha) while in case of Forage pollinators (OPVs), the highest green fodder yield (q/ha) was recorded by ICMV 05222 (684 q/ha) followed by ICMV 1710 (623 q/ha). Different Hybrids were developed from crossing of Bajra x Bajra and Bajra x Napier on two different dates of sowing. The interspecific hybrids between Bajra x Napier in first date of sowing (16.8.20) were BxN1 (384 q/ha) BxN2 (379 q/ha) and BxN3 (456 q/ha). The Number of crosses developed between Bajra x Bajra on two different dates of sowing i.e. 16.8.20 and 30.8.20. Several crosses were developed. Out of them, B2xB23 (656 q/ha) recorded highest yield followed by B2xB25 (546 q/ha). In the second date of sowing B6xB12 (634 q/ha) recorded highest yield followed by B2xB23 (578 q/ha).

Keywords: Genetic, characterization, Interspecific, Hybrids, Pearl Millet, Napier

O-V 18

Genetic diversity studies in maize (*Zea mays* L.) for green fodder yield and its quality traits

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Maize (*Zea mays* L.) is an important fodder crop which produces better nutrition quality along with good quantity of biomass. Fodder crops are an important component of agricultural economy as they help in sustainable development of livestock sector. In India, it is used as green fodder, hay and silage for animals. The experimental material for present study consisted of 32 genotypes of maize for genetic diversity. Observations were recorded on five quantitative and one quality parameters during *Kharif* 2022 at RVC Fodder Farm, Birsa Agriculture University, Ranchi (Jharkhand) in three replications and in RBD design. The genotypes were significantly different for all the characters; this indicates that there is scope for further genetic studies.

All the genotypes were grouped in to seven clusters. Cluster-I having the largest genotype (i.e eighteen genotypes), Cluster-II having six genotypes, Cluster-IV having four genotypes and Cluster-III, V, VI and VII having one genotype each. The maximum inter-cluster distance was observed for cluster between II & IV (262.94) followed by cluster II & III (169.20), followed by cluster II & V (144.90) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. The maximum contribution towards divergence was observed by Plant height (56 %) followed by Days to 50 % Flowering (18.75 %), Leaf /Stem ratio (15.24 %), Crude protein (12.38 %), Green Fodder Yield (3.02 %) and Dry matter yield (q/ha/day) (1.61 %). The genotypes MAH 15-84, IFH 10-21 K2, ADFM-4 and KDFM-8 were the most promising ones and their adaptation to the agro-ecological condition of Jharkhand. This can bring substantial increase in green fodder yield and crude protein (%). This study gives an insight into diversity pattern of advance maize lines which will be helpful for further utilisation in breeding programme.

Key words : GCV, PCV, Diversity, Heritability



Theme -VI

Breeders and farmers right and public awareness for IPR Entical issues and regulation of Biosafety



O-VI 1

The protection of plant varieties and farmers' rights act, 2001

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Under the Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS) of the World Trade Organization (WTO) India took the lead and became one of the first countries to develop a *sue generis* legislation to preserve and protect the way farmers have been practicing agriculture in the country since time immemorial. This is one of the few legislations in the entire world which mentions the word “farmers’ rights” in the legislation itself. PPVFRA under the aegis of Ministry of Agriculture & Farmers Welfare, Government of India, provides an effective system for protection of plant varieties, the rights of farmers and plant breeders, and to encourage the development and cultivation of new varieties of plants. Plant varieties are registered with PPVFRA (Protection of Plant Variety and Farmers Rights Authority), enabling farmers with exclusive right to produce, sell, market, distribute, import and export the variety. The preamble to the PPVFR act, 2001 clearly defines the reasons for its existence viz., protection of breeders and farmers rights, accelerated agricultural development and facilitation of growth of seed industry in India. The PPVFR act, 2001, empowers the Government of India to create a legal and governance framework for protection of plant varieties including transgenic plant varieties and a benefit sharing mechanism to reward plant breeders and farmers.

India has consciously chosen to keep plants, varieties and seeds outside of the Patent Act by inserting Section 3(j) in the Indian Patent Act (IPA), 1970 under category of inventions which cannot be patented. All in all, it is a win-win for the farmers and the Indian seed industry.

Keywords Plant variety protection (PVP), intellectual property rights (IPR), farmers’ rights, plant varieties, breeders rights

O-VI 2

Birsa soybean-4 (BAUS-96)- a high yielding variety of soybean developed for different agro-climatic region of Jharkhand

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In India, which is predominantly a vegetarian society, fats and proteins of vegetable origin acquire special significance. Soybean provides a cheap source of high quality protein suitable for human



consumption as well as edible oil. Besides, it fixes atmospheric nitrogen in the soil at the rate of 65-100 kg/ha with the help of *Bradyrhizobium Japonicum* bacteria.

The agroclimatic condition of Jharkhand provide ideal condition for Soybean production. Jharkhand is largely inhabited by tribal population. The whole region is socio-economically backward, quite a large section of tribal population is still practicing primitive type of agriculture. Protein calorie malnutrition is posing a serious threat to the over growing population. Increased production and consumption of Soybean is one of the best way to overcome protein malnutrition among poor tribal farmers of Jharkhand.

Considering the importance of development of high yielding improved varieties of Soybean for the State Scientists of Birsa Agricultural University, Ranchi working on Soybean have developed a high yielding variety of Soybean, namely, Birsa Soybean-4 (BAUS-96) in 2022 after extensive testing in different Co-ordinated trials, Station trials, Multilocation trial over the years as well as locations. It is found suitable for rainfed upland areas of Jharkhand . Birsa Soybean-4 has yield potential of 28-30q/ha and matures in 105-110 days. It has 40.30 percent protein and 17.5 percent oil content. It is found tolerant to Rhizoctonia Aerial Web Blight disease. It is also tolerant to major pest viz., Stem fly, girdle beetle & defoliators in Jharkhand. Its performance was also evaluated in front line demonstration. In farmer field Birsa Soybean-3 showed 10-36% increase in yield over farmer's variety over the year 2018-2020.

O-VI 3

Assessment of indigenous rice varieties under the rainfed condition of lohardaga district of Jharkhand

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This study was Carried out to assess five (5) Indigenous Rice Varieties viz: Kalamdani , Ranikajar , Ketki , Karaini , Laldhan at the KVK farm under the rainfed condition of Lohardaga district of Jharkhand. During the Kharif Season 2022-23 to assess the four local Rice varieties for five various attributes viz: plant height , Panical length, No. of tillers/ plant , 100 seed weight , Grain yield /ha . Two characters viz : Plant height , 100 seed wt. were found non- significant effect whereas rest of these three characters viz : number of tillers/plant , Panicle length and grain yield/ha were showed significant effect . Grain yield was found significant superior in the variety kalamdani over rest of the varieties with the highest value of 48.5 q/ha followed by Ranikajar 44.8 q/ha , Lal Dhan 40 q/ha, Ketki 22.67 q/ha and Karani 20.75 q/ha). Panicle length is greater in Kalamdani followed by Ranikajar , Ketki, LalDhan and Karaini number of tillers /plant was found highest in the variety of Kalamdani (7.5) followed by Lal Dhan (5.6) , Ketki (5.5) , Ranikajar (3.5) and Karaini (2) . Whereas Days to maturity was earlist in the variety karaini (75

DAS) followed by Ketki (100 DAS) , Laldhan (115 DAS) Kalamdani (125 DAS) and Ranikajar (130DAS)

O-VI 4

Prospects of early pigeonpea varieties in Jharkhand

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Introduction-

Pigeonpea occupies a prominent place in the Jharkhand agriculture. The total area of Pigeonpea in Jharkhand is 2.3 lakh hectares, and production is 240.0 thousand tons. The productivity of Pigeonpea in the state is (1049kg ha⁻¹). Mostly Late and medium duration varieties are preferred by the farmers. However, it causes grazing problem as it is only standing crop in the field. Although, early maturing (125-140 days) varieties are grown in various inter cropping systems along with cereals, millets and oilseed..

The productivity of Pigeonpea in Jharkhand has remained stagnant since last few decades. This is mainly due to lack of high yielding varieties grown in the regions and other major constraints including poor adaptability of the exiting varieties to different agro-ecological zones, erratic rainfall, non availability of quality seeds of the improved varieties and biotic stresses such as Fusarium wilt and sterility mosaic diseases, insect pests such as *Helicoverpa* pod borer, and *Maruca*. Drought is also a major bottleneck in Pigeonpea production. The trends of area, production and productivity fluctuates regularly in Jharkhand and it will remain fluctuating in Jharkhand due to higher and erratic rainfall, use of poor quality seed, non- adaptation of improved technologies and non-practicing of adequate plant protection measures by the poor farmers of the region. The research is conducted for early maturing genotypes to escape the high rain fall during flowering and pod initiation stage.

Results-

The several trials were carried out from 2016-2017 to till date where several early maturing genotypes were subjected to testing for yield and yield parameters including biotic factors (Wilt, Mosaic and Pod borer). In each year observation were recorded for grain yield, days to maturity, wilt percentage, pod borer percent and sterility mosaic. These observation for 2016-17 were found in the ranged of [yield(9.37 q – 13.43 q /ha), maturity (132-152 days), Wilt Incidence (5.0-21.6 %) , Mosaic (0.8-2.1 %) , for 2017-2018 [yield (5.55 q – 12.36 q/ha), maturity (117-143 days), Wilt incidence (1.0-3.1%),Mosaic (1.0-3.5%)],for 2018-19, yield (2.58-9.83 q/ha), maturity (105-122 days), wilt (2.5-18.5%) pod borer (2.1-7.7%) mosaic (2.5-18.5%), for 2019-20 [yield (4.65 q – 7.12 q/ha), maturity (112-163 days), Wilt (0.0-4.5%), pod borer (7.5-19.6%) ,Mosaic (2.2-20.8%)], for 2020-21, [yield (6.29-24.29 q/ha), maturity (161-196 days), wilt (6.8-



56.9 %), pod borer (1.4-2.9%)], for 2021-22, [yield (4.61-14.98 q/ha), maturity (154-161 days), wilt (0.4-17.3%) ,pod borer (3.7-6.4 %) mosaic (0.3-1.1 %)].

Conclusion-

It was concluded in 6 year trials that yield varied between 2.58 to 24.29 q/ha, maturity 105-196 days. This suggests that wide variation in yield and days to maturity was due to several abiotic (Rainfall, Climate, soil condition) and biotic factors (Pest such as *Helicoverpa* pod borer, and *Maruca*, and diseases such as *Fusarium* wilt and sterility mosaic). This wide variation can be exploited in breeding for early maturing varieties of Pigeonpea with resistance to biotic and abiotic stress as early maturing varieties can increase the cropping intensity and land will be made available for Rabi crop as well which will further enhance the economy of farmers.

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O-VI 5

Birsa kamrenga-1 (rwb-13) a promising genotype of wingedbean in jharkhand under rainfed and alfisol

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The genotype "RWB-13 (Birsa Kamrenga-1)" has different phenotypic traits than the check variety *i.e.* AKWB-1, RMDWB-1 and IWB-1 having suitable for rainfed and irrigated alfisol of Jharkhand. With objective high yielding and short duration, selection is done in local germplasm collected from farmer's field. Its average height is 310 cm and having blue flowered (having few white flower) and pod setting in 72 days. It matures in 162 days early and average damage by pod borer is 6.4%. RWB 13 produced highest grain yield among the tested entries of winged bean. Recommended dose of fertilizers (20 kg N, 40 kg P₂O₅, 20 kg K₂O and 20 kg S/ha) was found to be optimum. The entry, RWB 13 recorded 20.8 and 46.2 % increase in yield compared to the check varieties RMDWB-1 and AKWB-1 under 100% recommended dose of fertilizers under agronomical practices trial. The entry, RWB 13 recorded 1.23% and 34.44% increase in yield compared to the check varieties RMDWB-1 and AKWB-1, respectively in coordinated breeding three consecutive years trials. Damage by pod borer was less than Checks AKWB-1, IWB-1 and

RMDWB-1. RWB-13 was earlier than checks IWB-1, RMDWB-1 and AKWB-1. On the basis of field demonstration, the farmers can be convinced to grow on their field due to its importance as a vegetable with nutritional value.

O-VI 6

BAUMH-5, medium maturity maize (*Zea mays* L.) hybrid for Jharkhand

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Maize (*Zea mays* L.) is an important food, feed as well as raw material for producing large number of industrial or commercial products. It is adapted to all agro- ecological condition in India and grown in 3 crop seasons (rainy, winter, summer). Maturity period ranges from 80 to 180 days depending upon genotypes and climatic conditions. Varieties/hybrids of different maturity groups are needed to maximally exploit the agro- ecological environment for maize production.

In Jharkhand it is mainly grown as rainfed crop during rainy season in an average area of 0.29 million ha. having state average productivity of 18-20 q/ha. Seeds of maize hybrids developed by different private companies are available in local market comparatively at higher rate. Considering the poor adaption and higher cost of hybrid seed for Jharkhand state, efforts have been concentrated to develop medium maturity single cross hybrid under maize research project at BAU, Ranchi and develop BAUMH- 5. After extensive testing in Co-ordinated trials (NIVT), station trials, multi-location trials and farmer's field in different years and locations, it was found suitable for Jharkhand condition. The average yield potential of BAUMH-5 has been recorded more than 60 q/ha and maturity 85-90 days. It was also evaluated under agronomical trials, and with RDF yielded more than 65 q/ha having B : C ratio 2.07. In farmers field it was recorded that average yield varied from 55 to 65 q/ha.



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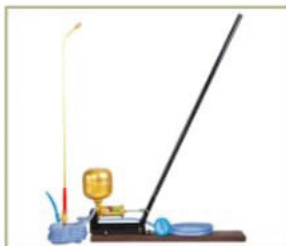
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