5th INTERNATIONAL GROUP MEETING (IGM)

Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability

(March 27-29, 2024)

BOOK OF ABSTRACTS

Organised by:

Society for Advancement of Wheat & Barley Research (SAWBAR), Karnal
&
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal

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on

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&
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal

Venue:
ICAR-Indian Institute of Wheat & Barley Research (IIWBR)
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Book of Abstracts: 5th International Group Meeting on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability

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PREFACE

The cereal crops occupy a major share in the world cropped area and have been supplementing the nutritional requirements of both humans and animals by providing food, animal feed, and fodder. Boosting cereal food production to meet the escalating demand without distressing the environment is a major challenge of the current time. In the past few years, a number of effects related to climate change have become increasingly prevalent. These include alterations in temperature, occurrences of flooding, periods of drought, waves of extreme heat or cold, prolonged lack of rainfall, and rises in insect or pest populations. The Key purpose of the 5th International Group Meeting (IGM) on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability is to create a forum where researchers, academics, extension workers, and students involved in cereal crop research can come together to exchange and explore the most recent developments, ideas, and applications in this field. The most effective approach to address climate risks is to enhance our ability to adapt and become more resilient, which can provide immediate advantages and mitigate the negative consequences of climate change.

We believe that the meeting will brings together researchers from all over the world to present and discuss the latest research, contribute to sustainable environment, technology and sustainable development and energy resources, and encourage more research cooperation. The will of the authorities, together with the important role of scientists in creating various opportunities is to strengthen the research culture and downstream research outputs, ultimately solving problems related to cereal crops.

We express gratitude to the participants for their immense enthusiasm in sharing and discussing their research findings, which have the potential to benefit other researchers and peers worldwide. The abstracts of all participants chosen for presentation during the 3-day event have been compiled and published as a book. I express my gratitude to the sponsors for their kind contribution, acknowledge the organizing committee and all individuals, including members of the Society for Advancement of Wheat and Barley Research (SAWBAR). We express our gratitude and extend a warm welcome to all the delegates. We anticipate productive and valuable discussions during this meeting.

I look forward in successful organization of the 5th International Group Meeting.

(Gyanendra Singh)

सत्यमेव जयते

डॉ. हिमांशु पाठक
DR. HIMANSHU PATHAK
सचिव (डेयर) एवं महानिदेशक (आईसीएआर)
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Director General (ICAR)

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MESSAGE

I am happy to know that the Society for Advancement of Wheat & Barely Research, Karnal, and ICAR-Indian Institute of Wheat & Barley Research, Karnal are hosting the 5th International Group Meeting (IGM) on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability during March 27-29, 2024 at Karnal, Haryana. Cereal crops play a crucial role in providing nutrition for both humans and livestock worldwide. However, the impacts of climate change pose significant challenges to cereal agriculture, potentially threatening global food and nutritional security as well as agrarian economies. Mitigation and adaptation strategies are essential for making agriculture more sustainable and resilient in the face of climate change. The 5th International Group Meeting addresses the pertinent topic 'Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability'. Research and innovations could provide a crucial stride for moving forward. The meeting will surely delve into the burning issues via a multi-disciplinary and multi-stakeholder approach to arrive at research technologies, policy support, package of practices for alleviating the adverse consequences of climate change.

I hope that the technical deliberations will provide a roadmap for innovations to combat with the effects of climate change and make agri-food systems more robust to realize the Sustainable Development Goals by 2030. Moreover, the meeting will provide an interface for fostering the linkages and collaborations to accentuate scientific innovations for the betterment of agriculture.

I wish the 5th International Group Meeting a grand success.

Yours sincerely,

(Himanshu Pathak)

Dated the 18th, March, 2024
New Delhi

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Dr. T. R. Sharma, Ph.D
FNA, FNAAS, FNASc, JC Bose National Fellow
Deputy Director General (Crop Science)

Message

I am pleased to know that the Society for Advancement of Wheat and Barely Research, Karnal and ICAR-Indian Institute of Wheat and Barley Research, Karnal are hosting the 5th International Group Meeting (IGM) on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability during March 27-29, 2024 at Karnal, Haryana. The topic and the themes selected by the group are very inclined for discussing the thrust areas of research in cereals.

As we are facing unprecedented environmental challenges, it is imperative that we take decisive action to safeguard our food systems against the impacts of climate change. Cereal agriculture, as the cornerstone of global food security, must be fortified with innovative strategies to ensure its resilience in the face of increasingly erratic weather patterns and extreme events. The urgency of this matter cannot be overstated. With each passing year, we witness the effects of climate change on our agricultural lands from droughts and floods to heat waves and pest infestations. These disruptions need attention to meet growing global population but also jeopardize the livelihoods of millions of farmers who rely on cereal crops for their sustenance. In response to these challenges, it is incumbent to embrace a holistic approach to climate-proofing cereal agriculture. This entails leveraging cutting-edge technologies, adopting sustainable farming practices, and fostering collaborative partnerships across disciplines and sectors.

I hope, this group meet will provide an excellent forum to discuss some of these issues and evolve future strategies that will enable us to deal with the problems of cereal's food and nutritional security at the national and international level.

I wish grand success for this scientific event.

(T.R.Sharma)

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Dr. Suresh Kumar Chaudhari
Deputy Director General (Natural Resources Management)

21.03.2024

Message

Climate-smart agriculture encompasses a range of strategies aimed at increasing resilience to climate variability, reducing greenhouse gas emissions, enhancing the sustainable use of natural resources and thereby the agricultural production and productivity across the ecologies. The varietal resilience to climate change not only reduce the dangers caused by unpredictable weather patterns but also improve the long-term viability and efficiency of farming practices. This endeavor demands collective action, interdisciplinary collaboration, and a steadfast commitment to embracing new technologies and methodologies. It is also eminent to prioritize climate-proofing of cereals as a fundamental component of agricultural agenda in the country.

On this note, I would like to acknowledge and congratulate ICAR-Indian Institute of Wheat and Barley Research for organizing 5th International Group Meeting on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability. I am sure, this platform will provide opportunities for knowledge sharing/exchange of information among stakeholders.

I wish grand success for this scientific event.

(Suresh Kumar Chaudhari)

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अध्यक्ष

Dr. Sanjay Kumar FNA, FNASc, FNAASc, FCISI
Chairman

Dated: 22.03.2024

MESSAGE

I am delighted that the 5th International Group Meeting (IGM) on Climate-Proofing Cereal Agriculture, organized by the Society for Advancement of Wheat & Barley Research (SAWBAR) and ICAR-Indian Institute of Wheat and Barley Research (IIWBR) during March 27-29, 2024, is taking place. This timely event represents a crucial step towards ensuring global food security in a changing climate.

The IGM brings together a dedicated community of researchers – committed scientists, passionate extension workers, and visionary research leaders. Their combined expertise will be instrumental in tackling the pressing challenges facing cereal production.

The focus on climate-resilient strategies resonates deeply with the current need for sustainable agricultural practices. The chosen themes promise to ignite vital discussions on advancements in efficiency and environmental friendliness. By fostering knowledge exchange and collaboration, the IGM has the potential to pave the way for significant improvements in cereal production and productivity.

This gathering holds immense promise for the future of agriculture. The insights and collaborations generated here have the power to empower young minds and contribute meaningfully to bolstering our global food security.

I extend my warmest wishes for a highly successful 5th IGM!

(Sanjay Kumar)

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डॉ. डी. के. यादव
सहायक महानिदेशक (बीज)

No. F. CS.29/2/2021-Seed
Dated: 22.03.2024

MESSAGE

To ensure food security for the ever growing population, agricultural production needs to be increased by 50% by 2050 with the dwindling natural resources. Recently, crop yields are stagnating due to narrow genetic base, climate change, biotic and abiotic stresses. Development of climate resilient varieties and other technologies in crops is a continuous process which needs proper programmes and roadmap for achieving the future targets. I am glad to know that the Society for Advancement of Wheat and Barley Research and ICAR - Indian Institute of Wheat and Barley Research, Karnal are collaborating to host the 5th International Group Meeting (IGM) on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability during March 27-29, 2024. I have high hopes that this meeting will have a significant impact on creating a more interconnected and collaborative global community by engaging in scientific discussions. Furthermore, IGM will present a highly valuable chance to foster new partnerships and connections among professionals and experts from different locations, working together to develop a holistic approach to develop climate resilient, biofortified and resource efficient varieties.

I am glad to see that several topics related to innovative approaches, new tools and techniques find a considerable place in the agenda of this meet for deliberations. I believe that the discussions and resulting suggestions made during the meeting will greatly improve the efficiency and profitability of various cereal crops. I am confident that this exclusive group will not only discuss the research agenda but also devise the road map for future thrust areas.

I wish the meet a grand success.

देवेन्द्र कुमार यादव
(D.K. YADAVA)

डॉ. अनिल कुमार
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Message

I am glad to learn that 5th International Group Meeting on Climate-Proofing Cereal Agriculture: Strategies for Resilience and Sustainability organized by the **Society for Advancement of Wheat and Barely Research and ICAR**-Indian Institute of Wheat and Barley Research, Karnal is being convened during 27-29th March at Karnal.

India's success in cereal production, particularly in crops like rice, wheat, and maize, has been crucial in meeting the food needs of its large population and contributing to global food security. The Green Revolution, which began in the 1960s, marked a turning point in India's agricultural landscape, especially in cereal production. With nearly 288 mmt of cereal production in the year 2022, Indian cereal agriculture ranks 2nd in the world contributing 25% of world cereal production. Climate proofing cereal agriculture with sustainable practices is crucial in continuing this success amidst several challenges such as extreme weather conditions, erratic rainfall, drought, heat waves, increased greenhouse gases and resource depletion. Sustainable practices and technological innovations will be key in further enhancing cereal production to meet the evolving needs of the future.

The 5th International Group Meeting has emphasized and set its goals towards addressing the current challenges through several technological interventions reflected in its theme to ensure food and nutritional security.

I am sanguine that the suggestions generated from the exchange of ideas during the scientific discussions will assist in establishing the plan for enhancing the production, efficiency, and quality of cereal crops globally. I convey my good wishes for the success of the 5th International Group Meeting.

Anil Kumar
(Anil Kumar)

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A rapidly changing climate is posing serious risks to sustainable rice production in the future. Biotechnological tools like molecular markers and genomics can add precision to breeding and accelerate breeding efforts towards development of climate change resilient rice varieties. Most of the mega-varieties of rice, which are grown across India, for e.g., Samba Mahsuri, MTU1010, Swarna, CR1009, etc. are susceptible to most of the pests and diseases including the deadly disease of bacterial blight. Towards this objective, our research team at ICAR-IIRR, in collaboration with CSIR-CCMB has applied molecular breeding for improvement of multiple traits in the mega-varieties like Samba Mahsuri, Swarna and MTU1010, viz., resistance/tolerance against three major diseases, viz., bacterial blight (BB), blast and sheath blight, resistance against the two insect pests, viz., gall midge and brown planthopper, (BPH) and tolerance to salinity, low soil phosphorus, drought and submergence along with improvement of yield related traits in order to develop climate resilient breeding lines/varieties in the genetic background of the above mentioned elite mega-varieties. Initially, through marker-assisted backcross breeding (MABB), we introgressed three major BB resistance genes (viz., Xa21, xa13 and xa5) into Samba Mahsuri, resulting in the development and release of a high-yielding, bacterial blight resistant rice variety possessing fine-grain type and low glycemic index (GI), named Improved Samba Mahsuri (ISM). Two novel BB resistance genes, Xa33 and Xa38 have been identified from the wild rice Oryza nivara along with another novel gene from distant wild species of rice, Oryza officinalis, Xa48 and transferred to Samba Mahsuri. Through these efforts, a breeding line of ISM possessing Xa38 and having 10 % more yield as compared to Samba Mahsuri along with broad-spectrum resistance against bacterial blight has been released as a new variety, called DRR Dhan 53, has been recently released along with a few other breeding lines of ISM having Xa33 and Xa48 in the pipeline for release. Additionally, gene-pyramid lines of ISM, possessing resistance against blast and tolerance to salinity and low soil P tolerance have also been developed in the genetic background of ISM and released as new varieties under the names, DRR Dhan 62, DRR Dhan 58 and DRR Dhan 60, respectively. We are also pyramiding major QTLs associated with tolerance to drought and submergence along yield enhancing genes and improved breeding lines of ISM possessing multiple traits are being evaluated in multi-location trials of All India Coordinated Research Project on Rice (AICRPR) and few such lines are in final year of testing.

Indian Wheat Improvement Program – Insights from Past and Way Forward

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Wheat (*Triticum aestivum* L.) is the second most important cereal crop of India and plays a vital role in food and nutritional security of the country. The diverse environmental conditions and food habits of people in India supports the cultivation of three types of wheat (bread, durum and dicoccum). Among these, bread wheat is major one contributing approximately 95 per cent to total production. Wheat crop in India is grown across different agro-climatic zones, based on climatic conditions, soil types and growing duration of wheat. An important milestone in the history of wheat cultivation in India was the establishment of the All India Coordinated Wheat Improvement Project (AICWIP) in 1965 by the ICAR. Through coordinated research efforts made under AICRP, nearly 550 wheat varieties suited to different agro-ecological conditions and growing situations have been released so far. These genotypes are very successful in increasing the wheat production from a mere 12.5 million tons in 1964 to around 110.6 mt million tons during 2022-23. Indian wheat has not witnessed any diseases epidemic of rust or any other disease pathogen during past five decades. Presently, the most serious constraint to wheat production in this region is climate change that can have significant effects on wheat production due to its sensitivity to temperature, precipitation, and other environmental factors. Extreme heat events during critical growth stages can also lead to heat stress and spikelet sterility, resulting in lower grain quality and yield losses. Besides, changes in precipitation patterns due to climate change can impact water availability for wheat cultivation. Shifts in the timing and intensity of rainfall can lead to water stress during crucial growth periods, affecting grain development and overall yields. To mitigate the negative effects of climate change on wheat, adaptation strategies are essential. These may include developing and adopting heat-tolerant and drought-resistant wheat varieties, implementing improved water management practices, promoting conservation agriculture techniques, and investing in climate-resilient agricultural infrastructure. Increased production is a prime concern for attaining sustainable food security and becoming world leader in wheat production.

Barley Improvement as Multi-Purpose Crop for Climate Change

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Barley is globally an important crop grown across 51.6 m ha area, producing 157 m MT with an average productivity of 3.04 T/ha. It is one of the geographically most diversely cultivated crops ranging from deserts to mountains and around 50% of cultivated in dry areas, which is highly prone to climate change. Similarly, in India also it is traditionally considered as crop for poor and marginal soils with minimum input, however, recent increased industrial requirement in restricted irrigation situation in north western plains. International Center for Agricultural Research in the Dry Areas (ICARDA) with global mandate for barley improvement, for >19 m ha dry areas across the globe, is collaborating with ICAR to supplement for new diversity through elite breeding lines for grain quality, biotic and abiotic stresses tolerance. The huskless barley for increased nutritional (specifically Zn, Fe, and β-Glucan contents) and hulled barley with higher biomass for green forage/ grazing in dry areas are the recently added components. The use crop wild relatives, *Hordeum spontaneum* and *H. bulbosum* is helping for drought, heat and cold tolerance. The doubled haploid populations for net blotch resistance and Fe, Zn contents. The ICARDA-NARS networking for effective phenotyping of several biotic stresses across different regions resulted in identification of novel sources of resistance and QTL identification through GWAS. The climate change with increasing temperature, decreasing/ irregular rainfall is posing a global challenge for small holder farmers with limited resources and barley is one of the best possible options for sustaining their lively hood.

Modifying Trehalose 6-Phosphate (T6P) Content in Wheat as A Means to Combining Drought Resilience and Yield Potential

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Water supply is a universal factor that affects agricultural productivity. For cereals drought is the most important abiotic stress limiting yield. Most agricultural crop production relies on rainfall during the growing season, so droughts can have potentially catastrophic and unpredictable impacts on crop yields. Breeding is a main mitigation strategy for drought resilience with targeting specific traits having benefit as traits can often be selected by markers and are more heritable than the yield trait itself. Genetic modification (GM) and gene editing for drought resilience are likely to be more difficult because drought resilience is a complex trait unlikely to be affected significantly by single genes or stacking of single genes. Although good outcomes may be possible. There is one example of a commercially available drought-resilient GM wheat variety.

Reproductive development is strongly affected by drought resulting in loss of grain. Understanding regulation of grain number as a specific trait throughout reproductive development would provide insight into specific strategies for resilient crops. In our work we have focused on the trehalose 6-phosphate (T6P) signalling pathway which regulates sucrose use and allocation within reproductive development as part of the regulation of both grain numbers and grain size. We can modify amounts of T6P in crops using light activated T6P compounds sprayed onto the crop. Using this approach, we have increased wheat yields in field conditions over four seasons in rainfed water-limited and water-sufficient conditions increasing both grain number and grain size. Spraying T6P at 10 days after anthesis at the start of grain filling stimulates expression of genes for the whole starch synthesis pathway within developing grain increasing sink strength which also results in more flag leaf photosynthesis. Yield is increased per unit of water and fertiliser input with no dilution of grain protein percentage. Enhancement of the whole source-sink pathway by T6P provides an effective mitigation strategy for drought and also enhances yield potential with no requirement for extra inputs.

Rhizosheath Formation in Contrasting Wheat Genotypes for Drought Stress Tolerance, and its Relevance in Drought Stress Tolerance

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Less water and unpredictable weather threaten wheat production. Researchers must develop drought-resistant crops or new farming practices to adapt. The literature cites that rhizosheath formation is an adaptive trait mainly in desert plant to cope with the drought conditions, and is basically are the soil particles that remain bind to the surface of plant roots after excavation. It's the outcome of the interaction between plant roots and the soil microbiota. During the interaction, the exopolysaccharide-producing bacteria transform the plant root exudates leading to soil aggregation and increase in volume of the rhizosheath, which improves absorption of minerals and water by plants. Consequently, it helps in abetting water and nutrients stress in plants. In preliminary studies, the wheat cultivars with enhanced rhizosheath formation could survive better under severe drought condition by sustaining their transpirational and nutritional demands compared to cultivars with poor rhizosheath formation. Here, we have initiated one DBT funded project wherein we have planted 200 diverse panel of wheat germplasm under rain-fed conditions in field to study the variability in the rhizosheath volume and root architecture at booting and anthesis stages of wheat growth. Similarly, we have planted 30 contrasting wheat genotypes for drought stress tolerance in pot conditions with watering at 40, 70 and 100% field capacity. All these genotypes have been studied for variations in their rhizosheath volume along with root architecture. The average score of rhizosheath volume in drought tolerant genotypes at booting stage of wheat growth was higher at all three watering levels compared to drought sensitive genotypes, and it decreased with decreasing watering levels starting from 100% field capacity to 40% field capacity in both types of genotypes. It was 3.0, 2.6 and 2.27 at 100, 70 and 40% field capacity, respectively in drought tolerant genotypes compared to 2.43, 2.47 and 2.06, respectively in drought sensitive genotypes. However, at post anthesis stage, the rhizosheath volume increased with decreasing field water capacity levels in drought tolerant genotypes, and it was 2.33, 2.43 and 2.73 at 100, 70 and 40% field water capacity. The trend was opposite in drought sensitive genotypes and it decreased with decreasing field water capacity and it was 2.70, 2.43 and 2.20 at 100, 70 and 40% field water capacity. The 200 genotypes planted under rain-fed condition in field also exhibited variations in their rhizosheath volume within the genotypes and the stages of plant growth. It varied 1.5 to 3.5 in different genotypes at pre-booting to 2.0 to 4.0 at post-anthesis stage. The increasing volume of rhizosheath with decreasing field water capacity in drought tolerant genotypes at post anthesis stage of wheat growth, prove its relevance in survival of the wheat plants under water stress conditions.

Mitigation Strategies engaging high throughput genotyping and Phenotyping for heat stress tolerance in wheat

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Wheat (*Triticum aestivum* L.) is a staple crop that nourishes billions of people daily. Although enormous improvement in wheat production has been made, yet due to climatic instability and abiotic stresses, its productivity is significantly threatened. Among all the stresses that wheat crop face, heat and drought are the prominent ones. At reproductive stages especially in heat stress wheat yield gets reduced due to reduction in spikelet fertility, grain number, grain weight, and grain filling duration. Genome wide association studies (GWAS) has been used to identify relationships between target traits and genetic markers. Identifying genetic loci associated with these traits facilitate physiological breeding for increased yield potential under high temperature stress condition. However, high throughput genotyping and phenotyping with precision, is important to lead into outcome. Single Nucleotide Polymorphisms (SNPs) are the best choice among markers for genomic studies as they meet the criteria of being in large number with whole-genome coverage. Precision field phenotyping is one of the key areas for successful crop varietal development programs. Keeping in view requirement of precision ambient temperature dynamics and micro-environments to avoid phenotyping bottleneck, particularly for screening against heat stress response, an innovative structure was created. One of such efforts was made in the form of a temperature-controlled phenotyping facility (TCPF) created at the ICAR- Indian Institute of Wheat and Barley Research, Karnal, India. Both high throughput array based SNP genotyping and precision field phenotyping, has been helpful towards genetic improvement for heat stress tolerance as a mitigating strategy.

Expression of Rust Resistance in Wheat at Different Growth Stages and Temperature Regimes

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Rust resistance in wheat has been demonstrated to express in two broad mechanisms and these are referred to as all stage resistance (ASR) and adult plant resistance (APR). These two broad categories however have been differentiated into further subgroups based on the developments of enabling technologies including advanced phenomics and genomics. None of these technologies can explain disease resistance in total alone. Many researchers believed that only APR genes should be deployed in future wheat cultivars to achieve durable rust resistance; however, my philosophy has been to combine ASR (army) and APR (air force) to achieve long lasting rust resistance in wheat. Here are two examples, where genes differing in expression at different growth stages and temperature regimes, were combined in a single genotype through breeding and have contributed towards durable stripe rust control in Australia. Common wheat cultivar Sentinel carries three stripe rust resistance genes, of which one expresses at the 4th leaf stage and the other two condition resistance after the jointing stage. Similarly, a durum wheat cultivar Wollaroi, carries four stripe rust resistance genes of which three express in a similar manner as the genes in Sentinel. The phenomics (ground force) and genomics (laboratory force) expertise among our research team led us to uncover the stripe rust resistance architecture of these commercially grown cultivars.

Global Warming and Climate Change Effects on Pest Management: Implications Crop Production and Food Security

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Global warming and climate change will have serious implications for pest associated losses, and effectiveness of pest management technologies. Climate change may result in breakdown of host plant resistance to certain insect pests, and thus, there is need to develop crop cultivars with stable resistance to insect pests across seasons and locations. Climatic change may also disrupt the balance between insect pests and their natural enemies. Temperature, relative humidity, elevated atmospheric CO_2, and UV radiation also alter effectiveness of of entomopathogenic fungi and nematodes for controlling insect pests. Insect viruses are also inactivated by high temperatures, sunlight and ultraviolet rays. High rainfall reduces the effectiveness of insecticides. Therefore, there is a need to have a concerted look at the likely effects of global warming on the efficacy of different crop protection technologies, and devise appropriate strategies to mitigate the adverse effects of climate change on the bio-efficacy of IPM technologies for sustainable crop production and food security.

Wheat Earhead Diseases Under Changing Climatic Scenario with Special Emphasis on Fusarium Head Blight in India

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Wheat is one of the most important cereal crops grown all over the world including India. The total production of wheat grains harvested in India during crop season of 2022-23 was 112.74 million tonnes from an area of 34.50 mha and the country is regarded as second largest producer of wheat in the world. Since the initiation of the ‘Green Revolution’ in the mid-sixties, India achieved remarkable increase in production and productivity of wheat. Wheat production in India has increased many folds from 6.4 mt in 1950 to 112.74 mt during 2022-23. The most serious constraints to the wheat production in India are biotic stresses (diseases) such as rusts, spot blotch, powdery mildew, Karnal bunt, loose smut, flag smut and head scab etc. The expected onslaught of climate change is also a worrisome aspect so it is very important to keep different biotic stresses under check for harvesting maximum yield potential of wheat varieties. In India, among foliar and head diseases of wheat *viz*., Fusarium head blight (FHB) or head scab is likely to become most important disease in South Asia in near future due to global climate change and adoption of minimum tillage practices. Among different *Fusarium* spp. causing FHB in India, *F. graminearum* is the most dominating spp. in India. Pathogenic variation among *Fusarium* spp./isolates have been studied by inoculating on a set of wheat varieties under artificially inoculated conditions. Genetic variation among *F. graminearum* isolates have been detected with microsatellite and RAPD markers. Genetic/molecular chemotyping of *F. graminearum* isolates was also accomplished with toxin specific primers. All the twenty-two isolates were tested negative for the genes responsible to produce DON toxin whereas all the isolates showed a positive result for genes responsible for 15-ADON, 3-ADON and NIV toxin. Presently, most wheat cultivars currently grown in different agro-climatic zones India are susceptible to FHB. Evaluation of more than 6500 wheat lines (indigenous germplasm, released varieties and exotic lines) during 2001-2024 led to identification of some resistant lines to FHB pathogen. Management of the disease has been difficult, because of the complex nature of the host/pathogen/environment interaction. Systematic study is required on different aspects of pathogen and interaction with the host for developing FHB resistant wheat varieties and devising eco-friendly management of disease for sustaining global wheat production.

Mainstreaming Grain Zinc in CIMMYT Wheat Germplasm

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CIMMYT's Wheat Breeding programs have continued to modify breeding and phenotyping strategies over time to best serve the targeted wheat growing countries in Asia, Africa and Latin America through the partnership called International Wheat Improvement Network. This has resulted in releases and cultivation of many varieties in various countries that have enhanced wheat productivity through grain yield potential and stability combined with climate resilience, disease resistance and appropriate end-use quality. CIMMYT is in the process of piloting and adopting new approaches to increase the current rate of genetic gain for grain yield while simultaneously mainstream high grain Zn in CIMMYT elite lines. The purpose of the document is to provide status of the breeding program and proposed schemes to further reduce cycle time and parents recycling aiming to achieve higher genetic gain and Zn mainstreaming while continuing to make progress for climate resilience and disease resistance.

Millets Post-Harvest Processing, Value Addition and Marketing

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Cereal grains are among the oldest grains and have been a constant in human diets. They are the primary source of energy for good health worldwide. Some cereals, especially colored rice, colored wheat, colored maize, and some millets, have functional bioactive components such as polyphenols, tocopherol, oryzanol (antioxidants), and vitamins. These cereals have functional properties and ultimately fight against diseases and prevent or control some diseases in the body.Millets or Nutri-Cereals are highly nutritious, small-grained, dryland cereals. Millets are remarkable cereals that store complex carbohydrates, protein, polyphenols, dietary fibre, antioxidants, minerals, and phytochemicals. This nutritious mixture of millets is the elixir for modern-day problems such as diabetes, cardiovascular diseases, and obesity. Millets can also solve the current global phenomena of climate change owing to their high production capacity, lower cost of production, and high tolerance to drought and heat. India is one of the top millet-producing countries. Various millets are produced in India. Regular millet consumption hydrates the colon, prevents constipation, and promotes serotonin production for mental well-being. Additionally, millets boast magnesium content, which may mitigate cardiac risks and migraines, while niacin lowers cholesterol.

Millet grains can be utilized as novel foods by cooking them decorticated or whole or transforming them into flour. Unlike other flours, millet flour does not yield elastic and extended dough when mixed with water due to the absence of gluten. Therefore, fortification with additional ingredients is often necessary to prepare ready-to-eat foods. Millets can be processed into various forms such as flour, porridges, popped grains, ready-to-eat cereals, sprouted cereals, roasted dishes, malted products, different Ready to Eat (RTE), and Ready to Cook (RTC) millets products to minimize the cooking time and make it convenient.Food security isn't just about having enough to eat; it's about getting the right nutrients. Millets, packed with vitamins, minerals, and fiber, offer a powerful alternative to common grains. These "nutri-rich" grains can combat malnutrition and improve overall health. Including millets in traditional dishes and exploring new ways to incorporate them can be a game-changer for global food and nutrition security.

Wheat for Human Nutrition: Facts and Misconceptions

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Wheat, one of the oldest and widely cultivated crops, plays a crucial role in ensuring global food and nutritional security. In addition to providing calorie and protein, wheat contains significant amount of dietary fibre, minerals, vitamins and bioactive compounds required for human health. Bioactive secondary metabolites provide anti-inflammatory, pharmacological, and antioxidant properties, gaining popularity for its health advantages. Insoluble portion of dietary fibre provides protection against conditions like constipation, obesity, cancer, heart disease, and diabetes (especially arabinoxylan). No other food crop supplies humans with such a huge diversity of products from bread to other baked goods and pasta products all over the world. Despite huge benefits, recently, electronic and print literature has cast doubt on wheat's role in our diet, suggesting that it leads to health issues including diabetes and obesity by its continuous use. Despite media skepticism, wheat remains essential in diverse products globally, providing energy, fibre, and micronutrients. In this presentation details of the significant findings are given to evaluate the merits and demerits of wheat consumption. Scientific facts are clearly against the rumours (collectively referred as wheat skepticism) related to negative aspects of wheat consumption. Additionally, there are compelling evidences that consistent intake of whole-grain products including correlates well with weight and diabetes management. Over all consumption of wheat have certain advantages over other cereals providing nutrition and energy.

Rice Bran Oil (RBO): A Rich Source of Bioactive Compounds

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Rice is one of the major staple foods for human consumption. Especially Asian countries are the major producers as well as consumers of rice. Rice bran is produced as a byproduct of the milling process and most of the functional compounds are localized within it. Rice bran contains 15%–23% oil, 12%–16% protein, 21%–27% fiber, and many micronutrients. Rice bran provides rice bran oil (RBO). India represents the world's largest producer accounting for 62.75% of the total global production of RBO. Leading health organizations such as World Health Organization (WHO), the American Heart Association (AHA), the National Institute of Nutrition (NIN) in India, the Indian Council of Medical Research (ICMR), the Japanese Oil Chemists' Society (JOCS), and the Chinese Cereals and Oils Association (CCOA) have declared RBO as "healthy oil". The underlying reason is RBO has the balanced fatty acid composition with a saturated (SFA), monounsaturated (MUFA), and polyunsaturated fatty acid (PUFA) ratio of approximately 0.6 (SFA): 1.1 (MUFA): 1 (PUFA), which is very close to the WHO recommended ratio of 1:1:1. In addition, the unsaponifiable component of RBO also has several health benefits. The most important one is γ-oryzanol, a mixture of ferulate esters of phytosterols having antioxidant properties. Other valuable micronutrients of RBO are the vitamin E derivatives; tocopherol (0.04%) and tocotrienol (0.07%) especially γ-tocotrienol. Tocotrienol helps to prevent obesity and diabetes in animal models through the suppression of inflammation and oxidative stress. Phytosterols are important nonsaponifiable constituents found in RBO. Phytosterol and γ-Oryzanol conjugates have important antioxidant, antiproliferative and anticholesterol activities.

Blending of two or more oils is an effective and economical method to get optimized fatty acid composition and physicochemical properties. In blending, oil deficient in one component is mixed with the oil having the same component to get the desired composition. Rice bran oil (RBO) is deficient in omega-3 fatty acids but rich in antioxidants. However, algal oil is a good source of omega-3 fatty acids particularly long-chain omega-3 fatty acids (EPA-eicosapentaenoic acid and DHA-docosahexaenoic acid) which is not found in other vegetarian sources. Due to the presence of polyunsaturated fatty acids (EPA and DHA), algal oil has low stability. In this study, the blending ratio for rice bran oil and algal oil was optimized to get superior physicochemical characteristics and omega-3 fatty acid content.

Climate Change Mitigation Strategies for Cereal Based Cropping System

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Climate change poses significant challenges to agricultural productivity and food security, particularly in cereal-based cropping systems. The impacts of climate change on cereal crops includes altered precipitation patterns, increased frequency of extreme weather events, and rising temperatures, all of which can lead to reduced yields and compromised crop quality. Previous research indicates that the Earth is projected to experience escalating temperatures in the coming decades, with an estimated rise of approximately 0.2 °C per decade over the next 30 years. Additionally, forecasts suggest that global temperatures could surge by 2.5 to 4.5°C by the end of the 21st century due to the increasing levels of greenhouse gases, such as carbon dioxide (CO_2) and methane (CH_4), in the atmosphere. To address this pressing issue, there is need to explore various mitigation strategies aimed at minimizing the adverse impacts of climate change while enhancing resilience and sustainability in cereal cultivation. One primary approach involves adopting climate-smart agricultural practices that promote resource-use efficiency, conserve soil and water, and reduce greenhouse gas emissions. Conservation agriculture, integrating minimal soil disturbance, crop residue retention, and diversified cropping systems, has shown promise in enhancing soil health, water retention, and carbon sequestration in cereal fields. Additionally, the use of improved crop varieties, such as drought-tolerant and heat-resistant cultivars, can enhance the resilience of cereal crops to climate variability and extremes. Breeding programs focused on developing climate-resilient traits offer long-term solutions to mitigate the impacts of changing climatic conditions on cereal production. Furthermore, precision agriculture technologies play a crucial role in optimizing input use and improving productivity in cereal-based cropping systems. Remote sensing, Geographic Information Systems (GIS), and precision irrigation systems enable farmers to monitor crop growth, detect stress factors, and manage resources efficiently, thereby reducing environmental footprints and enhancing yield stability. Moreover, agroforestry systems, which integrate trees with cereal crops, offer multiple benefits including carbon sequestration, biodiversity conservation, and improved microclimate regulation. By harnessing the synergies between trees and crops, agroforestry contributes to sustainable intensification and climate resilience in cereal farming landscapes. Overall, effective climate change mitigation strategies for cereal-based cropping systems require a holistic approach that integrates agronomic innovations, genetic advancements, technological interventions, and policy support. Implementing these strategies enables farmers to adapt to changing climatic conditions, enhance food security, and contribute to global efforts towards mitigating climate change impacts on agriculture.

Sowing Sustainability: Harnessing Carbon Credits for Cereal Farmers

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Farmers, especially cereal producers, face a daunting task on sustainability front in managing the adverse effects of climate change. Conventional cereal production, owing to large area under cultivation, leads to a significant amount of greenhouse gas emissions and hence the pressure to mitigate carbon footprint escalates while ensuring sustainable food security. In this context, this paper attempts to explore the concept of carbon credits as a potential option to incentivize sustainable practices among the cereal producers. Further, the implications for environment and farmers' livelihood owing to the carbon credits have been highlighted. Carbon credits provide cereal farmers an opportunity to earn additional income by sequestering carbon into the soil from the surrounding environment via sustainable farming practices *viz.,* reduced tillage, cover cropping, nutrient management, and agro-forestry. Adopting such sustainable practices ensures carbon sequestration and in turn these carbon credits can be sold to the companies that look to offset their greenhouse gas emissions. Carbon credit programs benefits both farmers and the environment. This process enables the cereal producers not only in mitigating the adverse effects of climate change but offer a new stream of revenue generation, improves soil health, conserve scarce resources like water, and promote biodiversity. However, the process has its own challenges in a developing country like India and those challenges like lack of awareness, robustness in measurement, monitoring protocols, and equitable access to carbon credit programs especially for small holders have been discussed in brief. Overall, carbon credit programs provide financial incentives to farmers and build ecosystem resilience through adoption of sustainable farming practices. Harnessing carbon credits contribute to the global efforts in sowing sustainability and ensuring climate-smart cereal production.

IIWBR Seed Model for Accelerated Genetic Gain and Deployment of Climate Resilient Varieties in Wheat

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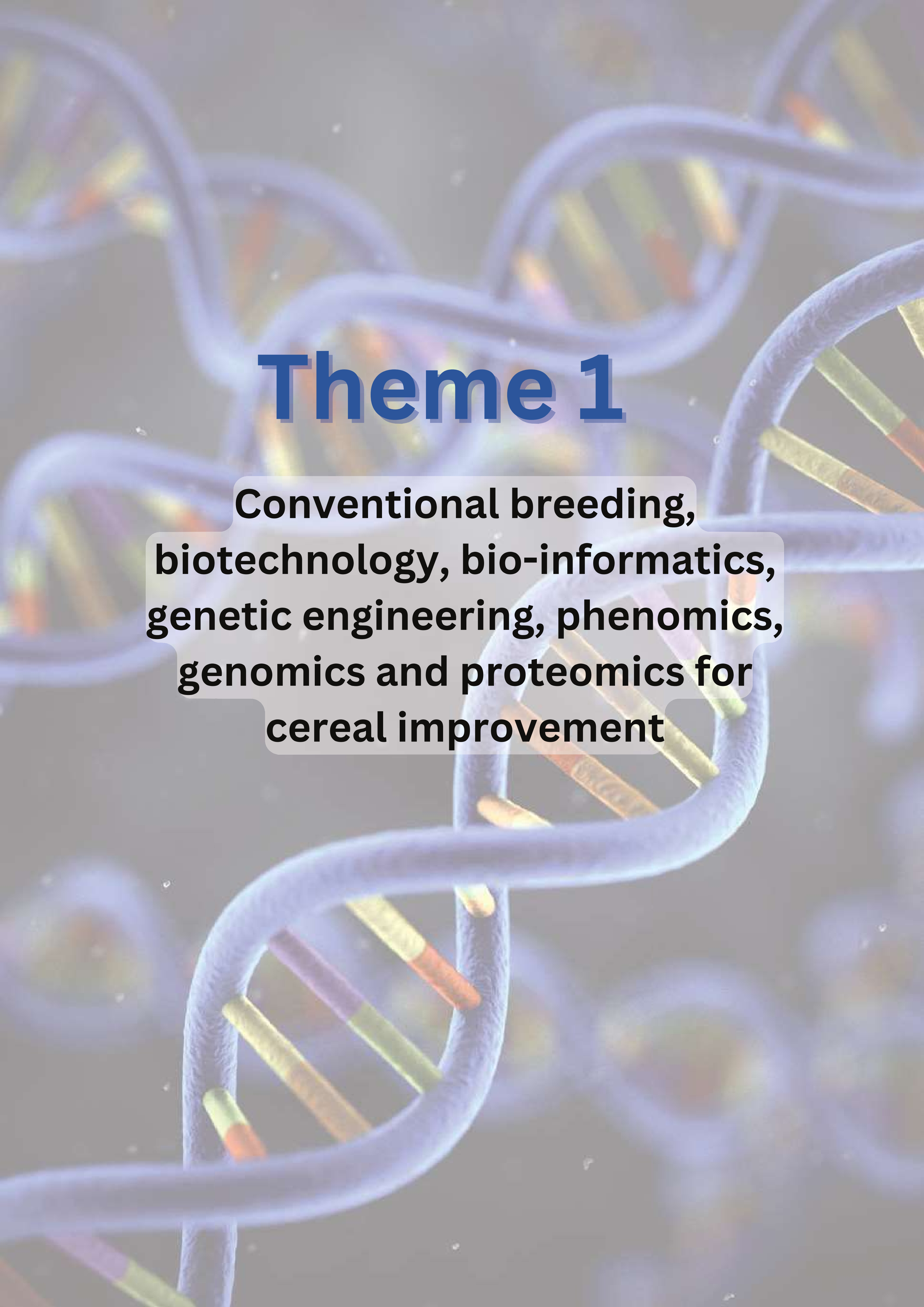
Seed is the basic input and fundamental component in agricultural production. Genetic gains achieved from targeted breeding programs will not be realized until quality seed of improved varieties are supplied to farmers at a reasonable price. Green revolution witnessed by India during 1970 is achieved through development of high yielding varieties and distribution of quality seed of such varieties to the farmers. Any variety takes about five years to reach its peak adoption since release and is attributed to the number of factors viz., seed availability, extension activities and farmers' outreach. However, as wheat is self-pollinated crop, farmers tend to use farm saved seeds which leads to delay in adoption of new varieties. Therefore, special efforts and arrangements are needed for rapid promotion of varieties at farmers' doorstep. The productivity of wheat is also increasing steadily in India and corelated with increased availability of quality seed of improved varieties. In case of wheat, genetic gain achieved by the robust breeding programme resulted in elevated productivity nationally. Overall wheat grain production is increased owing to robust breeder seed production system, higher seed replacement rate (SRR) and varietal replacement (VRR), meticulous planning of maintenance breeding and seed multiplication system, state of art infrastructure facilities for seed processing and storage, synergy of public & private sector in distribution and marketing.

Development, Deployment, Dissemination, Distribution and Dividend are integral components of IIWBR Seed Model. It is now well recognised as a 5D Model of seed production and distribution. ICAR-IIWBR signed MOU's with different ICAR institutes/ Agricultural Universities for faster dissemination of new varieties developed by the institute. This initiative helped to supply the seeds of new varieties to different wheat growing regions at a faster pace. IIWBR seed portal is equipped with the facility for registration of farmers, private seed companies, farmers producer organisation (FPO) willing to collaborate with ICAR-IIWBR for licensing of varieties. IIWBR seed portal supported by single window system for seed delivery and distribution. Supply of quality seeds of biofortified varieties and climate resilient varieties helped to support the nutritional security and stabilisation of wheat production during varying climatic conditions in recent times.

Presentations



Theme 1

Conventional breeding, biotechnology, bio-informatics, genetic engineering, phenomics, genomics and proteomics for cereal improvement

Oral

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The ICARDA Durum Wheat Program for Resilient Dryland Farming

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In India, durum contributes about 10% of all the wheat that is farmed. The aim of the study is to deliver novel durum wheat lines adapted to the restricted moisture conditions with the incorporation of various elite genotypes/germplasm worldwide with diverse traits in the parent pool. As a part of this, multi-year and multi-locations trials were conducted to assess the performances of potential advanced breeding lines and to define critical traits for adaptation. Moderate to high heritability, ranging from 24.0% to 91.0%, was recorded for the grain yield across the environment. Indore, Dhanduka and Udaipur were the top yielding locations in the year 2020, 2021 and 2022, respectively. Genotypes INL-18AREC_301, Kenzera, Tillejihan, Saraverves, IDON 43-21 & Ouzzjihan were found to be the most adaptable and best yielding genotypes across environments. Among cluster the five clusters, E5 containing Dhanduka location in year 2021, showed highest average grain yield (5234.1 kg/ha). Grain yield was found have positive correlation with 1000 grain weight and number of tillers, whereas negative correlation was observed with days to heading and maturity in all the season. Molecular markers are more effective and accurate in describing the genetic features for the identification and purity assessment of genotype. We assessed the distinctness and uniformity of spike morphology for Global Durum Panel (765 entries) over 3 seasons for six important spike morphological characters (viz., Lower glume beak shape, Lower glume shader shape, ear shape, ear colour, awns attitude and awns colour) using 90K SNP genotyping array. A total of 29 markers and were found to be strongly associated with different traits. A subset important KASP markers distributed across the chromosomes were used to screen for variety homogeneity along with morphological and phenotypic assessment. These findings highlight the importance of markers in validating the effect of each SNP to make better decisions about its suitability in the DUS characterization, breeding and registering high yielding potential plant varieties across the environments.

1OP-2

Unlocking the Potential of Early Maturity Genotypes

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Wheat provides one-fifth of the world's calories and protein thereby playing a vital role in ensuring global food and nutrition security. Early maturity genotypes in wheat refer to varieties or cultivars of wheat that have been bred or selected to reach maturity earlier than traditional varieties. In regions where the growing season is limited, early maturity genotypes allow farmers to plant and harvest wheat within the available timeframe. It enables farmers to plant a second crop after harvesting the wheat, thus increasing overall productivity and profitability. Farmers can plant early maturity wheat varieties within a broader window of time, allowing them to optimize planting dates based on weather forecasts and soil conditions. Since, early maturity genotypes have a shorter growing cycle, they may require fewer inputs such as water, fertilizer, and pesticides, leading to cost savings for farmers. Early maturing wheat varieties may fetch premium prices in markets where early harvests are desirable, such as for meeting specific market demands or export schedules. Early maturity reduces the risk of yield losses due to adverse weather conditions such as drought, heat stress, or frost, as the crop can reach maturity before the onset of such conditions. Developing early maturity genotypes involves breeding and selection for traits such as long coleoptiles, reduced tillering, early vigour, accelerated growth, reduced photoperiod sensitivity and tolerance to environmental stresses. Wheat's growth and developmental phases are governed by vernalization, photoperiod response, and earliness genes. So, breeders aim to combine early maturity with desirable agronomic and quality traits to ensure the overall performance and suitability of the variety for target environments. Traditional and modern methods, such as pure line selection, mass selection, backcross breeding, molecular-assisted selection (MAS), quantitative trait locus mapping (QTL), field phenomics, and speed breeding, have the potential to produce earliness and short duration wheat genotypes. Farmers need to consider various factors such as local climatic conditions, disease and pest pressures, soil types, and market demands when selecting wheat varieties for cultivation.

1OP-3

Improving Popular Sharbati Wheat Varieties (HI 1500 And HI 1531) Through Mutation Breeding

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Wheat is one of the most important staple crops which provide food for more than one-third of the world's population. With the ever-increasing population, increasing the yield and quality of wheat varieties in a short time is the need of the hour. In central India, bread wheat cultivars, HI 1500 (Amrita) and HI 1531 (Harshita) are most popular in central India as *Sharbati* wheat due to their excellent quality traits under limited irrigation conditions. However, these varieties are terminal heat sensitive and tend to lodge due to their tall stature under the winter rains and additional irrigation conditions. Therefore, to reduce the height, improves terminal heat tolerance, maintain their quality traits and improve yield under irrigated conditions, a large-scale population of mutants in the background of HI 1500 and HI 1531 was developed by irradiation with gamma rays. A total of 3000 single plant M_1 progeny lines of each variety were screened for identifying mutants for desired agronomic traits in M_2 generation. Identified putative mutants were confirmed and stabilized in M_3 and subsequent mutant generations. The developed mutant lines were 20-30 cm shorter than wild parents and were 7-8 days earlier without a negative effect on yield. These mutant lines were screened for rust responses under artificial epiphytotic conditions, and all improved mutant lines showed resistance to prevalent rust diseases. A high yielding dwarf mutant (85 cm plant height) in the background of HI 1531 was found promising and advanced to national varietal trial for further multilocation testing.

1OP-4

Problems and Prospects of Naked Barley Improvement in India

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Due to changing climates as well as lifestyles, humans are suffering from several diseases like diabetes, coronary heart disease, cancer,mineral defficiency etc. Hulless barley (*Hordeum vulgare* L. var. nudam) is enriched with nutrients and has medicinal properties. The whole grain of hullless barley is a good source of the soluble fiber beta-glucan, which is useful in human diets. ß-glucan plays a critical role in lowering the sugar levels of diabetic patients and also decreasing the risk of coronary heart disease. In addition, it .contains appreciable quantities of protein, minerals, and vitamins Nowadays, hulless barley is gaining importance as a raw material for food industry due to its highly nutritive value. However,Hulless barley has major problemsto reveal the potential grain yield. Six rowed genotypes of hulless barley, in the majority of cases, has a tall plant height with a weak stem, low tilleringcapacity, panicle bears small to medium grain size , low 1000- grain weight, diseases and insect-pests. Hence, it is imperative to improve these yield-attributing traits, along with resistance to major diseases and insects for .enhancing grain yield in hulless barleyBarley Improvement Division, under the aegis of ICAR-Indian Institute Wheat and Barley Research, Karnal, is approaching to mitigate these bottlenecks for improving the grain yield of hulless barley and increasing the area under this crop.

1OP-5

Harnessing the Potential of Sdn1-Crispr/Cas9 Genome Editing for Wheat Improvement

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Over the past decades, numerous efforts were made towards the improvement of cereal crops mostly employing traditional or molecular breeding approaches. The current scenario made it possible to efficiently explore molecular understanding by targeting different genes to achieve desirable plants. In this regard, technologies upgradation in the field of genome editing looks promising. Clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 is a rapidly growing genome editing technique being effectively applied in different crops. Further, the removal of regulation on Site Directed Nuclease1 (SDN1) and SDN2 products has made it more friendly technology for adoption in crop improvement. Though, the gene editing technique is widely used in various crops, wheat is lagging behind in its utilization due to complications associated with its hexaploid, large genome size and recalcitrant nature in terms of tissue culture. At ICAR-IIWBR, an effort has been made to establish the facilities and methods for SDN1-CRISPR/Cas9 genome editing in Indian wheat genotypes, starting from efficient gRNA designing to precise validation of edited plants. The comprehensive strategies have been developed for the first time to design efficient gRNA for genome editing in wheat. The MS1 and GW2 genes have been edited successfully for obtaining male sterile and grain weight improved edited plants respectively. Further, editing of ITPK1, ARE1, GAD3 and ProDH gene in widely grown wheat varieties (DBW187 and DBW303) are under progress. Thus, developed edited plants will have high potential in improving yield, quality, input use efficiency and stress tolerance in wheat. Further, several promising genes validated through RNAi or tilling can serve as a potential candidate for SDN1-CRISPR/Cas9 genome editing for wheat improvement.

1OP-6

Enhancing Barley Breeding for Arid and Semi-arid Regions Through Multilocation Testing and Root Architecture Analysis

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Barley is one of the drought-hardy crops grown worldwide. To increase the adaptation of the new germplasm to the target conditions the Global barley Breeding Program of ICARDA uses of key-location testing sites in Morocco, Egypt, Lebanon and India. Each of these sites represent a target population of environments and are hot-spots for major biotic and abiotic constraints. A total of 200 selected superior lines along with international check varieties, were evaluated using a spatially-arranged alpha lattice design in five different locations representing some of the most important barley growing conditions in the Drylands (JMA: Jemaa Shaim, MCH: Marchouch, SEA: Sidi el Aidi, Morocco; KFR: Kfrdan, Lebanon; and AMH: Amlaha, India. AMMI and GGE biplot analysis were conducted and found that SEA and AMH are the most representative environments of all the 5 environments, while KFR was found to have different environmental conditions compared to MCH and JMA. Genotypes such as ASA2200080, ASA00300, ASA2200908, and ASA2200582 were found to be well adopted to the KFR location, whereas ASA2200821, ASA2200761, ASA2200369, and a check Khnata were well adapted to MCH and JMA. However, some genotypes ASA2200795, ASA2200310, ASA2200793, and ASA2200312 were poorly adapted to all the test environments. Performance of the lines under limited water content is influenced by root architecture. Thus, the seminal root angle of the genotypes was studied. A regression analysis found a significant positive correlation of the seminal root angle with plant height (r=0.27) and grain yield (r=0.18). Overall, the utilization of diverse germplasm in breeding and evaluation of advanced breeding lines across diverse environments with adaptability and stability analysis can help to identify suitable lines for varietal release in diverse locations. Suitable lines with better performance were distributed with national partners to release varieties according to the national seed system.

1OP-7

Making Super-Sweet Corn '*Sweeter'* and '*Healthier'* Through Genomics-Assisted Breeding

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Sweet corn is a popular choice worldwide for its unique taste, sweetness, pleasant flavour, and known for its bioactive properties. The recessive *shrunken2* (*sh2)*, *brittle2* (*bt2*) and *sugary1* (*su1*) are three major genes being extensively used for development of sweet corn cultivars. The *sh2* and *bt2*-based sweet corn also known as 'super-sweet' corn contains 10-fold more sugar, whereas *su1*-type sweet corn possesses 3-fold more sugar and 10-fold more water-soluble phytoglycogen (WSP). In a journey of making sweet corn 'sweeter', *sh2* and *su1* genes were pyramided in the genetic background of two released super sweet corn hybrids *viz*., PSSC-1 and PSSC-2 through genomics-assisted breeding. Gene-based functional markers specific to *su1* and *sh2* were developed through full-length gene-sequencing approach in diverse mutant and wild-inbreds. Three allele-specific SNP markers (SNP583 and SNP755 in 5' UTR, SNP5112 in intron 12) for *sh2*; and one each of InDel (36 bp deletion in promoter) and SNP (SNP2703 in exon-2) marker for *su1* genes were developed. These markers were further validated in five F_2 populations, and 230 diverse inbreds. These markers were then successfully utilized in BC_1F_1, BC_2F_1 and BC_2F_2 populations which led to the development of double recessive sweet corn (*sh2sh2/su1su1*) hybrids through marker-assisted selection (MAS). Background selection using >100 SSRs led to the recovery of >90% recurrent parent genome (RPG). The sucrose among the reconstituted hybrids (*sh2sh2/su1su1*) was 46.3% compared to 29.7% among the original *sh2*-based sweet corn hybrids. This amounts to 53% enhancement in kernel sweetness among the pyramided sweet corn hybrids. The *sh2sh2/su1su1*-based sweet corn hybrids developed through MAS were first of its kind in India. In addition, traditional sweet corn lacks anthocyanins, vitamins and essential amino acids. Thus, to make sweet corn kernels more '*healthier'*, *bt2* gene was combined with genes for anthocyanins (*A1, Pr1, C1* and *R1*), lysine and tryptophan (*o2*), provitamin-A (*crtRB1* and *lcyE*) and vitamin-E (*vte4*) genes in the genetic background of four multinutrient-rich maize hybrids (Pusa HQPM-1-TI, Pusa HQPM-4-TI, Pusa HQPM-5-TI and Pusa HQPM-7-TI) using molecular breeding. The gene-based markers for *bt2, o2, crtRB1, lcyE* and *vte4* were used for foreground selection in BC_1F_1 and BC_2F_1 generations. The BC_2F_2 seeds possessed anthocyanins in kernel. Use of 100-110 SSRs led to the recovery of >90% RPG. The improved sweet corn genotypes possessed high degree of similarity for plant, ear and grain characteristics to their respective recurrent parents. The anthocyanin-rich multi-nutrient-rich blue sweet corn is first of its kind effort across the globe.

1OP-8

Evaluation of G×E Interaction and Yield Stability in Elite Genotypes of Bread Wheat (*Triticum aestivum* L.) using AMMI Model

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Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops that meet the hunger of most of the population in the world. Genotype-by-environment (G×E) interaction is a major factor limiting the success of germplasm selection and identification of superior wheat genotypes for use in climate resilience breeding programs. To determine stable bread wheat genotypes with high grain yield, field experiments were conducted with 49 genotypes for two consecutive years (2019-21) at 5 environments in a randomized complete block design with three replications in each environment. Combined analysis of variance for yield showed highly significant differences for the GxE interaction indicating the possibility of selection for stable entries. The results of AMMI (additive main effect and multiplicative interaction) analysis for yield indicated that the first four Interaction Principal Component Axes (IPCA1-IPCA4) were highly significant ($P<0.01$) and the first two IPCAs (IPCA-1 and IPCA-2) cumulatively explained 85.95% of total GEI sum of square. The partitioning of TSS (total sum of squares) exhibited that the environmental effect was a predominant source of variation. Genotype, WH 1105 had lower IPCA-1 (-0.0455) and IPCA-2 (0.1001) values, and present at a lesser distance from the center of AMMI-2 biplot, displayed less G x E interaction and minimum AMMI stability value (0.1664) among the genotypes, indicating WH 1105 was the most stable for yield. Based on both mean grain yield and stability index in a single criterion called Genotype Selection Index (GSI), of the forty-nine genotypes, the top five genotypes were WH 1105, BRW 3765, QLD-31, BW-5872 and QLD-46.

IOP-9

The Non-brittle Rachis in Barley: Genetic Insight into the Key Domestication Trait

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The insight into the genetics and molecular mechanism of domestication syndrome traits is imperative for success of breeding programmes in most crops. The study of these traits assumes an increased importance in the context of global climate change and its effect on these traits where reversal of these traits due to extreme environmental fluctuations cannot be ruled out entirely. Along with the reduced tillering, decreased seed dormancy, synchronized seed maturity, increased grain size and larger inflorescences, the reduced seed dispersal (non-shattering phenotype) include the domestication syndrome traits in cultivated barley *Hordeum vulgare*. The ancestral species *Hordeum spontaneum* and the closely related *Hordeum agrithicon* retain these traits and are thus considered to be non-domesticated types and consequently unsuitable for organized commercial agriculture. Since shattering does not allow harvesting to be carried out after physiological maturity, the selection of non-shattering types is considered to be a key barley domestication event. The non-shattering phenotype in the cultivated barley results from the non-brittle rachis which in turn originated from deletion mutation in two loci located 100 kb apart on chromosome 3H and designated as Btr1 (1 bp deletion) and Btr 2 (11 bp deletion). Apart from these two genes, chromosomes 5H and 7H in barley have been reported to harbour secondary QTL for brittle rachis. Independent recessive mutations in any of the Btr genes i.e., Btr1 or Btr2, turn the brittle rachis into non-brittle type. Recently, a point mutation in Btr1 has also been discovered which conditions the non-brittle rachis trait in cultivated barley. These studies are indicative of complex origin of this trait as well as polyphyletic origin of cultivated barley. Genetic screening of the world barley collections can add more such mutations to the list which eventually will shed light on the path through which the cultivated barley has evolved in its present form i.e a hardy crop capable of ensuring food and nutritional security of the world under climate change scenario. The study of genetics of Btr1 and Btr2 loci is also important in the context of hybrid barley programme where crossing of genotypes with different loci has been found to result in shattering type hybrids and thus constraining upon the type of crosses that could be attempted.

1OP-10

Identification of Novel Marker–Trait Associations for Stripe rust Resistance in Diverse Wheat Germplasm Using DArt Markers

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) is one of the most destructive diseases of wheat worldwide causes huge yield losses every year. Development and deployment of resistant varieties is the most economical and environment friendly approach for controlling this disease. However, because of the continuous evolution of the pathogen, resistant genes are easily overcome by new virulent *Pst* races, which necessitates a continuous identification and introgression of resistance genes to develop resistant wheat varieties. To identify effective source of resistance, a genome wide association study was performed using 652 diverse wheat genotypes based on 1938 polymorphic Diversity Arrays Technology (DArT) markers. Adult-plant-resistance was evaluated under field conditions for yellow rust resistance at four locations *i.e.*, Karnal, Hisar, Gurdaspur and Wadura. Genome wide association studies (GWAS) was done using Genralized linear model (GLM). Four DArT markers were identified using GLM model on chromosomes 2A, 3B and 5B which are significantly associated with stripe rust at all four locations. These highly resistant genotypes and linked molecular markers are recommended for further gene introgression and pyramiding purposes in the wheat breeding programs.

1OP-11

Evaluation of Wheat Germplasm for Stripe Rust Resistance Under Field and Controlled Conditions

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Wheat is vastly affected by stripe rust disease, principally under cooler environments, and the losses may reach up to 100 percent liable on the severeness of infection and the susceptibility of the genotype. The utmost promising approach to tackle this disease is the use of resistant varieties. In the present study, a set of 192 wheat genotypes was evaluated for stripe rust resistance under field conditions. These lines included pre-breeding germplasm developed for rust resistance and some high-yielding commercially grown wheat varieties. Out of 192 genotypes, 53 were found to be resistant, and 29 showed moderate resistance reaction under field conditions, whereas the remaining genotypes were all either moderately susceptible or susceptible. Under controlled conditions, out of 109 genotypes, only 12 were found to be resistant to all the six virulent/pathogenic pathotypes. Additionally, a selection of 97 genotypes were found resistant in field screening and were subjected to molecular validation using the markers linked to major R-genes, *viz*., *Yr5*, *Yr10*, *Yr15* and *Yr17*. Nine genotypes possessed the *Yr5* gene, twelve had the *Yr10* gene, fourteen had the *Yr15* gene and thirty-two had the *Yr17* gene. The resistance genes studied in the present experiment are effective in conferring resistance against stripe rust disease. The genotypes identified as resistant under both field and controlled conditions can be used as sources in stripe rust resistance breeding programs.

1OP-12

Multi-Locus Genome-Wide Association Studies to Identify Resistance Genes/Qtls Associated with Fusarium Head Blight Resistance in Indian Durum Wheat Germplasm Accessions

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Most wheat varieties presently in cultivation in India are susceptible to Fusarium head blight (FHB) or head scab (*Fusarium graminearum)*. Due to the complex nature of pathogen, it is very difficult to control the disease. Identification of resistance genes/QTLs for effective FHB resistance could greatly enhance our ability to breed durably resistant varieties. We performed a 90K SNP genotyping assay on an association panel of 196 diverse durum wheat genotypes including Indian wheat landraces. The genotypes were evaluated for FHB resistance during 2020-21 and 2021-22 under controlled poly-house conditions at IARI, New Delhi while, same set of lines were evaluated for FHB resistance under natural field conditions at IARI Regional Station, Wellington (Tamil Nadu) during 2021 and 2022. Nine indigenous germplasm lines *viz.*, IC335992 (Karnataka), IC079040 (Himachal Pradesh), IC266978 (Uttar Pradesh), IC585643(Uttarakhand), IC585659(Uttarakhand), IC356111(Uttarakhand), IC145983, IC138554 and IC0111899 having the Relative AUDPC values of <20% were considered resistance to FHB. Association analysis using four different multi-locus GWAS models (MLMM, CMLM, ECMLM and BLINK) identified a total of 15 significant SNPs which were identified on the threshold –log10 (H&B P-value) >4.0. These were mainly distributed on chromosomes 1A (1), 2B (3), 3A (1), 3B (2), 5B (1) and 7B (6). Three SNPs *viz*., wsnp_Ex_c16963_25554400, RAC875_s118711_102 and Excalibur_rep_c104999_171 were consistently detected in all the four models used in GWAS analysis. Identified candidate genes and highly favourable alleles showed their role in FHB resistance directly or indirectly. The information generated in this study will be of potential value for improving FHB resistance in wheat cultivars using marker-assisted selection.

1OP-13

Identification of Novel Genomic Regions Associated with Seedling and Adult Plant Stage Leaf Rust Resistance in Bread Wheat (*Triticum aestivum* L.) Through Genome-Wide Association Studies (GWAS)

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Leaf/brown rust (caused by *Puccinia triticina*) is one of the major diseases threatening wheat production. Genetic/host resistance is the most economic, reliable, environmentally safest, and sustainable way to manage leaf rust disease. The objective of this study was to map quantitative trait nucleotides (QTNs) linked to resistance against different leaf rust pathotypes (13 nos.) at seedling stage in controlled condition and adult plant stages at field situation. To accomplish this, a diverse collection of 105 exotic wheat germplasm accessions were subjected to a multi-locus Genome Wide Association Study(ML-GWAS) utilizing a 35K SNP genotyping assays. By employing six ML-GWAS models, association analyses successfully identified a total of 75 significantly associated QTNs for seedling/all stage resistance(ASR) and five QTNs for adult plant resistance (APR).Among the identified QTNs, nine were found to be reliable for seedling resistance, and five were identified for APR. These QTNs consistently appeared in at least two GWAS models, establishing their status as reliable QTNs A total of 35 putative candidate genes (CGs) associated with ASR resistance and16 putative CGs related to APR were identified. These genes could play a role in disease resistance mechanisms, including serine-threonine/tyrosine-protein kinases (STPK), leucine-rich repeat receptor-like (LRR) protein kinases, and P-loop containing nucleoside triphosphate hydrolase. The QTNs identified in this study can prove useful in wheat molecular breeding programs aimed at enhancing resistance to leaf rust and developing next-generation leaf rust-resistant cultivars. Wheat genetic resources can play a crucial role in mitigating the impact of this leaf rust disease on wheat production.

Poster

1PP-1

Genetic Analysis for Quantitative Traits in Bread Wheat (*Triticum aestivum* L.)

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An experiment was conducted on wheat to estimate the combining ability, gene action, heterosis, correlation analysis and path analysis for yield and its related characters. Ten genetically diverse lines namely; PBW 725, HD 3226, HPBW 01, DBW 88, PBW 550, UP 2425, WB 2, DBW 173, PBW 723 and WH 1105, and three testers namely; HD 3086, DBW 187 and DBW 222 were selected for the current study. On the basis of GCA effects, an overall evaluation showed that the parents DBW 222, DBW 88, PBW 550, UP 2425 and WB 2 were emerged as good general combiners for grain yield per plant with simultaneous consideration of other characters. An overall appraisal based on SCA effects revealed that the crosses PBW 725 × HD 3086, PBW 725 × DBW 187, HD 3226 × DBW 187, DBW 88 × DBW 222, PBW 550 × HD 3086, UP 2425 × DBW 187, WB 2 × HD 3086, DBW 173 × DBW 187 and WH 1105 × HD 3086 emerged as good specific cross combinations for grain yield per plant and other related characters. Among the crosses, DBW 173 × HD 3086, DBW 173 × DBW 222, PBW 723 × DBW 222 and WH 1105 × HD 3086 were emerged as good standard heterotic as well as heterobeltiotic crosses for grain yield per plant and some other more characters. The mean sum of squares due to differences among generations within each cross were significant in almost all the characters except for spike length in cross DBW 88 × DBW 222, and number of productive tillers per plant and peduncle length in cross WB 2 × HD 3086. The duplicate epistasis was observed for almost all the characters. While the complementary type of epistasis was also observed in few cases, viz., peduncle length in WB 2 × HD 3086 and for grain yield per plant in WB 2 × HD 3086. Among the main effects (d & h), magnitude of dominance (h) effect was observed higher than additive (d) effect in some characters in both crosses. The correlation study showed that grain yield per plant showed a positive and significant correlation with number of productive tillers per plant, spike length, peduncle length, plant height, number of spikelets per spike, number of grains per spike, number of grains per plant, test weight, biological yield per plant and harvest index at genotypic and phenotypic levels. The highest positive direct effect on grain yield per plant was observed for biological yield per plant followed by harvest index, peduncle length, spike length and days of anthesis. Thus, these traits may be considered of prime importance in formulating selection strategy for improvement of grain yield in wheat.

IPP-2

Relative Fertility Frequency of First-Generation Doubled Haploids in Wheat using Chromosome Elimination Approach

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Doubled haploid breeding using chromosome elimination has been employed in wheat improvement programmes for rapid development of new improved cultivars. However, the genetic origin of the uniparental elimination following intergeneric hybridization is not always certain. Hence, it becomes essential to evaluate the reproductive performance of the DHs developed to validate their fertility behavior. Therefore, the present investigation was carried out to determine reliable and efficient approach of DH breeding and estimate relative fertility frequency of the first-generation DHs induced in wheat. Hybridization was done using sixteen bread wheat genotypes, seven durum wheat genotypes and three wheat × rye derivatives (BC_1F_3) which were crossed with *Zea mays* L. and *Imperata cylindrica*. Various haploid induction and doubled haploidy parameters were computed *viz.,* pseudo seed formation frequency, embryo formation frequency, haploid regeneration frequency, haploid formation efficiency and doubled haploid formation frequency. Results indicated that *I. cylindrica* outperformed maize for all the haploid induction and DH parameters evaluated. A total of nineteen DHs were obtained out of which, 15 DHs were formed with *I. cylindrica* and four with maize indicating *I. cylindrica* as a reliable pollen source for DH production in wheat, whereas no doubled haploids were formed in wheat × rye derivatives using both pollen sources. These DHs were further evaluated for seed setting frequency and DHs *viz.,* NDH1, NDH3, NDH6, NDH9, NDH12, and NDH13 were found significantly superior. The results showed that seeds of first generation doubled haploids are true to type and can be used for various varietal developmental programmes.

1PP-3

Recent Advances and Breeding Techniques for Biotic Stress in Cereals

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Cereal crops face significant threats from biotic stresses such as pests, diseases, and weeds, jeopardizing global food security. Recent advancements in breeding techniques offer promising solutions to mitigate these challenges. Genomic selection and marker-assisted selection (MAS) expedite the breeding process by identifying and incorporating resistance traits efficiently. Transgenic approaches, including the integration of insecticidal proteins and genes conferring pathogen resistance, provide effective pest and disease management strategies. Genome editing technologies, particularly CRISPR-Cas9, enable precise modifications of target genes associated with stress resistance, enhancing the development of resilient cereal varieties. Bioinformatics and computational biology facilitate the analysis of genomic data, aiding in the identification of candidate genes underlying stress resistance. Phenomics and high-throughput phenotyping platforms enable rapid and accurate characterization of cereal crop responses to biotic stresses, enhancing breeding efficiency. Integration of these cutting-edge techniques offers unprecedented opportunities to develop cereal varieties with enhanced resilience to biotic stresses, ensuring sustainable cereal production and global food security.

1PP-4

Screening for Pre-Harvest Sprouting Tolerance in Bread Wheat

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Climate changes that are occurring at present will have and are already having adverse effect on agriculture. Rainfall at harvest is the major threat which hampers wheat production. Pre-harvest sprouting in wheat is one of the adverse effects of increasing temperatures, irregular rainfall that limits wheat productivity and causes enormous economic losses due to reduction in grain yield, quality and viability of seed, leading to price downgrades. In North Eastern Plain Zone and many areas receiving rainfall during maturity which affects both grain yields and quality. An investigation was initiated to evaluate PHS among 180 advanced breeding lines with 7 checks. The experiment was carried out in alpha-lattice design at AB Block Farm, BCKV, WB. Morphological traits like awn length, spike head angle, seed dormancy, seed-coat color, spike morphology had great impact in PHS resistance. Primary screening was done by artificial sprouting of intact spikes and germination tests in laboratory condition. From weighted germination index inherent seed dormancy was measured. Clustering was done based on resistance and susceptibility to PHS by scoring in sprouting method. Few SSR markers were identified for many genetic loci attributed to PHS resistance. Based on the experiment's outcome superior parents were selected and crossed to retrieve potential PHS lines in advanced generations.

1PP-5

Bridging Phenomics and Genomics gap through Artificial Intelligence: A smart approach to develop climate resilient crops

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Artificial Intelligence (AI) technology, notably Machine learning (ML), is now a pivotal component in the cultivar selection for specific or multiple major environments. Linking genotype to phenotype is a huge challenge that requires an accurate application of high-throughput field phenotyping, genomics, and enviromics. Several machine-learning algorithms are accelerating the activity of breeding new plant varieties, utilizing high-throughput genomics and phenomics for advanced breeding. The high-throughput phenotype systems have successfully documented phenotyping of disease resistance, image segmentation, semantic segmentation, biomass productivity. Using data fusion and an ensemble learning framework, low altitude UAV-based multi-sensor data can accurately predict early grain yield. Large-scale breeding operations can benefit from this high-throughput phenotyping method to increase selection efficiency. The coefficient of determination (R^2) values for Cubist, Support vector machine (SVM), Deep neural network (DNN) and Random regression (RR) models regarding grain yield prediction were observed from 0.527 to 0.670 in wheat. Moreover, across the multi-sensor data, the ensemble learning predictions displayed strong R^2 values up to 0.692, which was greater than individual ML models. Using multiple spectral traits collected from high-throughput phenotyping resulted in better Genomic selection (GS) accuracies for grain yield (GY) compared to using only single traits for predictions in wheat. For genomics studies, DeepBind and DeepSEA represent go-to models for identifying protein-coding genes, gene expression, protein-protein interaction, gene ontology, and genomic prediction. All comprehensive databases integrate resources with AI technology, such as phenotypic diversity of crops, SNPs polymorphisms, QTL analysis, GWAS analysis, genomics selection, and genome sequence. When harnessed in unison, phenomics, genomics, and AI technologies directly enhance the achievement of climate resilient crop varieties with improved yield potential and stability and enhanced tolerance/resistance/resilience to anticipated and simultaneous abiotic and biotic environmental stresses. In summation, we provide a succinct overview of the transformative role of ML and AI in genomics and breeding. It also highlights the commercial implications and trajectory of future research endeavours in these dynamic fields.

1PP-6

Agro-morphological Characterization for Examining the Variability in Global Durum Wheat Panel

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Durum wheat (*Triticum durum*), an allotetraploid (2n = 28, AABB), is a worldwide staple crop and the second most important wheat type after common bread wheat. Durum wheat production represents 5% of total wheat production with a area of 16 mha globally. Germplasm characterization is an essential step to identify the promising genotypes and assessment of variation present in the germplasm. A global panel of 752 durum wheat accessions were obtained from ICARDA, Morocco and evaluated at ICAR-IIWBR, Karnal along with four checks (DDW47, DDW55, PDW 291 and DDW48). The crop was sown during second first fortnight of November in a 3 rows plot of 2 meter length in augmented block design. Data were recorded as per distinctness, uniformity and stability guideline for durum, dicoccum and other wheat species. In the present study, a wide range of variation was observed for DTH (91-139), DTM (136-167), FLL (16.0-46.2 cm), FLB (1.1-2.9 cm), PH (67-181), PL (18.1-85.7 cm), EL (4.2-18.2 cm), SPS (16-32), GPS (11-103), GWPS (0.12-3.95 g) and TGW (10.1-55.9 g) GY (38-1202 g). Eight accessions hade more than 50g TGW, out of which two accessions {DWGIGSSALATFINA053 and ESDCB-2015/2016-100-yousef (Pharoan)} had more than 55g TGW and one accession (Ceedur) has 50.7 g TGW. Furthermore, five accessions (Simeto, Levante, Alemanno, Bronte and BRADANO) have TGW (51.2-51.9 g) and PH (92.2-98.7 cm) found superior from DDW55 for TGW (50.2 g) and at par or superior for PH (96.94 cm). These both traits (TGW and PH) play important role in improving grain yield, thus these identified genotypes could be used as a donors in active durum wheat breeding programme.

1PP-7

Decoding Rust Resistance Genes from Wild Wheat Germplasm: Utilizing Genomics Approach Enhancing Resistance Against Rust in Wheat

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Leaf rust (LR), caused by the fungal pathogen *Puccinia triticina* Eriks., is the most prevalent rust disease affecting wheat, particularly in Northern India where LR pathotypes Pt11, Pt16-1, Pt77-5, Pt77-8, Pt77-10, Pt104B, Pt106, and Pt162-2 are highly prevalent. Addressing the cyclical outbreaks of this pathogen requires swift exploration of resistance genes. While cultivated germplasm often lacks sufficient resistance, the diverse wild wheat germplasm offers a promising avenue. This study focuses on transferring LR resistance from three wild wheat species: *Ae. triuncialis* (UC) *acc pau*3460, *Ae. mutica* (T) *acc pau* 9996, and *T. lorenti* (UM) *acc pau*3536, resulting in the development of hexaploid LR-resistant introgression lines (IL*tri*, IL*mut*, and IL*lor*). The stability of these ILs is evident from their normal chromosome count (2n=42), consistent chromosome pairing, and phenotypic resemblance to typical wheat plants. Genetic investigation of the transferred resistance involves generating F2 mapping populations by crossing ILs with LR-susceptible wheat WL711. Subsequent screening with LR pathotype Pt77-5 revealed significant segregation. In the F2 population from IL*tri*, 219 plants displayed resistance (R) and 95 were susceptible (S), conforming to a 3R:1S ratio (χ2 (3R:1S) = 4.6). Similarly, the F_2 population from IL*mut* comprised 136R and 22S plants (χ2 = 5.4), and IL*lor* produced 238 R and 68 S plants (χ2 = 4.7), consistent with the expected ratios. The consistent transmission of LR resistance from these wild species suggests cryptic alien introgression, offering promising prospects for protecting wheat against LR. Ongoing efforts focus on mapping these newly acquired LR resistance genes using the Affymetrix 35K SNP chip array.

1PP-8

Marker Assisted Backcross Breeding Approach for Introgressing Rust Resistance in Developed Wheat Varieties

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Wheat is one of the major and important staple foods for Foliar infections are one of the major problems in wheat production. Wheat rusts are caused by Puccinia spp., which are the most common and dangerous fungal diseases of wheat worldwide. Creating wheat lines resistant to rust is the primary objective of any endeavour aimed at improving wheat. These days, the process of improving the production of such lines is called molecular marker assisted selection. In order to select for the target allele or gene, foreground selection involves the use of markers that are closely associated with the gene of interest. The method of selecting against other donor parent DNA using markers not closely related to the gene of interest is known as background selection. These decisions are made in breeding programs to increase the effectiveness or efficiency of selection for the targeted traits. In our study, DBW90, DBW187, DBW222 were used as recipient's and YR47*Mace as donor parents. We have made the crosses for incorporating rust resistance and has utilized BC_1F_1 in present study while attempted BC_2F_1 in this season. Using MABB approach, we evaluated the developed BC_1F_1 lines by Simple Sequence Repeat markers for foreground and background selection. Superior selected lines based on the molecular, agronomical and seedling resistance test (SRT) levels will be evaluated and further explored for wheat breeding improvement programme.

1PP-9

The Differential Expression Patterns of miRNAs Under Salt Stress in Salt Tolerant and Salt Susceptible Wheat Genotypes

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A better understanding of the role of miRNAs during salt stress opens the door of possibilities for using miRNA mediated gene regulation to enhance plant stress tolerance. Therefore, to identify salt stress responsive miRNAs in wheat, a salt tolerant wheat genotype KRL210 and salt susceptible HD2009 genotypes were grown under salt and control conditions. The flag leaf, spike and root were collected at Z73 stage. The samples were collected and immediately deep feezed in liquid Nitrogen and sequenced on Illumina platform using paired end sequencing. The total number of reads obtained for spike, root and flag leaf were 16,766,776, 21,538,963, 18,923,432, 12,915,081, 24,120,277, 27,548,354, 18,238,347, 20,752,234 in the three biologically replicated salt treated materials, while the number of fragments obtained in the control group was 16,477,620, 21,347,342, 18,057,239, 9,398,123, 23,862,810, 27,345,139, 17,987,253, 20027,221. We identified a total of 25, 34 and 61 novel miRNAs in the flag leaf, root and spike respectively of KRL210 genotype. Similarly, 42 flag leaf, 90 root and 65 specific miRNAs were reported in the susceptible genotype. A total of 23, 34 and 61 novel miRNAs were found to be exclusively expressed in flag leaf, root and spike of salt treated KRL210 genotype. Known and novel miRNA were further targeted to the Wheat reference genome for target prediction using psRNAtarget server. Identification of these salt stress responsive miRNA in wheat will contribute to better understanding the role of miRNAs in post transcriptional regulation of salinity tolerance in cultivated wheat.

1PP-10

Decoding the Timeline of Bread Wheat Improvement from Plant Domestication to Modern Genetic Innovations

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Bread wheat (*Triticum aestivum* L.) stands as a pivotal crop, playing a crucial role in the inception and evolution of agriculture, nourishing a substantial portion of the global population across centuries. Its domestication coincides with the beginning of agriculture, subjecting it to continuous human-directed selection. Over millennia of cultivation, inadvertent selection on adaptive traits occurred, followed by intentional but empirically driven selective pressures. Wheat breeding, rooted in science for over a century, has dynamically evolved through on-farm agronomy and advancements in breeding programs. Throughout its history, breeding objectives focused on enhancing yield potential, fortifying resistance/tolerance to biotic and abiotic stresses, and refining baking quality. Recent goals, including biofortification enhancement, have surfaced. The limited genetic diversity and genomic intricacies posed challenges for breeding, hindering the application of biotechnology. Old approaches, such as the introgression from relative species, mutagenesis, and hybrid breeding are strongly reappearing, motivated by an accumulation of knowledge and new technologies. A transformative shift has occurred with the routine use of molecular markers, enabling the genotyping of thousands of plants for numerous loci. The completion and accessibility of the wheat reference genome sequence and annotation mark a significant milestone for the scientific community. While transgenics remain a potential tool for wheat improvement, gene editing is emerging as a more prominent option. This, coupled with genomic selection, speed breeding and high-throughput phenotyping, constitutes the forefront of future wheat improvement, opening new avenues for agricultural innovation.

1PP-11

Utilization of Genetic Resources for Enhancing Quality for Food and Malt in Indian Barley

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The small grain cereals like barley have undergone strong selection pressure from the time of early domestication through today's modern plant breeding, resulting in the loss of valuable genetic diversity. This loss of crop diversity, coupled with changes in climate, present new and serious constraints for cereal production and quality. Barley genotypes with high beta-glucan and protein contents are desirable for the health food industry due to their potential health benefits. Beta-glucan, a soluble fibre, has been linked to improved heart health by lowering cholesterol levels and blood pressure. Protein is essential for building and maintaining tissues, and adequate intake can support weight management and satiety. On contrary, lower content of beta glucan is one of the most desirable traits for beer industry. It is an important criterion to determine malt quality of barley and less than 4% is analytic value desirable for malting purpose. Its level has been shown to have direct relationship with viscosity; speed of filtration, Kolbach Index and may affects malt extract value. Therefore, its two-way approach to improve barley quality to address demands of both food and beer industry. The goal of our research is to improve barley with genes derived from wild relatives, landraces and exotic genotypes that are rich sources of nutritional value, and adaptation. Recently we have developed novel two-row hulled genotypes utilizing exotic genetic sources (Shebac and SLOOP SAWL3167) for food and malt purposes. DWRBG-4, is a two-row hulled barley genotype derived from a cross DWR30/Shebac and advanced through pedigree selection. This genotype has shown significantly higher beta-glucan content (7.5% dry weight basis) and protein content (13.2% dry weight basis) as compared to beta glucan (4.2-6.2%) and protein (11.5-12.3%) content available in barley varieties. For malt quality improvement, genotype DWRBG19 is developed from backcross DWRB101*2/SLOOP SAWL3167 and selected through MAS. It has shown least level (3.7% dwb) grain β-glucan as compared to released Indian malt barley varieties including latest variety, DWRB182 (4.5% dwb) which is very much desirable for malting during beer production. DWRBG-4, unique combination of high protein and high beta-glucan content and DWRBG19 having least beta glucan content can be a valuable resource to serve as a donor parent for the introgression of these desirable quality traits for food and malt barley breeding programs.

1PP-12

Perspective of Transformation Methods for Developing Transgene-Free Genome Edited Wheat Crops

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Newly emerging flexible techniques are seen as superior options for enhancing crops, as they target multiple aspects to enhance the economic value and resilience of crop species in response to changing climates. Although genome editing technology remains somewhat constrained, its potential to expedite large-scale crop improvement endeavours is significant. Wheat's hexaploid genome, its size, and its resistance to tissue culture pose significant challenges to implementing genome editing in this crop. Recent advancements in various techniques for introducing CRISPR/Cas9 components into the wheat genome have been summarized visually, incorporating the latest updates on methods such as vector-mediated delivery, ribonucleoproteins (RNPs)-mediated delivery, *Agrobacterium tumefaciens*-mediated delivery, biolistic transformation, transfection, and electroporation. Furthermore, recent developments in transgene-free strategies for genome editing in wheat and other crops worldwide have been highlighted, emphasizing the importance of increasing accessibility on a global scale. Various transgene-free approaches for addressing foreign DNA and RNA have been comprehensively discussed and illustrated diagrammatically. Additionally, several countries have recently eased their regulations regarding genetically modified organisms (GMOs) concerning genome-edited crops, underscoring the necessity of adopting modern, cutting-edge technologies to meet the future demands of crop development.

1PP-13

Molecular Analysis and Phylogenetic Relationships of *Indeterminate Gametophyte1* (*ig1*) Gene for *In Vivo* Paternal Haploid Induction in Maize

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Doubled haploid (DH) technology has revolutionized the pace of maize breeding worldwide. The *indeterminate gametophyte1* (*ig1*)-based paternal haploid inducer (HI) line has immense potential to convert a maize inbred to its cytoplasmic male sterile (CMS) form. Here, entire *Ig1* gene (5431 bp) was sequenced in two mutant (*ig1*/*ig1*) and eight wild-type (*Ig1*/*Ig1*) maize inbreds. The gene structure analysis indicated two exons in wild-type (*Ig1*) and one exon in mutant (*ig1*) allele. The *Hopscotch* retrotransposon insertion in exon-1 along with 19 InDels differentiated the wild-type and mutant allele. In contrast to 260 amino acid-based wild-type IG1 protein, the insertion of *Hopscotch* resulted in truncated protein of 138 amino acids in mutant. Protein structure analysis revealed that the alteration of leucine-zipper-like motif (LZLM) and complete absence of product of exon-2 in mutant IG1 protein cause of the non-functionality of mutant *ig1* gene. The *Hopscotch* insertion was exploited to develop a PCR-based functional marker which was successfully used in genotyping five F_2 populations. Further, 15 InDel markers developed from the sequence analysis revealed 17 haplotypes of *ig1* among 48 diverse inbreds. The analysis also identified 10 *Ig1* paralogues and 31 orthologues in monocots. The phylogenetic analysis revealed that *Ig1* gene clustered with *Ig1-7*, *Ig1-8* and *Ig1-10* paralogues. The novel information generated here assumes great significance in understanding the molecular mechanism of *ig1* and accelerate the breeding cycle using genomics-assisted breeding in maize.

1PP-14

Identifying the Genomic Landscape of Disease Resistance Genes (R Genes) in Wheat: A Comprehensive Genome-wide Exploration

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Plant resistance genes (R genes) encode proteins that detect pathogen-specific molecules and trigger immune responses. Despite the identification of R genes in various plant species, their presence in wheat remains elusive. Therefore, finding NB-ARC encoding R genes in wheat and investigating their genomic organisation and possible functional divergence were our main goal of the study. Through a thorough genome-wide analysis, revealed a rich reservoir comprising 268 putative R genes present within the wheat genome. We observed an uneven distribution of all NBS candidates across the 21 chromosomes. Phylogenetic and synteny analyses highlighted evolutionary conservation among R proteins from wheat's wild relatives. Furthermore, our investigation indicated that the expansion of the wheat R gene family was driven by both segmental and tandem duplication events, highlighting the dynamic nature of these genetic elements. Moreover, we delved into the molecular dynamics and structural characteristics of wheat R proteins, providing insights into their functional diversity and potential modes of action against pathogens. The identification of these R genes in our study holds significant implications for plant breeding, serving as valuable reservoirs of resistance traits that could contribute to bolstering crop resilience and productivity in wheat cultivation.

1PP-15

Understanding Lodging Tolerance in Wheat: Insights from Morpho-Biochemical and Molecular Studies

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Lodging is a problem in wheat production that chronically limits grain yield. Extensive stem lodging destroys the normal canopy structure of crop, causing reduced photosynthetic activity and reduced efficiency of mechanized harvesting which result in grain yield losses. Wheat cultivars' ability to withstand lodging is primarily influenced by biological and anatomical characteristics of the root and stem systems, as well as environmental variables. Therefore, the meticulous selection of cultivars exhibiting resistance to lodging holds paramount importance for ensuring food and feed security. To address this concern, screening of 14 wheat genotypes was conducted to assess their tolerance to lodging within a controlled polyhouse environment at ICAR-IIWBR, Karnal. The evaluation involved subjecting the wheat plant to artificially induced lodging conditions with the help of glasshouse sprinkler system and high velocity farrata pedestal fans. Concurrently, excessive irrigation was administered to saturate the soil to maximum field capacity, creating a conducive environment prone to lodging. Various plant traits such as plant height, length and width of internodes, lodging score and plant biomass were recorded. Based on the data recorded lodging has been found positively correlated with plant height and spike length. Anatomical studies were conducted using thin sections from first and second internode areas. The observed plant height ranged from 75 to 136 cm and average length of first, second and third internodes measured was observed 5.12, 9.43 and 12.32 cm respectively. A positive correlation was recorded between plant height and weight of three lower internodes. Notably, the length of second basal internode and the thickness of third internode exhibited positive correlation of 0.10 and 0.27, respectively, with lodging percent. Furthermore, biochemical analysis of lignin synthesizing enzymes, specifically Phenylalanine ammonia-lyase (PAL) and Tyrosine ammonia-lyase (TAL) was analyzed. PAL enzyme activity demonstrated a significant positive correlation (0.34) with lodging. Additionally, up-regulation of the PAL during lodging stress, as evidenced by qRT PCR, underscored the pivotal role of this enzyme in the lodging tolerance mechanism.

1PP-16

Elucidating Molecular Marker for Photosynthesis in Wheat

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The molecular markers identification for photosynthesis is highly challenging, due to lack of availability of contrast lines for photosynthesis and also owed to complexity associated with its phenotyping. Such kind of studies are very much limited in major crops including wheat. At ICAR-IIWBR, through EMS mutation of the variety DPW 621-50, EMS-98 was identified, which was showing low photosynthesis compared to its parent. Both DPW 621-50 and EMS-98 were extensively phenotyped for photosynthesis associated traits. The DNA samples of contrast lines were genotyped with 35K Axiom® Wheat Breeder's Array (Affymetrix UK Ltd., United Kingdom). Genotypic data of EMS-98 was compared with the genotypic data of DPW 621-50 and the markers having SNPs were identified from these photosynthetically contrast wheat genotypes. Identified SNP's were annotated for putative candidate genes using BLASTn with the International Wheat Genome Sequencing Consortium (IWGSC) and 28 promising SNPs were identified. Primers were designed from these annotated SNPs and the marker were used for validation in contrast parents. Cysteine proteinase inhibitor 6(CPI6) (AX-94861179) and Dehydrin DHN4-like (AX-95135353) were found as the most promising SNP's for differentiating contrast parents for photosynthesis. The identified markers were further validated in a fixed population developed using these contrast lines. CPI6 has showed promising results in the tested population. Thus, CPI6 can be used as a potential molecular marker in differentiating high and low photosynthetic genotypes in wheat.

1PP-17

Importance of Leaf Azimuth in Wheat Crop Canopy

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Spatial orientation of leaf on stem of wheat plant can be considered in two ways. Firstly, the inclination angle and secondly as an Azimuth (angular measurement in a spherical coordinate representing the horizontal angle from a coordinal direction). Azimuth is important for understanding light interception by leaves in the crops, wheat not being an exception. Being a cumbersome trait in terms of data recording, there are not many publications available on this aspect in wheat. With the objective to understand leaf Azimuth in wheat, an experiment was conducted with more than two hundred wheat Genotypes. The orientation was recorded with reference to the flag leaf. Direction of two additional leaves below flag leaf (FL-1 and FL-2) and that of spike were recorded. Considering coordinal direction of flag leaf, the two leaves below were given an angle of 0 degree (if parallel), 90 degrees, 180 degrees or 270 degrees in the clockwise direction while for spike it was either parallel or perpendicular. The experiment was conducted for two years. In addition to this, a subset of 16 genotypes (from the panel) was also planted in perpendicular directions. Data was recorded on individual tiller basis taking nine random tillers per Genotype. Preliminary findings of this experiment will be shared in the international group meeting.

1PP-18

Evaluation of Red rice (*Oryza sativa* L.) Germplasm of Himachal Pradesh using Agro morphological and Molecular Markers

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The present investigation was undertaken to identify and characterize the rice genotypes by assessing the nature of variation and extent of genetic diversity among the genotypes using morphological and molecular markers in order to identify promising red rice genotypes so that these genotypes could be further used in crop improvement programme. 43 genotypes including two checks were evaluated in RBD during *Kharif* 2021 with three replications. The morphological analysis was done as per the standard statistical procedures and molecular analysis was done using NTSYS-pc, DARwin and STRUCTURE softwares. Analysis of variance revealed the ample amount of genetic variability in the material under study. D^2-statistics grouped the genotypes into four clusters indicating the presence of considerable genetic diversity among all the genotypes. The highest inter-cluster distance was recorded between cluster III and cluster IV. Hence, it the genotypes belonging to these clusters are genetically diverse. More the genetically diverse parents used in the hybridization program, greater will be the chances of obtaining high heterotic hybrids.

On the basis of SSR data, 43 red rice genotypes were grouped into three clusters. Furthermore, 35 genotypes were common between D^2-analysis and molecular analysis showing the congruence of molecular markers with the morphological descriptors and hence, providing a powerful tool to characterize and identify the genotypes of rice. Three genotypes namely Desidhan, HPR-2913 and Sukara Red were found promising on the bases of their mean performance and resistance to leaf blast and neck blast, therefore, could be further used in crop improvement programme.

IPP-19

Preserving the Past for the Future: Sustaining Ancient Barley germplasm in Modern Agriculture

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Barley (*Hordeum vulgare*) has been cultivated for thousands of years, with evidence of its domestication dating back to ancient civilizations such as the Sumerians and Egyptians. These varieties often possess traits such as drought tolerance, disease resistance, and adaptability to marginal growing conditions, honed through centuries of natural and human selection. By maintaining and reintroducing these traits into modern breeding programs, we can develop crops better suited to withstand the challenges of a changing climate. Furthermore, ancient barley varieties offer nutritional and culinary diversity that is increasingly appreciated in today's food landscape. With growing consumer interest in heritage grains and traditional foods, there is a renewed demand for barley varieties with unique flavours, textures, and nutritional profiles. By preserving and promoting these varieties, we not only celebrate cultural diversity but also enhance culinary experiences and promote healthier diets. However, the conservation of ancient barley varieties is not without its challenges. Rapid urbanization, industrial agriculture, and market pressures have led to the decline of traditional farming practices and the abandonment of landraces in favour of high-yield, monoculture crops. Additionally, the loss of agricultural biodiversity threatens the resilience of our food systems, leaving them vulnerable to pests, diseases, and environmental shocks. To address these challenges, concerted efforts are needed at local, national, and global levels. This includes the establishment of seed banks and germplasm repositories to safeguard genetic resources, support for in-situ conservation initiatives that involve farmers in preserving traditional varieties on-farm, and the promotion of policies that incentivize the cultivation and marketing of heirloom crops. Collaboration among farmers, researchers, policymakers, and consumers is essential to ensure the continued conservation and utilization of ancient barley varieties. In conclusion, preserving the past for the future is not just a romantic notion-it's a pragmatic approach to building resilient, sustainable agricultural systems. Ancient barley varieties embody the wisdom of our ancestors and offer hope for a more resilient, diverse, and flavourful agricultural future. By sustaining these treasures of our agricultural heritage, we can cultivate a healthier, more sustainable world for generations to come.

1PP-20

Exploring Genetic Potential in Wheat Varieties: Unveiling the Potential of Diverse Germplasm

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Wheat is a major crop of India which is being affected due to various stress conditions created by the ongoing climate change. The present study aims to explore the genetic potential in wheat varieties: unveiling the potential of diverse germplasm for breeding resilient wheat varieties. The study was conducted at Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh in India for two *Rabi* seasons 2022-23 and 2023-24. The study aimed to look at the importance of heterosis in diverse wheat germplasm using the half-diallel mating design. Nineteen parents were selected initially based on their qualitative and quantitative traits and divided into two sets each having 10 genotypes as parents. SHUATS-W15, SHUATS-W13, HP-1014, HD-2967, SHUATS-64, SHUATS-W50, SHUATS-W6 and SHUATS-W89 are high-yielding genotypes among the parents, whereas Paigambari (*Triticum sphaerococcum*), Kalicharan are among the farmer's varieties, and multiple crosses like AAI-W6×AAI-W10×AAI-W6, AAI-W6×MR3014/1/4, MR-1010/34×D4.iii, WR-1451×K.SONA.15KR-4/1, W6×MR-3014/1/4×WR-1451×MDR-30KR/31 are taken as parents which justifies the diversified nature of the experiment. It was prioritised to find out the best parent in terms of combining ability and offsprings which are superior to their parent in terms of yield, stress resistance (abiotic and biotic), and nutritional content. A number of progeny like those from the crosses between Paigambari and Kalicharan (Black Wheat), AAI-W6×MR3014/1/4 and HP-1014, MR-1010/34×D4.iii and W6×MR-3014/1/4×WR-1451×MDR-30KR/31 have shown significant change in their F1 offsprings that can be identified phenotypically. The study needs to be taken further to have a better understanding of the genetics involved.

1PP-21

Web Based Wheat Germplasm and Genetic Resource Database

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The breeding and development of varieties with desirable traits and enhanced characters is benefited by the availability of molecular markers linked to the trait of interest. The availability of markers allows linkage mapping, QTL discovery, foreground selection of donor plants, rapid screening of progenies and background selection. Therefore, at ICAR-IIWBR, a web Based system is developed with comprehensive database having catalog of chromosome-wise SSR of all the three sub-genomes (A, B, D) coupled with the option of designing primers for genotyping. It is also equipped with searching tool option of the 54 DUS features of 381 Indian released wheat varieties & information on released wheat varieties and registered genetic stocks.

MS-SQL (Microsoft SQL Server Management Studio Ver. 12) is used to create the RDBMS to store genotypes data in form of SQL Database files. Germ_Database file contains data of 381 wheat varieties with 54 DUS traits and is used by first Wheat Germplasm module. SSR_DB file has data of wheat SSR markers with 242 markers for 10 different traits & is fetched by SSR/SNP module.SQL database files used for third Variety & Genetic Stocks module are Wh_Gen_Stock, SVRC_DB, CVRC_DB. Visual Studio (Microsoft Visual Studio 2022 (64-bit) Version17.6.5) with C# is used for this web-based data retrieval system modules development.

1PP-22

Marker-Assisted Selection (MAS)-*Yr36* Gene Introgression in Indian Bread Wheat Cultivars

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Wheat is one of the most important crops for global food security; it is widely cultivated on more than 200 million ha of land and produces more than 781 million tonnes annually to feed the world (Wheat Initiative 2019). Grain protein content (GPC) in wheat has been a major trait of interest for plant breeders since it has enormous end use potential. High grain protein content (GPC) governs the nutritional and quality traits of the end-product in bread wheat. In the present study, marker-assisted selection (MAS) was successfully used to improve GPC into an elite wheat variety of North Western Plain Zone viz., DBW327, DBW372 and DBW332. The genotype *Avocet Yr36* was used as the donor parent for introgression of the gene Gpc-B1 that confers high GPC. In cross (DBW327 x A. *Yr36*) screening of F2 generation (123 lines), with five Simple sequence Repeats (SSR markers) viz., *XGWM132, XCFD190, XGWM193, XGWM361* and *XGWM219* were found polymorphic between parents and closely linked to Gpc-B1, used for foreground selection to select plants carrying Gpc-B1. We found 38 positive plants out of 123 lines in the cross (DBW327x *Yr36*) with allele size of 118bp, 191bp, 182bp, 123bp and 153bp respectively. This study thus suggested that MAS in combination with phenotypic selection is a useful strategy for development of wheat genotypes with high GPC associated with no loss in yield.

1PP-23

Climate Resilient Agriculture: A Holistic Approach

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Climate change poses significant challenges to global agriculture, threatening food security and livelihoods worldwide. In response, the concept of Climate Resilient Agriculture (CRA) has emerged as a holistic approach to mitigate risks and build resilience within agricultural systems. At its core, CRA integrates various strategies and practices to adapt to and mitigate the impacts of climate change. This holistic approach encompasses a range of techniques, including agroforestry, crop diversification, soil conservation, water management, and the use of climate-resilient crop varieties. By diversifying crops and planting trees, farmers can enhance biodiversity, improve soil health, and mitigate the risks associated with extreme weather events such as droughts and floods. Moreover, CRA emphasizes the importance of integrating traditional knowledge with modern science to develop context-specific solutions. Indigenous practices, passed down through generations, often hold valuable insights into sustainable land management and adaptation strategies. Investment in research and development is crucial for advancing CRA practices and technologies. This includes breeding crops that are more tolerant to heat, drought, and pests, as well as developing innovative irrigation techniques and climate-smart farming practices. Policy support and institutional frameworks play a vital role in promoting CRA adoption at scale. Governments, international organizations, and NGOs must collaborate to provide farmers with the necessary resources, incentives, and technical assistance to transition to climate-resilient agricultural systems. Furthermore, education and capacity-building initiatives are essential for empowering farmers with the knowledge and skills to implement CRA practices effectively. By fostering resilience at the individual, community, and institutional levels, CRA holds the potential to safeguard food production, enhance rural livelihoods, and contribute to global efforts to combat climate change. Through a concerted effort and commitment to sustainability, CRA offers a pathway towards a more resilient and food-secure future.

1PP-24

Enhancing CRISPR/ Cas9 Mediated Genome Editing Efficiency through gRNA Design Optimization in Wheat

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The groundbreaking CRISPR-Cas9 genome editing technology has opened new avenues in agricultural research. However, its application in wheat crop has faced significant hurdles due to the crop's hexaploid nature, extensive genome size, and repetitive DNA elements. To overcome these challenges, a specialized method was developed at IIWBR, Karnal, focusing on precise guide RNA (gRNA) design for wheat genome editing using the Site Directed Nuclease 1 (SDN1) approach. This method involves a meticulous three-phase process: gene verification, gRNA design, and gRNA analysis. In the gene verification phase, conserved regions across wheat sub-genomes were identified through Multiple Sequence Alignment. Subsequently, WheatCRISPR software was employed for gRNA design, emphasizing factors like on-target efficiency and minimizing off-target effects. The designed gRNA sequences were assessed for potential off-target hits against the wheat genome using BLAST analysis. Additionally, gRNA analysis included predicting secondary structures and evaluating single-stranded propensity using advanced computational tools like Mfold software. gRNA analysis steps ensured the integrity of the designed gRNA sequences, including checks for interference from vector backbones and the absence of transcription terminator sequences. This methodology was successfully applied to design gRNA for key wheat genes, such as *proDH*, *TaARE1*, *ITPK1*, *GAD3*, *SBEIIa*, and *SBEIIb*, highlighting its effectiveness in enabling precise genome editing in wheat, thus underscoring the pivotal role of CRISPR-Cas9 technology in revolutionizing agriculture.

1PP-25

Stability Analysis for Canopy Temperature using Different Models among Bread Wheat Genotypes

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GEI study is a very important for developing a stable variety in diverse environmental conditions. This study was conducted to explore the stability and G × E interactions of canopy temperature of 100 wheat cultivars using two statistical models *viz*; Eberhart and Russell model and AMMI bipot. On the basis of experimental results, the genotype WH 711 with lower mean value (low canopy temperature), bi > 1* and non-significant deviation from regression was found to be suitable for low canopy temperature for better (E5) environment whereas the genotype PBW 729 having low canopy temperature, regression coefficient less than unity and non-significant deviation from regression were found to be suitable for low canopy temperature for poor environment. According to AMMI biplot analysis, genotypes WH 1129, PBW 721, WH 1139, PBW 560 and PBW 527 were plotted near the origin of biplot and had a smaller share of the GEI which indicates its constant performance over the environments. Only E6 present on the leftward of midpoint of the main effect axis and can be called as most favourable for this trait. The data generated from this trial determines stability and the pattern of genotypic response across environments; and at last provides reliable guidance for selecting the best genotypes for planting in future years and at new areas.

1PP-26

Diversity of Durum Wheat (*Triticum durum* Desf.) Genotypes based on Agro-morphological Traits

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The present study was aimed to assess the diversity in durum wheat genotypes and identification of elite genotypes for future genetic improvement. In this investigation, 52 durum wheat genotypes along with 5 checks were evaluated in Augmented Block Design with 4 blocks wherein each block contains 18 genotypes including 13 test entries and 5 checks (randomly allocated). All the 57 durum wheat genotypes were grouped into nineteen clusters based on their D^2 values. The maximum intra-cluster distance was noted in cluster X followed by cluster IX and VI. Maximum percentage of contribution to the genetic divergence was displayed by number of followed by plant height. Maximum inter-cluster distance exhibited by cluster XII and XIV followed by clusters XVI and XVIII indicated that the genotypes associated with these clusters has wide genetic diversity and breeding between genotypes of these clusters could produce superior segregants and better recombinants for durum wheat development programmes. Six PC$_s$ accounted for 79.05% of total genetic variability using PCA. Furthermore, the promising genotypes *viz*., 50th IDSN 7100, 50th IDSN 7049, GW (D) 2019-972, 50th DYN 729, GW (D) 2019-975, 50th IDYN 744, GW (D) 2019-980, 50th IDYN 740 were recognized for yield and yield related attributes. These genotypes can be used as parents in future hybridization programme.

1PP-27

Genome-wide Association Study for Morpho-physiological Traits in Bread Wheat under Contrasting Production Regimes

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Conservation Agriculture (CA) presents a promising approach to sustainably enhance wheat yield in response to the increasing food demands of the global population amidst the challenges posed by climate change. To unravel the genetic basis of 19 morpho-physiological traits potentially contributing to the improved adaptation and performance of wheat genotypes under CA, we conducted Genome-Wide Association Studies (GWAS) to identify Marker-Trait Associations (MTAs) across four distinct production regimes: conventional tillage timely sown (CTTS), conservation agriculture timely sown (CATS), conventional tillage late sown (CTLS), and conservation agriculture late sown (CALS) using an association panel comprising 183 advanced wheat breeding lines, along with 5 checks. The GWAS, utilizing the BLINK model, detected 80 MTAs for the studied traits across four production environments. These QTNs accounted for phenotypic variations ranging from 2.15 to 40.22%. Gene annotation revealed informative SNPs associated with Phi2, NPQ, PS1, and RC, which were linked to genes crucial for physiological adaptation in both CA and CT. Through gene annotation studies, candidate genes essential for trait development, such as the Chloroplastic Photosystem II reaction center W protein for Phi2 and the Bidirectional sugar transporter SWEET1a for GL, were identified. Moreover, stress-responsive factors like UDP-glucose 4-epimerase, Heat stress transcription factor B-2c, and Ethylene-responsive transcription factor ERF071 were detected in the LD region for NPQ-associated QTNs. Upon validation, these identified QTNs have the potential to be integrated into marker-assisted breeding programs, aiding in the development of wheat varieties suited for Conservation Agriculture.

1PP-28

Genetic Insights in to Seed Germination Rate through Genome-wide Association Studies Earmarks Coleoptile Length as the Deciding Trait.

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Seed germination in wheat is an important agronomic trait that affects crops early vigour, uniform crop stands and in turn the yield and quality. Rapid and uniform seed germination are the most critical traits required for proper crop establishment and efficient and timely use of agricultural inputs. Understanding the genomic regions governing these traits proves to be an effective way of improving crop plants for these traits. In wheat, there are limited number of studies to dissect the genetic basis of seed germination related traits, we conducted a genome-wide association study on the genetic architecture of five germination traits. The study observed high phenotypic and genotypic variance for the traits under consideration with a significant difference. The correlation analysis of the seed germination parameters indicated strong and positive correlations between the related traits studied under this work. The GWAS studies on a panel of 220 advance breeding lines with 35k genotypic array information indicated significant QTLs for seed germination and its parameter traits. We identified genomic variants that were associated with the seed parameter traits, and many of these were shared between the many of these traits, indicating partial genetic similarity. Accumulation of favourable variants shortened germination time and improved uniformity in maize inbred lines. These findings contribute significantly to understanding the genetic basis of wheat seed germination and will contribute to the molecular breeding of wheat seed germination.

1PP-29

Character Association and Path Analysis for Yield and Yield Attributing Traits in Bread Wheat [*Triticum aestivum* (L.) em Thell] Genotypes

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The current study was conducted in *Rabi* 2021- 2022 at Instructional Farm, of the Rajasthan College of Agriculture, MPUAT, Udaipur to estimate the association among yield components and their direct and indirect influence on grain yield of bread wheat. For the overall traits under investigation, significant genotypic differences were found indicating the presence of huge amount of variation among studied genotypes. At both the genotypic and phenotypic levels, there was positive and significant correlation between grain yield and days to 50% heading, plant height, length of main spike, number of spikelets per spike, number of grains per spike, grain weight per spike and biological yield per plant. Plant height had the greatest positive direct impact on grain production per plant, followed by biological yield per plant, number of grains per spike, days to maturity and 1000-grain weight. It is therefore, feasible to increase the grain yield per plant in bread wheat by taking into account certain traits, plant height, biological yield per plant, number of grains per spike.

1PP-30

Integrative Deep Learning and Bioinformatics Approach for In Silico Characterization of UGPase Structure in Rice (Oryza sativa L.)

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In silico exploration of UDP Glucose Pyrophosphorylase (UGPase) in rice, crucial for sucrose synthesis, through the fusion of bioinformatics and the latest deep learning techniques. UGPase operates as a monomer in photosynthetic organisms, catalyzing the Mg+2-UTP + Glu-1-P ↔ PPi + UDP-Glu reaction in a manner dependent on the metabolic state of the tissue. The investigation begins with the extraction of the UGPase gene sequence, followed by a detailed analysis of its physicochemical properties. The approach combines traditional homology modelling with modern deep learning algorithms, such as AlphaFold2 and RoseTTAFold, significantly enhancing structural prediction accuracy.

Dynamic simulations, conducted via GROMACS, assess the enzyme's stability across various environmental conditions. A key innovation is the comparative analysis between traditional computational models and deep learning predictions, employing Ramachandran plots and RMSD metrics to highlight the advanced capability of deep learning in capturing the complex dynamics of protein folding. This approach not only improves the precision of structural predictions but also enriches the understanding of UGPase's functional dynamics and evolutionary insights. Highlighting the transformative impact of merging deep learning with bioinformatics, the exploration opens new avenues in structural biology, offering deep insights into protein function and regulation mechanisms. The implications of this research are profound, marking a significant leap forward in the understanding of biological complexities

1PP-31

Foreground Selection for Stripe Rust Resistance in Hybrid Wheat

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The presence of wheat stripe rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici* Erikss. (Pst) a fungal disease, can lead to a significant decline in the quantity of wheat harvested across the globe. Gene pyramiding strategy helps to stack resistant genes in hybrids while incorporating multiple genes separately into their parents. An attempt has been made to introgress the stripe rust resistance genes *Yr10* and *Yr15* into two maintainer lines (2851B and 365B) and two restorer lines (1752 R and 2003 R) to optimize the yield potential of hybrids developing at IARI, New Delhi. B (maintainer) and R (Restorer) lines were crossed with their respective donors for *Yr10* (Avocet *Yr10*) and *Yr 15* (HD2967 + *Yr15*) genes. F1 and backcross generations were screened with linked and validated SSR markers X*psp3000* for *Yr10* in B lines and *Xgwm*273 for *Yr15* in R lines. Based on marker-trait association, plants carrying *Yr10* in B lines and *Yr 15* in R lines in each backcross generation. BC3F1 is selfed to obtain BC3F2.Marker assisted breeding helped to reduce the time and effort to improve the parental lines. The improved B lines will be used to incorporate *Yr 10* for conversion as A-line using molecular approaches. The resultant A-line and R lines will be used for hybrid development that is expected to provide better disease resistance leading to enhanced yield levels in hybrids.

1PP-32

Character Association and Path Coefficient Analysis for Yield and its Component Traits in Bread Wheat [*Triticum aestivum* (L.) em. Thell] Genotypes

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The present investigation was aimed to determine the correlation and path coefficient analysis for seed yield and its attributing traits in wheat (*Triticum aestivum* L. em. Thell). In this study, seventy-six diverse genotypes of wheat were evaluated for fourteen quantitative traits in Augmented Block Design at Rajasthan College of Agriculture, MPUAT, Udaipur. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for all the characters under study. The grain yieldplant^{-1} exhibited positive and significant correlation with biological yield plant^{-1}and harvest index at both genotypic and phenotypic levels, while it showed positive and significant correlation with number of spikelets spike^{-1}, grain weight spike^{-1}, 1000-grain weight, protein content and sedimentation value at genotypic level only. The path coefficient analysis revealed that the maximum positive direct effect on grain yield plant^{-1} was exerted by days to 50% heading followed by biological yield plant^{-1}, sedimentation value, protein content and plant height. It is suggested that these characters can be considered as selection criteria in improving the grain yield of wheat.

IPP-33

A Study of diversity and Selection Indices in Barley Genotypes

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The present experiment was carried out using 36 barley genotypes at the Instructional Agronomy Farm, Rajasthan College of Agriculture, Udaipur during *Rabi,* 2022-23. The genotypes were evaluated in Randomized Block Design with three replications for 12 characters. Analysis of variance demonstrated a significant difference among genotypes for all the traits showed that the experimental material under investigation has a good amount of variability. The path coefficient analysis showed that the maximum positive direct effect on grain yield per plant was exerted by biological yield per plant, number of effective tillers per plant, 1000-grain weight and grain protein content. So, these characters can be considered as selection criteria in improving the grain yield. The discriminant function selection had higher genetic gain and relative efficiency over straight selection for grain yield per plant alone. There was an increase in genetic gain and relative efficiency with inclusion of an additional trait in the character combination. Selection index involving grain yield per plant, number of effective tillers per plant, 1000-grain weight and biological yield per plant could be advantageously exploited in the barley breeding programmes. Based, on multivariate hierarchical cluster analysis genotypes were grouped into nineteen clusters. The maximum number of genotypes was grouped into cluster I which had 8 genotypes while the cluster II to V had 3 genotypes, cluster VI and VII had 2 genotypes and cluster VIII to XIX having single genotype. The maximum intra-cluster distance was showed in cluster VII followed by cluster VI, V, I, II, IV and III. Maximum inter-cluster distance was observed between cluster XIV and XVI indicated that the genotypes associated with these clusters has wide genetic diversity and these genotypes could be used in future for barley crossing programme for the upliftment in grain yield. In the present investigation, genotypes *viz*., RD 2035, RD 2592, RD 2624, RD 2786, RD 2907, K 1055, PL172 and DWRB 182 were superior not only in terms of grain yield per plant but also in terms of traits like days to maturity, plant height, number of effective tillers per plant, grain weight per spike, number of grains per spike, 1000-grain weight, biological yield per plant and grain protein.

1PP-34

Estimation of Genetic Components for Yield and Related Characters in Five Diverse Wheat (*Triticum aestivum* L.) Crosses by Six Parameter Model

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The aim of this research was to examine the gene action that controls the expression of various traits in bread wheat by using generation mean analysis. Six generations (P1, P2, F1, F2, BC1 and BC2) of five crosses, cross I (HI 8627 x HI 8498), cross II (DBW 17 x JW 3211), cross III (HD 2993 x HD 4758), cross IV (MP 3269 x HI 1500) and cross V (HW 1900 x UP 2847), were used for this purpose. The results revealed that the estimated mean effects (m) of all the traits in all crosses were highly significant, indicating the quantitative inheritance of the traits. The epistatic interaction was present for all the eight traits in the crosses. Generally, the value of dominance effect (h) was higher than additive effect (d) in all the traits. Digenic interaction suggested that the inheritance was complex and involved non-additive gene action. The selection in early generation could be beneficial. For grain yield and most of the traits, the dominance type gene effects were more significant than additive gene effects. In the five crosses, the different traits showed a large and negative dominance x dominance degree, while the additive x additive gene actions were high and positive. In wheat breeding, the selection for enhancing grain yield and its related traits should be delayed until later generations because additive x dominant gene effects were less significant.

1PP-35

Introgression of BNI- trait in Indian Wheat Genotypes for Enhancing NUE

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Present wheat agricultural methods depend on nitrogen fertilizers, which contain the reactive or biologically accessible nitrogen in the soil. Reducing nitrification via effective management is desired to minimize nitrogen losses and enhance nitrogen fertilizer use efficiency. There are two main approaches to managing nitrification: controlling the supply of ammonium substrate and actively inhibiting nitrifiers. A successful approach is to directly suppress nitrifiers by using Biological Nitrification Inhibitors (BNI). BNI are promising tools to limit nitrogen (N) pollution derived from agriculture. Varieties of wheat don't possess the ability to release BNIs. However, a recent development occurred when the chromosomal region (Lr#n-SA) responsible for BNI production in *Leymus racemosus*, a wild cousin of wheat, was incorporated into three high-quality wheat cultivars, ROELFS, VOROBEY, and MUNAL. These BNI-derived lines of ROELFS, VOROBEY, and MUNAL were evaluated with three checks DBW 303, DBW 187, and DBW 371 at four nitrogen levels (0%, 50%, 75%, and 100%) of recommended nitrogen. The result showed that by utilizing the BNI trait, the nitrogen application in wheat can be reduced by 25-30% without compromising yield.

In order to transfer the Biological Nitrification Inhibitor trait, F4 crosses have been developed with BNI-MUNAL as donor parent with different recipient parents DBW 187, DBW 222, DBW 303, DBW 110, etc to incorporate specific features. The marker 24S81287 has been utilized to screen the F4 generation for the presence of the BNI gene and the presence of the gene has been observed in 55 plants. The markers' efficacy in characterizing wheat-BNI chromosomal introgression lines demonstrates their dependability, and their notable transferability broadens their scope of potential uses. Integration of these markers with appropriate cytogenetic methods would accelerate the development and characterization of wheat-alien chromosome introgression lines.

1PP-36

Genetic Variability Studies in F_2 Generation of Bread Wheat (*Triticum aestivum* L.)

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Wheat [*Triticum aestivum* L.] is key food crop in the world which belongs to genus *Triticum* and family poaceae. Genetic variability is a crucial factor from evolutionary point of view for crop species. Grain yield in wheat is a complex character and is dependent on its component traits. The genetic variability in a population can be divided into heritable and non-heritable variation. In present study, the estimates of heritability, coefficient of variability, genetic advance were computed in F_2 segregating population of three crosses their six parents and one check for 10 characters including yield and contributing traits during *Rabi* 2021-2022. Analysis of variance indicated that the mean sum of square due to genotypes was found significant for all of the characters under this investigation showing that huge amount of variability is present between crosses and their parents for all the traits. The estimates of PCV were little higher than their corresponding GCV pointing out that the environment had minor effect on the expression of the different traits. Higher estimates for GCV and PCV were revealed for grain yield per plant followed by number of effective tillers per plant, spike length, biological yield per plant and harvest index. The characters had high heritability along with high genetic gain were grain yield per plant, number of effective tillers per plant.

1PP-37

Genetic Analysis of Seedling Vigor Traits in Bread Wheat (*Triticum aestivum* L.) Using Genome-Wide Association Studies

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Seed vigor is one of the important traits. More importantly, in wheat, this helps in the better emergence of seedlings from deeper planting depths, which is very much essential to avoid lodging. Genetic variation for different seedling vigor traits was studied in a diverse panel of 220 wheat accessions under deep planting (DP) conditions, using a genome-wide association study. We observed large variations for all the measured seedling vigor traits, and broad sense heritability was found to be highest for the seedling dry weight (0.99) and coleoptile length (0.94). Association analysis yielded a total of 50 loci across the genome for all the measured seedling vigor traits. Further, we identified seventeen putative candidate genes which include a potential candidate gene *TraesCS7D02G040300* which is known to be associated with nutrient uptake and root architectural development pathways. Other potential genes namely, *TraesCS6D02G193000*, *TraesCS5A02G023600*, *TraesCS4A02G307900*, and *TraesCS2D02G126300* are found associated with the genes coding for Elongation Factor Tu (EF-Tu) and translational elongation, glycosyltransferase activity, polysaccharide catabolic process, and bulb-type lectin domain superfamily, respectively. The proteins encoded by these genes play an important role in seed germination and lateral root development. The identified SNPs and candidate genes associated with seedling vigor traits are important in breeding wheat varieties with better adaptation and seedling establishment.

1PP-38

Estimation of Correlation and Path Coefficient Analysis in Bread Wheat Genotypes *Triticum aestivum* (L. em. Thell).

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A research study was initiated to assess the correlation and path coefficient analysis of yield and yield contributing traits in 90 wheat cultivars with 4 check varieties grown in Augmented Design with three replications at the Main Experimental Station of Acharya Narendra Dev University of Agriculture and Technology, Ayodhya (U.P.) in *Rabi* season of 2021-22. The statistical technique of analysis of variance was employed to investigate the significance of the treatments on the various characters. The results indicated a high level of significance for all the characters under study. The results of the study indicate a strong positive correlation of grain yield per plant was observed for traits like Tiller per plant, Flag leaf area, Number of grains per spike, Biological yield and Harvest index. The findings of the study indicate that the harvest index exhibited the most significant direct positive impact on grain yield, with biological yield per plant, number of grains per spike, days to maturity, tiller per plant, peduncle length and flag leaf area following closely behind. These factors were identified as the primary contributors to the overall grain yield, as evidenced by the results of the path analysis.

1PP-39

Assessment of Genetic variability, Heritability and Genetic advance for some quantitative characters in bread wheat (*Triticum aestivum* L.) genotypes in Central plain Agro-climatic region of Uttar Pradesh, India

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Thirty-six genotypes of bread wheat comprise twenty-eight F1s and eight parents were assessed for genetic variability, heritability and genetic advance per cent over mean for eleven traits using a Randomized Block Design (RBD) with three replications for yield and its contributing characters at Crop Research Farm, Nawabganj, C.S Azad University of Agriculture and Technology, Kanpur, U.P, India during rabi 2021-2022. Analysis of variance revealed highly significant differences among genotypes for each of the characters studied, demonstrating a wide range of genotype variability. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were found in the number of productive tillers per plant, while biological yield and grain yield per plant had moderate PCV and GCV values. High heritability coupled with high genetic advance estimates for biological yield per plant and grain yield per plant, revealing the presence of additive gene effects and showing the effectiveness of the selection method of breeding for enhancing these characteristics in wheat.

1PP-40

Genetic Evaluation of Exotic Rice Germplasm for Yield and its Components Characters for Future Food Security

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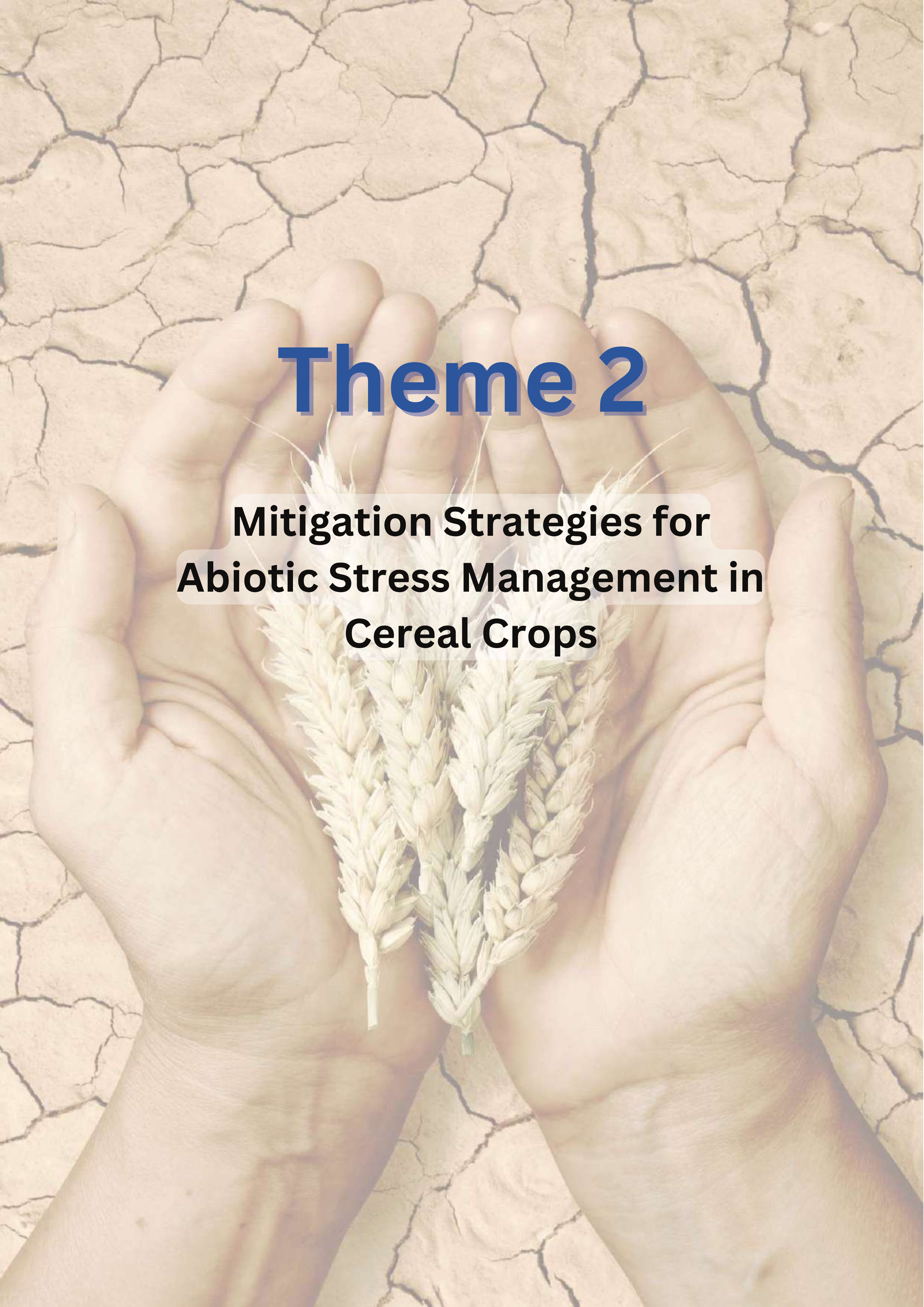
Rice, also known as *Oryza sativa* L., is the primary food crop globally, providing sustenance to millions. There are two types of cultivated rice, *Oryza sativa* and *Oryza glaberrima.* India is the leading global producer, but yields are low. To increase productivity, high-yielding, disease-resistant varieties are needed. A study at Allahabad School of Agriculture's Field Experimentation Centre examined genetic variability, heritability, and genetic advance of exotic rice genotypes during the 2010 kharif season. The analysis of 12 quantitative features revealed high heritability and genetic progress for desirable traits. The study found that certain varieties, IR72860-74-1-2-1, CHAITE4, IR82786-43-3-2-1, and CT15675-7-1-7-3-1-M, had the highest seed yield per hill, with significant heritability and genetic progress. Seed yield per hill was positively and significantly associated with biological yield and harvest index at both genotypic and phenotypic levels. Genotypes with better biological yield and harvest index result in increased seed production per hill. The study suggests using specific genotypes to enhance grain yield per hill: IR72860-74-1-2-1, CHAITE4, IR82786-43-3-2-1, CT15675-7-1-7-3-1-M, and CT17381-16-1-2-4-3-M. The findings reveal the genetic potential of the rice genotypes tested and provide guidance for breeding projects to develop high-yielding varieties with desired agronomic traits.



Theme 2

Mitigation Strategies for Abiotic Stress Management in Cereal Crops

Oral

2OP-1

Selection and Characterization of Candidate Parental Lines of Barely for Sodicity Stress Tolerance

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Barley has domesticated from the beginning of human civilization, and subsequently flowed with human migration into different continents. In the present investigation, genetic variation for physiological and morphological traits for alkalinity specific effects in barley cultivars were evaluated, to hunt out the higher alkalinity-tolerant parental lines, which could be utilized the barley improvement program for sodicity tolerance. Therefore, a diverse panel of 120 different barley cultivars released during (1945 to 2020) in India and adapted to various agro ecologies of the country was evaluated under control and sodicity stress (pH = 9.3 ± 0.12, ESP = 41 ± 13.25) in the field conditions. The trials were conducted in augmented randomized block design with the plot sizes of 1 meter^2. The quantitative observations were recorded on a total of 28 morpho-physiological traits under control and sodicity stress conditions. The analytical results reflected that significant reduction of 86.90, 56.72, 53.05, 48.89, 48.53, 46.82, and 39.61%, were observed in K^+/Na^+ ratio, stomatal conductance, above ground biomass, Assimilation rate, and grain yield/ plot respectively. Oppositely the expression of sodium content, vapour pressure deficit, flag leaf area, flavonoids content and days to 50% heading increased in the tune of 485.18, 32.07, 10.54, 10.25 and 4.82% respectively. Under control condition barley cultivars i.e. PRB-502, RD-2749, RD-2899, DL-88, Pargati, DWRB-137 attained the maximum grain yield in descending order. However, the cultivars VLB-56, RD-57, DL-88, NDB-1173 and RD-2899 attained the higher yield under sodicity stress, the performance of the cultivars is strongly linked to proper Na^+ and K^+ discrimination in leaves. On the basis of discriminant function and multiple traits association analysis we can emphasized that the cultivars RD57, K24, K603, NB3, NB5, RATNA, RS56, NDB1173, DL88 and RD2907 are sodicity tolerant compare to other released cultivars. The tolerant genotypes acquired a better ability to maintain stable NDVI, chlorophyll and photosynthetic rate, resulting in significantly higher grain yield production under sodicity stress. These identified cultivars can be utilized as salt tolerant candidate's parental lines for transferring alkalinity tolerance to improved cultivars as well as in further genetic studies to uncover the genetic mechanisms governing alkalinity stress response in barley.

2OP-2

Controlled Release Bionanoconjugate: A Smart and Sustainable Attribute to Mitigate Chilling and Terminal Heat Stress on Wheat

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Advancements in agriculture have made significant strides, but challenges remain in crop resistance to environmental changes and human density. Agrochemicals' prolonged use leads to yield loss and reduced nutrient uptake. In this scenario, nano-biotechnology combines nanoscience with biogenic polymeric materials to address stress damages in agriculture. Chitosan biopolymer, is the widely studied, safe, and environmentally friendly. Utilizing cross-linking ability of chitosan and TPP the study thus focused on the synthesis of controlled release bionanoconjugates (BNCs) encapsulating micronutrient (Zn) and plant hormone (SA) to enhance plant innate immunity and yield under stress. The BNCs were designed to prevent excessive loss, rapid leaching, and toxicity in the field and environment. The study also reveals the in-vitro release profile (pH and time-dependent) and kinetics of the ingredients in BNCs. First-order kinetics estimates that entrapped Zn and SA were released at rates of 0.579 and 0.559% per hour, respectively. The Zn and SA releases had a half-life ($T_{1/2}$) of 119.7 and 124.0 hrs, respectively. In combination with their slow-release capability, BNC resulted in more pronounced effects on seed germination, and grain filling of lately sown wheat (WH 542) facing chilling and terminal heat stress, respectively. Study reports that germination rate (GR) was increased (>20%) in contrast to mean emergence time (MET) which was reduced (20%). Further, the BNCs co-encapsulating zinc and SA, which extend grain filling duration by up to 57%, resulted in a 45% increase in yield, making them ideal substitutes for soluble fertilizers. These BNCs enhance plant growth, yield, and seed germination, enhancing crop tolerance to climate stress.

2OP-3

Heat Stress-Responsive SSR Markers to Assess the Genetic Diversity in Wheat for Heat Tolerance Breeding

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Being a major staple food crop of the world, wheat provides nutritional food security to the global populations. Wheat, as a key staple food crop, provides nutritional security to the world's inhabitants. Heat stress is a key abiotic stress that has a negative impact on wheat productivity all over the world, especially the Indo-Gangatic Plains. As a result, identifying heat stress-responsive molecular markers is critical for marker-assisted breeding programmes. Information regarding trait-specific gene-based SSRs is accessible, however there is a paucity of information on non-coding regions based SSRs. we developed 177 heat-responsive gene-based SSRs (cg-SSR) and MIR gene-based SSR (miRNA-SSR) markers from the wheat genome to assess genetic diversity analysis of thirty-six different wheat genotypes for heat tolerance. Of the 177 SSR loci, 144 produced clear and repeatable amplicons, however, thirty-seven were polymorphic with mean PIC of 0.35. The number of alleles produced per primer ranged from 2 to 6, with an average of 2.58. The UPGMA dendrogram analysis divided all wheat genotypes into four groupings. The markers produced in this work have the potential to be used in MAS-based breeding programmes to develop heat-tolerant wheat cultivars and to analyse the genetic diversity of wheat germplasm. Identifying noncoding region-based SSRs will be useful for identifying trait-specific wheat germplasm.

2OP-4

Native Arbuscular Mycorrhizal Fungi (AMF) For Enhancing Wheat Productivity and Tolerance Under Salt-Stressed Conditions.

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Salt stress mainly causes damage to plants through osmotic stress and ion toxicity. When the soil salinity increases, the water potential of the soil solution becomes lower than the water potential of the plant root cells, resulting in osmotic stress. As a result, the roots cannot absorb water and results to plants experiencing a physiological shortage of water. Arbuscular mycorrhizal fungi (AMF) have been shown to alleviate the toxic effects of salt stress in plants. However, more studies on AMF combined with other functional microorganisms are needed to further improve salt tolerance in different crops. Hence this present was planned to propagate the native AMF of salt affected areas and evaluate its efficacy in wheat crop. Two different host viz. Sorghum and maize were studied which readily form association with AMF and commonly used for AMF propagation. Mycorrhizal association and colonization increased significantly with time in both the cycles in both the host *viz.* maize and sorghum. However, significantly higher propagation during second cycle and colonization during both the cycles were also observed in maize roots than those of sorghum showing higher affinity of AMF in maize roots compared to sorghum crop. The same trend was observed for arbuscules abundance. The higher root percent colonization rates in maize are mainly due to the specific composition of root exudates secreted by it. Plant growth and yield of AMF inoculated plants were greater in normal soil followed by sodic and saline soils. The P content, P uptake, and K^+/ Na^+ were greater in AMF inoculated soils. The increase in Olsen's-P in AMF inoculated soils was observed. Dehydrogenase, alkaline phosphatases enzymes and glomalin were greater in AMF inoculated soils. Effect of AMF on different form of phosphorus in soil was also evaluated. The calcium bound phosphorus was found to be most abundant in both normal and saline soil. These results suggest that AMF inoculants may play an important role in improving wheat productivity in salt affected soils.

2OP-5

Comprehending Wheat Lodging by Analyzing Stem Architectural Traits

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Lodging refers to the permanent displacement of plant stems from their upright position, caused by external forces like wind, rain, or hail. It is estimated that wheat lodging can cause a reduction of up to 80% in grain yield. Lodging resistance is directly related to the morphological structure and physiological efficiency of stems. Improving stem mechanical strength can significantly enhance the ability of crop to withstand lodging. Therefore, a group of seventy-five newly released wheat varieties, few novel wheat genotypes, dwarfs and synthetic wheat genotypes were utilized to study the occurrence of lodging. The initial screening for lodging tolerance was done during early grain filling stage under artificially induced lodging conditions with the help of high speed wind blower. During the time of second screening *i.e.* during third week of March heavy rain fall and windy weather make the crop flattened naturally. To access the lodging tolerance, stem architectural traits like plant height (76.3-142 cm), spike length (8.33-13.93 cm), length of third internode (4.8-18.6 cm), culm thickness of 3rd Internode (0.86-2.30 mm), lodging score (0-5) and average lodging percentage (54.8%) were recorded. Based on the collected data lodging has been found positively correlated (r =0.75) with plant height and spike length. The study found a direct relationship between the height and weight of the three lower internodes, however a negative correlation was observed with wall thickness. Considerable variability in culm characteristics have been noted among the tested wheat genotypes, suggesting potential for utilizing these variations in wheat breeding initiatives aimed at enhancing wheat's ability to withstand lodging.

2OP-6

Evaluation of Morpho-Physiological Traits for Improving Adaptation under Terminal Heat and Drought Stress in Bread Wheat (*Triticum aestivum* L.)

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High temperature and drought stress disturb agricultural crop production and nutritional quality which is a significant threat to food security. Heat and drought stresses are major constraints to wheat crop cultivation in dry and semi-arid regions. The production potential of wheat is greatly impacted by heat and drought stress. To address the issue present study was conducted to identify genotypes with better adaptation under heat and drought stress conditions. A total of 108 diverse wheat genotypes including three checks (HD 2967, DBW 222 and WCF 12-07) were evaluated with 18 morpho-physiological traits under three contracting environments (i) optimum environment (OE) timely sown (ii) heat stress environment (HSE) late sown and (iii) drought stress environment (DSE) timely sown under rainout shelter during two consecutive *Rabi* season 2021-22 and 2022-23. The ANOVA revealed significant differences for almost all recorded traits except number of tillers (NT) in all three environments and canopy temperature at the booting stage (CT_{BS}) under a heat-stress environment. Seed yield is significantly impacted by stressful environmental conditions, with a decrease of 58.31% under heat stress and 27.52% under drought stress. Chlorophyll content (CC), Normalized Difference Vegetation Index (NDVI), and Chlorophyll Content Index (CCI) exhibited positive correlations with seed yield across all environments. On the other hand, Canopy temperature (CT) showed a negative correlation with seed yield in stressful environments, indicating valuable traits for identifying tolerant lines. Based on STI and SSI stress indices, genotypes IC 55718, IC 73575, and IC 0594378 were identified best-performing genotypes heat-tolerant and IC 73575, IC 0443622, and IC 104617 exhibited drought tolerance. Genotypes IC 55718, IC 73575 and IC 0594378 were found tolerant under both heat and drought stress environments. Identified tolerant genotypes can be used for the development of RILs population to decipher the genes conferring tolerance as well as understanding the molecular basis of tolerance.

2OP-7

Ammonium Transporter Gene Family in Wheat (Triticum Aestivum L.): Bioinformatics, Physiological, Evolutionary and Expression Analyses Under Nitrogen Stress

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Ammonium, the primary nitrogen source for plant growth, is acquired from soil through specialized plasma membrane proteins called ammonium transporters (AMT). In this study, 21 putative AMT genes were identified and classified into two subfamilies AMT1 and AMT2 (AMT2/AMT3/AMT4) in wheat. The molecular weight and isoelectric point ranged from 46.92 kD (TaAMT3.2c) to 53.47 kD (TaAMT3.1a) and 6.6 (TaAMT3.2b) to 9.13 (TaAMT2.3a), respectively. Wheat AMT genes were distributed on fifteen chromosomes (Chr1A, 1D, Chr2A, 2B, 2D, Chr3A, 3B, 3D, Chr4A, Chr5A, 5B, 5D, Chr6A, 6B, 6D) and has ammonium transporter domain (PF00909) with occurrence of diverse transmembrane helices (9 to 11). TaAMT1 and TaAMT2 subfamilies showed differences with regard to conserved structures and protein motifs. TaAMT2 have introns in their structure while TaAMT1 were intronless. The differences in TaAMTs were evident from presence of helices (53-63%), beta (1-7%), coil (31-42%) and turn (5-18%) structures. Gene ontology (GO) enrichment analyses of TaAMTs showed that the biological as well as molecular functions were related to ammonium transportation. The protein-protein interaction showed that AMT1 and AMT2 interacted with other proteins involved in nitrogen transportation (high-affinity nitrate transporter) and metabolism (glutamine synthetase). Ka/Ks analysis and circos plots established that segmental duplications have contributed largely in the evolution TaAMTs. Phylogenetic classification Poaceae members including the parent species using the amino acid sequences of AMT1.1 gene confirms the speciation patterns shown by matK sequence. Synteny blocks in ‘best score’ matching of circoletto showed best matches among TaAMTs and AMTs of the B. distachyon and H. vulgare subfamily thus, supporting the taxonomic evolution. Promoter analysis of TaAMTs showed presence of cis-elements related to light response, anaerobic induction, growth hormones, drought stress, biotic stress and several endogenous signals related to plant growth and development. Gene expression pattern of AMT genes at different developmental stages of the two varieties namely, Chinese spring and Azhurnaya was studied. It was found that ten out of twenty-one AMT genes shown differential gene expression viz. root, leaf/shoot, grain/spike and three of the AMTs showed root-specific expression. The response of all AMTs towards N starvation and recovery showed that the expression of AMT genes was found to be varying in these conditions.

2OP-8

Identification and Characterization of Heat Tolerance in Wheat Using Stress Indices

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Wheat (*Triticum aestivum* L.), a crucial staple globally, faces mounting challenges from climate change-induced heat stress, compounded by biotic and abiotic stresses. Projections indicated significant yield losses, including a 4.5% reduction in India's 2022 wheat yield due to heat stress, highlighting the urgent need for heat stress-tolerant wheat genotypes. Therefore, development of heat stress-tolerant wheat genotypes is crucial to mitigate yield losses and enhance productivity. An experiment was conducted involving two environments, i.e., non-stress (irrigated normal sown) and stress condition (irrigated late sown) with 30 diverse genotypes in randomized block design using three replications in both conditions at ICAR-IIWBR, Karnal and CCSHAU Hisar. The heat tolerance indices were calculated based on grain yield under normal sowing (Yp) and late sowing (Ys) conditions. The combined analysis of variance revealed significant impacts of heat stress on grain yield, along with notable differences among genotypes in both grain yield and heat tolerance indices, including Heat Susceptibility Index (HSI), Heat Tolerance Indices (HTI), Geometric mean productivity (GMP), Tolerance index (TOL), and Mean productivity (MP). Notable genotypes like Raj 4083, DBW 90, HD 2932, Raj 4037, Raj 4079, DBW 71 and PBW 590 showed high yield potential under both normal and heat-stressed conditions, suggesting suitability for cultivation in high-temperature environments or as parent sources for heat stress tolerance breeding programs. This study underscores the importance of developing wheat varieties resilient to heat stress to sustain and enhance productivity in the face of climate change challenges, informing future breeding programs and agricultural strategies.

2OP-9

Impact of Restricted Irrigation Condition on Morphological Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes

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Wheat (*Triticum aestivum* L.), is known as the king of cereals and consumed as a staple crop by one-third of the global population. Drought has the most injurious effects on the growth and development of wheat. There is a need to develop drought-tolerance lines for wheat. For this purpose, 30 distinct wheat genotypes were investigated under two environmental conditions i.e., optimum and restricted irrigation in Randomized Block Design with three replications at the Wheat farm of Dr. RPCAU, Pusa, Samastipur, Bihar, during *rabi* (2022-23). Bread wheat lines for their response to drought stress under restricted irrigation conditions and the selection of good-performing genotypes under this stress condition were evaluated with 16 morphological traits. Population has shown significant variation among all the studied lines under both conditions. Path analysis under both conditions revealed that no. of grains per spike, relative water content, and leaf thickness have a positive direct effect on grain yield. Hence, the selection of these traits might be effective for the indirect selection of grain yield. D^2 Statistical analysis revealed the presence of 5 and 4 clusters in optimum and restricted irrigation conditions respectively. The selection of genotypes from different clusters as a parent in the hybridization programme will be beneficial for the production of superior hybrids. From this study, selected wheat genotypes towards water stress evaluated different yield contributing traits under stress conditions and the presence of diversity among all genotypes. Improvement of all the above-studied yield contributing traits under water stress conditions will ultimately improve yield either directly or indirectly, so the selection of these traits will be effective in future breeding programmes.

2OP-10

Comparative Analysis of Cytosine Methylation Levels Induced by Heat Stress in The Rca (Rubisco Activase) Coding Region in Leaves of Contrasting Wheat Genotypes

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DNA methylation is crucial epigenetic alteration that modulates gene expression in plants under diverse abiotic stresses. Rubisco, a heat-sensitive protein present in chloroplasts, is rendered inactive when exposed to high temperature conditions. Wheat crop is inevitably affected by higher temperature at various phases of growth throughout its life cycle, which is detrimental to its growth, development and overall yield. In this study, bisulfite sequencing was carried out for a comparative analysis of cytosine methylation in the coding region of the Rubisco activase (Rca) gene in heat tolerant (RAJ3765) and heat susceptible (HUW510) wheat genotypes at four growth stages under control and heat-stressed conditions in CG, CHG, and CGG contexts. We found that the overall 5-mC levels increased due to heat stress in HUW510 during tillering (25%), boot stage (25%), heading (48%) and anthesis (50%) as compared to RAJ3765 during tillering (21%), boot stage (4%), heading (4%) and anthesis (11%). Furthermore, gene expression profiling using qPCR at several plant growth stages revealed that its expression in the HUW510 genotype decreased by 1.9, 2.7, 2.5, and 3.3-fold at tillering, booting, heading, and anthesis stages, respectively. In RAJ3765, the expression of the gene decreased by 1.7, 2.0, 2.2 and 2.8-fold at tillering, booting, heading and anthesis respectively. The study will increase the knowledge on the underlying epigenetic modifications controlling Rubisco and Rca concentrations in wheat so as to enhance the photosynthetic potential as well as the yield in the backdrop of increasing environmental temperatures.

2OP-11

Assessment of Morphological Variability in Indigenous and Exotic Rice (*Oryza Sativa* L.) Under Sodic Soil Conditions

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Genetic variability for quantitative traits is the key component of breeding programme for broadening the gene pool of rice. The experiment was conducted to evaluate eighty-five genotypes including four checks, in Augmented Block Design at Genetics and Plant Breeding Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during kharif, 2021. The entire experimental materials were divided into five blocks and twenty-one plots accommodated in each block. Each plot was consisted of 17 genotypes along with 4 checks. Computing means, range, heritability, and genetic advance were used to examine existing variability within the 85 germplasms, as well as four checks.

The highest grain yield per plant produced by genotypes WHM-1024 followed WHM-1016, TCN-2071, and TCN-2114. L:B ratio had the highest GCV value, followed by grain yield per plant, biological yield per plant. Moreover, L:B ratio had the highest magnitude of phenotypic coefficient of variation (PCV), followed by grain yield per plant. The heritability (%) in broad sense for 13 characters studied, which has wide range among which biological yield per plant shows highest heritability. Maximum genetic improvement provides the best selection conditions. L:B ratio, grain yield per plant showed maximum genetic improvement. So, after further validation these germplasms may be used for future crop improvement programme to create desirable recombinants for the development of high yielding varieties.

2OP-12

Unravelling Genetic Variability Through Principal Component Analysis for Drought Responsiveness in Durum Wheat Germplasm

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Durum wheat (*Triticum durum* Desf.) is an important species in wheat where, drought poses a significant challenge for its productivity and food security worldwide. This study aimed to investigate the genetic variability and associations between morphological and drought-responsive traits for grain yield in durum wheat collected across the globe. Germplasm mini core of 220 durum wheat germplasm lines selected from global durum panel were evaluated during *rabi* 2021 and 2022 for drought responsiveness. Pooled data was subjected to analysis of variance revealed high significant variation among genotypes. Phenotypic and genotypic coefficient of variation was higher for the traits like tillers per meter, peduncle length, number of grains per spike and grain yield with high heritability. Trait correlation study revealed under moisture stress, a strong correlation is observed between grain yield with number of grains per spike, plant height, tillers per meter, and flag leaf area. In the absence of moisture stress, there is a strong positive correlation between grain yield with number of grains per spike, peduncle length, plant height, and tillers per meter. Conversely, under both stress and non-stress conditions, there is a notable negative correlation between the days to flowering and maturity, suggesting that early maturity is favorable for achieving higher grain yield. Principal Component Analysis (PCA) explained under PC_1 and PC_2 showed insight for selecting traits and genotypes to improve grain yield under moisture stress where, the direct selection is ineffective. Eleven distinct principal components were identified, with the first four accounting for approximately 60 percent of the variation under moisture stress conditions. The positioning of genotypes along each vector serves as an indicator of the significance of these traits for the respective genotypes. For instance, under moisture stress conditions, GDP2022-105 demonstrates importance for grain yield, while GDP2022-171 is noteworthy for its trait related to the number of grains per spike. The utilization of principal component analysis and correlation coefficient analysis in durum wheat landraces aids in the identification of desirable traits and their associations with yield, enabling a dependable classification of genotypes. The first two components exhibited strong associations with phenological, agronomic, and yield-related characteristics selecting representative genotypes from these specific groups for hybridization programs can be instrumental in enhancing drought tolerance mechanisms and the development of exceptionally drought-resistant wheat varieties.

Poster

2PP-1

Mitigation Strategies for Abiotic Stress Management in Cereal Crops

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Abiotic stresses such as drought, salinity, heat, and cold, significantly affect the growth, development, and yield of crops worldwide. These stresses are expected to increase in severity and frequency due to climate change, posing a serious threat to global food security. Understanding the molecular mechanisms underlying stress tolerance and the application of modern biotechnological tools have enabled the development of stress-tolerant cereal varieties. Genetic improvement of stress tolerance is a key focus area, with researchers identifying and characterizing genes and molecular pathways involved in stress responses. Genetic engineering for stress tolerance continued research into the molecular mechanisms underlying stress tolerance will enable the development of genetically engineered crops with improved resilience to abiotic stresses. CRISPR-Cas9 technology offers a precise and efficient way to introduce desirable traits into cereal crops, enhancing their adaptability to changing environmental conditions. Omics technologies Advances in omics technologies, such as genomics, transcriptomics, proteomics, and metabolomics, provide powerful tools for understanding the complex networks regulating stress responses in cereal crops. Integrating omics data with bioinformatics and systems biology approaches can lead to the identification of key genes and pathways involved in stress tolerance, facilitating the development of stress-tolerant varieties. Future research directions should focus on the following areas to further enhance stress tolerance in cereal crops. Integrating these strategies into crop management practices can improve the resilience of cereal crops to abiotic stresses, ensuring sustainable food production in the face of changing climatic conditions.

2PP-2

Performance Comparison of Rice Genotypes under Different Environments

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Rice (*O. sativa*) is a staple food of the South Asian region with a high starch value that needs an ample water supply to complete its life cycle. Over half of the world's population depends on rice, making it an essential crop for ensuring global food security. This study was conducted in the agro-climatic region of Prayagraj, Uttar Pradesh, to observe morphological differences that occurred due to variations in water supply from July to November 2023. The study focuses on irrigated, rainfed, and drought conditions as it explores the diversity in rice traits under various growing environments with a set of five genotypes that were evaluated in a randomly selected block design for five parameters, *i.e.,* days to flowering, days to maturity, plant height, tillers per plant, and economic yield. It was evaluated that in irrigated conditions, genotypes took a minimum number of days to maturity and showed maximum plant height and economic yield in comparison to the other two environments, while in contrast, genotypes in rainfed and drought conditions showed reduced height and maximum duration. The study concludes that Shyamla performs better in rainfed conditions than in irrigated and drought conditions, whereas for yield SHIATS DHAN 4 performs in irrigated, in contrast for days to flowering and maturity genotypes SHIATS DHAN 3, SHIATS DHAN 4, and SHIATS DHAN 5 of drought condition perform better than other two. With these observations, the genotypes can be used for further breeding programmes, depending upon their performance.

2PP-3

Assessing Phenotypic Variability in Bread Wheat Root Systems at Reproductive Stage

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Water availability is a major limiting factor for wheat (*Triticum aestivum* L.) production in rain-fed agricultural systems worldwide. Root architecture is important for water and nutrition acquisition for all crops, including wheat. Understanding root system morphology in bread wheat is critical for identifying root traits to breed cultivars with improved resource uptake and better adaptation to adverse environments. To precisely understand the contribution of root traits towards yield, 30 wheat genotypes were evaluated to access the drought tolerance level for two seasons (2017-2018 and 2018-2019) under drought and irrigation conditions. In this study, these genotypes were characterized for root traits at reproductive stage in polyvinyl chloride (PVC) pipes of 1.5 m in length. These diverse genotypes were evaluated for variability in root morphological traits, such as root length density (RLD), root projected area (RPA), root surface area (RSA) and root volume (RV), at later growth stages in different soil depths (0–30cm, 30–60cm, 60–90cm, and 90–120cm) using WinRHIZO root scanner. The results of analysis of variance (ANOVA) indicated that significant amount of genetic variation was present and behavior of studied germplasm showed different behavior in both the conditions. Correlation coefficients revealed a significantly positive association between root length density (0-60cm) and grain yield under both the treatments while RLD, RPA, RSA and RV (60-120cm) were found negatively correlated with grain yield, thousand grain weight and grain number per spike under drought condition. Under irrigated condition, grain yield and grain number per spike were found negative correlated with RV. Overall, strong positive correlations were identified among all root traits (i.e., RLD, RPA, RSA and RV at different depths). The multivariate analysis showed that out 20 principal components only six and four PCs were significant and has eigenvalue > 1, cumulatively showed 83.3 and 78.9% of total variation under irrigated and drought conditions, respectively. Phenotypic differences in and trait correlations among some interesting root traits may be considered for breeding wheat cultivars with efficient water acquisition and better adaptation to abiotic stress. The best performing genotypes can be used in future breeding programs. The selection on the bases of studied attributes is effective for development of drought-tolerant and high-yielding varieties for sustainable food security.

2PP-4

Integrated Strategies for Mitigating Abiotic Stress in Cereal Crop Production: From Traditional Breeding to Precision Agriculture

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Abiotic stresses, including drought, salinity, heat, and nutrient deficiencies, exert significant constraints on cereal crop productivity, posing substantial challenges to global food security. We delve into the mechanisms underlying the physiological and molecular responses of cereals to various abiotic stressors, elucidating their impacts on growth, development, and yield. Strategies for mitigating abiotic stress encompass a multifaceted approach, integrating traditional breeding techniques, molecular breeding, and biotechnological interventions. We discuss the importance of developing stress-tolerant cultivars through conventional breeding methods, emphasizing the identification and introgression of stress-responsive genes and quantitative trait loci (QTLs). Additionally, we explore the potential of emerging biotechnological tools, such as genome editing and marker-assisted selection, in accelerating the development of stress-tolerant cereal varieties. Furthermore, agronomic practices, including irrigation management, soil amendment, and crop rotation, are evaluated for their effectiveness in alleviating abiotic stress impacts and enhancing crop resilience. Sustainable agricultural practices, such as conservation tillage and organic farming, are also discussed in the context of mitigating abiotic stress while promoting soil health and ecosystem sustainability. Moreover, we highlight the importance of leveraging precision agriculture technologies, remote sensing, and predictive modelling to optimize resource use and mitigate abiotic stress risks at a field scale.

2PP-5

Variation for Heat Tolerance in Wheat Genotypes

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Climate change is being considered a major obstacle to food crops in the country. Wheat is vulnerable to terminal heat stress due to sudden rise in temperature and suffer significant yield loss (~25%) because it coincides with the flowering period. In the present changing climate scenario, heat stress has attracted a lot of attention hence development of heat tolerant wheat varieties and genetic stocks is the need of the hour. Therefore, the present study was conducted during *Rabi*, 2022-23 at ICAR-IIWBR, Karnal. Total 72 diverse wheat genotypes were grown under timely and late sowing conditions. Observations were recorded for different phenological, agronomical and physiological traits. Grain yield showed the highly significant positive association with thousand grain weight (TGW), Grain per spike (GP), Biological yield, Vegetative stage NDVI, heading NDVI and grain filling NDVI under late sowing condition. Based on grain yield, heat susceptibility index (HSI) was calculated to detect the tolerant genotypes. Genotypes with HSI less than 0.55 were considered highly tolerant (HT) and from 0.55 to less than 1.0 as moderately tolerant (MT), while with HSI greater than 1.0-1.50 was considered moderately susceptible (MS) and above 1.50 as highly susceptible (HS) one. Based on this study, 13, 17, 33 and 9 genotypes under heat stress were identified as HT, MT, MS, and HT, respectively. Analysis of variance revealed the significant genetic variance for all studied traits. After validation, these genotypes can be used in wheat breeding programs for heat stress tolerance.

2PP-6

Genetic Variation for Terminal Heat Tolerance in *Emmer* Wheat Germplasm and Diversity Analysis using SSR Markers

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Enhancing germplasm utilization in breeding programs relies on characterizing germplasm, creating core collections, and identifying promising donors. Crop improvement program depends upon the use of wild relatives for introgression of traits of interest into elite cultivars and creation of variability which necessitate genetic diversity assessment. Tetraploid wheat (*Triticum turgidum* L., 2n = 28, AABB) is an important genetic resource for economically important traits including biotic and abiotic stress tolerance. In this study, 96 *dicoccum* wheat accessions from the Indian National Genebank were evaluated for terminal heat stress tolerance using agronomic, physiological, and molecular analyses. Significant variation was observed among accessions for traits across different locations and sowing conditions. For instance, under timely sown conditions, grain yield showed highly significant positive correlation with FLW, GS, GWS, BY, HI, while under late sown conditions, HI, PH, FLW, NDVI, and BY were highly correlated. Principal component and cluster analyses further elucidated variation and grouping among accessions, with 77.40% and 68.52% cumulative variation explained under timely and late sown conditions, respectively. Molecular profiling revealed polymorphism in SSR markers, with 35 out of 63 markers showing variation and 139 alleles detected. Notably, the barc10 marker exhibited the highest PIC value and cfd39 the lowest. Population structure analysis classified accessions into distinct groups, suggesting high similarity among *dicoccum* accessions but indicating a need for introducing diversity from other sources. Promising genotypes for heat tolerance and stability across traits were identified, with heat-tolerant genotypes (<0.5 Heat Susceptibility Index) and stable yielders highlighted for potential use in breeding programs aimed at improving heat tolerance in wheat. In conclusion, our findings not only contribute to the understanding of terminal heat stress tolerance in *dicoccum* wheat but also offer valuable insights for breeders and researchers aiming to develop heat-tolerant varieties to ensure global food security in the face of climate change.

2PP-7

Unravelling the Role of Potential Root Endophytic Bacteria in Inducing Drought Stress Tolerance in Sensitive Wheat (*Triticum aestivum*) Genotype Under Drought Condition

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Bacteria are free-living organisms, living in every possible habitat on the planet and playing a vital role in recycling of nutrients and fixation of nitrogen from the atmosphere. Moreover, the endophytic bacteria inhibiting roots of the plant play pivotal role in stimulating plant growth even under adverse growth conditions. Therefore, to unravel the role of potential endophytic bacteria in abetting drought stress in wheat, endophytic bacteria isolated from the roots of contrasting bread wheat genotypes for drought stress tolerance were evaluated in susceptible wheat genotype DBW303. Out of 43 endophytic bacteria, 12 exhibiting superior growth in presence of 15% PEG 6000, were inoculated in seeds of drought sensitive cultivar DBW303 and planted in pots under drought condition maintained in pots by limiting the water application. The effects of endophytic bacteria were evaluated on growth of plants and compared with non-inoculated plants during wheat growing seasons of 2021-22 and 2022-23 under Rain Out Shelter (ROS) and rain-fed condition. Endophytes treatment increased wheat growth as longer plant height, root length, higher fresh and dry weight were recorded at seedling stage, and physiological parameters like higher NDVI, Chlorophyll fluorescence, longer spike length, more number of tillers, higher grain yield, more plant biomass and thousand grain weight with few exceptions were recorded in stressed plants as compared to the non-inoculated plants. These endophytes exhibited one or more plant growth-promoting properties, such as solubilization of phosphate, potassium, and siderophore production. Molecular identification of potential drought tolerant bacterial strains was done using 16S rRNA sequencing and five out of 12 endophytes belonged to genus *Priestia* while seven endophytes belonged to genus *Bacillus*. The study revealed that application of endophytic bacteria enhanced the drought tolerance in drought sensitive wheat genotype DBW303 and was more evident as compared to non-inoculated plants. These strains could be effective bioenhancer and biofertilizer for wheat cultivation, and a promising, novel way to improve plant growth, grain yield and drought tolerance in drought prone regions.

2PP-8

Screening Wheat Genotypes for Drought Tolerance through Morphological and Physiological Traits Characterization

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Wheat (*Triticum aestivum* L.) is one of the most widely cultivated crops in rainfed areas, where drought is the main limiting factor on yield. Wheat like other crops adopt various morphological, biochemical, and physiological responses to mitigate the effect of drought stress. Drought tolerance is a big challenge and grain yield is a direct indicator of resilience of the tolerant genotypes grown under water deficit conditions. Screening for drought-tolerant genotypes is crucial to ensure food security. Therefore, the present study was conducted during two consecutive *Rabi* seasons, 2021-22 and 2022-23. This study aimed to identify drought-tolerant genotypes in bread wheat by evaluating the morphological and physiological traits under both drought (rainfed) and irrigated conditions. A total of 500 genotypes were planted under irrigated and rainfed conditions in augmented design. Observations were recorded for fifteen morphological and physiological traits for each genotype and condition. The results revealed significant variations among genotypes for all traits under drought conditions. Genotypes Quaiu-1 (EC637486) and IC533733 were the highest grain yielder under drought and irrigated conditions, respectively. Grain yield showed the highly significant positive association with phonological traits, thousand grain weight, NDVI and CT at heading, anthesis and grain filling under drought condition. Drought Susceptible Index (DSI) and Drought Tolerant Index (DTI), and Tolerance (TOL) were estimated to identify drought-tolerant genotypes. DSI ranged from -0.78 in BCN-179 (IC539415) to 1.6 in genotype IC47797. Overall, 43 genotypes were identified as highly tolerant with DSI < 0.5. The study provides valuable insights into identifying and selecting drought-tolerant genotypes in wheat, contributing to sustainable wheat production under drought-prone environments.

2PP-9

Biopriming for Improving Seed Germination Potential and Seedling Vigour in Different Wheat Cultivars

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Bio-priming is a process of biological seed treatment that refers to a combination of seed hydration and inoculation of the seeds with beneficial microorganisms. It increases plant growth, seed viability, germination, vigour indices, subsequent disease protection and crop yield. Considering this, experiment "Biopriming for improving seed quality parameters, seedling vigour and biochemical parameters in different wheat cultivars" conducted during 2023 at ICAR-IIWBR, Karnal. During the study, four biopriming agents *viz*., *Trichoderma harzianum, Trichoderma asperellum, Bacillus subtilis* and *Chaetomium globosum* were isolated and used as biopriming agents for improving seed quality parameters and biochemical parameters in DBW187, DBW303, DBW327 and DBW 332.

Out of five bioagents studied, *Bacillus subtilis* was found to be most effective in improving seed quality parameters in all four varieties *i.e.* DBW332, DBW327, DBW187 and DBW303. Bacilli group can synthesize phytohormones and enhanced levels in plant which are involved the initial processes of lateral and adventitious root formation and elongation (Erturk et al., 2010). Among the four varieties, DBW332 had significantly higher germination percentage under control as 80.67, (%) followed by DBW 327 as 77.67 (%) and DBW 303 (74.0 %) whereas the lowest germination percentage was observed in variety DBW 187 as 67.67 (%). Among the different biopriming agents, *Bacillus subtilis* was found most effective in increasing number of normal seedlings and reducing the abnormal seedlings percentage over the non-treated seeds in the all four varieties. Seed treated with *Bacillus subtilis* recorded significantly higher germination percentage, seedling length, seedling dry weight, vigour index-I and vigour index-II.

2PP-10

Strategies for Improving Salinity Stress in Wheat

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Recently, climate change and global warming have directly affected the crops yield and quality by intensifying the frequency and extent of numerous stresses. Among these major cereals, wheat is ranked at the first position due to its domestication and contribution as the primary staple food crop globally. Salinity stress is a major threat to global food production and its intensity is continuously increasing because of anthropogenic activities. However, wheat productivity is adversely affected by salt stress, which is associated with a reduction in germination, growth, altered reproductive behavior and enzymatic activity, disrupted photosynthesis, hormonal imbalance, oxidative stress, and yield reductions. Management practices are still helpful to improve the wheat performance under salinity stress. The development of salt-tolerant cultivars along with appropriate agronomic practices can help to improve crop production under salt stress conditions. Use of arbuscular mycorrhizal fungi, plant growth-promoting rhizobacteria, and exogenous application of phytohormones, seed priming, and nutrient management are important tools to improve wheat performance under salinity stress. Se proved beneficial in enhancing proline and sugar accumulation in normal and NaCl-stressed seedlings providing extra osmolarity to maintain RWC and protect photosynthesis. Biochar is an activated carbon soil conditioner that can alleviate the negative impacts of salinity. Therefore, soil and agronomical (drainage system management, leaching of salt, nutrient managements), physiological (osmotic adjustment, seed priming, improve photosynthesis efficiency, and water relation), biochemical (redox, ion, and hormonal homeostasis) are the crucial step in wheat salinity stress tolerant program.

2PP-11

Evaluation of Wild Wheat Accessions for Drought Tolerance using Plant Morphological and Physiological traits

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Drought is one of the major abiotic factors that negatively affect wheat production. It is estimated that drought causes a 50–90% reduction in wheat yield. Like other crops, wheat undergoes diverse physiological, biochemical, and morphological reactions to lessen the impact of drought stress. However, drought stress remains a significant concern, and grain yield directly reflects the resilience of the tolerant genotypes cultivated in water stress conditions. In present study, during rabi 2022-23, wild wheat accessions of *Aegilops peregrina* (4x) were evaluated for drought tolerance under drought stress in rainout shelter (ROS) and irrigated (control) condition. The observations for each genotype were recorded for twelve morphological and physiological traits. Analysis of variance (ANOVA) and mean comparison were performed using R tools. Descriptive statistics and correlation analysis were performed using Meta-R software. For the identification of drought tolerant genotypes, the drought susceptibility index (DSI) was estimated using grain yield. Genotypes exhibiting a DSI value less than 0.55 were considered highly tolerant (HT), moderately tolerant (MT) with values between 0.55 and 1.0 while with DSI values greater than 1.0 were categorized as susceptible (S). Analysis of variance revealed that genotypes possess significant genetic variability at $p < 0.01$ for nine traits *i.e.,* days to 50% heading (DH), anthesis (DA), and maturity (DM), plant height (PH), tiller number (TN), spike length (SL), peduncle length (PL), grain yield (GY) and NDVI under drought stress. It was also observed that genotype PI 603931 had recorded highest grain yield of 6.97 g/plant while PI604186 recorded minimum yield of 1.14 g/plant under drought condition whereas under irrigated condition, the average grain yield was ranged from 6.19 to 19.46 g/plant. A significant positive correlation was observed among yield and five morpho-physiological traits *i.e.,* PH, TN, SL, PL, and NDVI. On contrary, yield and DH, DA, DM, 100 grain weight and spikelet length revealed a negative correlation under drought condition. The drought susceptibility index for grain yield ranged from -0.07 to 1.36 and two, seven, and six genotypes were categorized as HT, MT, and S, respectively. Based on the drought susceptibility index, the genotypes PI 603247 and PI 603931 were found to be HT, while the genotypes PI 487275, PI 604162, PI 604167, PI 604172, PI 604176, PI 604189, and PI 604192 were found to be MT. The identified genotypes will be further confirmed for effective utilization in breeding programs.

2PP-12

Recent Strategies for Abiotic Stress Management in Cereal Crops: A Genetic Perspective

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Abiotic stresses such as drought, salinity, heat, and cold significantly constrain the productivity and quality of cereal crops, posing a major threat to global food security. This abstract provides an overview of recent genetic strategies employed for abiotic stress management in cereal crops.Marker-assisted selection (MAS) and genomic selection (GS) have enabled breeders to identify and introgress stress-tolerant genes into elite cultivars more efficiently. Additionally, the availability of high-throughput sequencing technologies has facilitated the identification of key genes and regulatory networks underlying stress tolerance. Furthermore, advances in genetic engineering have opened new avenues for enhancing stress tolerance in cereal crops. Transgenic approaches involving the introduction of stress-responsive genes from diverse sources have shown promise in conferring tolerance to multiple abiotic stresses simultaneously. CRISPR/Cas-based genome editing techniques have emerged as powerful tools for precise manipulation of endogenous genes associated with stress responses, offering the potential to develop stress-tolerant varieties with minimal off-target effects. Integration of omics technologies, including transcriptomics, proteomics, and metabolomics, has provided valuable insights into the molecular mechanisms governing stress responses in cereal crops. Systems biology approaches have enabled the elucidation of complex gene regulatory networks and metabolic pathways involved in stress perception, signal transduction, and physiological adaptations. Moreover, exploiting natural genetic variation through association mapping and genomic studies has facilitated the identification of novel stress-responsive alleles and quantitative trait loci (QTLs) for further utilization in breeding programs. Multi-parent advanced generation inter-cross (MAGIC) populations and nested association mapping (NAM) populations have emerged as powerful resources for dissecting the genetic architecture of complex traits related to abiotic stress tolerance. In conclusion, recent advancements in genetics offer promising opportunities for developing cereal crops with improved resilience to abiotic stresses. Integrating diverse genetic strategies, including traditional breeding, molecular breeding, genetic engineering, and omics-assisted approaches, holds the key to addressing the challenges posed by abiotic stresses and ensuring sustainable cereal production in the face of changing climatic conditions.

2PP-13

Metabolite Profiling and Physiological Response of Wheat (*Triticum aestivum* L.) in Response to Salinity Stress

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The increasing world population requires more food to fulfill the nutrient requirements of humans. Wheat (*Triticum aestivum L.)* is one of the world's most consumed cereal grains and is a source of protein, carbohydrate, fat and fiber. However, the wheat productivity is challenged by increasing incidences of salt stress. In the present study, effect of salinity on growth and physiological parameters of wheat genotypes (AAI W6, AAI W9, AAI W10, AAI W13 and AAI W15) was studied by growing them in a hydroponics system under controlled environmental conditions in a growth chamber. The five genotypes evaluated showed significant differences with respect to germination percentage, plant height, shoot length, root length, chlorophyll content (SPAD value), photosynthetic rate and stomatal conductance. Based on the growth and physiological response, the genotype AAI W13 was found to be salt sensitive whereas AAI W10 was salt-tolerant. Higher salinity levels (340 mM) reduced the protein content whereas at lower levels of salinity (170 mM) slight increase in the protein content was observed. Metabolite profile of five genotypes was performed and a variable importance in projection (VIP) plot was created for the identification of differentially expressed compounds with maximum abundance. Fifteen (15) compounds were identified with VIP score, based on Partial least square- discriminate analysis (PLS-DA), ranging from 2 to 8. These compounds may be involved in the salinity stress response of the wheat varieties. Further experiments are in progress to understand the molecular mechanisms underlying the salinity stress tolerance in the tolerant wheat cultivar.

2PP-14

Exploring Fungal Endophytes for Mitigating Abiotic Stresses in Wheat

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Wheat stands as the second most crucial staple food crop globally, facing various abiotic stresses amidst a changing climate. These challenges significantly impact its quality and yield on a global scale. Over time, diverse conventional, agronomic, and molecular approaches have been devised to address abiotic stress in crops. One particularly promising strategy that has gained attention in recent years is the utilization of endophytes to enhance abiotic stress tolerance in various crops. However, the application of endophytes in wheat remains significantly under explored. In this study, we investigated the role of fungal endophytes in imparting abiotic stress tolerance in wheat. Two strains of endophytic fungi, namely PMB1 and PMB2, previously isolated and characterized at the University of Agricultural Sciences, Bangalore, exhibiting promising abiotic stress tolerance in rice, were employed. The initial step involved assessing the colonization of these endophytes in wheat, specifically using the HD2009 genotype. Once colonization was confirmed, treated seedlings were subjected to evaluation for stress tolerance under multiple abiotic stresses. We also tested the role of endophytes in two widely grown wheat varieties, DBW187 and DBW303. The effectiveness of these endophytes in inducing heat, drought, and salt stress tolerance in wheat was comprehensively evaluated through the quantification of various physiological and biochemical parameters associated with stress tolerance. These assessments were conducted in both pot and field conditions. The selected fungal endophytes exhibit promises in enhancing multiple abiotic stress tolerances in DBW187 and DBW303 genotypes. Ongoing investigations are focused on reaffirming their stress tolerance capabilities in field conditions. The fungal endophytes identified in this study hold potential as bioformulations to alleviate abiotic stress in wheat, particularly in the context of natural and organic farming systems, addressing critical needs in future agriculture

2PP-15

Overexpression of Multiple-Stress Responsive Genes in Indian Wheat via *Agrobacterium*-mediated Transformation

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Wheat grain quality and yield are affected by various biotic and abiotic stresses, especially in the current changing climate. These concerns attract attention to the urgent need to find a solution to meet the future global food demand. Plant genetic engineering is a quick solution where we can transfer or edit the resistance genes from close wheat relatives and/or other plant species. In this direction, we have transferred multiple stress-responsive genes (*AhBTF3, AhNF-YA7, EcSAP-ZF*) into Indian wheat HD3086 genotype through *Agrobacterium*-mediated transformation. We have obtained transformation efficiencies of 10% and 12.56% using mature and immature embryos, respectively. The transgenes cassette integration in the wheat genome was confirmed by PCR and southern blot. Transgenic plants were assayed for different abiotic stress drought, heat, and salt. Physiological and biochemical data analysis suggested a higher stress tolerance capacity in transgenic plants compared to the wild type. To verify the transgene inheritance, T_1 seedlings were grown under controlled conditions and analyzed by PCR for the transgene presence. Positive seedlings (33, 42, 48, 50, and 60) were further subjected to stress-tolerance assays. T_1-positive plants showed 20-30% higher tolerance compared to the wild type. Through this study, it has been established that multiple stress-responsive gene transformation can provide a fast way to validate the gene interactions and alter the existing pathways to generate better resistance against multiple stresses in crops.

2PP-16

Role of Abiotic Stress Management Practices for Improving the Properties of Cereal Crops

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Abiotic and biotic stress is one of the major challenges which is being faced in agriculture. To sustain higher yield of crop plants under prevailing abiotic stress condition is an important task for agriculture researchers. It acts as a hurdle to inhibit plant growth under changing climatic conditions. The severity of loss in yield varies according to the dissimilarities among various biotic and abiotic stresses. Conventional breeding program and molecular approach is one of the potent approaches against abiotic stress in plants. Plants have also self-defence mechanism against theses stresses which improves physiological properties of plant under extreme environment. There also exist some cross-talks in pathways of abiotic stress which can enhance plant's resistance and cross tolerance. To ensure sustainable production under changing climatic condition focus must be given on abiotic and biotic stresses management practices.

2PP-17

Breeding Strategies to Combat Heat Stress in Wheat

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Heat stress, is a significant environmental element that restricts wheat crop yields worldwide. Heat stress is characterized as a temperature rise above a saturation level for a period of duration strong enough to induce irreparable loss to plant growth and development. Heat stress may enable the crop's anatomy, morphology, biochemistry and physiology to deteriorate partially or completely. Due to elevated rising temperatures, wheat terminal heat stress is also expected to rise in the coming years. Besides terminal heat, early heat is also posing barrier for stable yield. As a result, wheat breeding for heat resistance is a big global priority.

For each degree rise in temperature, wheat production is estimated to reduce by 6%. Heat stress have negative impacts on wheat production by reducing tiller numbers, grain filling period, size of kernel, biomass and other factors. A rise in temperature of upto 0.5°C shorten the crop length for seven days and reduce yield by 0.5 t/ha^{-1} in Northern India. The terminal heat impact occurs when grain filling phase in the Indo-Gangetic plains combines with greater temperatures slowing photosynthesis and grain filling rate, resulting in reduced grain sizes and low yield.

Wheat is exposed to heat stress in differing rate at various levels of its development, yet reproductive heat stress is far more dangerous unlike vegetative heat stress. Heat stress during the final stages of development is a concern in 40 % of wheat growing regions in temperate zones. Even briefly exposing to elevated temperatures (>35 °C) will severely reduce yield by triggering premature senescence and accelerating assimilation in grain. Heat stress throughout the post anthesis disrupts photosynthate supply and translocating to advanced grains, as well as starch synthesis and accumulation inside the kernel, leading to decreased weight of grain and damaged grain content. Grain yield loss of 33.6% was observed in major wheat cultivars due to heat stress in late sown conditions indicating that there is a need to incorporate heat tolerance mechanisms. Therefore, breeders are focused on developing genotypes and various crucial management strategies to address the heat stress situation in wheat.

2PP-18

Abiotic Stress Management in Cereal Crops

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With devastating increase in population there is a great necessity to increase crop productivity of staple crops but the productivity is greatly affected by various abiotic stress factors such as drought, salinity, high and low temperature. Abiotic stresses negatively impact plant growth, development, reproduction, and ultimately crop productivity. Physiological process such as flowering, grain filling and maturation was highly effected abiotic stresses. Plant metabolisms which include photosynthesis, enzyme activity, mineral nutrition, and respiration are affected by abiotic stress. Crops can tolerate certain environmental stresses through their innate adaptation mechanisms, which are driven by various physiological and metabolic processes at the cellular level and are manifested in the whole plant. It is necessary to understand the adaptive mechanisms of plants to identify traits associated with tolerance to abiotic stresses. Several proteins and genes involved in abiotic stress adaptation and mitigation have been integrated to develop varieties that are tolerant to abiotic stresses. The genetic engineering of crop plants with stress-responsive genes has been demonstrated to enhance the adaptation to various abiotic stresses. Much of the gene identification efforts can be traced to model plants like *Arabidopsis*, and this basic knowledge needs to be accelerated to make the crop plants resilient to abiotic stresses in target growth environments. Advancement in physiology, genetics and molecular biology, have greatly improved our understanding of plant responses to stresses.

2PP-19

Enhancing Wheat Drought Tolerance: Cost-Effective Root Architectural Phenotyping at Seedling Stage

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To ensure global food security amidst climate change-induced water scarcity, increasing wheat and staple crop production is vital. Roots, often called the "hidden half" of plants, play a critical role in improving plant growth and productivity, especially under stressful conditions. However, traditional methods available for Root System Architecture (RSA) phenotyping are often low throughput, expensive, labour-intensive, and time-consuming. The development of robust and cost-effective phenotyping techniques, such as the one presented in this study, is crucial. In this study, we introduced a novel approach, a modified clear pot method (MCPM), to screen 500 diverse wheat lines from the NBPGR, New Delhi, for their precise quantification of RSA traits. Transparent plastic cups filled with soil-cocopeat and vermicompost media, with black cloth separating the cups and media. Visible seminal roots (SR) were imaged using a digital camera and EPSON Scanner on the 10th day after sowing and analyzed in the Adobe Photoshop and RhizoVision software.

Our results revealed significant RSA diversity for all the traits studied suggesting the scope for the establishment of a relationship with drought response data from the field plot. Correlation analyses of RSA traits and RWC indicated significant associations with indicative drought tolerance parameters. The MCPM demonstrated notable advantages over other techniques, including cost-effectiveness, high precision, and suitability for seedling-stage root phenotyping. By allowing roots to grow on the cloth, nearly all SRs were visible for high-quality imaging. This study underscores the importance of exploring and utilizing the root architectural diversity to enhance resilience to drought.

2PP-20

Abiotic Stress Management in Wheat: Strategies and Challenges

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Wheat, as one of the primary staple crops worldwide, faces significant challenges from various abiotic stresses, including drought, salinity, heat, and cold stress. These stresses severely affect wheat productivity, leading to substantial yield losses globally. This abstract provides an overview of current strategies and challenges in managing abiotic stress in wheat.

Conventional breeding efforts aim to develop stress-tolerant wheat cultivars through the selection and crossing of genotypes with desirable traits such as drought tolerance, salt tolerance, and heat resilience. However, the slow pace of traditional breeding methods necessitates the exploration of alternative strategies to expedite the development of stress-tolerant varieties.

Biotechnological approaches, including marker-assisted selection (MAS), genetic engineering, and genomic studies, offer promising avenues for accelerating the breeding process and enhancing stress tolerance in wheat. Genetic engineering techniques, such as gene editing and transgenic approaches, allow for the precise manipulation of target genes associated with stress tolerance, offering unprecedented opportunities to engineer wheat varieties with tailored traits.

In conclusion, effective management of abiotic stress in wheat requires a coordinated effort involving conventional breeding techniques, biotechnological advancements, and genomic studies. By integrating these approaches, researchers can accelerate the development of stress-tolerant wheat varieties capable of withstanding adverse environmental conditions, thus ensuring global food security in the face of climate change.

2PP-21

Study of *T. sphaerococcum* (Indian Dwarf Wheat), A Boon for Stress and Nutritional Resilience

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Climate change has become a significant problem for global agriculture as it has led to an increase in abiotic stress. In India, also, climate change has drastically affected agriculture with an increase in drought spells, flooding, and drastic temperature variations. One of the crops which has been significantly affected is wheat because of drought and heat stress. Wheat has been a part of the Indian civilisation since ancient times as can be seen both physically through excavations and in literary context through ancient texts. One can find references of wheat as "*Godhuma*" in ancient Sanskrit texts. It finds references in *Ayurveda* too as can be seen in *Charaka Samhita* and *Susrutha Samhita*. One of the species of wheat (*Triticum)*, *T. sphaerococcum* (Indian Dwarf Wheat) has been prominently found in excavations of ancient India like Mohen-jo-daro etc. The *T. sphaerococcum* (AABBDD 2n=6x=42) which originated in India was grown in primitive Punjab, Sindh and the Gangetic plains. As the generic name, *Paigambari*, suggests it was assumed to have been introduced from Arabia. However, studies in the field of genetics and genomics have clearly shown that this species has evolved in South Asia. The Indian dwarf wheat had a major role in the overall wheat productivity during the neolithic period and there are evidences that show it as the major crop during 3000 B.C. but now this grain is almost out of cultivation because of its low productivity. However, it is known to have several advantages such as heat and temperature tolerance, short and strong culm, better tillering capacity, resistance to several biotic and abiotic stress, and can be grown in rainfed conditions as well. Nutritionally it has been found to be rich in protein, minerals and amino acids compared to common bread wheat, making the Indian Dwarf Wheat a potential source for breeding nutritionally rich wheat varieties. Even after having remarkable qualities and being endemic to India, it has still not been fully utilised. *Triticum sphaerococcum* has a plethora of prospective uses and its genes can be used in the advancement of wheat varieties which are climate and nutritionally resilient. In the present study we have characterised two landraces of *T.sphaerococcum* grown in Prayagraj region and discuss the history, significance, advantages, and prospects of *T. sphaerococcum*.

2PP-22

Mitigating Abiotic Stress in Wheat through Rice Straw Biochar

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Wheat, the “King of Cereals,” is called so because of its importance as a staple crop throughout the world. Though high-yielding wheat varieties have the potential ability to provide sufficient food to feed the worldwide growing populations through their huge productivity. Although wheat occupies the largest total harvested area (38.8%) among the cereals including rice and maize, its total productivity remains the lowest. The main constraint toward global wheat production is the adverse effects of many biotic and abiotic stresses. Abiotic stresses, such as, water stress (both waterlogging and drought conditions), temperature stress (i.e., cold stress as well as high temperature or heat exposure), heavy metal (metalloid) toxicity, salinity stress etc. adversely affect different growth and developmental stages of wheat. As the global population continues to rise, the urgency to develop sustainable agricultural practices becomes paramount. Rapid global warming directly impacts agricultural productivity and poses a major challenge to the present-day agriculture. Current climate change models predict severe losses in crop production worldwide due to the changing environment, and in wheat, this can be as large as 42 Mt/°C rise in temperature The utilization of rice straw biochar (RSB) offers a sustainable solution for managing agricultural waste while enhancing soil health and crop productivity. RSB application enriches soil properties essential for stress tolerance in wheat. It improves soil water retention capacity, thereby alleviating drought stress by ensuring optimal moisture levels for plant growth. Additionally, RSB aids in ameliorating soil salinity, facilitating better root penetration and water uptake in wheat plants under saline conditions. Moreover, RSB serves as an effective tool in mitigating heavy metal toxicity in soil, reducing the bioavailability of metals and safeguarding wheat crops against metal-induced stress. Additionally, RSB application promotes soil microbial activity, fostering nutrient cycling and improving soil structure, which further contributes to stress tolerance in wheat. Despite its potential benefits, challenges such as determining optimal application rates, addressing long-term effects on soil fertility, and optimizing biochar production methods need consideration. Nonetheless, integrating RSB into wheat farming systems holds promise for sustainable agriculture, offering a practical approach to enhance crop resilience and ensure food security amidst changing environmental conditions. Overall, the promising role of RSB in sustainable agriculture as a tool for enhancing wheat abiotic stress tolerance while addressing environmental concerns associated with agricultural waste management.

2PP-23

Effect of Terminal Heat Stress on Spikelet Fertility and Grain Filling in Durum Wheat under the Agroclimatic Conditions of Prayagraj

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Durum wheat (*Triticum durum*) is a vital crop especially in the central part of the country, but its productivity is significantly impacted by heat stress, especially during the terminal stages of growth. We investigated the impact of terminal heat stress on spikelet fertility and grain filling in 130 genotypes of ICARDA Durum wheat in the Prayagraj region. Two sets of data, timely and late-sown, were collected to assess the responses under varying climatic conditions. The study employed comprehensive field experiments and detailed physiological analyses to evaluate spikelet fertility and grain filling parameters.

Preliminary analysis revealed a significant reduction in spikelet fertility and grain filling under terminal heat stress conditions, particularly in the late-sown genotypes. Late-sown crops exhibited a pronounced decline in spikelet fertility and grain filling rates compared to timely-sown crops, indicating the heightened susceptibility of Durum wheat to heat stress during the critical reproductive stage. Our findings underscore the urgent need for heat-tolerant Durum wheat varieties tailored to the specific agroclimatic conditions of Prayagraj to mitigate the adverse effects of terminal heat stress on yield and quality.

This study contributes valuable insights into the physiological responses of Durum wheat to terminal heat stress, offering a basis for the development of resilient cultivars and adaptive agronomic practices to ensure sustainable wheat production in heat-prone regions like Prayagraj. Understanding the mechanisms governing spikelet fertility and grain filling under heat stress conditions is crucial for enhancing the resilience of Durum wheat and ensuring global food security in the face of climate change challenges.

2PP-24

Estimation of GR_{50} Values of ACM-9, Axial, Total and Leader Herbicides to Control the Resistant Population of *Phalaris minor Retz*. Collected from Four Districts of Punjab.

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The field experiment was conducted at experimental farm of Lovely Professional University Phagwara, Punjab, during *Rabi* season of 2022-2023 and 2023-2024. GR_{50} values of prominent herbicides viz. ACM-9 29WG (metribuzin + clodinofop) 174g a.i/ha Axial 5EC (pinoxadin) 50g a.i/ha, Total 75WG (sulfosulfuron + metsulfuron) 30g a.i/ha and Leader 75WG (sulfosulfuron) 25g a.i/ha were used to control the resistant population of *Phalaris minor* collected from different districts of Punjab was calculated. Four experiments were conducted with each herbicide separately. In first experiment, ACM-9 (clodinofop+metribuzin), was applied at 0, 1/2R, R, 2R and 4R levels in main plots and four biotypes viz. B1-Ferozepur, B2-Ropar, B3-Fazilka and B4 -Ludhiana in sub plots. Second, third and fourth experiment was conducted with Axial 5EC (pinoxadin), Total (sulfosulfuron+metsuluron) and Leader (sulfosulfuron) respectively with similar doses and biotypes as in experiment 1. All herbicides were applied as post emergence at 35 days after sowing.Total (sulfosulfuron+metsuluron) at 4R recorded highest mortality % (72.2% and 23.6% during 2022-2023 and 2023-2024 respectively) and dry matter was (6.9 g/sqm and 147.8 g/sq m during 2022-2023 and 2023-2024.) At the recommended level the mortality percentage was observed (37.6% and 15.0%) during both years respectively with dry matter (20.26 g/sqm during first year and 183 g/sqm during 2023-2024) which was significantly more than 4R respectively. Among the biotypes the Biotype-3 Fazilka showing highest mortality % (47.7% and48.0%) and lowest dry matter (25.8 and 112.7) during both the years respectively. The highest mortality % and lowest dry matter of *P. minor* was found in Leader (sulfosulfuron) at 4R (43.5% in 2022-2023 and during 2023-2024 19.6%) having dry matter (49.09 g/sqm.in 2022-2023 and during 2023-2024 168.3 g/sqm.) and at the recommended level the mortality percentage was (36.4% in 2022-2023 and 11.6% 2023-2024) and at the recommended level the dry matter was observed (52.1 g/sqm during 2022-2023 and during 2023-2024 dry matter was recorded 190.3 g/sqm.) the highest mortality percentage (64.0% and 44.3%) lowest dry matter (29.6 g/sqm and 111.3 g/sqm) was obtained in Biotype -3 (Fazilka) during both the years respectively. Dry matter of B3 was found to be significantly less than all other biotypes during both years.

2PP-25

Appraisal of High Yielding Drought Tolerant Transgressive Segregants in Crosses of Two Rows and Six Row Barley (*Hordeum vulgare* l.) in Early Segregating Generation

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In pursuit of enhance productivity along with drought tolerant barley cultivar; a line x tester (6 x 4) crosses involving rainfed cultivars was made. Of the 24 crosses, 10 crosses from diverse parents were selected in next *rabi* season and 10 F_2's originating from a selected crosses were grown under two environments. Data recorded on grain yield per plant relating to 10 F_2's originating from these crosses were subjected to screening drought tolerant transgressive segregants. The cross/ genotypes which shows least drought susceptibility index values (<1) is identified as drought tolerant/ resistant and therefore, it might be concluded on the basis of Y_d, Y_p, GM and S values that plant derived from the cross BCU 4956 x K 603 and BCU 4922 x K 603 were drought tolerant. The cross BCU 4922 x K 603 was most promising as it yielded highest number of recombinants (18 in irrigated and 17 in rainfed conditions). Next to this, BCU 4910 x K 603 yielded 15 segregants in irrigated and 15 segregants in rainfed conditions. A total of 92 and 53 promising F_2 recombinants in irrigated and rainfed conditions, respectively from 10 crosses were evaluated for yield, number of effective tillers, thousand grain weight, harvest index, stomatal conductance, chlorophyll content and proline content. All the recombinants selected under rainfed condition (including a few from irrigated condition) showed enhanced level of proline content coupled with high grain yield and harvest index. Further, the segregants (culture no. 20, 41 & 4 in irrigated and culture no.14, 15 & 9 in rainfed) derived from cross BCU 4910 x K 603 and (culture no. 14, 37 in irrigated and 17, 19 & 7 in rainfed) from BCU 4922 x K 603 gave maximum percentage increase in grain yield over check coupled with other drought tolerant traits.

2PP-26

Assessing Heat Response for Wheat in Central India: Examining Genetic Variability, Genotype-environment Interactions, and Optimal Trait Selection

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This study aimed to boost wheat productivity in central India under high-temperature stress by exploring genetic variability, understanding the influence of diverse environments on wheat production, and identifying heat-responsive traits. New wheat lines were developed by crossing heat-sensitive (MACS2496) and heat-tolerant (WH730) varieties at IIWBR Karnal. Total 240 wheat lines were evaluated at three locations (Jabalpur, Narmadapuram, and Sagar) over two years (2019–20 and 2021–21) and under two planting conditions (timely and late). Significant differences were found in traits across locations, years, and planting conditions. Traits like days to heading and thousand kernel weight were strongly affected by terminal heat stress. traits such as tiller number per plant, kernel weight per spike, and thousand kernel weight were found to be closely linked to grain yield. Path and multiple regression analysis helped identify which traits contribute most to grain yield under heat stress. Another study identified stable wheat varieties for both normal and high-temperature planting conditions via univariate and multivariate stability analysis. Genotypes JW3288, L8, and L13 showed consistent grain yield stability, with L13 being the most reliable across all conditions. The location of Jabalpur was identified as the most influential environment. These findings suggest promising opportunities for breeding heat-tolerant wheat varieties, with a focus on understanding how genes interact with the environment and ensuring stability across different growing conditions.

Theme 3

Biotic Stress dynamics under changing environments

Oral

3OP-1

Biological Control of Sheath Blight Disease and Plant Growth Promotion in Rice by using different isolates of *Trichoderma harzianum* and Fluorescent Pseudomonads

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This study aimed to evaluate the impact of *Trichoderma harzianum* and *Pseudomonas fluorescens* isolates on the growth of rice (*Oryza sativa* L.) and the development of sheath blight disease caused by *Rhizoctonia solani*, a major threat to this vital staple crop. This investigation was carried out through a pot experiment. The maximum increase in rice plant height was observed in treatments where seeds were bio-primed and seedling roots were dipped in *T. harzianum* (IRRI-1), followed by *T. harzianum* (SV-3) and *P. fluorescens* (PF-2). These particular isolates were also highly effective in enhancing rice root growth when applied via seedling root dipping. Both application methods—seed bio-priming and seedling root dipping—with *T. harzianum* (IRRI-1) followed by *P. fluorescens* (PF-4) and *T. harzianum* (SV-3) resulted in the highest fresh and dry weights of roots. The highest fresh weight and dry weight of rice shoots were observed in plants treated with bio-priming using *T. harzianum* (IRRI-1), *T. harzianum* (SV-26), and *Pseudomonas fluorescens* (PF2). Regarding sheath blight disease reduction in rice, the most significant decrease was noted in plants subjected to bio-priming with *T. harzianum* (IRRI-1), *T. harzianum* (SV-3), and *P. fluorescens* (PF4). However, the efficacy of these bioagents differed slightly when applied via seedling root dipping, with *T. harzianum* (IRRI-1) followed by *P. fluorescens* (PF4) and *T. harzianum* (SV-19) showing the highest effectiveness in reducing sheath blight disease levels in rice. In summary, seed bio-priming appeared to be comparatively more effective for promoting rice growth, whereas seedling root dipping showed greater efficacy in managing sheath blight disease.

3OP-2

Unlocking Sugar Transporters: Paving the Way to Sustainable Wheat Rust Management

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Wheat (*Triticum aestivum* L.), the second most vital food crop worldwide, faces significant challenges from biotrophic fungi of the *Puccinia* genus, causing wheat rust. Pathogens extract sugars, a vital carbon source, from host cells, underscoring the pivotal role of sugar transporters (*STP*s) present on the plasma membrane. *STP*s regulate sugar transport, exchange, and allocation at plant-pathogen interfaces, influencing the resistance or susceptibility of wheat plants to rust. This study conducts an in-depth analysis of the genetic diversity and clustering patterns of sugar transporter genes in wheat. International Wheat Genome Sequencing Consortium (IWGSC) database searched for identification of Sugar Transport Protein (STP) gene family in wheat by using Sugar_tr Hidden Markov Model (HMM). Total of 476 *TaSTP* proteins with E-value of <1e−5, these sequences checked for presence of the Sugar_tr domain using Pfam database. 86 candidate STP proteins were discarded due to either a partial or complete absence of the *STP* domain and remaining 390 putative *TaSTP* sequences used for phylogenetic analysis along with 14 *AtSTPs* (Sugar transporter proteins from *Arabidopsis thaliana,* named as *AtSTP1* to *AtSTP14*. Phylogenetic tree, constructed based on the protein sequences of these 390 putative *TaSTPs* and 14 *AtSTPs*, revealed three subgroups. Second subgroup exclusively housed all *Arabidopsis* sugar transporter proteins. This group represents monosaccharide transporters, and further we investigated only monosaccharides of this group in wheat. Within this subgroup, 81 wheat genes shared structural similarities with *Arabidopsis thaliana*. Chromosomal mapping of 81 STPs revealed an uneven distribution of these *TaSTP* genes on the long or short arms of the A, B, and D chromosomes. Conserved Motifs of STPs- Pfam analysis gives conserved motifs present in STPs and this comprehensive exploration provides valuable insights into the distribution of conserved motifs among *TaSTP* proteins, shedding light on their potential functional significance. Understanding the genetic diversity and clustering patterns of sugar transporter genes in wheat offers valuable insights into their role in regulating sugar transport at plant-pathogen interfaces, crucial for enhancing wheat resistance against rust pathogens. Furthermore, it explores the potential implications of a deeper understanding of *STP*-mediated wheat-rust interactions in devising effective strategies for wheat rust management.

3OP-3

Application of Omics Technologies in Molecular Mechanism of Cereal's Host-Resistance against Biotic Stresses

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Cereal crops play a pivotal role in global food security, serving as primary sources of nutrition for a significant portion of the world's population. However, these crops face constant threats from a myriad of pathogens, posing substantial challenges to agricultural productivity. Genomics has significantly contributed to unravelling the genetic basis of host-resistance in cereal crops. Genomics approaches also facilitate the development of molecular markers such as RFLP, SSR, SNP, etc. for accelerated and precise breeding, ensuring the transfer of desirable traits in a targeted manner. The use of such technologies has gained importance in identifying disease resistant genes in three major cereals viz. rice, sorghum and maize, but it is very difficult in case of wheat and barley because of their large genomes sizes.Transcriptomics provides a dynamic perspective on the host response to pathogen invasion. High-throughput RNA sequencing allows the simultaneous analysis of gene expression levels, unravelling the intricate regulatory networks activated during the plant defense response. The identification of key genes involved in defense pathways and signaling cascades enhances our understanding of the molecular events that contribute to host resistance. Additionally, transcriptomic studies shed light on the temporal and spatial regulation of gene expression, offering insights into the fine-tuning of defense responses in cereal crops.Proteomics plays a pivotal role in uncovering the functional proteins involved in host-resistance mechanisms. By analysing the plant proteome in response to pathogen attack, researchers can identify stress-responsive proteins, post-translational modifications, and protein-protein interactions critical for effective defense. The integration of proteomic data with other omics datasets enhances our understanding of the molecular crosstalk between different components of the defense machinery. Furthermore, proteomics aids in the identification of potential targets for genetic manipulation to enhance host resistance.

The integration of multiple omics technologies offers a systems biology approach to deciphering the molecular mechanisms of host-resistance in cereal crops. The crosstalk between genomics, transcriptomics, proteomics, and metabolomics provides a comprehensive and nuanced understanding of plant defense responses. This integrated approach not only accelerates the identification of key molecular players but also enables the development of targeted strategies for crop improvement. Ultimately, the implementation of omics technologies in elucidating the molecular mechanisms of host-resistance in cereal crops is instrumental in developing resilient crop varieties, sustainable pest management practices, and ensuring global food security in the face of evolving biotic challenges.

3OP-4

Genetic Association Study for Blast Resistance Using *Ssr* Markers in Rice Varieties

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Rice blast is one of the foremost destructive rice diseases causing serious yield losses under conducive conditions. The most ideal, cost effective and environmentally friendly approach to manage blast disease is the use of resistant cultivars. However, due to high variability, the blast fungus overcomes resistance after a couple of years, so identification of novel broad spectrum resistance genes is indispensable. In this study, a set of 81 National Rice Research Institute released varieties (NRVs) spread over eight ecologies were screened against leaf blast resistance at NRRI, Cuttack for two consecutive years. The disease reaction showed that twenty varieties were highly resistant, twenty-one showed moderate reaction and forty varieties were found susceptible. Based on cluster and structure analysis, 81 NRVs were categorized into three groups. The NRVs showed 96% variation among individuals and 4% variation among the population. The principal coordinate analysis partitioned the resistant and susceptible NRVs into different groups. The genome wide association study (GWAS) was performed using 135 SSR markers to identify the *R* gene/QTLs conferring resistance to the rice blast. The GWAS study identified 15 genomic regions significantly associated with the leaf blast disease resistance. This study would help in the identification of the potential function, and validation of the candidate *R* genes/QTLs. The associated genes could be used in developing blast-resistant cultivar through marker-assisted selection.

3OP-5

Genetic Diversity, Phylogeographic Relationships, And Population Structure of Wheat Loose Smut Fungus *Ustilago tritici* From the Hill and Plain Terrains of India

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Ustilago tritici (UT) is a fungal pathogen that cause in loose smut disease in wheat. There is very little information known about its genetic variability and phylogenetic relationships of *U. tritici* causing wheat loose smut disease in hill (HT) and plain terrains (PT) of India. The current work performed to know the phylogeographic patterns of *Ustilago tritici* isolates obtained from wheat growing HT and PT regions of India. In this study, two sequences (ITS and RPB2) were amplified and sequenced in 112 isolates from two different populations (HT and PT) in India to determine their genetic diversity, genetic differentiation and pedigree geographic structure in order to provide information necessary for deveining effective disease protection strategies. In total, 5 haplotypes were obtained. The gene flow (Nm) among the population populations was 0.7, and displayed low overall genetic diversity. Analysis of molecular variance (AMOVA) showed that genetic variation in UT occurs mainly within populations (77.27%) rather than between populations (22.73%). Furthermore, the UT populations exhibited a large degree of genetic differentiation ($F_{st} = 0.2273$). A mismatch analysis curve and neutrality test indicated that the UT populations recently expanded. The phylogeographic patterns of species based on two-gene analysis, as well as the predominance of a single haplotype, suggested that human-mediated dispersal may have played a significant role in shaping this pathogen's population.

3OP-6

Virulence Analysis of *Bipolaris sorokiniana*, Fungal Incitant of Spot Blotch Disease in Wheat

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Wheat (*Triticum aestivum* L.) is a crop of great significance globally not only because it is one of the premier cereal crops, but also due to its high nutritive value and huge acreage dedicated to wheat cultivation around the word. It is considered as the second most staple food crop next to rice in India. Wheat cultivation is affected by many biotic and abiotic stresses. But biotic stresses or diseases are major obstacles in the realization of yield potential of the promising high yielding wheat cultivars. Among the diseases spot blotch caused by *Bipolaris sorokiniana*, is one of the major threats to the wheat production especially in the humid warmer regions of Indo-Gangetic plains. This pathogen besides the established NEPZ regions is emerging as threats in some other regions also like NWPZ regions under wheat cultivation. *B. sorokiniana* affected wheat leaves samples were collected from both NEPZ and NWPZ regions, the pathogen was isolated and purified. Out of the different isolates of *B. sorokiniana* collected from various locations, total 14 isolates were screened on susceptible wheat cv. WH 147 for virulence analysis of the fungal incitant. Among the isolates, *B. sorokiniana* BS 8 was found most virulent isolate, which resulted in maximum avg. lesion length= 35.2 mm, avg. lesion breadth = 5.4 mm, max. avg. AUDPC = 1162.5, and minimum NDVI value 0.21 on susceptible wheat cv. WH 147. Isolates dependent variation in the virulence pattern was noticed. NEPZ isolates were found more virulent.

3OP-7

Identification of Genomic Regions Associated with Stripe Rust Resistance in W8627 x PBW343 derived Wheat Recombinant Inbred Population

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Stripe rust in wheat is caused by *Puccinia striiformis* f. sp. *tritici*, which affects the grain yield, quality and nutrition. So, detection of the quantitative trait loci (QTLs) related to these traits becomes highly important for wheat breeders to implicate genetic resistance by using various molecular breeding approaches in wheat against rust. In order to dissect the genetic basis of resistance, 212 recombinant inbred lines have been developed with the single seed descent method via crossing between resistant (W8627) and susceptible (PBW343) parents. This study was conducted at experimental field of ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana were screened at seedling and adult plant stage against stripe rust during the year 2021-22 and 2022-23. Data for various agro-morphological traits was recorded. The parents and RILs were genotyped using a 3.9K DArT Array. Only 602 markers were found polymorphic on both the parents, which were used for construction of linkage map. QTL analysis was done using ICIM v.4.2. We detected 2 QTLs for all stage resistance effective against the pathotype 78S84. A total of 2 QTLs for adult plant resistance were identified. Of these, 1 QTL was found consistent and stable over the years (2021-22 and 2022-23). Analysis of variance revealed significant differences for various traits studied over sowing conditions and years. These markers could be utilized for marker assisted selection for screening germplasm and breeding for stripe rust resistant cultivars.

3OP-8

Nanoparticle Mediated Spray-Induced Gene Silencing (SIGS): A Novel Tool to Control Spot blotch Disease of Wheat

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Wheat is a major staple food crop affected by several fungal diseases. Among them, spot blotch caused by *Bipolaris sorokiniana* poses a significant threat to wheat production and grain quality. Breeding approaches and chemical fungicides have made commendable progress in protecting wheat from spot blotch. However, the continuous evolution of *B. sorokiniana* strains and the negative effects of fungicides on human health necessitates more effective and sustainable strategies for spot blotch management. Two RNAi approaches, Host induced gene silencing (HIGS) and Spray induced gene silencing (SIGS), have been employed to target pathogenesis-related genes to control plant diseases. Since HIGS is a transgenic approach, it is less preferred than SIGS. The SIGS is an environment-friendly approach that involves spraying double-stranded RNAs (dsRNAs) specifically targeting the virulence genes of pathogen. However, the unstable nature of dsRNA employed in SIGS poses a major constraint to its wide-scale application. With this background, in the present study, three pathogenesis-related genes from *B. sorokiniana* were selected for designing the dsRNAs. dsRNAs targeting the fungal genes were designed using the software PssRNAit. The dsRNA sequences were synthesized and isolated using the *TRIzol* method. They were bound to nanoparticles, and *in-vitro* and *in-vivo* bioassays were performed to test their efficacy on fungal growth and disease symptoms, respectively. Nanoformulated dsRNAs targeting fungal virulence genes significantly reduced fungal growth under both *in-vitro* and *in-vivo* conditions. Reduction in disease severity was also observed under only dsRNA and nano-formulated dsRNA treatments. A substantial decrease in the expression patterns (validated using qRT-PCR) of dsRNA-targeted genes validated the role of these genes in pathogenicity and their potential in SIGS. The application of SIGS-mediated RNAi technology in wheat holds immense potential for improving resistance against spot blotch by suppressing the expression of critical genes involved in pathogen virulence.

3OP-9

Management of Footrot Disease in Rainfed Wheat by using the Combi product (Carboxin 37.5%+ Thiram 37.5%) WP

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Foot rot of wheat caused by *Sclerotium rolfsii* is serious problem mainly in the rainfed areas of Karnataka, Gujarath and Madhya Pradesh. The pathogen is soil borne and damaging the crop by causing pre and post emergence death from seedling stage to maturity of the crop and also causes 25-50 per cent loss through infection of seedlings. The recommended fungicide Carboxin 37.5% is not available in the market. In this context experiments were conducted during rabi 2021-22 & 2022-23 in the All India coordinated wheat improvement project, MARS, UAS, Dharwad to evaluate the effective molecule for management of the foot rot disease. The treatments consist of seed treatment with biocontrol agents and fungicides which were evaluated in the sick plots of foot rot of wheat. All the treatments were found significantly superior to the untreated control pots. Among the biocontrol agents *Trichoderma harziaum* recorded least foot rot incidence (46.54 %) followed by *Neofascicoccum purvum* (50.33). However, the fungicide Carboxin 37.5%+ Thiram 37.5%) WP @ 3 g/kg was found significantly superior (13.78%) in management of the foot rot disease and the yields were also found superior (39.77q/ha) as compared to other treatments and untreated control (15.51q/ha). The maximum net returns of Rs 52785.00/ha and benefit cost ratio (1:1.97) were found in the same treatment. Thus, the combi product (Carboxin 37.5%+ Thiram 37.5%) WP) @ 3g/kg may be recommended for the management of the foot rot disease of wheat.

3OP-10

Advances in Genomics of Karnal Bunt Pathogen in Wheat

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Fungal pathogens are emerging or/ remerging in climate change scenarios. In the era of molecular biology, there is a need to understand pathogen evolution, biology, lifestyle, and novel disease management using molecular techniques. The *T. indica* genome assembly size of 33.7 MB was generated using Illumina and Pac Bio platforms with a GC content of 55.0%. Till date, no reference or complete genome of Tilletia indica is available, and reported genomes are variable in size ranging from 26.7 to 43.7 Mb. The population of T. indica was highly diverse. The population of T. indica in India was divided into three subpopulations the presence of 13 SNPs associated with Karnal bunt virulence. The genes like Ti3931, *Ti6828, Ti7098, Ti7462, Ti7522, Ti 9289, Ti 8670, Ti 7959, Ti 7809*, and *Ti10095* may have a role in the germination of teliospores. The sequenced genomes provide insight into which potential virulence factors were identified and from which genes associated with different pathogenic strategies could be predicted. Few putative pathogenicity-related genes in Tilletia indica were identified in the genome. Further research still needs to be discovered in the genomics of fungal plant pathogens and functional studies to identify and characterize pathogenicity-related genes and their targets in the host.

3OP-11

Differential Silicon Regime Earmarks Distinct Genomic Regions for Yield Traits and Leaf Rust Resistance in Bread Wheat Though Association Analysis.

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The biotic and abiotic stresses along with water stress and soil nutrient deficiencies, production, and grain quality of Bread wheat (*Triticum aestivum* L.) are affected. And hence, it is important to develop drought-tolerant wheat varieties with high yield potential and enhanced grain nutrients for food security. Silicon (Si) which is an important mineral present in soil and there has been an understanding that genotypes with different genetic makeup or species can have differential response to Si, in terms of its uptake and deposition. The present study, therefore, was planned in a two subsidiary experiments with the objective to determine the effects of Si on wheat varieties under timely and late sown conditions, and then to characterize unexplored breeding materials for their response to Si in terms of yield related agronomic traits and disease resistance and then to identify genomic regions through genome wide association studies. The core set of 205 genotypes with 35K genotypic data were analysed for Si response and its impact on yield related traits and under leaf rust disease epiphytotic conditions. The findings revealed a significant genetic variation for different yield and biotic traits under different Si regimes, indicating present of genotype differences in terms of Si response. With the different algorithms of association mapping viz., BLINK and FarmCPU, 12 unique QTLs under Si+ and 07 QTLs for Si- conditions for various yield and disease resistance traits were identified. Some of these QTLs were captured by both the algorithms. Our results thus provide an important insight into understanding the genetic basis of Si response and can in developing molecular markers for selection and integration.

3OP-12

Thematic Area: Biotic Stress Dynamics Under Changing Environments

Uncovering Genomic Region Associated with Rhopalosiphum Maidis (Fitch) Resistance in Wild and Synthetic Wheat Using Genome Wide Association Mapping

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Corn-leaf aphid (CLA), *Rhopalosiphum maidis* (Fitch) is one of the serious insect pests of wheat posing a considerable economic threat to wheat production worldwide. Developing resistant cultivars is considered a cost-effective and environmentally friendly method of pest management. Utilizing DNA markers associated with genes conferring insect resistance, marker assisted selection has been proven to be a very useful method in the development of resistant varieties. This study employed Genome-wide association study on 287 wild and synthetic wheat genotypes to assess genetic resistance against *R. maidis* over two consecutive years. The analysis of population structure and kinship has revealed the existence of three distinct subpopulations among the genotypes. Subpopulation 3 was identified as the most diverse group, as indicated by distinct allelic patterns. Molecular variance analysis revealed a significant variation both within and among subpopulations. Although no significant linkage disequilibrium was detected between single nucleotide polymorphic markers, however, genome D demonstrated the highest level of linkage disequilibrium at the genomic level when compared to genomes A and B. Fifteen and nineteen significant marker-trait associations positively linked to *R. maidis* resistance were identified in wild and synthetic wheat genotypes under field and screenhouse conditions, respectively. In silico analysis pinpointed these marker-trait associations to putative candidate genes regulating biotic stress tolerance, especially against insect pests and diseases. Thus, identified marker-trait associations and associated genes offer valuable resources for future wheat breeding programs, facilitating the development of resistant cultivars against *R. maidis*.

Poster

3PP-1

Dynamics of Adaptation: How Wheat Pathogens Respond to Climate Shift

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Climate change is profoundly impacting global environmental conditions, including agricultural ecosystems and the dynamics of plant pathogens in crops like wheat. Rising global temperatures, particularly in regions vulnerable to heat and reduced precipitation, pose a significant threat to wheat cultivation. This shifting climate is anticipated to affect both abiotic and biotic stresses affecting wheat, with diseases such as rusts, blast, spot blotch, and powdery mildew becoming critical constraints in achieving future production targets. Statistical analyses highlight alarming trends in wheat disease incidence and severity, with climate change contributing significantly to production losses according to the Food and Agriculture Organization (FAO). Elevated carbon dioxide levels in the atmosphere further complicate matters, influencing plant physiology and pathogen virulence, potentially leading to more aggressive strains. Changes in weather patterns, such as warmer winters, can facilitate the survival and earlier infection of fungal pathogens, while erratic rainfall patterns create favorable conditions for soil-borne pathogens like Rhizoctonia solani. Simulation studies combining data and models provide insights into future disease impacts, projecting increased severity in some cases, such as Fusarium head blight, while others, like Septoria tritici leaf blotch, may decrease. However, uncertainties exist due to variations in climate models and emission scenarios, necessitating more collaboration among researchers to enhance understanding and develop effective management strategies. In conclusion, addressing the complex challenges posed by climate change on plant disease management requires a holistic approach emphasizing sustainable practices to ensure the long-term viability of wheat production and global food security.

3PP-2

An Overview on Recent Advancement of Spot Blotch (*Bipolaris sorokiniana*) in Wheat

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Spot blotch (SB) disease in wheat, caused by *Bipolaris sorokiniana*, have made significant strides in both conventional and molecular approaches. Despite its global impact in warm, humid wheat-growing regions, no wheat variety is immune to SB. Genetic resistance to SB is predominantly quantitative, governed by Quantitative Trait Loci (QTLs), with only four major QTLs identified so far (Sb1 through Sb4). Recent studies in South Asia have identified stable QTLs contributing to significant phenotypic variation, aiding in SB resistance breeding. Advances in wheat genome assemblies, functional genomics, and gene cloning have accelerated SB resistance breeding efforts. The mapping of the Sb4 gene and identification of 21 putative genes on chromosome 4B represent notable milestones. Stacking QTLs with minor effects has notably reduced SB severity, highlighting the importance of combining multiple resistance loci. Integrated disease management strategies combining fungicide use, particularly triazoles, with cultural methods like crop rotation and early sowing, has proven effective in mitigating disease impact. These advancements promise more resilient wheat varieties, enhancing food security in affected regions. Ongoing collaboration between breeder and plant pathologists remains crucial for further progress in combating spot blotch disease.

3PP-3

The Battle against Cereal Cyst Nematode: Comprehensive Management Strategies

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Cereal cyst nematode, *Heterodera avenae* is one of the most economically damaging nematodes to wheat in lighter soil of Rajasthan and Haryana. Most of the small grain cereals and some grasses are hosts of this nematode. Common symptoms appear on wheat as stunting and poor plant growth in patches across the field, reduced number of tillers, and plants looking more yellow than surrounding healthier plants. Recognizing the economic implications, a field trial was executed on a farmer's field to investigate integrated management strategies for managing *Heterodera avenae* in wheat. In present investigation integration of Fluopyrum 5 ml/kg seed and Soil application of *Metarhizium anisopliae, Beauveria bassiana* and *Glomus fasciculatum* at 4 kg/ha, Fluensulfone at 5 kg/ha + Soil application of *Metarhizium anisopliae, Beauveria bassiana* and *Glomus fasciculatum* at 4 kg/ha have been tried for the management of cereal cyst nematode, *H. avenae* on wheat. The study employed a Randomized Block Design with four replications. Result indicated that Fluopyrum 5ml/kg seed +Soil application of *Glomus fasciculatum* at 4 kg/ha was most effective, followed by Fluensulfone at 5 kg/ha + soil application of *Glomus fasciculatum* at 4 kg/ha.

3PP-4

Entomological Perspectives on Biotic Stress: Understanding Insect Dynamics in a Changing Environment

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The intricate relationship between insects and their environment is a cornerstone of entomological research, particularly when considering the impacts of changing environmental conditions on insect dynamics. Biotic stressors, such as insect populations, play a pivotal role in ecosystem functioning, agricultural productivity, and human well-being. In this abstract, we delve into the complexities of how insect dynamics respond to environmental changes and explore the implications for entomology. Climate change stands out as a primary driver of environmental transformation, exerting profound effects on insect populations. Alterations in temperature regimes, precipitation patterns, and extreme weather events significantly influence insect phenology, distribution, and abundance. These changes can disrupt synchronized interactions between insects and their host plants, leading to mismatches in timing and potentially disrupting critical ecological processes such as pollination and herbivory. Moreover, land-use changes, driven by agricultural expansion, urbanization, and habitat fragmentation, reshape insect habitats and alter resource availability. Fragmented landscapes may impede insect movement, leading to genetic isolation and reduced population resilience. Understanding the responses of insect populations to changing environmental conditions is paramount for devising effective management strategies. Integrated pest management approaches, grounded in ecological principles, offer sustainable solutions by leveraging natural enemies, crop diversity, and habitat restoration to suppress pest populations while minimizing ecological impacts. In conclusion, elucidating the dynamics of insects under changing environmental conditions is essential for safeguarding biodiversity, ensuring food security, and mitigating the impacts of biotic stressors on ecosystems and human societies. Entomologists play a critical role in this endeavour, bridging scientific knowledge with practical solutions to address the challenges posed by insect dynamics in a rapidly changing world.

3PP-5

Study of Stage-Specific Field Life Tables of Pink Steam Borer (*Sesamia Inferens*) (Walker) on Wheat

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The study, conducted at the Research Farm of the Department of Agricultural Entomology, College of Agriculture, Latur (MS) during the *rabi* season of 2021 and 2022, aimed to investigate the stage-specific field life tables of wheat. Results revealed that *Sesamia inferens* (Walker) completed three generations during both 2021 and 2022. Field-life studies identified key mortality factors, including *Callibracon* sp. (Braconidae) (larval parasitoid), *Cotesia flavipes* (Braconidae) (larval parasitoid), and other unidentified causes, which regulated the population of *S. inferens*. Maximum mortality occurred during early instar larvae in all generations during both seasons. These findings underscore the utility of field-life tables in identifying indigenous natural enemies and devising strategies for mass multiplication techniques of natural enemies within Integrated Pest Management (IPM) frameworks.

3PP-6

Genetic Analysis of Spot Blotch Disease Resistance in Wheat (*Triticum aestivum* L.)

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The spot blotch disease, attributed to the fungus *Bipolaris sorokiniana* holds economic significance in Eastern India, particularly in West Bengal, which is the natural hotspot of the disease. 96 wheat genotypes were screened for spot blotch disease resistance in two consecutive years 2019-20 and 2020-21. Using the AUDPC value obtained through double-digit scoring, 21 genotypes were classified as highly susceptible, 47 genotypes as moderately susceptible, 19 genotypes under moderately resistant category and 9 genotypes categorized as resistant. Days to maturity, green leaf duration after heading, glaucousness index, yield showed significant negative association with AUDPC. 96 genotypes were evaluated for presence of three spot blotch resistance QTLs viz., *Sb1*, *Sb2* and *Sb3* by using markers *Xgwm148*, *Xgwm639* and *XWGGC12282* respectively. 5 genotypes were found to possess three QTLs, 8 genotypes with two QTLs and 11 genotypes with single QTL. Marker-trait association study through single marker analysis (SMA) identified 3 markers; *Xgwm374, Xgwm120* and *Xgwm156* to be significantly associated with spot blotch resistance. Consequently, the identified potential sources of resistance and linked markers from this study can be further utilized in transferring QTLs into favourable genetic backgrounds or incorporated into hybridization programs to select superior transgressive segregants.

3PP-7

Harnessing *Yr* Gene Linked SSR Markers to Identify Yellow Rust Resistant Wheat RILs

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Fungal diseases have always been a havoc impeding the crops from reaching their full genetic yield potential. *Puccinia striiformis*, a fungal pathogen causing yellow rust in wheat is prime target for breeding resistant genotypes in wheat. In such an attempt, the two parents, PBW698 (resistant) and WH711 (susceptible), were crossed and the progenies were selfed upto seven generations to produce a series of 210 recombinant inbred lines. To identify the lines carrying *Yr* genes, three *Yr* gene linked SSR markers were used *viz*. Xpsp3000 (*Yr*10), Xgwm11 (*Yr*15) and Barc181 (*Yr*24). Presence and absence of gene was scored on the basis of presence and absence of bands in susceptible and resistant parents in accordance with established relationships. The results depicted that maximum of the RILs (79) carried *Yr*24 gene along with the parent WH711. The gene *Yr15* was identified in 65 RILs along with parent PBW698 and the gene *Yr10* was present in 50 RILs. There were 21 RILs that carried all three studied *Yr* genes in their genomes. Mean performance of these resistant RILs was compared to the overall mean of F_7 progeny and they showcased a positive shift in few morpho-physiological traits. These resistant lines carrying *Yr* genes and surpassing the progeny mean for morpho-physiological traits can be used in wheat breeding programmes as source of stable resistance against yellow rust and high mean performance under stress conditions to create truly resilient wheat genotypes.

3PP-8

Management of Gloeocercospora and Colletotrichum graminicola by Fungal Endophytes of *Sorghum bicolor* L.

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In this study, we collected various healthy samples of sorghum and isolated 36 fungal endophytes from it. Then they were individually tested against *Gloeocercospora sorghi* (Zonate leaf spot) and *Colletotrichum graminicola* (Anthracnose) using dual culture approach and the result showed that T4, T6, T9, T15, T21, T22, T27, T39, G2 and G5 were found to be effective against *G. sorghi* and G1 and G3 isolates were effective against *C. graminicola*. Isolate T4, T6, T9, T15, T21, T22, T27, T39, G1, G2, G3, and G5 were taken for biochemical analysis and also examined under glasshouse conditions to determine their effect on plant's capacity to produce defense enzymes, PAL and PPO. The results showed that isolates T9, T15, T39, G1, G2, and G5 were found to be capable of eliciting an immunological response by inducing PAL and PPO. The entire investigation showed that the chosen fungal endophytes had potential for treating test pathogens. Therefore, we concluded that fungal endophytes affect the plant positively and can be an aid in promoting sustainable agriculture.

3PP-9

MutRenSeq: A Resistance gene capture technique to generate disease resilient plants

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MutRenSeq is a novel technology developed and successfully applied in crop plants to clone resistant genes. The RenSeq technique is based on the principle that sequence information of known resistance genes from sequenced genome is used as a bait to capture similar gene fragments in closely related crops and species. In plants, majority of the disease resistance genes known so far belongs to Nucleotide binding and Leucine Rich Repeat (NLR), kinase (receptor like kinase, receptor like proteins, wall associated kinase etc) and transporters families. Here we target NLR as it is the major class of R gene family conferring disease resistance in model and crop plants. Captured and enriched fragments are then subjected to next generation sequencing. As the goal is to create a de novo assembly based on wild type RenSeq data. Then, map RenSeq data from the susceptible mutants to the assembly.

3PP-10

Molecular Markers for the Detection of *Sitophilus oryzae* in Wheat and Barley

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Cereal grains in storage are impacted by a variety of pests, of which *Sitophilus oryzae* is one of the most commercially significant. In order to overcome heavy losses in post-harvest storage of grains, timely detection of this pest is of utmost importance. But traditional detection techniques are expensive, time-consuming and lack sensitivity for same species. In this context, molecular approaches could be instrumental in rapid detection of stored grain pests with precise accuracy. For the molecular detection of *S. oryzae*, genomic DNA from *S. oryzae* was isolated. DNA was also isolated from contaminated and uncontaminated wheat and barley grains with *S. oryzae.* The genomic DNA was amplified in vitro with already reported specific primers for molecular identification of *S. oryzae*. The specific primers of *S. oryzae* were designed using sequences on NCBI Blast by comparing them with unrelated species for cross amplification. PCR amplification of defined regions of cytochrome oxidase I (COI) gene followed by sequencing to identify the pest species in order to develop specific primers. As per the results, it was found that the primer in COI Region showed specific binding with *S. oryzae.* Therefore, the primer specific to *S. oryzae* were further tested through qPCR to check the sensitivity of the primers by using different dilutions. The results were confirmed using Melting curve analysis and Standard Curve. Thus, developed markers offer rapid detection of *S. oryzae* with precise accuracy, facilitating the timely and proper management of *S. oryzae* in wheat and barley grains.

Theme 4

Cereal quality, nutrition, post-harvest processing, value addition and marketing for food safety and global nutritional security

Oral

4OP-1

Deployment of Climate Resilient and Bio Fortified Wheat Varieties in Punjab and Haryana: A Status Report

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Wheat crop has always been challenged by climate change weather vagaries such as drought, heat, salinity, excessive rain, water logging, hailstorm and storm. At ICAR-IIWBR an effort has been made to survey the deployment of climate resilient and biofortified wheat varieties at farmers' field to assess their adaptation impact at final stakeholders' farm. During first fortnight of December, 2023 an extensive survey was conducted in Northern India Covering all the districts of Punjab and Haryana. A total of 1027 farmers involving 550 farmers from Haryana and 477 farmers from Punjab were interviewed on a pre designed interview schedule to elicit information on the adoption of climate resilient and bio-fortified wheat varieties at farmers' fields. Ten teams were constituted involving scientist of ICAR-IIWBR, Karnal and other line departments such as officials from State Department of Agriculture and scientists from Krishi Vigyan Kendra to know the category of farmers cultivating these wheat varieties. It was found that In Punjab 32.92 % of the wheat growers were medium category farmers where as in Haryana 30.18% of the farmers were small category farmers. During the survey it was recorded that 9.20% of total area in Punjab under wheat was early sown (25th October to 5th November) and in Haryana it was 15.29%. Under timely sown condition 83.34% and 81.19% area was recorded in Punjab and Haryana, respectively. Under late sown condition 7.46% and 3.52% area were recorded in Punjab and Haryana respectively. It is evident from the data that farmers in Haryana and Punjab state deployed climate resilient varieties at their fields to mitigate the impact of climate change on wheat cultivation. Another important strategy to counter the impact of terminal heat on wheat crop is early sowing which was largely adopted by farmers of both the sates; 94.54% in Punjab and 96.48% in Haryana. The overall deployment of climate resilient and bio fortified wheat varieties were 82.51% if we take both the states together. The state-wise data revealed that in Haryana, the adoption of these varieties was 83.20% whereas in Punjab it was 81.80%. This clearly indicated the preparedness of farmers as well as extension machinery against climate change. It was further observed that majority (54.20%) of farmers *i.e.* 48.99% in Punjab and 59.41% in Haryana adopted resource conservation technologies for sowing of wheat, which is one of the climate change mitigations strategies, to avoid negative impact on wheat crop.

4OP-2

Discovering Novel Genomic Regions Associated with Grain and Nutritional Quality Traits in an Ancient Indian Landrace *Triticum Sphaerococcum* Through ML-GWAS

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Exploring the utilization of Indian Dwarf Wheat (*Triticum sphaerococcum*) in breeding programs among freely threshing hexaploid species holds promise. This study aimed to characterize 116 Indian dwarf wheat accessions for grain and nutritional quality traits and identify quantitative trait nucleotides (QTNs) by phenotyping them across three distinct production conditions—timely sowing, restricted irrigation, and late sowing—over two consecutive years (2021-22 and 2022-23). *T. sphaerococcum* have 8.6 % higher Fe content and 48.8 % more Zn content than bread wheat. They also have more protein, wet and dry gluten content than bread wheat varieties. ML-GWAS analysis revealed 96 significant QTNs in timely sown (TS) conditions, 109 in restricted irrigation (RI) conditions, and 117 in late sown (LS) conditions for six key grain quality parameters (Grain hardness index, Gluten index, Wet gluten, Dry gluten, GPro, GFe, and GZn). Among the total QTNs identified, 74 were deemed reliable as they were consistent across at least two models. Additionally, three QTNs for Grain Hardness Index and one QTN for GZn were consistently observed across all three conditions. The gene annotation analysis for the highly reliable QTNs revealed putative candidate genes such as Flavanone 3-dioxygenase 3 and Superoxide dismutase for GZn, Peroxidase 52, U-box domain-containing protein 73, and Probable LL-diaminopimelate aminotransferase for GFe. Additionally, Ethylene receptor 2 was associated with DG, which has been reported to be upregulated in weak-gluten and downregulated in strong-gluten wheat. These findings suggest potential targets for further investigation and utilization in bread wheat breeding programs, facilitated by marker assistance.

4OP-3

A Multifaceted Analysis: Unveiling the Complexities of Wheat Genotype, Fortification, And Processing on Iron and Zinc Bioavailability in Whole Wheat Flour and Chapati

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This study investigated the impact of wheat cultivar selection and fortification with NaFeEDTA and ascorbic acid (AA) on Fe and Zn bioavailability in whole wheat flour (WWF) and chapatti. Nineteen hexaploid wheat cultivars were evaluated for their intrinsic Fe and Zn content (total content, solubility, and bioaccessibility). Significant variations ($p<0.05$) were observed among cultivars, with Fe content ranging from 34.8 mg.kg^{-1} to 41.8 mg.kg^{-1} and Zn content varying from 34.5 mg.kg^{-1} to 43.8 mg.kg^{-1} in WWF. Fortification with NaFeEDTA (T3) significantly ($p<0.05$) increased total Fe content in WWF by 85.0% (from 38.1 mg.kg-1 to 70.7 mg.kg-1), solubility by 51.2% and bioaccessibility by 165.5% compared to the control. AA fortification (T3) also increased Fe solubility by 98.7% and bioaccessibility by 130.6%, but to a lesser extent than NaFeEDTA. Interestingly, cultivar-specific responses were observed to both fortification strategies. When translating these findings to chapati, both NaFeEDTA and AA fortification (T3) improved Fe and Zn bioaccessibility compared to unfortified chapati. However, cooking resulted in substantial reductions ($p<0.05$) in Fe (39.5%) and Zn (23.9%) content. This emphasizes potential challenges in retaining micronutrients during food processing. Furthermore, the impact of fortification varied across wheat cultivars, with certain cultivars exhibiting superior performance in enhancing micronutrient bioavailability. Correlation analysis revealed complex interactions between Fe and Zn bioavailability parameters, highlighting the importance of judicious fortification strategies. Overall, this study highlights the effectiveness of NaFeEDTA and AA fortification in enhancing Fe and Zn bioaccessibility in WWF and chapatti.

4OP-4

Effective Use of Social Media Platforms for Digital Extension to Ensure the Sustainable Wheat Production

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An agricultural extension service provides technical aid to farmers on relevant agricultural issues and augments the supply with the essential inputs, services and support to increase their agricultural production. The new ideas and techniques developed by the agricultural scientific research organizations are dispersed among the farmers by the agricultural extension activities. There are over two lakhs extension workers in India in the agriculture, livelihood and the allied sectors. The shows and discussions *on* Radio and Television have played an important role in agricultural extension and in getting farmers in touch with key services. Moreover, the benefits of informative videos also to be useful in extension services for agricultural research and development stakeholders. Recently the initiative of digital green in the country have trained the youth of rural background to produce videos by farmers, of farmers, and for farmers to exchange most relevant agricultural practices to boost farm productivity and improve nutrition of human beings. Besides that there are many examples of the use of mobile phones in agriculture, the e-agriculture platform constantly cover these examples. Mobile phones either use voice, text or photos within the farmer and subject matter specialist interaction. The good number of Kisan Call Centres has been established at many locations across the country covering all states and UTs where the farmers can call on a toll-free number (1800-180-1551) and get information regarding their area of interest in agriculture. The aspect of timely and relevant information, especially with the role of Information Communication and Technology to connect farmers with the information has received much attention in the last decade. The social media platforms (Facebook, X, YouTube, WhatsApp, Instagram etc.) would be very effective and economically viable option in addition to the frontline demonstrations to host a digital curated information in multi-formats and multi-lingual contents to update the extension workers access to the curated content on the agriculture and rural livelihood missions through the online materials to pass on further to the farmers on the time.

4OP-5

Celiac Antigenicity Analysis of Indian Aestivum and Durum Wheat Varieties

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Wheat, the second most consumed staple food after rice, has evolved as primary staple commodity to ensure food security for millions across the globe due to its praiseworthy nutritional composition. Worldwide, wheat processing has proved to be a profitable venture in the form of bread, biscuit, pasta, porridge and flour. The presence of gluten extends wheat dough with remarkable viscoelastic properties, but due to the presence of gliadin as gluten component, wheat has been linked to celiac disease in genetically susceptible individuals. In this study, we analyzed Indian wheat varieties (8 each of aestivum and durum) to measure gliadin content and assess their antigenicity with a celiac disease-specific monoclonal antibody. The results demonstrated significant variation in gliadin content (4.33 to 7.33 g/100 g whole wheat flour), with the lowest in PDW 233 and highest in HD 3171 varieties. The correlation between gliadin *vs.* celiac antigenicity was found to be 0.598 (r= 0.77) for aestivum while no correlation in durum varieties. An overall positive correlation ($r^2 = 0.713$; r value = 0.84) was observed between antigenic gliadin to gliadin content across all the tested varieties, highlighting the role of gliadin in celiac disease progression.

4OP-6

Evaluation of Genetic Diversity of Hexaploid Wheat Cultivars for Total and Soluble Pentosan Content across Diverse Growing Conditions

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Pentosan is a non-starch polysaccharide, composed mainly of pentose sugars (arabinose and xylose), present mainly in the outer layer of the grains of wheat, rye, barley, etc. The major polysaccharide pentoses are, xylose, arabinose, small amounts of galactose, mannose, glucose and the like thereof. In wheat the total pentosan content is around 8-9 % while the soluble pentosans are generally around 1%. Due to high viscosity, oxidation and, gelation property pentosan proved to be useful as a thickener, laxative and, emulsifier in food industry. Pentosans are used in the baking industry to increase water holding capacity of the flour in effect slowing down the rate of time it takes the bread to go stale. Pentosans as soluble DFs have several health benefits such as lowering of blood cholesterol, improving gut health, reduction of blood sugar, prevention and control of cancer, improve immunity etc. In this study, we have determined the total and soluble pentosan content in wheat flour by the Orcinol-HCl colorimetric method.

In this study we have quantified total and soluble pentosan content in 17 different popular wheat varieties grown at different locations across two zones viz. NWPZ and CZ. The total and soluble pentosan in whole wheat flour was found in the range of 4-12 and 0.5-1.2 g/100g, respectively. Consistent variation was observed in the pentosan content for the same variety grown at different locations. It can be inferred that the pentosan content is affected by the growing location and environment of wheat crop.

4OP-7

Enhancing Wheat Grain Quality Through Application of Liquid Bioformulation Comprising *Pseudomonas Fluorescens* on the Wheat Grains Infected by Spot Blotch

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A field experiment was conducted at the Main Agricultural Research Station, Dharwad during *Rabi* season 2019-20 to assess the impact of liquid formulations of *Pseudomonas fluorescens* on the quality parameters of wheat infected by Spot blotch. The findings suggested that among the different formulations examined, seed treatment with a canola oil-based formulation at a rate of 10 ml/kg followed by the spray of same formulation at 0.5 per cent concentration recorded maximum Grain Protein Content (GPC) (11.44 %), Wet Gluten Content (WGC) (33.16 %) and Gluten Index (GI) (92.64 %) followed by seed treatment with soybean oil-based formulation at a rate of 10ml/kg and subsequent spray of soybean oil-based formulation at 0.5 per cent concentration which displayed GPC (10.95 %), WGC (31.78 %) and GI (89.86 %). However, regarding GPC, no significant variation was observed between all the treatments containing *Pseudomonas fluorescens* formulations. Conclusively, the application of liquid formulations led to a significant increase in grain quality in contrast to untreated plants. Thus, this study provides a significant information regarding the effectiveness of liquid bioformulations, filling a gap in the literature where numerous studies have explored the efficacy of various fungicide treatments on wheat quality, yet limited information exists regarding bioagents and their formulations. Moreover, these bioformulations serve as eco-friendly alternatives to chemical fungicides in managing spot blotch disease and positively affecting the quality attributes of wheat grains. Thereby, emphasizing their potential to improve the overall quality of wheat.

4OP-8

Functional, Nutritional and Textural Attributes of Pearl Millet *(Pennisetum glaucum)* Flakes

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There is an increased demand for nutritive and convenient foods of millets among the consumers these days due to increased awareness and admiration. India is largest producer of pearl millet in the world with 6.93 million ha area, average production of 8.61 million tones and productivity of 1243 kg/ha. Millets possess various functional and health benefits for processing into Ready-to-cook (RTC) foods to meet the consumption needs of modern consumers. The process for production of pearl millet flakes was standardized using different pre-treatments for softening the grain and partial gelatinization of starch followed by flattening in the developed roller flaking machine and effect of processing treatments on proximate composition, functional parameters, textural characteristics and polyphenolic contents. Roller flaking machine was used to prepare pearl millet flakes which consisted of feeding hopper, feeding agitator, set of two horizontal rollers, outlet tray, transmission assembly and prime-mover. Rollers were made of hard chrome steel (140mm Ø and 320mm length). Motor of 1.0 hp (0.746kW) with 1425 rpm was used, assembly was getting drive through V-pulley set in two stages to reduce roller rotation up to 100 rpm. The performance of flaking machine was evaluated with the variable clearance ranged between 0.1 to 0.5 mm between flaking rolls. As roller clearance increased from 0.1 to 0.5 mm, the length and width of flakes decrease from 5.2 to 3.09 mm and 4.44 to 2.76 mm respectively, whereas the thickness of flakes increased from 0.50 to 1.50mm. The bulk density of flakes was proportional with clearance ranged between 349.5– 590.7 kg/m^3 at the mean moisture content of 8.11±0.07 per cent. Based on the above finding, the rest of experiment on flaking was conducted at a roller clearance of 0.2 mm. Soaking (20 min) with steaming (15 min) treatment produced flakes with least bulk density 355 kg/m^3. Variations in physical, functional, textural and nutrient composition were observed using different pretreatments. Water absorption index of the flakes ranged from 2.20-4.10. The fat absorption capacity decreased with increase in the bulk density. Emulsion activity and emulsion stability of flakes improved significantly after steaming as pre-treatment. The ash and protein content ranged between 0.1-0.5g and 9.41- 12.89 g, respectively. Pressure cooking method resulted in the highest loss of total polyphenolic content.

Poster

4PP-1

Effect of Nutrient Enrichment through Zinc and Iron on Growth, Yield Attributing Characters and Yield of Wheat (*Triticum Aestivum*)

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The experiment entitled "Effect of nitrogen fertilizer and Ferti-fortification through zinc and iron on growth and yield attributing characters of wheat (*Triticum aestivum*)" at the Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, (U.P.) during *rabi* season of 2021-22 and 2022-23. The experiment comprises of twelve treatments *viz.* Control, No nitrogen + Soil zinc, No nitrogen + foliar iron (0.5%), No nitrogen + foliar zinc (0.5 %), No nitrogen + soil zinc + foliar zinc (0.5%), Recommended nitrogen, Recommended nitrogen + soil zinc, Recommended nitrogen + foliar zinc (0.5%), Recommended nitrogen +foliar iron (0.5%), Recommended nitrogen +foliar iron (1.0%), Recommended nitrogen + soil zinc + foliar iron (0.5%) and Recommended nitrogen + foliar zinc (0.5%) + foliar iron (0.5%) were tested in randomized block design with three replications. The result of the experiment revealed that the maximum plant height (98.10 cm & 96.81 cm), number of tillers (321.96 m^{-2} & 319.83 m^{-2}), dry matter accumulation (1255.85 g m^{-2} & 1234.05 g m^{-2}), effective tillers (311.14 m^{-2} & 304.04 m^{-2}), spike length (12.53 cm & 12.26 cm), grains spike^{-1}(45.68 & 45.06) and test weight (43.89 g & 43.26 g) was recorded with recommended nitrogen + foliar zinc (0.5%) + foliar iron (0.5 %) treatments during 2021-22 and 2022-23, respectively.

4PP-2

Genetic Improvement of Grain Texture and Agro-Morphological Trait Performance in Wheat through Gamma Ray-based Induced Mutagenesis

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Ensuring grain quality of cereals is crucial for maintaining food safety and global nutritional standards. Wheat being a self-pollinated crop suffers from adequate variability, whereas mutation breeding is a well-known technique to create variation and improve one or few traits without compromising the agronomic base of well-adapted varieties. Hence, a multi-year study was conducted to induce and isolate mutants for grain texture with superior agro-morphological performance from an elite soft textured wheat variety HPW 89. Based on LD_{50} dose, 9000 seeds were irradiated with three doses of 250 Gy, 300 Gy and 350 Gy of gamma rays. During M_1 generation, high frequency of biological damage and mortality for doses beyond 300 Gy was observed. Among 2219 M_1 plants evaluated in M_2 generation, 1862 progenies having higher trait performance were advanced to M_3 generation. A total of 293 screened mutants evaluated in M_4 generation showed that 287 mutants (GH 8.79 to 50.06) had higher grain hardness and 5 mutants (4.91 to 7.38) had lower grain hardness than HPW 89 (7.39). In M_5 generation, these 108 medium-hard mutants were assessed at genetic level using allele specific markers and variations in either *pina* and *pinb* or both genes suggested that genetic variation occurred at loci coding puroindolines. Also, simultaneous analysis of grain hardness trait with better agro-morphological and quality traits resulted in development of eleven elite mutants. These mutants are being evaluated in multi-location trials along with zonal/national checks and can serve as important genetic resource for developing texture-based bread wheat varieties.

4PP-3

Blending Millets-legumes with Whole Wheat Flour for Enhancing Nutritive Value of Biscuits

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Whole-wheat products have clear nutritional advantages over refined flour products. Its consumption is inversely associated with the risk of chronic diseases like obesity, type-2 diabetes, cardiovascular diseases, and cancer. However, manufacturing whole wheat products presents unique challenges. Accordingly, a study was carried out to find out the quality of biscuits prepared from whole wheat flour alone or in combination with chickpea, pearl millet, finger millet, and barley flour (0-100%). Whole wheat biscuits were prepared following the AACC 10-52 protocol. Further, a comparison was also made between the biscuit-making potential of whole wheat flour from var. DBW 187 and 296, as determined by the spread ratio. The spread ratio for biscuits obtained from DBW 187 and DBW 296, was found to be 4.66 and 6.45. The addition of chickpea flour at a 10% level, increased the spread ratio to both varieties, while further addition of chickpea flour (20-30%) decreased the spread ratio. The spread ratio for finger millet, pear millet, and barley incorporated biscuits ranged from 4.83-4.93, 4.73-5.33, 4.49-4.64, and 6.55-7.16, 6.43-6.79, 6.68-7.74, for DBW 187 and DBW 296, respectively. The spread ratio for biscuits prepared from 100% chickpea, finger millet, pearl millet, and barley flour were 4.94, 5.61, 5.80, and 4.85, respectively. The information could be utilized for manufacturing biscuits from whole wheat flour alone or blended flour by utilizing chickpea, finger millet, pearl millet, or barley flour for enhanced health benefits.

4PP-4

Golden Grains: Elevating Health and Nutrition through Wheat Biofortification

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The global population has surged to 8 billion, yet access to nutritious food remains unequal. Reports indicate that approximately 2.5 billion adults grapple with overweight issues, with 890 million classified as obese, while 390 million suffer from undernourishment. These challenges, compounded by the ongoing COVID-19 crisis, have exacerbated hidden hunger, stemming from insufficient intake of vital micronutrients such as iron, zinc, selenium, and provitamin A. Wheat, a staple providing about one-fifth of the world's energy and protein needs, also contributes to 30% of global iron and zinc intake, despite substantial nutrient loss during milling. Addressing this concern, biofortified wheat emerges as a promising avenue for delivering essential micronutrients like iron and zinc to consumers. Notably, the impact of biofortification is more pronounced in Asia and Africa, regions struggling with widespread micronutrient deficiencies and hidden hunger. In India, genetic biofortification shows greater promise compared to agronomic approaches, with its impact on wheat micronutrient concentration being threefold higher. Recognized as an economically and environmentally sustainable strategy, genetic biofortification holds considerable potential in combating malnutrition on a global scale.

4PP-5

Analysis of Water-soluble Carbohydrates in the Stem of Wheat Under Different Water Regimes

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Wheat (*Triticum aestivum L.),* a staple cereal crop with global cultivation, is highly susceptible to water scarcity during critical growth stages, leading to substantial yield losses. The efficacy of grain production in wheat during drought depends on the stored assimilates from reserve pools, reallocated before or during anthesis. Such stored assimilates, known as water-soluble carbohydrates (WSCs), accumulate mainly in stem and leaf sheath from stem elongation to the early grain-filling phase and remobilize to grains in the later grain-filling stage, which further depends on the genotypic potential and environmental factors. To elucidate the biochemical intricacies of WSC dynamics, an analysis was conducted in stem samples of 220 F_{10} recombinant inbreds lines (RILs) of a mapping population for two consecutive *Rabi* seasons sown under irrigated and rainfed conditions at ICAR-IIWBR, Karnal. The mapping population was meticulously phenotyped for accumulation of stem WSCs and their constituents, such as glucose, fructose, sucrose and fructans, 15 days after anthesis. Significant differences were observed between the parental lines (Dharwad dry and DPW621-50) in terms of WSCs and the component traits recorded. Dharwad dry exhibited a higher accumulation of WSC component traits as compared to DPW 621-50 under rainfed conditions. In contrast, under optimum conditions, DPW 621-50 showed higher accumulation as compared to Dharwad Dry. Similarly, the average WSC content observed across inbred lines revealed higher accumulation under rainfed conditions, with WSC ranging between 185.54-391.87 mg/g and its components, fructan (68.85-75.21 mg/g), sucrose (29.59-47.48 mg/g), glucose (17.86-38.46 mg/g) and fructose (14.23-49.73 mg/g) as compared under irrigated conditions where WSC ranged between 164.07-356.30 mg/g, fructan 64.94 (72.66 mg/g), sucrose (27.5-46.9 mg/g), glucose (13.80-34.24 mg/g) and fructose (10.38-46.73 mg/g). Among these sugars, fructans were predominating non-structural sugar, contributing about 70 to 75 percent to total WSCs. In contrast, sucrose, glucose, and fructose contributed nearly 19-21, 7-8, and 6-7%, respectively. QTL mapping is being carried out at ICAR-IIWBR, Karnal, using phenotypic and genotypic data to identify significant SNP markers (genomic regions) associated with carbohydrate accumulation, which could be used for marker-assisted selection of drought tolerance in wheat.

4PP-6

Inter-institutional Collaboration for Quality Seed Production of PB-1847 and PB-1692 at ICAR-IIWBR, Karnal

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During, *kharif* season 2023, under institutional collaboration programme of seed production of Basmati rice varieties *viz*., PB-1847 and PB-1692 was carried out at ICAR-IIWBR, Karnal. The breeder seed of PB1847 and PB-1692 was obtained through RS-IARI, Karnal as a source and nursery was raised on approx. 2000 square meter area separately at main and new farm, Karnal on 25th and 28th May, 2023 respectively. Seed treatment of rice seeds was done with carbendazim50 % WP @ 20 gram + streptocycline@ 1 gram per 10 litres of water and 8 kg seeds was soaked for 12 hours before sowing of nursery. *Trichoderma viride* @ 1 kg per acre was applied to control soil borne fungal disease. 10 kg of sand was mixed with 1 kg of *Trichoderma viride* and mixed in shade for effective control. Seed treatments were effective in controlling several seed borne and soil borne disease during early growth period. Transplanting of seedling was carried @ 25 days old seedlings which resulted in appropriate plant stand in the field. During the seed production programme, advanced technologies were deployed *viz*., drone-based insecticides application was done to control of rice leaf folder and stem borer. Genetic purity of seed plots was ensured by the rouging operation carried out under the guidance of rice breeders from RS-IARI, Karnal. In order to avoid breakage and seed germination losses, manual harvesting and threshing was carried out at 13.6 % moisture level. This ensured highest quality seeds with maximum germination potential. Overall, 20 quintal per acre of quality seed was harvested and total 820 quintals of quality seed of both the varieties were supplied to the RS-IARI, Karnal.

4PP-7

Development of Micronutrients Rich Lines through Pre-breeding in Wheat (*Triticum aestivum* L.)

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Malnutrition caused due to undernourishment has led to the important global health issue, affecting both physical and mental development, vulnerability to diseases, mental retardation, blindness, reduced cognitive ability, and general losses in productivity. Several health organizations have shown concern on this issue at global level despite the fact it is also covered under sustainable Developmental Goals (SDGs). Currently, more than 2 billion people are suffering from micronutrient deficiency across the globe. Particularly, three micronutrients, Iron, Zinc, and Vitamin A are recognized as the most limiting factors in assimilation of other nutrients and therefore responsible for malnutrition. Keeping in view, the wheat as a staple food in vegetarian diet, a breeding program is being carried at ICAR-IIWBR, wherein Synthetic wheats and other wild relatives have been used to tap the genetic diversity and enriching the segregants for important micro-nutrients. The promising accessions screened during previous years were used in hybridization programme and as per requirements back crosses were also attempted. A total of 36 promising advance lines involving wild accessions of wheat along with four check varieties were evaluated in two environments for two years. The experimentation was conducted at Karnal and Hisar locations. The range of Grain Iron Content (GFeC) was found 41.5 to 53.8 mg/kg while Grain Zinc Content (GZnC) ranged from 43.4 to 54.3 mg/kg in the advance lines. Similarly Grain Protein Content (GPC) ranged from 15.2 to 18.9% in the advance lines. The genotypes BFKW 10 showed highest GFeC (53.80); BFKW 3 showed highest GZnC (54.3). Two genotypes BFKW 7 and BFKW 3 were found stable for all the three studied traits while BFKW 4 was found to be stable for GFeC and GPC; BFKW11 was stable for GFeC and GZnC; BFKW-10 for GZnC and GPC. Therefore, these stable and high trait vale genotypes would be a potential source as high grain protein, iron, and zinc donor parents. This valuable germplasm may be utilized in breeding programs to develop bread wheat varieties with high protein and micronutrient content.

4PP-8

Halopriming for Improving Seed Quality Attributes and Biochemical Parameters in Wheat Cultivars

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Wheat (*Triticum aestivum* L.) is a crop of global significance not only because it is usually accorded a premier place among cereals, but also due to its high nutritive value and huge acreage devoted to its cultivation. Improving field establishment during early growth stages is critical aspect of successful crop production. Seed priming is a common agronomic technique shown to cause an increase seed vigour as well as synchronize and accelerate germination, improve stress resistance and enhances productivity. Keeping this in a view, four chemicals *viz*., GA_3, $CaCl_2$, Nano Chitosan and Ascorbic Acid were used as halopriming agents for improving seed quality parameters and biochemical parameters in DBW87, DBW303, DBW327 and DBW 332.

Among the four priming treatments, $GA_3$was found to be most effective in improving seed quality parameters in DBW332, DBW327, DBW 187 and DBW303. This might be due to priming increases reserve mobilization of food material, repair and re-synthesis of various enzymes and rapid growth of embryo results in enhanced germination.GA_3 occupies a prominent position in mediating a variety of plant physiological processes including seed germination, leaf expansion, flower set, dry matter production, photosynthesis, translocation of food material and synthesis of mRNA coding for hydrolytic enzymes.

Among the four varieties, variety DBW 303 had significantly higher germination percentage under control as (80.00 %) followed by DBW 332 as a 76.67 (%), DBW 327 as 75.00 (%) whereas the germination percentage was observed in variety DBW 187 as a 72.00 (%). Among the different seed treatments, $GA_3$was found most effective in increasing number of normal seedlings and reducing the abnormal seedlings percentage over the non-treated seeds in the all four varieties. Seed treated with GA_3recorded significantly higher germination percentage, seedling length, seedling dry weight, vigour index-I and vigour index-II followed by Ascorbic Acid and Nano chitosan. Seed treated with Nano chitosan was found most effective in increasing the SOD over the non-treated seeds in the all four varieties.

4PP-9

Biotechnological Tools for Improve Productivity and Quality of Cereal Crops

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The increase in food demand due to increasing population along with decline in the availability of arable land exerted a pressure on farmers to produce more with fewer resources. Biotechnological tools as a viable solution have the potential to release this pressure with improved and sustainable agricultural productivity which enhances the food security. Biotechnology refers to any technological application makes or modifies products or processes for specific usage using biological systems. Plant tissue culture, transgenic approaches, and molecular breeding methods are key areas of biotechnology in cereal crops breeding. Most popular and used method is the molecular breeding method, in which DNA markers utilized to improve variety through marker-assisted selection. The targeted introduction of desired genes into the crop could speed up breeding. Main goal of transgenic breeding is to improve agronomic and qualitative features of cereal crops. Herbicide resistant, salinity-tolerant, drought-tolerant crops and golden rice are examples of biotechnology's crop achievements. This genetically modified rice has a higher content of beta-carotene. These are the useful techniques for the selection of new desired characteristics for the nutritional improvement and stress. DNA markers complement conventional methods of breeding for developing novel cultivars with desirable attributes in less time.

4PP-10

Indian Traditional Rice Landraces (*Oryza Sativa L.*): Essential Medicinal Values for Global Nutrition and Food Security

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Rice (*Oryza sativa* L.) serves as a staple food source for a substantial portion of the global population. It constitutes a unique collection of traditional rice strains for their unique grain characteristics encompassing texture, aroma, taste, and nutritional value. These rice varieties hold significant economic and cultural value, particularly for regional and indigenous smallholder rice farmers. Through generations, farmers have dedicatedly cultivated landraces within their specific agro-climatic conditions, leveraging ancestral knowledge passed down from generations. These heirloom varieties not only enrich agricultural heritage but also stand as a testament to sustainable farming practices and resilience. The demand for rice that is high in nutrients has grown over the past ten years. The symbiotic relationship between landraces and smallholder farmers reflects a harmonious blend of tradition, sustainability, and the cultivation of crops that embody both historical and agricultural significance. This study aims at documenting the functional values of selected landraces, shedding light on their potential role in global nutrition and food security. Understanding the nutritional significance of these landraces is crucial for promoting their cultivation, consumption, and integration into mainstream diets, ultimately contributing to enhanced well-being on a global scale. This study was carried out with various rice landraces like Vishnubhog, Trombay Chhattisgarh Dubraj Mutant-1 (TCDM-1), CG Zinc Rice, CG Madhuraj, Mappillai Samba and Karupkauni. Five landraces viz Sathi, Albela, Sengar, Bhadai and barabanki were collected from Eastern Uttar Pradesh. Each landrace exhibits unique health benefits such as controlling high blood pressure, aiding heart health and diabetes management, combating malnutrition, increasing hemoglobin content, reducing asthma risk, detoxifying the liver, and preventing cancer. With a significant portion of the global population suffering from various forms of malnutrition, including undernutrition and deficiencies in essential micronutrients, the nutritional richness of these landraces could serve as a valuable resource in addressing this pressing public health issue.

4PP-11

Precision Breeding Techniques for Developing Low Gluten Biofortified Wheat Varieties

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Wheat (*Triticum aestivum*) is an important staple crop in India. Globally, India's share ~14% of production (2nd largest) but less than 1% of export. This is because of non-preference to high gluten content in Indian wheat varieties. In addition to this, nowadays there is rising concern among people regarding malnutrition and other health issues related with high gluten content grains like wheat. Thus, development of high yielding varieties with enriched micronutrient like Zinc and Iron and low gluten content is a noteworthy alternative to overcome the challenges of malnutrition and chronic coeliac diseases. However, development of such elite lines with a number of assembled genes or QTLs from various sources may take long spell of time *via* conventional breeding. Thus, for development of such improved cultivars at accelerated rate precision breeding technique *viz*. genome sequencing, gene editing, and marker assisted selection (MAS), etc. are more appealing and efficient both in time and resource utility. Newer innovations in genome sequencing offer novel insights in identifying diverse and new sources of variability. Similarly, the genome editing techniques (ZFNs, TALENs, and CRISPR/Cas9) can make targeted genetic changes to create novel variation at a much faster rate than the conventional breeding methods. MAS allow genetic evaluation of target trait independent of suitable environment for trait expression thus save time, money, labour and other resources. So, in a nutshell, it can be concluded that these advanced techniques can be utilised in identification and characterisation of genes for higher yield and micronutrient content but low gluten content in wheat and their subsequent transfer in target genotype or précised genetic modification of target genotype to increase its preference among the end users.

4PP-12

Assessment and Validation of QTLs Governing Iron and Zinc Accumulation in Hexaploid Wheat

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Quantitative Trait Loci (QTLs) linked to grain iron and zinc content in wheat have been extensively studied as they are crucial for improving the nutritional quality of wheat, particularly in regions where wheat is a staple food and iron and zinc deficiencies are prevalent. Two hundred sixteen wheat accessions were selected from 2300 germplasm lines based upon grain zinc and iron content and evaluated at five locations represented four different agro-climatic zones for various traits to identify superior and stable genotypes along with high grain nutrition value. These lines were grown in alpha-lattice design along with four high yielding commercial checks in three replicas during *Rabi*, 2022-23. Grain Zn and Fe content were determined using Non-destructive, Energy Dispersive X-Ray Fluorescence Spectrophotometer (ED-XRF). Phenotypic data was analysed using AMMI and GGE Biplot analysis. The wheat accessions PI-180974, VHC-6374, C-591, PI-176325 and LGM-238 performed well at all the locations in terms of high grain iron and zinc, grain yield, earliness and other agronomic traits. GGE biplot analysis revealed that genotype PI 126806, IC 78813, PI 180993, IC 60193-B, PI-166179, PI-163037, IC-78726, PI-176345, PI-322110-AL, LGM-115 and PI-183871 had high mean and stability across all studied environments for grain yield. The mean vs. stability biplot for grain zinc content showed the high mean and stabile genotypes, namely, IC-82402-A, LGM-238, IC 82432, NB 29-4-2-4, PI-180974, PI-176240-A, PI-164505, LGM-137, PI-182116 and PI-166192 across all studied environments. These lines were also subjected to molecular screening using SSR markers to validate the QTLs linked to grain iron and zinc concentration. Twenty eight out of forty-seven SSR primers were shown polymorphism (13 markers for zinc and 15 markers for iron) and used for marker trait association of grain iron and zinc concentration. Phenotypic data was subjected to BLUPs analysis before determination of marker-trait association. Five markers (Xbarc106, Xbarc184, Xgwm282, Xgwm537 and Xwmc617) identified in earlier studies showed significant association with grain zinc concentration pooled over locations. For grain iron content, a total five markers namely, Xbarc124, Xbarc186, Xbarc170, Xcfa2049 and Xwmc525 showed significant association with the character. These molecular markers can be used in future marker aided selection breeding program for grain iron and zinc content.

4PP-13

Recent Advances in Enhancing Cereal Nutrition through Agronomic Approaches

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Recent advancements in enhancing cereal nutrition through agronomic approaches have garnered significant attention in agricultural research. Agronomic practices play a pivotal role in optimizing nutrient availability, uptake, and utilization by cereal crops, thereby improving their nutritional content and overall yield. Crop rotation stands out as one of the most widely adopted agronomic strategies to enhance cereal nutrition. By alternating different crops in sequence, soil fertility can be improved, reducing nutrient depletion and enhancing the availability of essential nutrients for subsequent cereal crops. Intercropping, another key agronomic approach, involves growing two or more crops simultaneously in the same field. This practice not only diversifies crop production but also facilitates complementary nutrient uptake patterns among different crop species, resulting in improved overall nutrient utilization efficiency. Moreover, soil management practices such as conservation tillage, cover cropping, and organic amendments contribute to soil health and fertility, consequently enhancing the nutrient content of cereal crops. These practices help to maintain soil structure, minimize nutrient leaching, and promote beneficial microbial activity, all of which are crucial for sustaining long-term crop productivity and nutritional quality. Recent data and research findings have provided compelling evidence of the effectiveness of agronomic approaches in enhancing cereal nutrition. Studies have demonstrated increased nutrient concentrations in cereals grown under optimized agronomic management practices compared to conventional methods. Furthermore, agronomic interventions have been shown to positively influence crop resilience to environmental stressors, such as drought and nutrient deficiencies, further underscoring their importance in ensuring food security and nutrition. In conclusion, recent advancements in agronomic approaches offer promising avenues for enhancing cereal nutrition, thereby addressing key challenges in global food security and public health. By leveraging these innovative strategies and incorporating them into agricultural practices, we can work towards achieving sustainable cereal production systems that promote both agricultural productivity and human nutrition.

4PP-14

Unlocking Nutritional Potential of tetraploid wheats: Leveraging hybridization and Marker-Assisted Selection techniques

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The cultivation of wheat plays a crucial role in combating malnutrition in India. Three single crosses, namely DDK-1029 x GPM DIC 66, HW-1098 x GPM DIC 87, and NP-200 x GPM DIC 74, were created using the donor lines GPM DIC 66, GPM DIC 87, and GPM DIC 74, respectively, along with popularly cultivated varieties DDK-1029, HW-1098, and NP-200. Molecularly confirmed F1 progeny were self-pollinated to generate F2 populations. Additionally, two double-cross F1 hybrids, specifically (DDK-1029 x GPM DIC 66) x (HW-1098 x GPM DIC 87) and (DDK-1029 x GPM DIC 66) x (NP-200 x GPM DIC 74), were produced by crossing selected single crosses.The study assessed three F2 populations, two double-cross F1 hybrids, parental lines, and control varieties across various traits. Analysis of the results showed that the F2 populations displayed superior performance in yield characteristics compared to the parents, indicating promising trends. Traits such as plant height, tillers, spike characteristics, yield, and zinc content displayed high heritability and genetic advance across the F2 populations, indicating minimal environmental influence and effective selection. For the F2 population of the cross DDK-1029 x GPM DIC 66, targeted inter-mating is recommended to mitigate the negative correlation between grain nutrients and yield. Conversely, the NP-200 x GPM DIC 74 population demonstrated a favourable correlation, indicating its potential for simultaneous improvement in yield and micronutrient content. The F2 population of the cross NP-200 x GPM DIC 74 exhibited higher transgressive segregants for yield, while HW-1098 x GPM DIC 87 displayed higher grain nutrients. Notably, one of the double-cross F1 hybrids showed positive associations between iron, protein, and yield. In the F2 population of the cross HW-1098 x GPM DIC 87 cross, the validation of molecular markers revealed a strong association of Xbarc 67 with grain iron content and while gwm 271 with grain zinc content. These markers, reported for the first time in dicoccum wheat, indicate their potential for effective utilization in marker-assisted selection to develop micronutrient-rich dicoccum wheat varieties, as well as in durum and bread wheat after validation.

4PP-15

Barley: A Potential Cereal for Producing Healthy and Functional Foods

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Barley is the fourth largest cereal crop in the world. It is mainly used for feeding, beer production and food. Barley is receiving more attention from both agricultural and food scientists because of its special chemical composition and health benefits. In comparison with other cereal crops, including wheat, rice and maize, barley grains are rich in dietary fibre (such as β-glucan), which are beneficial to human health. It is well proved that diets rich in those chemicals can provide protection against hypertension, cardiovascular disease, and diabetes. Barley has been widely recognized to have great potential as a healthy or functional food. In this review, we present information about studies on the physical structure of the barley grain and the distribution of its main chemical components, nutrient and functional composition of barley grain and their health benefits, and the approaches of improving and utilizing the nutrient and functional chemicals in barley grain. With the development of processing technologies, functional components in barley grains, especially β-glucan, can be efficiently extracted and concentrated. Moreover, nutrient and functional components in barley grains can be efficiently improved by precise breeding and agronomic approaches. The review highlights the great potential of barley used as healthy and functional foods, and may be instructive for better utilization of barley in food processing.

4PP-16

An Examination of Wheat Grain Quality, Nutritional Characteristics, and Yield in Drought and Heat Stress Conditions Using Multiple Environments

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A set of 15 modern wheat cultivars was tested in nine environments including three different production conditions (normal, heat, and drought) during 2020-21. AMMI analysis of variance indicated significant differences among genotypes and environments, and the G × E interaction for all the traits under study except grain Fe content. The results of AMMI revealed that, of the total variance, a more significant portion was described by the environmental main effect for the traits, protein (51%), Moisture (80%), Zn (53%), and GY (81%) indicating that the environments were diverse and the influence of environment on these traits. At the same time, the G × E effect was more prominent for the traits Starch (51%), Wet gluten (49%), Fe (49%) and TGW (52%). Furthermore, it showed two PC with highly significant differences ($p < 0.001$) and accumulated first two PC (PC1 and PC2) interaction principal component of AMMI explaining >50% of the genotype-environment interaction for all the traits under study. Protein content decreased with increasing yield under both stresses. Under heat stress, grain iron decreases while zinc increases with yield. Conversely, under drought stress, grain zinc decreases with yield. Understanding these dynamics is crucial for enhancing crop resilience and nutritional value. Selecting zinc, starch, and kernel weight under stress can boost yield. Protein content and yield are inversely related, making it difficult for breeders to optimise both traits. G × E interactions and stability indices have found genotypes like G12 (MP 1358) and G5 (HI 1544) with high grain yield and iron content, making them crop improvement resources. G12 (MP 1358) has a high protein content (14.98 %). Also, notable zinc-rich are G11 (MACS 4058, 45.23 ppm) and G15 (WH 730, 42.44 ppm). Genotype G12 (MP 1358) has improved crop yield, nutritional quality, and stability, a "win-win" approach. Multi-trait stability index (MTSI) provided the desired selection differential (SD) for 8 out of 8 studied traits with a G10 (MACS 3949) and G7 (HI1636) were selected as the best high-value stable genotypes across the traits and environments. This study shows the complexity of nutrient metabolism under different stress conditions and suggests targeted breeding to improve wheat grain quality and micronutrient profiles without yield loss.

Theme 5

Climate change mitigation strategies, resource management, conservation agriculture, integrated farming for sustainable cereal production systems

Oral

5OP-1

Soil Color as a Tool for Solving Salt Related Problems of Rice-Wheat Growing Alluvial Soils

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Co-existence of salt affected soils and poor-quality groundwater for Irrigation affects rice-wheat production. Present study is investigating soil profiles (0-60 cm depth) located (30.11267N to 76.36173E) in Haryana state of India. The hypothesis of the research study is that the Acquired color origin in these profiles could reveal soil temperature and moisture regimes for the formation of salt. Soil auger and Munsell color chart were used to determine soil color for these soils of arid and semi-arid areas. Preliminary results show pH_s 8.5 to 9.3 and EC_e ranged from 0.36 to 1.60 dS m^{-1}. Significant changes in Chroma from 3 to 4 were observed at 50-60 cm depth while the Hue (5 YR) and Value (3) were found to be consistent throughout the profile. The research findings would help in solving the problems of salt affected areas for better rice-wheat production.

5OP-2

Impact of Rice Residue Management and Nitrogen Optimization on Wheat Productivity, Microbial Dynamics and Enzymatic Activities

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In response to the degraded soil health and lack of improvement in yield of rice–wheat cropping system in South Asia's Indo-Gangetic Plains, experiment was formulated in a split-plot design. It encompassed four rice residue management practices as the primary factor, alongside two nitrogen levels (150 and 180 kg/ha) and two nitrogen split levels (two and three splits) as sub-treatments. The findings revealed a notable enhancement in soil organic carbon (SOC), microbial count, and enzymatic activity in plots subjected to conservation tillage and residue treatment compared to those treated with partial residue (anchored stubbles) and conventional methods (residue incorporated with chopping). The collective analysis demonstrated a significant influence of rice residue management practices and nitrogen application levels on wheat yield attributes and productivity. Specifically, zero tillage with full residue (unchopped) in wheat exhibited a 5.23% increase in grain yield compared to conventional with full residue (chopped), concurrently boosting soil microbial count by 19.80-25%, diazotrophic count by 29.43-31.6%, and actinomycetes count by 20.15-32.99% over conventional. Moreover, applying nitrogen in three splits (at sowing, before 1st irrigation, and after 1st irrigation) led to a 6.25% rise in grain yield compared to two splits (at sowing and after 1st irrigation), significantly impacting wheat productivity in the soil. Furthermore, zero tillage-happy seeder with full residue, elevate dehydrogenase activity by 11.75% during study year, surpassing conventional plot. This enhancement in enzymatic activity was paralleled by a robust positive correlation between microbial population and enzymatic activity across various residue retention practices. In conclusion, the results underscored the efficacy of crop residue retention following conservation tillage, in tandem with nitrogen optimization and scheduling, in enhancing wheat yield within the rice–wheat cropping system.

5OP-3

The impact of Nano Urea on Nitrogen Economy in Fodder Oat (*Avena sativa* L.): A Comprehensive Study

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A field trial was conducted at the Research Farm of the Fodder Section, CSK HPKV, Palampur, during the Rabi season of 2022-23. The experiment involved eleven treatments, which included combinations of three nitrogen levels (100% recommended, 75% recommended, and 50% recommended dose of nitrogen), three doses of nano urea (2ml, 4ml, and 6ml/l of water) in conjunction with the recommended nitrogen dose (RDN) of 100kg/ha, RDN with water spray during nano urea application, and a control treatment with no nitrogen. The study followed a randomized block design with three replications, focusing on soils characterized by acidic pH, low available nitrogen, and medium levels of available phosphorus and potassium. The treatments, which included the RDN *i.e.,* 100kg/ha and 75% of the RDN + nano urea at 6ml/l of water, exhibited similar performance, leading to improved characteristics in yield attributes such as emergence count, shoot count, and leaf-stem ratio. Additionally, these treatments showed enhanced fodder yields (both green and dry), increased crude protein content and higher crude protein yield as compared to the control treatment.

Moreover, the application of 75% of the RDN + nano urea at 6ml/l of water resulted in an increase in the available NPK content in the soil beyond its initial values. Among the treatments, the application of the RDN *i.e.*, 100kg/ha proved to be the most economically advantageous, yielding the highest gross returns (₹ 88089/ha), net returns (₹ 51487/ha), and a benefit cost ratio of 1.41.

5OP-4

Protein hydrolysates: Transforming Waste into A Plant Biostimulant with Improved Rice Growth and Yield

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An investigation was conducted using protein hydrolysates obtained from enzymatic breakdown of animal and plant wastes, which contain substances that can help in controlling plant growth and increasing yield, in line with the circular economy concept. The research was carried out at the Agricultural research farm, Banaras Hindu University during the *kharif* season of 2021. The treatments consist of various doses of protein hydrolysates applied at specific timings during the crop growth stages, along with an untreated control. Throughout the study year, the growth parameters of rice, including plant height, number of tillers, and dry matter accumulation, remained consistent up to 30 DAT. Plant height, number of tillers per hill, total dry matter at 80 DAT, and harvest stage were significantly influenced by varying rates of protein hydrolysates application. The highest values were observed with protein hydrolysates at 1.5 L/ha, followed by 0.875 L/ha. The yield parameters including the number of panicles, panicle length and weight, number of filled grains per panicle, fertility percentage, grain, and straw yield were significantly influenced by various treatments. The highest values were observed with protein hydrolysates at 1.5 L/ha, followed by protein hydrolysates at 0.875 L/ha, compared to the untreated control. After analysing the results provided, it can be inferred that incorporating Protein hydrolysates (L) at a rate of 1.5 L/ha proved to be the most successful in enhancing rice growth and yield.

5OP-5

Agroforestry for Climate Change Mitigation and Adaptation in Cereal Based Agrosystems

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Climate change is expected to have an adverse effect on crop production across the globe. Agroforestry is widely recognized as an effective strategy for adapting to climate change conditions and is practiced extensively worldwide. Agroforestry systems involve the cultivation of different combinations of crops and trees in various spatial and temporal arrangements. Agroforestry has gained popularity among farmers due to its higher economic returns compared to traditional cropping systems. This has led to an expansion in agroforestry areas throughout the various countries. Farmers are also positive about adopting agro-forestry practices due to their better ecological and economic benefits. Research has shown that the majority of annual crops are vulnerable to climate change and that changes in air temperature at crucial developmental stages can lower agricultural grain yields. In particular, excessive summer heat can cause pollen sterility and lower seed yields. Trees work as buffers in agroforestry, which improves water use efficiency, ameliorate microclimate, and protect crops from heat stress, resulting in increased crop yield. In general, a great number of studies have revealed that agroforestry has enormous potential to increase agricultural productivity, improve farm income, enhance soil qualities, and store atmospheric carbon. Moreover, the introduction of tree plantations in agricultural landscapes through agroforestry may enhance crop resilience in the face of changing climatic conditions. Overall, it has reported that designing and practicing agroforestry systems enhances the resilience of crops against changing climatic conditions.

5OP-6

Management of Herbicide Resistant Weeds for Sustainability of Rice-Wheat System

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Rice-wheat cropping system is one of the major cropping systems and occupies about 13.5 mha area in south Asia. This cropping system is of significance importance in providing food and nutritional security in India. However, there are various constraints limiting production and productivity of this system and one of the major constraints is infestation of weeds. This problem has been further aggravated due to evolution of herbicide resistance in weeds. In wheat, five weeds (*Phalaris minor*, *Avena ludoviciana*, *Polypogon monspeliensis*, *Chenopodium album* and *Rumex dentatus*) have evolved herbicide resistance. Among these, *P. minor* has evolved multiple herbicide resistance to three modes of action [Photosynthesis at photosystem II site A (isoproturon), acetyl-coA carboxylase (ACCase) (clodinafop and pinoxaden) and acetolactate synthase (ALS) (sulfosulfuron, pyroxsulam and mesosulfuron) inhibitor herbicides]. *A. ludoviciana* has evolved resistance against ACCase and ALS inhibitor herbicides. Whereas, three weeds namely *Polypogon monspeliensis*, *Chenopodium album* and *Rumex dentatus* have evolved resistance against ALS inhibitor herbicides. While in rice, two weeds species (*Cyperus difformis* and *Echinochloa crusgalli*) have evolved resistance to ALS inhibitor herbicides (Bispyribac- Na, penoxsulam, ethoxysulfuron, metsulfuron). The evolution of herbicide resistance in multiple weeds is causing significant yield losses and is a major threat to rice-wheat production in India. Management strategies must be developed to prevent selection and spread of herbicide resistant populations. The impact of herbicide resistant weeds on rice-wheat productivity and farmer's income can be minimized if a range of non-chemical weed management strategies are integrated with alternate herbicides.

5OP-7

Performance of Different Genotypes on Growth and Yield of Wheat (*Triticum aestivum* L.) Under Irrigated Condition

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A field experiment was conducted during 2019-20 in *rabi* season at the Wheat Research Unit Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra). The experimental plot's soil was clayey in texture and somewhat alkaline in reactivity, with a pH of 7.64. The organic carbon content (5.8 g ha^{-1}) and available nitrogen content (212.72 kg ha^{-1}) were moderate and low respectively. Available phosphorus (22.27 kg ha^{-1}) was low while the soil was fairly rich in available potassium (368.45kg ha-1). The experiment was laid out in a factorial randomized block design with three replications. The treatments consisted of 15 treatment combinations comprised of three irrigation levels i.e., two irrigations (CRI, Flowering), four irrigations (CRI, Tillering, Flowering and Milk stage), six irrigations (CRI, Tillering, Jointing, Flowering, Milk and Dough stage) and five wheat genotypes viz., AKAW-4627, AKAW-4832, WSM 109-4, PDKV SARDAR and PDKV WASHIM.

The growth parameters and yield attributes of the wheat crop were much enhanced when it was irrigated with six different types of irrigation (CRI, Tillering, Jointing, Flowering, Milk, and Dough stage) as opposed to four types (CRI, Tillering, Flowering, Milk stage, and two types, CRI, Flowering). The grain yield was increased in case of six irrigations (CRI, Tillering, Jointing, Flowering, Milk, and Dough stage), noticeably. The performance genotype AKAW-4627 better than other genotypes like: test weight (g), grain yield (kg ha^{-1}), straw yield (kg ha^{-1}), number of tillers plant^{-1}, dry matter accumulation plant^{-1} (g), weight of spike (g), number of spike plant^{-1}, number of spikelet spike^{-1}, number of grains spike^{-1}, weight of grains spike^{-1}(g), number of functional leaves plant^{-1}, leaf area plant^{-1}(dm^{2}) and number of tillers plant^{-1}.

5OP-8

Integrated Use of Nano-Nitrogen with Prilled Urea to Improve Use-Efficiency and Minimize Environmental N Losses in Rice-Wheat System

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Nitrogen (N) is the most frequently limiting plant nutrient for crop growth and yield. A field experiment was initiated in 2020 at ICAR-Central Soil Salinity Research Institute (CSSRI), Karnal, India to develop strategies for integrated use of Nano-N with prilled urea to improve use-efficiency and minimize environmental N losses in rice-wheat system under different combination with prilled urea and precision application techniques. The present experiment was carried out with eight treatments in total: four treatments with replacement of prilled urea by nano-N namely, 33% replacement (R33), 50% replacement (R50), 66% replacement (R66), 100% replacement (R100); two precision-scheduling treatments namely, application of nano-N based on leaf colour chart (LCC) values after basal dose of prilled urea (M-LCC), and application of nano-N based on GreenSeeker (GS) values after basal dose of prilled urea (M-GS) and two control treatments included '100% recommended N through prilled urea' (R0; no replacement), and 'no N fertilizer at all' (No-N) treatment to observe their impact on environmental loses, yield parameters, and use efficiency of N under rice-wheat system. The findings showed that the incremental replacement of prilled urea with nano-N resulted in decreased environmental losses of reactive N (N_2O and NO_3). No decrease in the available soil N pool was noticed upto 33% replacement (1 split dose replacement) of urea with Nano-N. The available N in the soil showed a noticeable decrease when nano-N replaced conventional urea by 50% or more. Therefore, only one split dose replacement of conventional urea with nano-N would avoid N mining over time, unless N addition from any other source is provided. The overall assessment suggests that at least one dose of conventional urea (1 out of 3 splits) may be replaced with nano-N without a reduction in yield yet significant gain in use efficiency in rice-wheat system.

5OP-9

Effect of Biostimulants on Yield and Yield Contributing Characters in Wheat

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Biostimulants are natural or synthetic substances that can be applied to seed, plant and soil. These substances cause changes in vital and structural processes in order to influence plant growth through tolerance to abiotic stresses and increase seed or grain quality and yield. A field experiment was conducted to evaluate Yield and Quality Parameters of Wheat Affected by Biostimulants. The present investigation was carried out during *Rabi* season at experimental field of Wheat Research Unit, Dr. PDKV, Akola. The experiment was laid out in Randomized Block Design with three replications involving Ten different biostimulants treatments at 30-35 DAS, 60-65 DAS. It was observed that the treatment T_{10} : Compost 2.5 t / ha + combination of (fulvic acid 10% + humic acid 20 % + sea weed extract 5 %) + spraying of compost extract 5 % at 30-35 DAS, 60-65 DAS recorded significant result for morph physiological characters like plant height, No. of effective tillers per meter, No. of grains per spike, 1000 grain weight, Grain yield per plot and seed quality parameters, followed by treatment T_9: Compost 2.5 t / ha + potassium humate 80% at sowing + spraying of compost extract 5% at 30-35 DAS, 60-65 DAS and treatment T_3: compost 2.5 t / ha + spraying of compost extract 5 % + cow urine 2% at 30-35 DAS, 60-65 DAS both the treatments are as par with the treatment T_2 i.e. 100 % RDF. It will be helpful to identify the effective bio stimulants for obtaining the higher grain yield and seed quality parameters of wheat.

Poster

5PP-1

Conservation Agriculture: Cultivating Sustainability for Future Generations

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Conservation agriculture is a sustainable farming approach that promotes the use of practices such as minimal soil disturbance, permanent soil cover, and diverse crop rotations to improve soil health, conserve water, enhance biodiversity, and build resilience to climate change. By reducing erosion, enhancing nutrient cycling, and promoting natural pest control, conservation agriculture offers numerous environmental benefits. Additionally, it can lead to increased yields, reduced input costs, and improved profitability for farmers in the long term. Embracing conservation agriculture can help address the challenges of modern agriculture while safeguarding natural resources and ensuring food security for future generations. By adopting conservation agriculture practices, farmers can mitigate the negative impacts of conventional farming methods on the environment while also improving their own livelihoods through increased yields and reduced input costs. Overall, conservation agriculture offers a promising pathway towards a more sustainable and resilient agricultural system. It also discusses the challenges and barriers to adopting conservation agriculture practices, such as initial costs, knowledge and skills required, and resistance to change. Furthermore, it highlights the potential of conservation agriculture to contribute to sustainable food production, climate change mitigation, and rural livelihood improvement.

Overall, conservation agriculture offers a promising solution to address the challenges of modern agriculture while promoting long-term sustainability and resilience in farming systems. Further research and extension efforts are needed to promote the widespread adoption of conservation agriculture practices and support farmers in transitioning to more sustainable and environmentally friendly farming methods.

5PP-2

Exploring Advancements and Challenges in Organic Farming

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In recent years, organic farming has drawn a lot of attention as an environmentally sustainable substitute for conventional agricultural methods. In recent year a lot of advancements in organic farming techniques have been observed which includes precision farming, agroecology, and the integration of digital technologies. These innovations contributed for improving productivity, reducing environmental impact, and enhancing resilience to climate change. Additionally, some emerging practices like agroforestry, cover cropping, and biological pest control plays a vital role in enhancing soil fertility, pest management, and ecosystem services. The advantages of organic farming for the environment are then covered, including improved soil health, biodiversity preservation, ecological balance and decreased chemical pollution. It also looks at the social dimensions of organic farming, including food sovereignty, consumer awareness, and community involvement. Organic farming possesses plenty of advantages, but it also has difficulties. Some of them include lower yields than conventional farming, limited access to resources, and the on-going need for innovation and research. Overall, Organic farming is a viable strategy for sustainable agriculture that has the ability to solve major social, economic, and environmental problems affecting the world food system in the face of global environmental challenges.

5PP-3

Dissemination of Information About Wheat and Barley Crops on Social Media Under The Aegis of Agricultural Knowledge Management Unit (AKMU)

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New digital technology has allowed the sharing of ideas and information, including text and visuals, through virtual networks and communities conveniently known as Social media. The interactive technologies on social media would be utilized for sharing the consolidated content, ideas etc virtually by prominent networks. The applications are online platforms that enable users to participate in social networking. The text posts or comments, digital photos or videos that are generated by the users as generated through all online interactions have become the lifeblood of social media. The largest social media platforms worldwide are Facebook, YouTube, WhatsApp, Instagram, and WeChat. The participation of people has exploded in the recent years with the entry of Facebook and Twitter (now X platform). Entertainers use social media to engage with fans, politicians with voters, charities with donors. Governments often turn to social media to convey vital information during emergencies. These were the most widely used social media providers as of January 2023, AS the recent reports of the Data Reportal the number of users is more than 2.96 on Facebook (billion users) followed by YouTube with (2.51 billion users). The institute has started the posting of institute activities, developments and achievements in the field of wheat research on Facebook and as well by Youtube channel. The progress has been observed over the two years as exponentially increase has been account. The field preparation, sowing of latest varieties for various agro climatic zone of the country with appropriate seed rates as well the optimum tile of planting had helped to harvest the record production of wheat crop in last two years. The planners and policy makers had recognised the importance of wheat crop in food security of the country and the information dissemination on social media would be very well appreciated.

5PP-4

Optimizing Wheat Yields in the North Western Plain Zone: A Case Study on Farmer's Fertilizer Practices for High Productivity

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In a study conducted in Karnal district of Haryana, 100 farmers were examined to assess soil conditions, fertilizer practices, and wheat yields. Soil analysis revealed a slightly alkaline and non-saline nature across all fields. Of the surveyed areas, 25 showed low organic carbon, 37 had medium levels, and 38 exhibited high organic carbon content. Available nitrogen levels were uniformly low (52.9-170.5 kg/ha), while phosphorus varied (4.0-35.1 kg/ha), with 79 fields categorized as low, 20 as medium, and 1 as high. Available potassium ranged from 87.4-558.9 kg/ha, with 19, 54, and 27 fields falling into low, medium, and high categories, respectively. Examining farmer practices, 27% applied low nitrogen, while 71% used higher amounts. Phosphorus (P_2O_5) and potassium (K_2O) application fell below recommended levels. The inclination toward higher nitrogen resulted in lodging, impacting yields and cultivation costs.

To address this, farmers can adopt early wheat sowing, along with the recommended fertilizer dose (150-60-40 kg NPK/ha) and optimal farmyard manure usage. Farmers in the Indo-Gangetic plains, including Haryana, Punjab, and Western UP, face lodging issues during grain filling/harvesting. To mitigate this, two sprays of chlormequat chloride (0.2%) + tebuconazole (0.1%) at the first node (45-50 DAS) and flag leaf stage (70-75 DAS) can be applied in high-yielding tall wheat varieties. Implementation of these practices not only meets future wheat demand but also enhances farmer profits.

5PP-5

Analyzing the Influence of Urea and Nano Urea Applications on wheat: Revealing Growth, Yield Characteristics, and Crop Output

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A field trial was conducted in the *Rabi* seasons of 2021-22 and 2022-23 at the ICAR-IIWBR Research Farm in Karnal, Haryana. The experiment was designed with four soil application treatments (control, 50% recommended dose of nitrogen, 75% recommended dose of nitrogen, and 100% recommended dose of nitrogen at 150 kg N/ha) allocated to the main plot, and five foliar sprays (control, nano urea spray @ 4% at 25-30 days after sowing, two nano urea sprays @ 4% at 25-30 DAS and 45-50 DAS, urea spray @ 6% at 25-30 DAS, and two urea sprays @ 6% at 25-30 DAS and 45-50 DAS) assigned to the sub-plot. The arrangement followed a split-plot design with three replications. Among soil applied nitrogen, significantly higher plant height (106 cm), no. of tillers/m^2(474), dry matter accumulation (1356 g/m^2), spike length (10.44 cm), number of grains per spike (37.88), grain yield (5446 kg/ha), straw yield (7127 kg/ha) and biological yield (12573 kg/ha) were recorded with 100% RDNat harvest stage on pooled basis over the control (no nitrogen), 50% RDN and 75% RDN. Application of 100% RDN increased grain yield by75.70 and 78.94% over control during 2021-22 and 2022-23, respectively. Among foliar sprays, two spray of urea @ 6% at 25-30 DAS and 45-50 DAS resulted in significantly higher plant height (103 cm), number of tillers/m^2(436), dry matter accumulation (1216 g/m^2), spike length (9.55 cm), number of grains per spike (33.89), grain yield (4633 kg/ha), straw yield (6374 kg/ha) and biological yield (11007 kg/ha) over control, nano urea one spray, nano urea two spray and urea one spray at harvest stage on pooled basis. Moreover, theurea spray @ 6% at 25-30 and 45-50 DAS increased the grain yield by 11 and 11.48% as compared to control (no spray) during 2021-22 and 2022-23, respectively.

5PP-6

Sustainable Integrated Farming for Climate-Resilient Cereal Production

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Climate change presents formidable challenges to cereal crop production, jeopardizing global food security. Integrated farming approaches to sustainably produce cereals amidst changing climatic conditions. We assess climate change impacts on cereals, such as temperature shifts and extreme weather, affecting yield stability and agricultural sustainability. Mitigation involves holistic strategies blending climate-smart practices, agroecology, and innovative technologies. Integrated farming systems, fostering biodiversity and soil health, bolster crop productivity and climate resilience. Tactics like agroforestry, cover cropping and diversification mitigate climate risks, enhancing cereal systems' adaptability. Precision agriculture tools optimize resources, counteract climate impacts, and boost farm efficiency. Sustainable soil management, including conservation tillage and carbon sequestration, mitigates emissions and bolsters soil health. Interdisciplinary collaboration and stakeholder engagement are vital for promoting climate-resilient cereal production. Integration of climate mitigation with sustainable practices fortifies cereal production's resilience, aligning with broader environmental and socioeconomic objectives.

5PP-7

Selection of Bread Wheat Genotypes under Variable Environmental Conditions Based on Stability Analysis

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Sixteen bread wheat genotypes were tested for yield stability under five different locations E_1: Agricultural Research Station; Niphad, E_2: Agriculture Research Station; Dhule, E_3: Agricultural Research Station; Saval Vihir, E_4: Agricultural Research Station; Kasabe Digraj and E_5: Post Graduate Institute Farm, MPKV Rahuri under timely-sown irrigated condition. The yield data was analyzed using Eberhart and Russell (1966). Genotype X Environment (G X E) interactions were found to be significant. Stability was measured based on regression (b_i) and stability parameter (S^2d_i). On the basis of environmental index, Agricultural Research Station, Niphad (E_1) found to be favorable for grain yield. The genotype NIAW 4447 found as the most stable genotype on the basis of stability parameters with best per se performance. NIAW 4302, NIAW 4451, Phule Samadhan and NIAW 4454 were also found stable for grain yield. Among above mentioned genotypes, the genotype NIAW 4447 is the only genotype with regression coefficient more than unity (b_i>1) indicating that it is suitable for favourable environmental conditions while others have regression coefficient less than unity (b_i<1), means they are suitable for unfavourable or adverse environmental conditions.

5PP-8

Strategies for Mitigating Climate Change and Promoting Agricultural Sustainability through Integrated Soil Fertility Management

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Agriculture is a major source of greenhouse gas emissions, including emissions from animal husbandry (enteric fermentation and manure management) and agricultural soils (i.e., excessive N fertiliser use and organic material decomposition). Combined application of farmyard manure and mineral fertilizer is very economical than sole NP application in maintaining sustainable agricultural productivity. The highest sustained crop production (2.88 t/ha) was achieved when 69 kg of NP fertilizer was combined with 10 t/ha farmyard manure. The combined application of tie ridge, farmyard manure, and NP fertiliser contributes to agricultural sustainability. Using integrated soil fertility increases total nitrogen and accessible phosphorus in the soil, promoting agricultural sustainability. The highest carbon (12 mg/kg) was sequestered when farmyard manure was applied with NP fertilizer on maize and wheat crop. Implementing integrated fertility management decreases N_2O emissions by improving nitrogen-use efficiency. The use of animal dung and NPK fertilizer reduces CH_4 emissions into the atmosphere, which contributes to climate change mitigation. Integrated soil fertility management increases soil fertility and contributes to agricultural sustainability. Thus, it may be concluded that crop yield was improved by application of integrated fertility management which sustains agriculture. Integrated soil fertility management was on option for climate change mitigation.

5PP-9

INM Practices as a Strategy for Mitigating Climate Change, Sustainable Crop Nutrient Management, and Resource Conservation

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Climate change poses significant challenges to agriculture, impacting food security, cereals yield and overall farm productivity. In recent times demands of cereals grains have been increasing due to rapid increase in the population but cereals production is declining due to poor management system and climate change is another major factor to declining productivity. The reason behind this problem is the continuous degradation of soil and the increasing greenhouse gases in the environment. The avoidance of indiscriminately use of chemical fertilizer in India, can be given through the consumption and production of fertilizers at world level. India, a populous agrarian country, is the world's third-largest producer and consumer of chemical fertilizers. In recent agriculture management practices farmers increase the use of chemical and synthetic fertilizers in the practice of nutrient management in the agriculture system which is not the only polluted the environment but create the nutrient imbalance under the soil and becomes a harmful factor in climate change. INM results in significant improvements in soil health and agricultural production while also lowering greenhouse gas emissions and other associated issues. The INM practice in the cropped fields showed a 1,355% reduction in methane over conventional nutrient management. Thus, it may be concluded that the INM is an important practice for supplying all essential nutrients in the right proportion at the right time. INM can be increases 1.3% to 66.5% of cereals yield over the conventional nutrient management system.

5PP-10

Regenerative Agriculture: A Strategy for Mitigating Climate Change in Cereal Production System

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Climate change poses a significant challenge in the present-day agricultural system, resulting in notable shifts in agricultural production and posing obstacles to achieving food security. Climate change decreases crop yields as well as the nutritional value of produce. Global warming, primarily propelled by greenhouse gases, notably CO_2, is a key behind climate change. The concentration of these gases continues to rise steadily over time. While agriculture is a source of climate change, it also acts as a sink for substantial amounts of carbon. Agriculture and other land-use changes collectively contribute approximately 23% of net anthropogenic global greenhouse gas (GHG) emissions from different sources. Among them, enteric fermentation, fertilizer application to agricultural soils, rice cultivation, manure management, and crop residue burning contributed 54.5, 19.1. 17.5, 6.7, and 2.2 % GHG emissions respectively. While the production of GHG cannot be entirely halted, it can be controlled, or capture atmospheric carbon through carbon sequestration in soil. Several methods have been devised to tackle this problem, with regenerative agriculture emerging as one of the latest approaches. Numerous sustainable practices can be employed to regenerate agricultural ecosystems, including agroforestry, minimum tillage, zero tillage, conservation agriculture, crop residue management, biochar application, crop diversification, cover cropping, green manuring, integrated nutrient management, precision agriculture, improved technology (SRI, DSR, FIRB), natural farming, mulching, and enhanced water management. This is not an overnight task but the involvement of various stakeholders such as farmers, policymakers, and governmental support can facilitate these approaches in achieving their objectives.

5PP-11

A Comparative Study on Applying Machine Learning Techniques for Seed Classification

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The precise evaluation of seed viability holds immense importance for various sectors such as agriculture, biodiversity conservation, and ecological research. Conventional methods for determining seed viability often involve destructive techniques, which are not only labor-intensive but also result in wastage, especially when dealing with limited or valuable seed resources. Recent advancements in Near-Infrared (NIR) spectroscopy coupled with Machine Learning (ML) have opened up new avenues for non-destructive seed viability assessment. This study leverages the combined power of NIR spectroscopy and cutting-edge ML algorithms like Decision Trees, Support Vector Machines and Logistic Regression to classify seeds accurately based on their viability. By utilizing a diverse NIR spectra dataset encompassing a range of seed species, the research applied various ML techniques to analyze and predict seed viability with exceptional precision. This study not only highlights the successful integration of NIR spectroscopy and ML but also delves into the evaluation metrics used to assess the model performance. Accuracy, precision, recall and F1 score are meticulously analyzed to measure the effectiveness of the classification models in predicting seed viability. By embracing this non-destructive approach, the research streamlines the seed viability assessment process and significantly reduces seed wastage. This advancement represents a substantial leap forward in agricultural practices and conservation efforts.

5PP-12

Wheat Yield and Economics as Influenced by *Phalaris minor* Infestation Under Different Tillage and Residue Management Practices

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The rice–wheat cropping system is the largest cereal-based agricultural production system, providing considerable significance to national food, nutrition, and livelihood security. In South Asia, this agricultural system contributes to over 30% of rice and 42% of wheat production, covering approximately 113.5 million hectares of cultivated land. However, intensive tillage practices have led to a progressive reduction in soil organic matter. This decline is attributed to the oxidation and burning of crop residues, resulting in environmental pollution and the loss of essential plant nutrients. Conservation agriculture (CA) practices are widely acknowledged as effective solutions to counter the challenges associated with land and environmental degradation. *Phalaris minor*, a major weed in this rice-wheat cropping system, significantly affects the yield of wheat crops. Therefore, the primary objective of this study is to determine *Phalaris minor* distribution among different treatments. The study was conducted at the ICAR-IIWBR research farm, comprising five tillage and residue management practices, namely Zero tillage, zero tillage + residue retention, zero tillage + residue burning, Conventional tillage + residue incorporation, and Conventional tillage + residue burning. The study revealed that Zero tillage + residue retention recorded the least *Phalaris minor* density and also exhibited the highest growth attributes and significantly higher grain yield in wheat crops. This treatment also yielded the highest net returns and benefit-cost ratio due to comparatively lower cultivation costs over other treatments. In contrast, conventional tillage + residue burning recorded the highest *Phalaris minor* density, resulting in minimal growth attributes and grain yield. In conclusion, the treatment of Zero tillage + residue retention was found to be the best among all tillage and residue management practices in terms of output and economics.

5PP-13

Net Zero Emission in Indian Agriculture Its Possibilities and Scope

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Agriculture is an important sector of the Indian economy. It contributes about 20% of national gross domestic product, and nearly two – third of Indian population is dependent on agriculture for their livelihoods. Agriculture is one of the Major contributors of Green - house gases and hence climate change also but at the same time it is the sector which gets most affected due to climate change. India, at the 26th session of the United Nations Framework Convention on Climate Change (COP 26) which was held at Paris in November 2021, announced its target to achieve net zero by 2070. In the Paris Agreement, India's long-term low-carbon development strategy, has been submitted to the United Nations Framework Convention on Climate Change, and it reaffirms the goal of reaching net-zero by 2070. According to FAO, in 2018, world total agriculture and related land use emissions reached 9.3 billion tonnes of carbon dioxide equivalent (Gt CO2eq) in which livestock production dominated the total farm gate emissions. Nitrous oxide and Methane make up over half of total greenhouse gas emission from agriculture. A possibility or scope is seen in Agriculture Sector for achieving the committed target of net zero emissions by 2070. Sustainable agricultural practices can play a significant role in mitigating climate change. By implementing techniques like soil carbon sequestration, agriculture can become a part of the solution by not only reducing greenhouse gas emissions but also enhancing soil health and crop productivity. It's crucial to prioritize restoring and maintaining healthy soils to realize these benefits and ensure the long-term sustainability of our food systems. Carbon credits provide a mechanism for companies to offset their emissions by investing in projects that either reduce greenhouse gas emissions elsewhere or capture carbon from the atmosphere. This allows companies to compensate for activities that can't be made carbon-free on their own. In the most ambitious cases, carbon credits can help companies achieve carbon-neutral status by balancing out their environmental footprint. It's a valuable tool in the transition towards a more sustainable future. The concept behind carbon credits is straightforward: if one entity cannot completely eliminate its CO2 emissions, it can offset them by supporting projects that reduce, remove, or avoid emissions elsewhere. Although challenges persist in streamlining carbon verification and validation, a bespoke and integrated approach holds promise for enabling smallholder farmers to access the carbon market, ultimately benefiting both them and the planet.

5PP-14

Regenerative Agriculture: A Key Player in Sustainable Crop Production and Climate Resilience

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The Green Revolution, driven by intensive agriculture, caused soil degradation. Regenerative Agriculture (RA) counters this, enhancing soil health with practices like minimum tillage and cover cropping. RA integrates livestock and agroforestry, optimizing productivity sustainably. Rooted in biological principles, RA limits synthetic compounds, aiding climate change mitigation and offering holistic environmental benefits. Along with forestry and other land use, agriculture is estimated to contribute some 24% of global greenhouse gas emissions. Food production is also associated with ≈15% of global N_2O emission rates. Leguminous crops, for example, can increase crop productivity while having no effect on N_2O emissions due to their ability to fix atmospheric N. Cover crops, in addition to improving greenhouse gas emissions. Enhanced-efficiency of nitrogen fertilizers is used to reduce N_2O emissions. Plant diversity can also reduce N_2O emissions in restored agricultural soils. The type of cover crop used may also influence soil fertility, aid in carbon sequestration, and their widespread adoption could reduce agricultural GHG emissions by 10%. Regenerative livestock management practices like rotational grazing and improving feed quality reduces methane emission from livestock. Additionally, optimizes nutrient management minimize nitrous oxide emissions from fertilizers, contributing to overall greenhouse gas reduction. Climate change poses various challenges to agriculture, such as extreme weather events, water scarcity, and pest outbreaks. Regenerative Agriculture enhances soil health, pest control, nutrient uptake, and resilience. It yields nutrient-dense food, boosts biodiversity, resource efficiency, and long-term yields, while sequestering carbon, addressing food security and environmental concerns.

5PP-15

Optimizing Wheat Varietal Performance through Residue Retention and Different Tillage Techniques

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A field study was conducted during the Rabi seasons of 2017-18 and 2018-19 at the research site of the College of Agriculture, Kaul, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The experiment utilized a strip plot design, incorporating four distinct sowing methods: wheat sown with a turbo seeder under full residue retention (TS+IR+LR), wheat sown with a turbo seeder under intact rice residue (TS+IR), wheat sown with a zero till seed cum fertilizer drill under no residue (ZT+NR), and wheat sown under conventional tillage conditions with no residue (CT+NR). Additionally, six wheat varieties (HD 2967, HD 3086, WH 1105, WH 711, WH 1124, and WH 1142) were assigned to subplots, each replicated three times. Results indicated that the TS+IR+LR treatment exhibited the highest effective tillers, grain yield, and straw yield, which were statistically comparable to TS+IR and ZT+NR treatments and significantly higher than the CT+NR treatment. Spike length, number of grains per spike, and 1000-grain weight were numerically greater in the TS+IR+LR sowing treatment, although no significant differences were observed among the various wheat sowing methods. Regarding wheat varieties, HD 3086 displayed significantly higher effective tillers and grain yield, although it was statistically equivalent to HD 2967 and WH 1105. WH 1105 exhibited numerically higher straw yield, spike length, and number of grains per spike, while HD 3086 demonstrated the highest 1000-grain weight. In conclusion, the wheat variety HD 3086 sown with a turbo seeder under full rice residue retention showed enhanced productivity.

5PP-16

System of Wheat Intensification through Seed Priming and Spacing Optimization

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The field experiment was conducted over two consecutive Rabi seasons (2020-21 and 2021-22) at the Research Farm of All India Co-ordinated Wheat and Barley Improvement Project (AICW & BIP), MARS, UAS, Dharwad, and Ugar, to investigate the impact of precision nutrient management approaches on wheat cultivation. The experimental design involved a split-plot layout with four main plots representing different seed priming (No seed priming and seed priming) and bed types (Flat bed and raised bed), and three sub-plots representing varying spacing configurations (20 x 10 cm, 30 x 15 cm and 30 x 20 cm), each replicated thrice. Analysis of the pooled data from Dharwad and Ugar revealed significant effects on wheat growth, yield attributes, yield, and economics based on the treatment combinations. In Dharwad, this combination resulted in a higher number of tillers per square meter (457.67) and increased yield (48.77 q/ha) compared to other treatments. Similarly, in Ugar, it led to a higher number of tillers per square meter (440.67) and increased yield (50.00 q/ha). The combined analysis of Dharwad and Ugar data highlighted the superiority of the treatment combination of seed priming with a raised bed and a spacing of 30 x 15 cm, showing significant yield advantages of 49.38 q/ha, biomass yield of 149.19 q/ha, and test weight of 44.15 gm compared to other combinations.

5PP-17

Impact of Climate Change and Importance of Carbon Sequestration and Stabilization in Mitigation of Climate Change

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The accumulation of carbon dioxide (CO_2) and other air pollutants in the atmosphere causes the absorption of sunlight and solar energy that has reflected off the earth's surface, leading to global warming. The average global temperature for 2023 exceeded the pre-industrial (1850–1900) average by 1.35° C. Global Carbon dioxide emissions from energy combustion and industrial processes increased 18 times in 2020 compared to 1990's emissions. The Kyoto Protocol was an agreement under the United Nations Framework Convention on Climate Change (UNFCC) taken in December 1997 which aims to reduce carbon dioxide emissions and other greenhouse gases (GHG) to minimize the impacts of climate change. At the same time, the global agriculture sector generated 5.87 billion tonnes of CO2 equivalents in 2020. In agriculture excess CO_2 in the atmosphere can be stored above and below ground by adopting carbon sequestration practices. By 2050, agriculture is expected to feed a population of 9.1 billion. Carbon stabilization is the process of storing carbon for a longer time to mitigate climate change and also prevents the escape of sequestered carbon back into the atmosphere, thereby protecting the environment and promoting the sustainable development of nations. It is estimated that $3x10^9$tC/yr can be sequestered in soils of terrestrial ecosystems. In developing countries cereal and legume production could increase by 32 million Mg/yr depending on climate and other variables by adopting potential carbon sequestration and stabilization techniques.

5PP-18

Sustainable Resource Management Conservation Agriculture – INM

Influence of hydrogel application and zinc fertilization on nutrient content and uptake of pearl millet

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A field experiment was conducted at Agronomy farm, S.K.N. College of Agriculture, Jobner (Rajasthan) during the Kharif 2021 on loamy sand soil. The experiment was laid out in factorial randomized block design with four levels each of hydrogel (control, 2.5 kg ha^{-1}, 5.0 kg ha^{-1} and 7.5 kg ha^{-1}) and zinc sulphate (control, foliar spray of $ZnSO_4$ @ 0.25%, 0.5% and 0.75%). Pearl millet crop grown with hydrogel with all application rates yielded higher than control. Higher N, P, K and Zn uptake also recorded under application of pusa hydrogel 5.0 kg/ha in grain and stover. Results showed that foliar spray of 0.5% $ZnSO_4$ significantly higher yield over foliar spray of 0.25% $ZnSO_4$ and control. The pearl millet crop under the influence of foliar spray of $ZnSO_4$ did not have significant effect on NPK concentration in grain and stover. Foliar spray of $ZnSO_4$ 0.5 % significantly increased Zn concentration in grain and stover over foliar spray of $ZnSO_4$ 0.25 % and control which was remained at par with foliar spray of $ZnSO_4$ 0.75 %. Further foliar spray of $ZnSO_4$ 0.5 % significantly improved total NPK and Zn uptake over foliar spray of $ZnSO_4$ 0.25 % and control.

5PP-19

Modelling and Assessment of Superiority of Wheat Varieties Tested under Farmers' Fields through Front Line Demonstrations in Semi-Arid Vertisols of India

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Front-line demonstrations (FLD) were conducted on 122 farmers' fields in semi-arid Vertisols during 2012-19, including 11 improved wheat varieties. Observations were collected on holding size, FLD area, check area, yield, duration, irrigations, cost of cultivation, gross and net returns and BC ratio from farmers. Duration ranged from 106 to 119 days, while irrigations ranged from 4 to 6. Mean yield ranged from 14.8-20.6 q/acre; gross returns ranged from Rs. 31132/- to Rs. 42531/- with a BC ratio of 0.92-2.09. Yield increase of FLD over check varieties ranged from 15.7-66.4%. FLD varieties attained significantly higher mean yields in black cotton, heavy, medium black, and sandy loam soils than check varieties. A maximum yield of 17.9 q/acre was attained in black cotton, followed by 16.7 q/acre in heavy, 16.9 q/acre in medium black, and 14.9 q/acre in sandy loam soil. Grain yield is positively correlated with irrigations, cost of cultivation, gross and net returns, and BC ratio. Crop duration had a significant positive correlation with irrigations, net returns, and BC ratio and a negative correlation with the cost of cultivation. In contrast, irrigation positively correlated with gross returns and BC ratio. Heavy (Rs. 23103/acre) and saline (Rs. 9440/acre) among soils; and HW-1098 (Rs. 22383/acre) and MACS-6478 (Rs. 10945/acre) among FLD varieties were superior for attaining higher net returns. The regression model of the yield of FLD varieties through rainy days, rainfall, area and BC ratio gave R^2 of 0.326 with a prediction error (PE) of 2.28 q/acre, while a model of check varieties gave R^2 of 0.661 (PE of 2.15). Soil-wise sustainability yield index (SYI) of FLD varieties ranged from 36.5% (light black) to 61.6% (clay loam), while FLD variety-wise SYI ranged from 26.4% (MACS-4028) to 62.8% (HD-3090). A rank sum of soils ranged from 14 (black cotton) to 27 (heavy and loamy) in RS1, while it ranged from 5 (heavy) to 40 (light) in the RS2 group. Overall rank sum indicated that heavy and medium black soils were superior. Three principal components (PCs) of FLD varieties explained 69.5% variance, compared to 66.4% of check varieties in black cotton soil. Thus, HD-3090 with maximum SYI (62.8%), HW-1098 with maximum net returns (Rs. 22383/acre) and MACS-6478 with lowest rank sum (29) were superior and are recommended for large-scale adoption under similar soil and agro-climatic conditions.

5PP-20

Species Occurrence and Phenological Studies of Weeds under Diversified Cropping Systems

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The *study* was carried out in a continuing experiment under AICRP-IFS at Bhadearkhar farm CSK HPKV, Palampur. Ten cropping systems C_1–"Maize – wheat", C_2 – "Maize – Gobhisarson + Toria", C_3– "Dhaincha–Early cabbage – Frech bean", C_4– "Sunhemp – Vegetable Pea - French bean", C_5–"Maize + Soyabean – Chickpea + Linseed", C_6– "Rice – Wheat + Gram", C_7– "Hybrid Sorghum + Hybrid Bajra – Oats + Sarson", C_8 – "Hybrid Sorghum + Hybrid Bajra – Ryegrass + Berseem", C_9 – "Baby corn – Broccoli - French bean", C_{10} "Okra – Turnip - Tomato" in a RBD design with three replications were evaluated for appraisal on weeds floristic diversity, phenology and NPK depletion .Soil of experimental field was silty-clay loam in texture and acidic with PH 5.38. Weed flora was composed of 13 species in *kharif* 2021 and 13 in *rabi* 2022. In *kharif viz. Ageratum conyzoides* (24%), *Cyperus spp.* (20%), *Phyllanthus niruri* (11%) and *Galinsoga parviflora* (10%) which were the dominating weed species and remaining weed species found were *Alternanthera philoxeroides, Artemesia vulgaris, Commelina bengalensis, Coronopus didymus, Digitaria sanguinalis, Echinochloa spp., Ipomoea spp.* and *Monochoria vaginalis*. During *rabi* 2022, dominating weed species were *Poa annua* (25%),*Coronopus didymus* (15%), *Spergula arvensis* (14%) and *Trifolium repens* (10%)and the other weed species were *Anagallis arvensis*, *Avena fatua*, *Cynodon dactylon*, *Phalaris minor*, *Lolium temulentum*, *Raphanus spp*., *Stelleria media* and *Vicia sativa*.

N-P-K depletion due to weeds ranged from 39.8 – 43.9 kg/ha N, 10.4 – 15.6 kg/ha P and 19.3 – 25.5 kg/ha K under different cropping systems minimum being under cropping system C_1 – "Maize – wheat" for N, C_2 – "Maize –Gobhisarson + Toria" for P and C_7 – "Hybrid Sorghum + Hybrid Bajra – Oats + Sarson" for K and maximum under cropping systemC_7 – "Hybrid Sorghum + Hybrid Bajra – Oats + Sarson" for N, C_{10} "Okra – Turnip - Tomato for P and C_3– "Dhaincha – Early cabbage – Frechbean" for K.

5PP-21

Optimizing Wheat Yield Through Precision Fertilizers Application: A Soil Test-Based Approach for Targeted Results

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A survey was conducted during Rabi season of 2021 by ICAR- Indian Institute of wheat and barley in collaboration with ICAR-Indian institute of soil science (IISS), Bhopal in Haryana to determine the availability of NPK for its targeted recommendation to get the predicted wheat yield of 8t/ha. A total of 60 farmers were randomly selected, comprising 26 from Rasina village (Kaithal district) and 34 farmers from Gohida (Karnal district), for location-specific soil test-based recommendation of NPK for the wheat crop. The latitude and longitude of each specific field were also recorded with the help of GPS. ICAR-IISS, Bhopal team in collaboration with ICAR-IIWBR team, collected the soil samples for analysis of primary nutrients i.e., N, P and K. ICAR-IISS team analyzed the soil samples for available N, P and K. Using the soil nutrient levels from each field, ICAR-IISS Bhopal team developed an equation and a soil map to suggest the appropriate NPK fertilizer for each specific field. The required amount of N, P and K was calculated by putting value in the equations; for nitrogen: targeted fertilizer nitrogen (kg/ha) = [(5.31× 60) – (0.51× pixel value of soil nitrogen)], for phosphorous: fertilizer phosphorous (kg/ha) = [(3.45×60) – (5.55×pixel value of soil phosphorous)] and for potassium: fertilizer potassium (kg/ha) = [(2.75× 60) – (0.42×pixel value of soil potassium)]. The farmers were directed to apply targeted dose of nitrogen (in the range 130.6-144.5 kg/ha), phosphorus (0-60kg/ha), and potassium (9.8-91.6 kg/ha) in Gohida village for the wheat crop prior to sowing.While the farmers of Rasina village were directed to apply targeted dose of nitrogen (in the range 130.3-143.1 kg/ha), phosphorus (0-66.5 kg/ha) for the wheat crop prior to sowing. The data ondate of sowing, variety and other cultural practices were maintained. The readings of NDVI and CCI were taken from the farmers' field. These instruments-based readings were highly affected by date of sowing, NDVI values taken in first fortnight of January were ranged from 0.52 to 0.79 whereas CCI values were from 33.4 to 52.5. Based on the recommendations, it is expected to get at least 80% of the targeted yield (i.e., 8 t/ha) from the farmers' fields.

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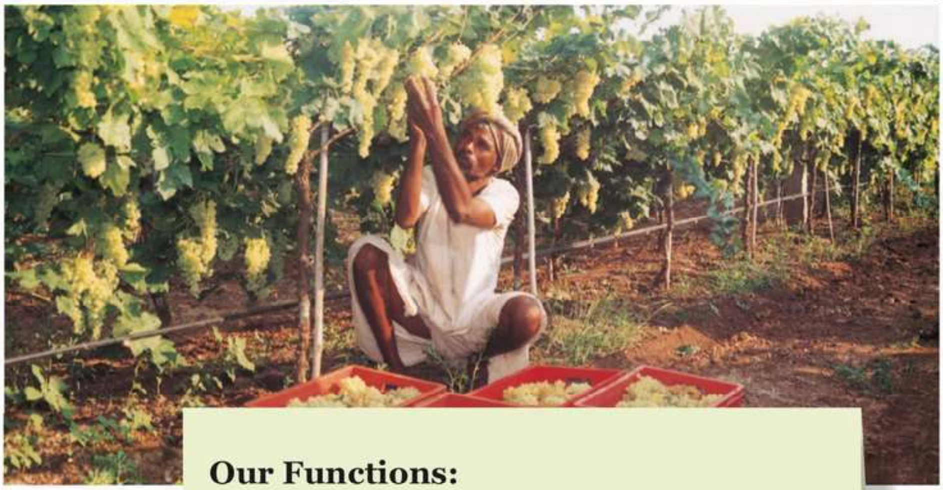

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