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Abstracts of 4th Internatonal Group Meeting on " Wheat Productivity Enhancement through Climate Smart Practices" at CSK HPKV, Palampur, HP, India (February 14-16, 2019)

Theme 1: Genetic manipulation to mitigate effects of climate change

KL 1: New technology and introgression strategies are enabling the systematic exploitation of genetic variation from wild relatives for exploitation in the production of high-yielding wheat varieties adapted to environmental change.

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The objective at the start of the introgression programme at the University of Nottingham was to transfer the whole genomes of a range of wild relatives (*e.g. Amblyopyrum muticum, Aegilops speltoides, Triticum urartu, Triticum timopheevii, Secale cereale, Thinopyrum bessarabicum, Thinopyrum elongatum and Thinopyrum intermedium)* into wheat in small, overlapping chromosome segments.

In this work we have generated F_1 interspecific hybrids between wheat (carrying the ph1 mutant or carrying Ph1 suppressors - the ph1 mutant and Ph1 suppressors enable interspecific recombination to occur between the chromosomes from different genomes) and a number of its wild relatives. The interspecific F_1 hybrids were effectively haploid for the three wheat genomes, *i.e.* A, B and D and also the genome(s) of the wild relatives. In the absence of homologous chromosomes from the same genome high levels of homoeologous recombination were expected to occur between the chromosomes from the three genomes of wheat and those of the wild relatives in the interspecific F_1 hybrids. In order to recover introgressions resulting from homoeologous recombination in the gametes each of the F_1 hybrids were recurrently backcrossed to the wheat parent and the progeny analyzed.

In the past one of the major bottle necks in wheat/wild relative introgression has been the absence of technology that facilitates the high throughput detection/characterization of introgressions. In order to overcome this problem we have used a new 35K Axiom SNP array specifically designed to detect introgressions. The introgression strategy we have employed coupled with the new Axiom array led us to believe that we would detect new introgressions. However, the number of introgressions we detected were far higher than we had predicted from previous work and represents a step change in the field of wheat/wild relative introgression, *i.e.* over 1000 new introgressions have been generated and detected from a range of species. This work has enabled us to develop genetic maps of the wild relatives based on the introgressions generated and in addition allowed the determination of the syntenic relationship between wheat and each of the wild relatives.

In collaboration with a network of global partners, work is presently underway to target introgressions carrying genetic variation for agronomically important traits. Targetted introgressions will be incorporated into breeding programmes for the development of superior wheat varieties that are adapted to climate change.

LL 1.1: Genetic manipulation of wheat for different quality traits

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Hexaploid wheat is one of the important food crops that has been improved for multiple traits through hybridization. To develop important traits in wheat, breeders have continuously strived to develop new and improved varieties by introgressing superior traits from germplasm resources to the commercial elite cultivars. In this direction, multi-faceted efforts have been undertaken at the National Agri-Food Biotechnology Institute (NABI) to improve nutritional and grain quality of bread wheat. In an attempt to develop nutritionally rich wheat grains an EMS induced mutants where developed to achieve high amylose in the grains of wheat variety C306. In this study, a set of 101 M4 EMS-treated TILLING mutant lines was obtained that show variation between ~3 to 76 % in amylose content. In these mutant lines, large variation for resistant starch was obtained in the wheat grains in M5 generation. These tilling mutant lines are being used for genetic mapping of the QTLs for high amylose contents and developing specific wheat varities for obese and diabetic individuals. In an attempt to develop anthocyanin rich wheat, a few coloured wheat lines *viz.* blue, purple and black grains with enhanced anthocyanin content (40-140 ppm) compared to white wheat (5-15 ppm) was developed in the genetic background of high yielding cultivars PBW550, PBW621 and HD2967. Utilizing mice studies it was observed that these colored wheat grains are rich in antioxidant affects thereby, improving the health promoting properties. To enhance the micronutrient (Fe and Zn) bioavaliability, RNAi based approach has been used to target the phytic acid (PA) biosynthesis pathway. PA is considered to be antinutrient since it has ability to chelate these micronutrients, thereby reducing its avilability for human body. During this study, multiple wheat lines with low phytic acid were generated by silencing ABCC13 (a putative transporter for phytic acid) and inositol pentakisphosphate kinases (*IPK1*). Silencing of these genes resulted in 28-56 % reduction of total

PA and enhancement of Fe and Zn contents in these silenced wheat lines. In addition to this, my presentaiton will also be providing some insight about the impact on some of these traits by increased CO_2 concentration and high temperature stress. It is therefore important to explore new plant breeding technologies to reduce the vulnerability of important crop like wheat to global climate change.

LL 1.2: Genetic manipulation of cereals for adaption to climate change

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Global climate change will alter many elements of the future crop production environment: an increase in atmospheric CO_2 concentration, average temperatures and tropospheric O_3 concentration, frequent and severe occurrence of drought, intense precipitation leading to flash flooding and soil degradation. Other than CO_2, N_2O and CH_4 are gases that directly contribute to global warming and climate change come from agriculture. All of these are widely recognized as important to crop production in the last few decades. The studies have also indicated that enhanced CO_2 leads to decline in quality in terms of C:N ratio, N and protein content and hence decreased nutritional value for humans. Biotic stresses are also becoming a challenge due to emergence of new diseases and pests due to climate change that need different strategies to tackle. Strategies to combat elevated atmospheric CO_2, high temperature, soil degradation, increased salinity, unpredicted floods and draught are extremely important in today's agriculture. Biotechnological tools, especially genomic selection, genetic engineering and genome editing will be greatly useful under this scenario for sustainable cereal production including rice and wheat. Manipulating Rubisco which is the key carboxylating enzyme and frequently the rate-limiting factor for photosynthesis, engineering and/or substituting Rubisco from other species, engineering plants to express different types of Rubisco in sunlit and shaded leaves and a better knowledge of source-sink relationship in terms of C acquisition and photosynthesis is essential if maximum yield potential is to be realized under elevated atmospheric CO_2. Genes for stress adaptive traits like water and nutrient use efficiency, spike photosynthesis, leaf morphology, pigments like chl a, chl b and carotenoids, antioxidant would be target for tolerance to most of the climate change induced stresses. Uniquely adapted crop wild relative species with enhanced tolerance to salt, drought, soil aluminum toxicity and cold stress have been identified through structural and functional genomics studies. Bio prospecting of novel genes and alleles responsive to climate change induced biotic and abiotic stresses is equally important to broaden the genetic base of the crop by incorporating the genes from land races and crop wild relatives, which can be introgressed through genomics-assisted backcrossing. The ultimate goal is to search for genes for resistant/sensitivity to adverse effects of global climatic changes across the plant and microbial kingdom and their deployment through MAS or transgenic technology. ICAR-NRCPB has been partner in genome sequencing of number of crop species including rice, wheat tomato, pigeonpea, flax, jute and mango. Use of the information obtained from structural and functional genomics studies will be useful for developing new climate resilient high yielding crop varieties. Examples climate resilient varieties developed in rice and efforts underway in wheat will be presented. Stacking of genes for multiple stress tolerance is the need of the day for developing future climate adaptive wheat varieties while maintaining their high yield potential and quality traits.

LL 1.3: Induced mutagenesis to sustain wheat production under changing climate

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Wheat is second important food crop of India. It is cultivated on 30.6 million hectares area with a production of 98.4 million tonnes in the year 2016-17. Wheat production in India showed consistent improvement after green revolution. Stagnation of yield experienced in present breeding programs is due to maximal utilization of existing genetic variability. Increasing wheat production is essential to keep pace with growing population under changing climate. However, genetic similarities in the cultivated wheat germplasm made it impossible to assemble new gene combinations to break yield plateau. This situation demands the creation of new genetic variability. Induced mutations uncover novel alleles that are harnessed to breed superior crop varieties. Continued development of agronomically superior wheat varieties, improved nutrition and processing quality, tolerance to biotic and abiotic stresses is essential to harvest stable yields for ensuring food security. Mutation breeding at BARC has resulted into the isolation of novel variability for rust resistance, drought tolerance, dwarf, early maturity, herbicide tolerance and pre-harvest sprouting tolerance. Specific traits and the mutant isolated are discussed here.

Rust resistance: Stripe, leaf and stem rust are the major biotic stresses of wheat. The losses due to rusts can be very large and vary from year to year and region to region. Therefore, the hunt for new resistance genes continues against incessantly evolving rust pathogen races. Mutation breeding programme to isolate rust resistant mutants has been isolated in popular variety HD2967. Screening of M2 population in stripe rust epiphytotic conditions resulted in isolation of two stripe rust immune and seven resistant mutants. Their yield potential is being evaluated.

Drought tolerance: Wheat genotypes capable of giving higher yield under moisture stress condition are considered desirable. An attempt has been made to isolate drought tolerant mutants in variety HD2967. The population was evaluated under moisture stress conditions. Eight drought tolerant mutants were confirmed in M3 generation based on yield and yield contributing traits over parent HD2967. These mutants will be further confirmed for physiological and biochemical traits.

Dwarf: Plant height is an important feature determining the lodging tolerance, fertilizer responsiveness and harvest index of wheat. Green revolution genes, Rht-B1b and Rht-D1b known for height reduction and were found in more than 95% of released wheat cultivars. Studies were carried out to identify new dwarfing genes in bread wheat to exploit in breeding programs. A series of dwarf mutants with height ranging from 65 to 85cm as compared to 95cm height of parent HD2967 have been isolated. These mutants are being characterized for yield potential and modifications in dwarfing locus.

Early maturity: Early maturity is desirable trait in the areas where the wheat crop is affected by terminal heat stress. Flowering in wheat is regulated by three set of genes *i.e.* photoperiod genes (Ppd), vernalization genes (Vrn) and earliness per se genes (eps). These genes are present in three copies on chromosomes of three genomes of wheat. Early mutants were identified and confirmed in M3 generation of two cultivars, PBW677 and HD2967. These early mutants will be utilized for genetics and molecular studies to decipher the nucleotide alterations responsible for earliness.

Herbicide tolerance: Glyphosate is an active ingredient in widely used brand name “Round up ready” and many other brands of herbicides. This herbicide controls broad spectrum of unwanted plant species in crop fields. The mode of action of glyphosate is to inhibit aromatic amino acid biosynthesis pathway with 5-enolpyruvyl-shikimate-3-phosphate (EPSP) synthase as its primary target[11]. The consequence of inhibiting EPSP is to impede biosynthesis of aromatic amino acids. Initial studies were carried out to isolate mutants tolerant to Glyphosate in wheat. A gamma ray induced putative herbicide tolerant mutants were isolated in M2 generation and will be confirmed in subsequent generations.

Pre-harvest sprouting (PHS) tolerance: Climate change is an inevitable risk to wheat yield and quality and calls for development of climate smart cultivars. Unpredictable rains during maturity experience total loss of yield and end use quality due to sprouting of wheat in the spike. PHS is a complex trait and largely influenced by environmental conditions. Putative mutants for PHS have been isolated from parent varieties WSN109-4 and HD2967. Their validation shall be confirmed in subsequent generations.

This novel variability is being exploited in hybridization to tailor desirable plant type suitable to changing climate.

LL 1.4: Innovations and new horizons in chromosome elimination- mediated dh breeding: five decades journey of speed breeding in wheat

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Dynamism of an innovative process of uniparental or preferential chromosome elimination occurring during wide hybridization in wheat when crossed with various Gramineae genera, has been recognized as a boon for wheat geneticists and opened new horizons for enhancing the speed of genetic improvement in wheat. Since the invention of bulbosum approach in 1970, some other potential systems *viz.*, wheat x Zea mays and wheat x Imperata cylindrica leading to the chromosome elimination have further enhanced the opportunities to increase the doubled haploid production efficiency manifolds in bread and durum wheats. Sensitivity of the pollen of Hordeum bulbosum to the crossability inhibitors (*Kr* alleles) restricted the applicability of the bulbosum approach for haploid induction in wheat whereas the insensitivity of that of *Z. mays* and *I. cylindrica* to these inhibitors opened a gateway to induce haploids in any wheat genotype. The *I. cylindrica*- mediated approach invented by our group in the year 2005 has emerged as an efficient alternative to the widely used *Z. mays*–mediated system in various aspects. The *I. cylindrica* is a wildly growing, weedy, perennial winter grass (n=x=10) and available under natural conditions in almost all parts of the world coincides well for flowering with that of wheat, rye and triticale. This pollen source has been observed as genotype non-specific for hybridization with any genotype of wheat, triticale and their derivatives and performed significantly better than Z.mays for all the haploid induction parameters. *Z. mays* has totally failed to realize haploids from triticale x wheat and wheat x rye derivatives whereas, I cylindrica yielded significant results. Cytological studies of *I. cylindrica*- mediated system has inferred that endosperm is not formed in wheat x *I.cylindrica* hybrid and all the chromosomes of this grass are eliminated in the first zygotic division during the process of seed development, thus allowing the production of embryo-carrying pseudoseeds. Various innovative protocols have further been developed in this Lab to break the barriers needed to save time and energy and recover higher frequency of doubled haploids in *Triticum aestivum*, *T. durum*, *T. tauschii* and triticale x wheat derivatives. Him Pratham has been developed and released as first DH wheat variety of the country. Although this unique phenomenon of chromosome elimination has opened an opportunity to shorten the breeding cycle y*et al.*o acts as a great hurdle during the situation when a breeder desires to introgress targeted genes from the potential pollen sources like *Z. mays* and *I. cylindrica*. The B and D genomes of wheat have been observed to trigger the elimination process. This paper will reveal the innovative protocols which can actually increase the DH production efficiency manifolds in hexa- and tetraploid wheats and open new vistas globally for speed and precision breeding in wheat.

LL 1.5: Harnessing the genetic variation from wild *Triticum* and Aegilops species for broadening wheat gene pool for biotic stress resistance

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Yield potential of wheat, a major cereal grain, is limited due to various biotic and abiotic stresses, reduced nutrient use efficiency and declining soil health complicated by unpredictable environmental fluctuations. Ancestral hybridization events involving only a limited number of accessions created a genetic bottleneck which led to a narrow genetic base of the modern wheat germplasm. This lack of genetic diversity, however, can be compensated by introgression of genetic variability from wild exotic species. Among biotic stresses, the fungal diseases pose major constraint to wheat production globally. Emergence of new pathotypes of major diseases and spread of diseases to new habitats due to climate change and human interventions further intensifies the threat. Appearance of a highly virulent stem rust pathotype in Kenya and Ethiopia led to wide spread crop loss. Recently in 2016, wheat blast, a devastating fungal disease from South America, emerged in Bangladesh putting whole of wheat growing area in the Indian subcontinent at risk. Continuous efforts have been made over last more than five decades to recruit genes/alleles from wild gene pools which harbour wide array of new genes and alleles against different biotic stresses. More than 300 resistance genes against leaf rust, stripe rust, stem rust and powdery mildew have been identified from these wild gene pools and successfully transferred to cultivated wheat. Only a handful though has been used in commercial cultivation due to impeding linkage drag. Recent advances in genomics could provide solutions for rapid discovery and targeted introgression of alien genes with minimal linkage drag. Genome wide association mapping using genome wide high density SNP markers based on SNP chips or skim sequencing presents an attractive scenario for mapping genes in the wild wheat background itself and for developing gene based/closely linked markers for targeted introgression of the alien genes to cultivated wheats in combination with chromosome engineering technologies. We at PAU, Ludhiana, have transferred a multitude of disease resistance genes from wild *Triticum* and Aegilops species using combination of approaches including use of bridging species, suppression of Ph1 locus and molecular marker technology. Five rust resistance genes introgressed in our programme have been designated as Lr57, Lr58, Lr76, Yr40 and Yr70. Ae. umbellulata rust resistance genes Lr76-Yr70 have been deployed at farmers' field in a recently released wheat variety Unnat PBW343. Advance breeding lines carrying a number of other genes introgressed in our wide hybridization programme are at various stages of evaluation. A coordinated effort to mine genetic variation from wild wheats in national wheat breeding programme has the potential to provide a broad genetic base for developing climate resilient wheat varieties.

OL 1.1: Speed breeding - a climate smart tool to accelerate research in wheat

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Most of the crops take several years to breed for an improved cultivar. This holds good for field crops like wheat that are limited to one to two generations per year. Moreover, environmental noise in the form of change in temperature, precipitation, light duration, relative humidity and disease pressure associated with climate change affect the rust diseases screening in the field. In such a situation, speed breeding (SB) provides a comfortable solution. SB greatly shortens the generation time with the use of prolonged photoperiods to accelerate the developmental rate of plants. SB is inspired by the NASA's experiments to grow wheat in space, using continuous light on wheat which triggers early reproduction in the plants. To understand the response of wheat to SB, a preliminary study involving ten cultivars of wheat species (six of *Triticum aestivum*, two each of *T. durum* and T. dicoccum) along with five leaf rust susceptible lines were subjected to extended photoperiod (22 hr of light and 2 hr of dark) using LED lamps in polyhouse condition. Temperature range of 17^{-2}20C and relative humidity of 75-80% was maintained. Under these conditions, depending on the species/cultivars, plants reached anthesis in 38-40 days and physiological maturity in 75-80 days, while the same set of cultivars under field condition took 60-65 days to reach anthesis and 110-115 days for physiological maturity. Leaf rust susceptible lines displayed 40-60S and 60-80S, leaf rust reaction under SB and field grown lines respectively. In

SB, selection can be performed at any time of the year and with five generations per year, faster development of rust resistant lines is feasible which is independent of climate. In addition, SB has great potential to integrate with other modern crop breeding technologies in wheat including high throughput genotyping/phenotyping, marker assisted selection and genomic selection.

OL 1.2: Genetic improvement for drought and heat tolerance in wheat

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Breeding for drought and heat tolerance is challenging due to its complex inheritance and difficulties in phenotyping. The working wheat germplasm collection available at the division of genetics IARI was phenotyped for component traits of drought and heat tolerance including physiological and morphological traits. Trait-wise donor genotypes for were identified. Among 25 different traits phenotyped, NDVI at boot and grain filling , canopy temperature at grain filling and milky stage, Leaf area index (LAI), Fv/Fm, stomatal conductance, grain weight, biomass and harvest index showed significant correlation and regression values with yield under heat and drought stress. QTLs validation and idtification was carried out in six different mapping populations. In the genetic background of GW322, GW366 and HD2733, 1-4 QTL (Meta QTLs) regions were transferred using Marker Assisted Backcross Breeding (MABB) strategy for heat and drought tolerance. To combine QTLs for drought and heat adaptive traits using four different bi-parental populations, Marker Assisted Recurrent Selection (MARS) was conducted in four different bi-parental populations;in each case both parents carrying positive alleles for drought and heat tolerance were used. Carefully chosen pair-wise inter crosses were attempted in order to combine QTLs using limited population size. Based on validated markers, wide range of inter crossed progenies in advanced generation with improved drought and heat tolerance were identified. Genotypes with high molecular score in MARS and more number of QTLs with MABB, out-performed the checks in multi-location testing. A MAGIC population consisting of 3894 individuals was developed for trait mapping of heat and drought tolerance involving eight founder parents.

PP 1.1: Relative efficiency of Imperata cylindrica and Zea mays – mediated induction of doubled haploids in wheat x rye derivatives

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Chromosome elimination mediated-doubled haploidy breeding via wheat x maize and wheat x Imperatacylindrica approaches serve as a highly efficient tool for acceleration of genetic improvement programmes in bread wheat. This approach was exploited in the wheat x rye backcross derivatives to allow recombination and fix desirable genes from the indigenous rye source in the wheat genetic background. The investigation comprised of wheat x rye (Lahaul Local) derived backcross generations BC1F1 and BC1F2 utilized as maternal parents, whereas maize (BajauraMakka) and *I. cylindrica* were used as pollen sources to compare respective pollen efficiency for the induction of haploids. Among the haploid induction parameters, the pseudoseed formation frequency was almost equal for all the backcrosses, however, mean embryo (17.91%) and haploid (4.74%) formation frequencies were significantly positive and high using *I. cylindrica* pollen in both generations. The mean doubled haploid (DH) efficiency (29.17 and 50%) was high with *I. cylindrica* pollen in both the backcross generations, where maize pollen could only induce DH's (50%) in BC1F2 generation. In BC1F1, backcross HPW 89 X RYE X HPW 89 showed higher frequency for embryo (32.92%) and haploid (13.01%) formation, whereas for DH formation (75%), backcross HPW 147 X RYE HPW 147 was highly efficient when crossed with *I. cylindrica.* Similarly, in BC1F2, *I. cylindrica* was highly efficient for the backcross BW 215 X RYE X BW 215 for embryo (6.87%) and haploid (1.55%) formation, whereas it was equally effective alongwith backcross HPW 89 X RYE X HPW 89 for DH formation (50%) frequency. Thus, BC1F1 generation proved to be more productive for haploid and DH induction parameters. *I. cylindrica* as the pollen source proved most efficient for induction of haploids and doubled haploids in both the backcross generations.

PP 1.2: Genetics of size of haploid embryos in wheat produced through intergeneric crosses with maize and Imperata cylindrica

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Wide hybridization with maize and Imperatacylindrica following chromosome elimination is a high precision approach for producing haploids in wheat genetic background. But during the adoption of these approaches, the size of haploid embryos was realized as the main hindrance for low regeneration of these embryos. The aim of present investigation, therefore, was to screen the parent genotypes of bread and durum wheats and to study the variability present in size of haploid embryos in different genotypes. The material used for study was comprised of eleven diverse genotypes of bread wheat, seven of durum wheat and two of triticale. The length of haploid embryos was used as the measure of embryo size. The haploid embryos obtained through wide hybridization were classified into three categories *viz*., small (<1mm), medium (1-2 mm) and large (>2 mm) embryos. The inheritance pattern of size was studied through wide hybridization in F1 and F2 of parents showing contrasting traits. A range of variation in size of haploid embryos was obtained from <0.5 mm to >3 mm in the segregating generation which could not be classified into discrete classes. The results revealed the quantitative nature of the character controlled by polygenes. The study of reciprocal crosses in F1 hybrids of wheat suggested the influence of maternal cytoplasm on the size of haploid embryos.

PP 1.3: Development of rust resistant wheat doubled haploid lines via imperata cylindrica mediated chromosome elimination technique and their molecular characterization

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Wheat rusts are the most destructive and widespread among all other diseases of wheat which result in serious yield losses. The molecular characterization of 140 wheat genotypes and 11 doubled haploid (DH) developed via Imperatacylindrica mediated chromosome elimination technique was investigated using gene specific primers for Lr34, Lr46, Lr24, Lr32, Yr5 and Yr10 genes. For Lr34 six DH and fifty wheat genotypes showed positive band; for Lr46 five DH; for Lr24 eleven wheat lines; for Lr32 thirty wheat genotypes; for Yr5 and Yr 10 no DH line showed positive bands.The developed DH lines were also screened in field and glasshouse for their resistant reaction and were found to be resistant to one or the other pathotypes. The current studyfound that SSR makers could distinguish and characterize the genotypes and DH lines for the presence of resistant gene and the idtification of rust resistant genes in Indian wheat germplasm and, thus, will help in accelerating the breeding program in future, including pyramiding of different wheat resistant genes.DH lines developed using *I. cylindrica* mediated chromosome elimination technique was also found to be resistant and could be registered as genetics stock.

PP 1.4: *In vivo* and *in vitro* colchicine manipulations for enhancing doubled haploid production efficiency in *Triticum durum* using Imperata cylindrica- mediated chromosome elimination approach

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The present research endeavour was executed to establish a standard protocol for colchicine application aimed at enhancement of doubled haploid production in durum wheat. The material for present investigation comprised of two durum wheat genotypes *viz*., A-9-30-1 and PDW 314 utilized as maternal parent whereas Imperatacylindricawas used as a pollen source. Durum wheat x *I. cylindrica* hybridization was carried out followed by in vivo and in vitro application of colchicine. At in vivo level various concentration of colchicine ranging from 500 ppm to 7000 ppm were injected to the pollinated spikes at different time interval *viz*., 24 hours, 48 hours and 72 hours after pollination. At in vitro level the haploid embryos were cultured on medium enriched with various concentration of colchicine ranging from 100 ppm to 3000 ppm for different duration *viz*., 24 hours, 48 hours and 72 hours before transferring them to normal growth medium. Application of 5000-7000ppm colchicine at 48 hours after pollination in vivo and 1000- 2500 ppm colchicine for 72 hours in vitro were established as the optimum colchicine doses for chromosome doubling in durum wheat using *I. cylindrica*- mediated chromosome elimination approach. Both the systems proved better than traditional approach of colchicine application to the haploid regenerants and exhibited similar efficiency when compared to each other with in vivo colchicine application having slight edge in terms of convenience and cost effectiveness. idtification of optimum dose of colchicine for application at in vivo and in vitro level for induction of doubled haploids has opened new vistas in durum wheat improvement programme.

PP 1.5: Synthesis of hexaploid and octoploid triticales by utilizing himalayan rye (*Secale cereale*) and their characterization for various morpho-physiological traits

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Himalayan rye posseses the diverse source of desirable genes which can be utilized to synthesize new triticale to be used as a bridge species to introgress the rye genes from diverse source into the targeted wheat varieties. Present investigation was conducted to synthesize new hexaploid and octoploidtriticales utilizing indigenous landraces of rye and to characterize the newly synthesized triticales for ploidy level, spike fertility and various morphological traits. The material comprised of seven durum and twelve bread wheat genotypes as maternal parent whereas the pollen sources involved diverse Himalayan rye genotypes. Hybridization was carried out and haploids generated following embryo rescue in case of hexaploid triticale and through seed in octoploid triticale. Further, the regenerants were subjected to colchicine treatment for the synthesis of primary triticale. Hexaploid and octoploid seeds so obtained were raised for the characterization of various traits.A total of three hexaploid and two octoploid triticales were synthesized. Chromosome doubling efficiency in these different hexaploid triticales *viz*, PDW-^{2}33 × Himalayan rye 3, HI-8498 × Himalayan rye 2 and HI-8498 × Himalayan rye 3 was 7.14, 7.41 and 37.50 per cent, respectively. Chromosome doubling efficiency in two different octoploidtriticales*viz.*, C-306 × Himalayan rye 1 and DH-100 × Himalayan rye 1 was 83.33 and 46.87 per cent, respectively. The newly synthesized triticales were characterized for various seed (seed size andcolour) and morpho-physiological traits (coloeoptilecolour, stem colour, shoot-base colour, auricle, early growth habit, waxy-leaf sheath and greenness of leaves). Synthesis of hexaploid and octoploidtriticales by utilizing Himalayan rye has opened new vistas to develop wheat varieties having diverse novel genes conferring durable and stable biotic and abiotic stress tolerance in bread wheat.

PP 1.6: Improving grain yield by transferring grain size from wild relative to hexaploid wheat

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Wheat is one of the world's most important food sources, alongside with rice and maize, directly providing about 50%of human food calories. Higher yield is one of the most important goals in wheat breeding.Larger grains not only directly relate to grain yield but also have favourable effects on seedling vigour and early growth,thereby promoting and stabilizing yielding ability. Large grain size has been an important trait and it is usuallymeasured by thousand grain weight (TGW), mainly determined by grain width (GW),grain length (GL).Milling and baking quality is also influenced by grain size. At Punjab Agricultural University, Ludhiana more than 300 Aegilopestauschii accessions was evaluated for more than 10 years and several potential donors for different traits have been identified.Aegilops tauschii, the D genome donor ofhexaploidwheathas an immense reservoir of favourable alleles for economic traits and have been considered as prioritized genetic resource for wheat genetic improvement. In the present study a set of wheat - Ae. tauschii advance backcross introgression lines derived from different accessions of Ae. tauschii in the background of wheatcvs. PBW550 and PBW621 were analysed for three consecutive crop seasons (2015-16, 2016-17 and 2017-18) to determine the phenotypic diversity and relations between TGWand other yield parameters such as grain number, tiller number, grains per spike and yield. Introgression lines derived from various Aegilops tauschii accession showed a wide variation of Grain weight, length and width as well as yield components consisting of tiller number, plant and plot yield to an extent of 1.12, 1.01, 1.02 ,1.06, 1.17 fold respectively. Introgression lines derived from Ae tauschii PAU accession pau3760 and pau14158 in PBW621 background gave overall better performance.The selected introgression lines can further be used in wheat improvement programme and mapping yield component traits.

PP 1.7: Development of thermo-tolerant wheat for climate resilient agriculture

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Wheat (*Triticum* sp.) is one of the most important cereals to be used as staple food worldwide. It occupies 17% of the world's cultivatable land with a world annual production of about 757.2 million tonnes (FAO 2018). To feed the ever burgeoning population, food production needs to be increased, which can be achieved by enhancing the productivity per unit area. 60% of the land for cultivation is under harsh environmental conditions and is increasing due to changing global climate resulting in reduced crop yield. The negative impact of global climate change is also visibly evident on wheat production. Thus, it is essential to develop wheat cultivars tolerant to abiotic stresses. The breeding programs using conventional methods have been successful in developing "climate smart" cultivars but in recent years breeders are restricted with the available gene pool within a species. Recombinant DNA technology followed by plant transformation has successfully revolutionized the method of transferring genes across the genomes. Inspite of efforts in numerous laboratories across the world, transformation efficiency in wheat is still much lower than that of other cereals. The large (17,000 Mb) and complex (hexaploid) genome, genotype-dependent tissue culture responses, transgene silencing continues to be the hurdles for efficient genetic transformation in wheat.In the present study abiotic stress responsive genes from tolerant plant systems as Prosopis cineraria, Ziziphu snummularia, Eleusine coracana, Penniset umglaucum as well as thermophillic microbes have been isolated, characterized and binary vectors harbouring these genes developed. Further, a few of these selected candidate genes are functionally validated in model plant systems. Inplanta (apical meristem) method of genetic transformation has been standardized in elite Indian wheat genotype, HD2894. Using the available gene constructs, transformation has been carried out and the transgenics obtained have been confirmed for stable integration of transgene at T1 generation by southern hybridization analysis. Functional validation for abiotic stress tolerance trait of the transgenic events in further generation is underway.

PP 1.8: Deciphering photosynthesis associated traits for improving yield in wheat

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India will need 140mt of wheat in 2050 for feeding 1.89 billion people. Wheat yields are approaching ceiling under high productivity areas in India. Among several plant processes photosynthesis is the key determinant of biomass production that in turn contributes to yield potential of a cultivar. Improved harvest index was the basis for yield gains in wheat till recently. As this has now reached theoretical optimum, further yield gain requires increase in biomass primarily resulting from photo¬synthetic efficiency. Potential yield increases of up to 45% are theoretically possible from improved photosynthetic efficiency in C3 crops.The available natural variation in photosynthetic efficiency is currently an unexploited genetic resource for potential crop improvement. Using gas-exchange analysis, the existing natural variation in photosynthetic efficiency in adiverse panel of 60released wheat cultivars grown in the field was examined in relationto growth traits, including biomass and harvest index. Significant variations in photosynthetic efficiency, biomass and yield were observed, although no consistent correlation was found between photosynthetic efficiency of the flag leaf and grain yield in this study of genotypes. The majority of the variation in photosynthesis could be explained by components related to maximumefficiency and operational rates of CO_2 assimilation, and to CO_2 diffusion. Variations were observed for stomatal density and stomatal structure along with sink associated traits like water soluble carbohydrates and grain filling efficiency.Variations were observed for expression of photosynthesis rate limiting genes among the genotypes.These findings suggest that there is significant underutilized photosynthetic efficiency among existing wheat varieties. Hence, exploiting natural variation in photosynthetic efficiencycan be used as a potential source to increase yield in wheat.

PP 1.9: Genome-wide idtification, cis-regulatory analysis and development of nitrogen responsive candidate gene SSRs from bread wheat

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Wheat (*Triticum aestivum*) is an important food crop of the worldfulfilling the energy, protein, and dietary fiber demandsof majority of humans.Globally, a largeamount of nitrogenous fertilizers areapplied to harvest the yield potential of the crop. Studies have shown that wheat utilizes only 40-50% of applied nitrogen (N) and the rest is lost into the environment in different forms causinghuman and animal health problems. Hence, improving the N use efficiency (NUE) of wheat becomes essential to reduce the footprints of excess N on environment.idtification of genes and regulatory elements controlling the N use is important for development of high NUEwheat genotypes.In this study, the protein sequences of functionally validated nitrogen responsive (NR) genes were used to identify wheat orthologous through blastP search against wheat genome database. Seventy-five NR genes distributed among 21 chromosomes of wheat were identified. Chromosome 6A carried a maximum of 10 geneswhile 7 genes were found on chromosome 2A. Tissue and developmental-stage specific and biotic and abiotic-stress responsive expression analysis revealed constitutive as well as inductive response of NR genes in wheat.Promoter analysis of NR genes showed the presence of biotic and abiotic stress (cold, drought and salt), light, hormone, cell cycleetc., responsive cis-regulatory elements in wheat. Out of 56 NR gene based SSR markers were screened on 26 wheat genotypes,one TaGATA5 SSR marker displayed polymorphism. Our results showed that the identified wheat NR genes play distinct roles in plant growth-development and biotic and abiotic stress tolerance. The data obtained from this study contribute to better understanding of role played byNR genes in wheat. Study also provides the basis for further studies aimed at dissecting the function of these genes in wheat NUE pathway.

PP 1.10: Molecular mapping of frost tolerance in wheat using SNP markers

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The 2017-18 Rabi (winter) crop season witnessed sudden drop in temperature in the month of January, 2018 after an initial relatively warm December month in the Northern wheat belt of India. This led to appearance of frost symptoms in the wheat crop which was at late tillering to booting stage (Zadok's scale 26-45). A typical dent imprints appeared on leaves, sometimes being as severe as leaf rolling and deformity. This finding was in conformity to earlier reports that climatic warming may actually increase the risk of frost damage to plants (Gu *et al.* 2008: Cannell and Smith 1986). A study was undertaken to map frost tolerance in which 298 wheat genotypes were used to constitute a diverse association panel. The genotypes were evaluated for frost at the experimental field of ICAR-IIWBR, Karnal during the crop season 2017-18. Phenotyping was done visually from late tillering to early booting stage (Zadok's scale 26-45). Based on spread of the symptoms in the plot as well as the severity of damaged leaves, scoring of the genotypes was done with a score value of '0' to those with no symptoms and '50' with very high damage. SNP genotyping was done with 35K Axiom Wheat Breeder's Array followed by quality processing. Association analysis was performed using compressed mixed linear model (CMLM) which took into account of K-PC model. Kinship (K) information together with the first three principal components (PC) as covariates was included for GWAS improving its statistical power. In total 14,612 markers were utilized for GWAS which led to idtification of 47 Marker trait associations (MTAs) at -log10 P ≥3, for single trait frost/ chill. Out of 47 MTAs, 13 markers were found on 1B, 2B, 5B, and 7A chromosomes with -log10P ≥ 4. Significant SNPs were annotated for being putative candidate genes using BLASTN with the International Wheat Genome Sequencing Consortium (IWGSC) reference sequence. To the best of our knowledge, this study is pioneer in reporting genomic regions for frost tolerance using diverse wheat genotypes from India and shall be useful information for scientists engaged in wheat genetic improvement.

PP 1.11: Mapping QTLs associated with physiological and agronomic traits under diverse water regimes in wheat using SNP and SSR markers

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Drought is major abiotic stress that adversely affects wheat production in many regions of the world including India. Objective of this study was to identify quantitative trait loci (QTLs) controlling yield contributing and other physiological traits under different water regimes, *i.e.*, well-irrigated, rainfed and drought conditions. A recombinant inbred line (RIL) population of 218 lines derived from cross 'Dharwar Dry' (drought tolerant) x 'DPW621-50' (drought susceptible) was used to identify genomic loci associated with agronomic traits including grain yield, thousand-kernel weight, grain number per spike, grains weight per spike, biomass yield and physiological traits. The mapping population was phenotyped at three locations *i.e.*, Karnal, Hisar and Powarkhera over three consecutive years (2015-2018) under drought and irrigated conditions. Four linkage groups (7B, 4B, 1B and 2D) were constructed with 112 SSR markers using software Join map 4.1 for map construction and Win QTL Cart for idtification of QTLs on above mentioned chromosomes using minimum LOD value 3. Genomic regions were found on chromosome 7B for grain filling duration under water stressed condition and for spike length under irrigated condition and chromosome 2D for thousand grain weight and grain number per spike under water stressed condition. Further genotyping of RILs with 35K wheat SNP array markers is being in process to saturate the linkage maps.

PP 1.12: Pyramiding of adult plant and seedling rust resistance genes in the genetic background of selected wheat cultivars by marker assisted backcross breeding

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Selection and development of wheat cultivars with effective and durable rust resistance constitute a global breeding objective in wheat. Adult plant resistance (APR) provides protection in a crop's post-seedling stages (typically between tillering and booting) while seedling resistance, by comparison, is effective at all growth stages. An attempt was made to transfer Adult plant resistance and seedling rust resistance genes by using different donors in the genetic background of high yielding genotypes UP2855 and UP2572 by using Marker Assisted Backcross Strategy. Known donor genotypes carrying specific APR genes was used to validate the known linked molecular markers. Different F1's produced during rabi 2016-17 were raised along with two recurrent parent (UP 2572 and UP 2855) and 11 donor parents in staggered manner at Crop Research Centre, GBPUAandT, Pantnagar during rabi 2017-18. Transmission of molecular markers linked to desirable genes to F1 heterozygotes was validated. Parental polymorphic survey was also carried out by using different SSR primers (Xbarc 8, Xcfd71, Xbarc200, Xwmc511, Xwmc830, Xcfd88, Cfa2190, Wmc238, barc40, gwm501, barc167, Wmc810, Xpsp3000, csLV34 and gwm273) on twelve parents [UP2572, UP2855, Avocet/Yr10, UP2425, Avocet/*Yr15*, FLW21, FLW22, FLW23, Agra Local, Lr46, PBW644 and HD3086]. Out of fifteen SSR primers used following eight primers namely Xbarc 8, Xcfd71, Xwmc511, cfa2190, Xwmc810, Xpsp3000, csLV34 and gwm273 showed polymorphism in our populations. SSR primers that were found to be monomorphic were Xbarc200, Xwmc830, Xcfd88, Xbarc167, wmc238, barc40 and gwm501. The parents and the respective F1's were also evaluated for various morphological traits and rust resistance. Back crosses were attempted with both the recurrent parents to produce BC1 generation. Foreground selection will now be practiced on the BC1 generation plants for idtification of desirable backcross progenies carrying the APR genes and Background selection will also be practiced for recovery of recurrent parent background.

PP 1.13: Mapping stem rust resistance (Sr+) in genotype CPAN4027

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Sixty indigenous wheat lines selected for stem rust study were screened at four screening site (Indore, Dharwad, Pune and Mahabaleshwar) for adult plant resistance and for gene postulation (SRT) at Flowerdale, Shimla. On the basis of APR and SRT data, promising genotypes carrying rusts resistance were selected to be used in crossing program to target novel rust resistance genomic regions. One of the promising stem rust resistant genotype CPAN4027 was selected for mapping stem rust resistance (Sr+) and RILs population was developed from a cross WL711 X CPAN4027. Bulk segregant analysis was done for segregating recombinant lines for chromosomal location of Sr+ in CPAN4027. Seedling resistance testing (SRT) was done with parental lines and segregating F2/ F3 RILs with predominant pathotypes 40A and 117-6 to identify homozygous resistant (HR) and susceptible lines (HS) in population for stem rust resistance. A set of 302 SSR markers was used to screen wheat genome using parents and homozygous contrasting bulks (HR/ HS) during bulk segregant analysis (BSA). The molecular and SRT information so generated indicated segregation for stem rust resistance at 2B chromosome for resistant parent CPAN4027. With the idtification of bin location of Sr(+), efforts will be made to map stem rust resistance major/minor genes in genotype CPAN 4027.

PP 1.14: Construction of linkage map using SSR markers and idtification of QTLs associated with salt tolerant traits in wheat (*Triticum aestivum* L.)

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Salinity is one of the major abiotic stress constraints affecting wheat production across the world.Therefore, development of wheat cultivars having tolerance to salinity stress is needed.However, breeding for salt tolerance by conventional means is difficult because of lack of selection criteria and complexity of the trait. However, idtification of QTLs and molecular markers associated with salinity tolerance can help breeding wheat varietiesforsalt stress. For this purpose a population (120 lines) of recombinant inbred lines (RILs) was developed using a cross between salt stress tolerant wheat cultivar Kharchia 65 and sensitive HD 2009, and evaluated for 2-years (2015-16 and 2016-17) under control (pH~8.1) and salt stressed (pH~9.2) conditions along with parents. A molecular genetic map covering 4725.16 cM with an average inter marker distance of 35.53 cM was constructed using 133 polymorphic microsatellite markers of which 49 SSRs mapped on D genome chromosomes, 44 SSRs on A genome chromosomes and 40 SSRs on B genome chromosomes. Genomic regions controlling traits related to salt tolerance were identified by using interval and composite interval mapping (using ICI Mapping) with a threshold of LOD 2.5. Twenty-fiveQTLs were detected for 10 different traits on 7-chromosomal regions (1A, 1B, 2D, 4D, 5D, 6A and 7D) which explained PVEs (2.6-15.1 %).Among these QTLs,QSNa+.iiwbr-1B, QSK+.iiwbr^{-2}D, QStn.iiwbr-4D, QSph.iiwbr^{-2}D.1, QSph.iiwbr-6A and QSdth.iiwbr^{-2}D were consistently reproducible in all environments and explained PVEs 2.6^{-2}.8 %, 10.2-12.6 %, 12.7-15.1 %, 4.8-11.4%, 9.8-13.1 % and 9.9-10.1%, respectively indicating strong genetic basis for salt tolerance. The information is useful in improving salt tolerance of wheat by using marker-assisted selection.

PP 1.15: Development of yellow rust resistant wheat lines using induced mutation breeding

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Although wheat has a wide range of climatic adaptability, it usually affected by many biotic factors the most devastating of which are the rust diseases. Wheat yellow (stripe) rust (caused by P. striiformis) is the major threat to whet production the wheat bowl of India. With recent emergence of new aggressive and virulent races of yellow rust, threat due to this disease has become an important concern. Induced mutations have been used as a tool to develop resistant lines in the wheat variety DBW 88. The variety was mutagenized by gamma rays at three different doses (*viz.* 250, 300 and 350 Gy), at

BARC, Trombay. M1 population (approx 3000 plants) was raised at Karnal and individual single plant harvests were advanced to M2 generation (approx 5000 plants) at during rabi 2015-16. The was screened for resistance to yellow rust under artificial epiphytotics with prevalent virulent races and nearly 92 putative variants showing resistance compared to parent were selected. To confirm the resistance in mutant progeny, putative mutant lines (M3) were advanced at IIWBR, summer nursery facility at DalangMaidan (HP) in offseason 2016. 72 mutant lines were advanced in M4 generation during rabi 2016-17 and in the M5 during offseason, 2017. The selected 50 lines were evaluated during rabi 2017-18 and the mutants were immune. The yellow rust resistant lines are being tested for yield and other agronomic traits (2018-19). The current success in identifying resistance to virulent races of yellow rust without altering favourable combination of genes responsible for yield related traits using gamma rays induced mutation breeding can be seen a successful method in wheat improvement.

PP 1.16: Developing wheat genotypes carrying resistance to pst. virulences through introgression of genes from diverse gene pools

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Wheat crop in India is affected by a large number of diseases, among which rusts are the most devastating and causing huge losses. Recently evolved virulences of stripe rust have created fear of rust epidemics in Northern India. Combining rust resistance genes is considered as one of the most effective strategies to achieve durable resistance to stripe rust. In this direction, 138 breeding lines of a three-way cross (HD3055/HS507//HPW349) were developed and evaluated at different generations for stripe rust resistance to a wide array of pathotypes at seedling and adult plant stage. The seedling reaction for infection type of stripe rust was recorded after a fortnight of inoculation along with parents and sets of differentials according to Stakman*et al*., 1962. Infection type at adult plant stage on flag leaf was recorded as per the method suggested by Roelfs *et al*., 1992 and disease severity was recorded as per modified Cobb's scale. DalangMaidan (HP), considered as hot spot for stripe rust, among 138 breeding lines, 26% of lines were recorded as resistant, 22% were moderately resistant, 28% were moderately susceptible and 24% were highly susceptible. But at Katrain (HP), 45% of lines were resistant, 27% were moderately resistant, 22% were moderately susceptible and 6% were highly susceptible. The genotypes were also challenged with new virulent pathotypes under green house conditions in three different sets of pathotypes *viz*., 110S119, mixed pathotypes (238S119, 78S84, 46S119) and (110S84, 110S119, 238S119) and we found variation for infection types. In our preliminary results, several recombinant inbred lines including SW765, SW780, SW816, SW840, SW841, SW842, SW867 and SW881 showed higher level of seedling andadult plant resistance than the parents, indicating accumulation of rust resistance genes for expressing broad spectrum resistance to stripe rust. These recombinant inbred lines will be developed as useful plant genetic resources to new virulences of stripe rust in India.

PP 1.17: Introgression of rust resistant genes in indian wheat cultivars using MABB approach

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Biotic and abiotic stress factors are the major constraints to wheat production and productivity. Among the biotic factors rusts are the most devastating pathogens that have hindered global wheat production since the domestication of the crop and still continue to threaten the world's wheat supply. Our study was aimed at targeting introgression of rust resistance genes in three wheat cultivars released from ICAR-IIWBR *viz*., DBW88, DBW107 and DBW110 for improving rust resistance through marker assisted backcross breeding. Leaf rust gene Lr32 was selected for introgression in all the three varieties; yellow rust gene *Yr15* was selected for incorporation in DBW88 and DBW107 and the stem resistance gene Sr26 was to be incorporated in DBW110. Five cross combinations *viz*., DBW88/PBW703, DBW107/PBW703, DBW107/FLW15, DBW110/FLW15 and DBW110/Sunlin were successfully attempted. Foreground selection for the presence of leaf rust resistant gene Lr32 was done using two SSR markers *viz*.wmc43 and barc135; for the idtification of yellow rust resistant gene *Yr15*, SSR marker gwm413 was used and for the idtification of stem rust resistant gene Sr26based markers *viz*. Sr26#43 and BE518379 were used for confirming presence and absence. For background selection the number of markers found polymorphic for different parental combinations were DBW88/PBW703 (79), DBW107/PBW703 (79), DBW107/FLW15 (86), DBW110/FLW15 (69), DBW110/Sunlin (59) were used. During the cropping season 2017-18 the BC1F3 populations were screened for background selection. Individuals with significant background recovery were identified in each combination, *i.e.* DBW88/PBW703 (up to 72.7 per cent), DBW107/PBW703 (up to 76.2 per cent), DBW107/FLW15 (up to 68.2 per cent), DBW110/FLW15 (up to 63.6 per cent), DBW110/Sunlin (up to 81.8 per cent). Till now a total of one hundred twenty polymorphic markers have been used on different crosses for Marker assisted backcross breeding technique which has helped in rapid idtification of desired resistant plants in the segregating progenies.

PP 1.18: Integration of gpc-B1 allele in two bread wheat genotypes also provides adult plant resistance against yellow rust

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Wheat (*Triticum aestivum* L. em.Thell.) is one of the oldest and most important globally cultivated cereal crops in the world. It's production worldwide is challenged by several biotic and abiotic factors, the condition being worsened by climate change. Out of various biotic stresses, stripe (yellow) rust, caused by Pucciniastriiformis f. sp. tritici (Pst), has been major concern with the changing climate particularly in northern latitudes. The disease spreads in epidemic form in cooler and humid environments as the rust spores have the capacity for wind dispersal over thousands of kilometers under high inoculum pressure from the initial infection sites. Lassik cultivar has Gpc-b1 allele for high grain protein content and Yr36 gene is tightly linked to it. Marker assisted breeding program was undertaken to improve grain protein content and yellow rust resistance. CAPs and ASA markers for Gpc-b1 were used for foreground selection. Background selection was also undertaken and agronomic performance in F8 generation was recorded. All lines were sown in replicates of three along with four checks *i.e.* DBW88, HD2967, HD3086 and WH1105. Four lines derived from WH711 × Lassik and two lines derived from PBW343 × Lassik were found promising in terms of grain yield and agronomic traits which can be further tested in IPPSN/ station trials developing improved wheat cultivars.

PP 1.19: Development of new diversified cytoplasmic male sterile (CMS) lines for hybrid wheat technology

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Wheat is one of the mainstays for global food security and it is necessary to increase the wheat production and productivity through new technologies. Indian wheat production is a success-story but most productive parts in India are now facing a kind of stagnation in productivity. Hybrid wheat technology is one of the innovative technologies which can play an important role in fulfilling the future need. For a successful hybrid wheat technology, CMS based hybrid development programme is promising. The primary requirement for successful implementation of this technology is availability of best CMS and restorer lines in Indian wheat background. A CMS development programme was initiated with diversification of male sterility source into Indian wheat background. For this purpose we used the CIMMYT originated male sterile line as a recipient parent and Indian wheat variety as a donor. After 7-8 generations of backcrossing with Indian wheat variety, 22 CMS lines were developed in the background of PBW 343, DBW 17, DBW 16 and PBW 502. Later 59 more lines were developed in 14 different Indian wheat backgrounds. These CMS lines were evaluated for extent of male sterility, days to heading and plant height as these traits are crucial for their utilization. Extent of male sterility was determined by bagging of five randomly selected spikes at heading stage and the seed setting was recorded in these spikes after harvest. All the 81 lines showed no seed set confirming to complete male sterility. Out of the 81 diversified CMS lines, 29 were selected based on the agronomic features, for further utilization as female parent in the hybrid development programme. These diversified CMS lines may be potential parent in development of successful hybrid cultivar that may enhance productivity due to their inbuilt capability to mitigate the effects of climatic changes.

PP 1.20: Genetic diversity studies over environments for yield attributes and some morpho-physiological traits in wheat *(Triticum aestivum* L.*)*

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Fifty six diverse wheat genotypes were evaluated for moisture-stress tolerance and to conduct diversity analysis in α- design with three replications under three environments *viz.*, irrigated (E1) and rainfed/moisture-stress (E2 andE3) environments. Data were recorded on grain yield attributes, phenology and morpho-physiological traits like excised leaf water loss (ELWL), stem reserve mobilization (SRM),dry matter accumulation (DMA), membrane stability index(MSI), drought response index (DRI) and drought susceptibility index (DSI). Analysis of variance revealed highly significant mean squares due to genotypes for all the characters across the environments. Pooled analysis of variance over environments indicated highly significant mean squares due to genotypes and genotype X environment interaction for all characters. On the basis of low DSI and high DRI values and relative ranking for other traits, wheat genotypes *viz.*, HPW 368, NI 5439, CM 33, CM 19, HPW 236, CM 11 and HPW 349 were found to be moisture-stress tolerant. On the basis of D2 statistics, the genotypes were grouped into 15, 19, 17 and 12 clusters in E1, E2, E3 and pooled analysis over environments, respectively. Under E2, cluster IX showed maximum value for grain yield/plant, tillers/plant, grains/spike and thousand-grain weight, while Cluster XVIII showed maximum mean values for biological yield and DMA. Under E3, Cluster XIV showed maximum mean values for ELWL and SRM, whereas, cluster XV had maximum mean values for seedling vigour and DMA. Cluster XVI included maximum values for grain yield / plant, thousand-grain weight and harvest index. Thousand-grain weight followed by MSI, seedling vigour and flag leaf area exhibited maximum contribution towards genetic divergence under E2, whereas, under E3, biological yield, grains/spike, DMA and thousand-grain weight were the main contributors. HPW 277, HPW 297, HPW 147, HPW 301, VL 892, NIAW 1415, NIAW1689 and Kanku were found to be superior and diverse for most of the traits, so these genotypes can be used in hybridization programme to obtain transgressive segregants under moisture stress environments.

PP 1.21: Evaluation of diverse set of bread wheat *(Triticum aestivum* L.*)* genotypes for grain yield

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Fifty advanced bread wheat genotypes of 24th semi-arid wheat yield trial (24th SAWYT) of CIMMYT were grown at16 locations in India during rabiseason of 2016-2017. The genotypes were planted in an alpha lattice design with two replicates per genotype and six rows of 3m length per replication with a plant-to-plant distance of 10cm and row-to-row distance of 25cm (gross plot size of 4.5 m2). Grain yield from four middle rows was measured (net plot size of 3.2 m2)and converted into ton ha-1. The yield data was analyzed by the stability models namely, Russel and Eberhart (1966), AMMI and GGE biplot. The experiment results showed that the genotypes G14 and G26 were most stable genotypes in Eberhart and Russel model of stability analysis. Whereas genotypes G10, G14, G18, G23, G26, G30 and G47 were found out to be stable in AMMI stability model. Stable genotypes identified in GGE model were G26, G23, G10, G43 and G14. Genotypes G14 and G26 turned out to be the most stable genotypes in all the three stability models. Genotypes G48 ranked best for (Durgapura, Pantnagar); G29 (Powarkheda); G35 (Hisar, Delhi and Ludhiana) and were top performers for grain yield.The GGE bi-plot indicated that Durgapura was an ideal environment followed by Hisar, Ludhiana, Delhi, Pantnagar and Powerkheda. These sites can be further used as representative environments for yield evaluation.

PP 1.22: Preliminary evaluation of emmer wheat in North Western Plains Zone (NWPZ) of India

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Emmer wheat (*Triticum dicoccum* (Schrank) (Schulb) is known for various therapeutic and nutritional qualities. Its products are in great demand both in India as well as abroad. However, in India, dicoccum wheat cultivation is restricted to Karnataka, Southern Maharashtra and Sourashtra region of Gujarat. Considering the potential use of dicoccum wheat in various health foods, the demand for dicoccum may arise in near future. There is a possibility that farmers of North Western Plains Zone (NWPZ) may start cultivation of dicoccum wheat in near future. 61 diverse genotypes of dicoccum wheat were obtained from UAS, Dharwad and evaluated at ICAR-IIWBR, Karnal during 2015-16, in order to identify superior genotypes. A wide range of variation was observed for various traits namely days to heading (86-102 days), leaf length (27.6-31.2 cm), leaf width (1.3-2.3cm), peduncle length (19.8-57.6cm), spike length (6.8-11.9), number of spikelets/spike (16-24), plant height (85-127.2 cm) and yield per plot (123-462g). Genotypes DDK GPM 50, 52 and 53 for plant height ≤ 85 cm, DDK GPM 58 and 59 days to flowering (≤ 86 days), DDK GPM 1 and 58 for spike length and spikelet per spike and DDK GPM 7, 11, 16 and 28 for yield per plot were found promising. The results suggest for inclusion of these genotypes in dicoccum breeding for NWPZ region of the country.

PP 1.23: Combining ability study for yield and its contributing traits in bread wheat *(Triticum aestivum* L.*)*

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Wheat is one of the most important crop amongst the cereals. It is a major staple food crop of the world after rice. Eight diverse genotypes *viz*, HD 3171, WH 147, K 906, K 307, K 1006, K 7903, DBW 14, and PBW 502, were crossed in diallel mating design excluding reciprocals for studying of combining ability analysis in F1 generation of wheat.The experimental material consisted of 36 genotype (28 F1s + 8 parents) was sown in Randomized Block Design with three replications at Crop Research Farm, Nawabganj of C. S. Azad University of Agriculture and Technology, Kanpur during Rabi

2017-18. Observations on twelve characters namely, day to heading (75%), plant height (cm), days to maturity, number of tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike (g), 1000 gains weight (g),biological yield per plant(g), grain yield per plant (g) and harvest index (%) were recorded in each treatment of all replications on five randomly selected plants. Analysis of variance (ANOVA) for combining ability revealedhighly significant variances for both general and specific combining abilities for all the characters indicating the importance of both additive and non-additive gene action in the inheritance of most of the traits. On the basis of per se performance and gca effects good general combiners were HD 3171, K 307 and PBW 502 for grain yield per plant. Parent HD 3171 was good general combiner for four other traits like, number of spikelets per spike, spike length, grain weight per spike, biological yield per plant and K307 for three other traits like number of spikelets per spike, spike length, biological yield per plant while PBW502 for one other trait biological yield per plant. On the basis of per se performance and sca effects good specific combiners was WH 147/K 1006, WH 147/DBW 14, K307/K 1006, K1006/ K7903 and K 7903/ DBW 14 for grain yield per plant. Cross WH 147/ PBW 502 was good specific combiner for five other traits like days to heading, number of spikelets per spike, number of grain per spike, grain weight per spike, biological yield per plant and K7903/ DBW 14 for four other traits like days to heading, plant height, number of grain per spike, biological yield while WH147/K1006 for three other attributes like number of grain per spike, 1000 grain weight and harvest index. Biparental mating followed by recurrent selection may be utilized to exploit both additive and non-additive gene actions and to obtain transgressive segregants in advanced generations for characters governed by such type of gene action.

PP 1.24: Assessment of genetic diversity amongst winter × spring wheat and triticale × wheat derived wheat doubled haploids using molecular and morpho- physiological markers

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Bread wheat is an important cereal crop of India and plays a vital role in nutritional and food security. Genetic diversity is a pre requisite for an efficient breeding programme that aims at the improvement of wheat productivity. The present investigation was conducted to assess variability, infer genetic relationship among yield and related traits and to characterize wheat genotypes using morpho- physiological and SSR markers. The experimental material comprised of 196 genotypes along with two checks which were evaluated for different morpho- physiological traits in Simple Lattice Design of 14 × 14 with two replications. Sufficient genetic variability was observed for seed yield and its component traits suggesting the scope of selection for these traits. High PCV and GCV along with high heritability and high genetic advance were observed for seed yield per plant and harvest index indicating additive gene action suggested selection would be effective for these traits. Genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients, indicating the inherent association among the various traits. Seed yield per plant showed significant and positive correlation with plant height, tillers per plant, grains per spike, 1000-grain weight, biological yield and harvest index. Biological yield per plant and harvest index were observed as best selection indices for increasing seed yield per plant. Principal component analysis revealed 65.33 per cent variation which was elaborated by the first four significant principal components. D2 statistical analysis grouped genotypes into six clusters whereas molecular analysis delineated them into three clusters thereby revealing that the population structure was mainly based on genetic origin along with moderate to high gene flow. On the basis of mean performance for seed yield, four genotypes *viz*, TWDH-6, HPW^{-2}36, HPW-147 and HS490 were superior to the best check HPW- 360.

PP 1.25: Assessing the variability in yield attributing traits among Indian wheat genotypes

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The projected global and India's wheat demand is 1090 and 140mt by 2050 respectively and this target can be achieved with annual production growth of 1.7 percent. The wheat yields and genetic gains in high productive areas are approaching ceiling and hence the trait based breeding is the need of the hour for future yield improvement. A study was conducted at the experimental farm of ICAR-IIWBR, Karnal with 21 high yielding wheat varieties released during last three decades. Plant traits like flag leaf area, plant height, culm thickness, spike length, stomatal density, Canopy temperature, chlorophyll a and b, nitrate reductase activity were recorded along with culm internal structure. The wheat genotype NIAW1415 recorded highest value of leaf area 68.85 cm2 and nitrate reductase activity (0.41 µmol NO2 h-1g-1FW), but highest stomatal density (213) was found in DBW 39 with lowest Canopy temperature. HD 2967 recorded highest value of chlorophyll a (24.3µg/g)and chlorophyll b (13.1µg/g)at 15 days after anthesis and also relatively high heat stress tolerance both at seedling and adult stage (based on TIR technique and HSI value). K 307 was identified with longest spike (14cm) with multilayered sceleranchyma along with well-developed conducting tissue. GW 322 has a maximum culm diameter of 4.55mm, a desirable trait for stem strength. These identified traits of high yielding wheat varieties can be efficiently used in future breeding programmes for improving yield gain in wheat to meet the future food demand. These traits in combination not only improve crop yielding efficiency but also reduce yield losses under climatic vagaries.

PP 1.26: Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.*)* under temperate climatic conditions

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Wheat is one of the most significant crops among the major cereals at the international level. Plant genetic diversity decides their eventual proficiency and uses for breeding, to augment and advance for production particularly during the current changing climate

Therefore, we investigated the extent of genetic variability present in wheat genotypes for various traits and the phenotypic correlation coefficients between yield and its component traits. Wheat genotypes were sown and evaluated under rainfed condition during rabi season of 2016-17 in a randomized complete block design with three replications with a plot size of 3.5x1.2 m. Analysis of variance (ANOVA) and mean comparison were performed using SAS ver. 9. Descriptive statistics and correlation analysis were performed Using SPSS Ver. 23. Cluster analysis and PCA was performed using R, PAST and STAT graphics Ver. XVI*I*. In the present investigationtwenty-four bread wheat (*Triticum aestivum* L.) genotypes were evaluated to estimate the extent of genetic diversity. Analysis of variance revealed that genotypes possess significant genetic variability for all traits at $p <$ 00.1. It was also observed that HPW 447 had recorded the highest value of 35.16 (q ha-1) whereas, HPW446 exhibited the lowest value (23.78 q ha-1) for yield. A significant positive correlation was observed among yield and biological yield traits. On contrary, yield and days to maturity revealed a negative correlation. Days to heading revealed a significant positive correlation with plant height (0.40) and a negative correlation with biological yield (-0.45), respectively. Diversity analysis classified the evaluated wheat genotypes into four distinct groups based on an index of similarity and dissimilarity of attributing traits. Group I and II have one genotypeeach *viz*., HS637 and HPW447, respectively whereas in third group 6 genotypes including HPW441, HPW444, HPW446, VL2030, HS634, and VL2025 are clustered together. The fourth group had two sub-groups. The first sub-group had five genotypes and the second sub-group had eight genotypes. The first three principal components based on the Euclidean similarity matrix explained 45.13, 17.85 and 14.71 percent of the total variation, respectively. Wheat genotypes (HS631, HPW 442, HPW 447, VL 2027 and VL2028) possess significant genetic variability and indispensable potential for use in breeding as candidate wheat genotypes under temperate conditions.

PP 1.27: Genetic divergence study in six rowed barley (*Hordeum vulgare* L.)

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Genetic variation is prerequisite for any crop improvement programme. Therefore it is important to have idea about the genetic divergence in available material for success of the breeding programme. Keeping in view an experiment involving fifty genotypes of barley was conducted during Rabi 2014-15 at Crop Research Farm, Nawabganj, Kanpur in Randomized Block Design (RBD) with three replications. Data was recorded on eleven characters such as days to 50% flowering, days to maturity, plant height, number of productive tillers/plant, spike length, number of grains/spike, grain weight /spike, 1000-grains weight, biological yield/plant, harvest index and grain yield/ plant.Analysis of variance revealed significant differences among genotypes for all the traits. High estimates of genotypic co-efficient of variation were recorded for grain yield/plant, biological yield/plant, number of productive tillers/plant, number of grains/spike, grain weight/spike and plant height.The fifty genotypes were grouped in to the eight clusters I, II, III, IV, V, VI, VII, and VIII using D2 analysis which consisted 6, 9, 6, 5, 4, 4, 10 and 6 genotypes respectively. Maximum inter-cluster distance was recorded between cluster V and VII (612.52) followed by III and V (484.64) and V and VII (383.41). Therefore crosses developed involving the genotypes belonging to these groups may give better transgressive segregants and heterosis. Maximum contribution towards expression of genetic divergence was exhibited by grain weight/spike followed by productive tillers/plant, grain yield/plant, plant height and biological yield/plant. This suggests that these traits played important role in conditioning the total divergence between the genotypes.

Theme 2: Biotic stresses in changing climatic scenario

KL 2: Discovery of diverse sources of rust resistance to win the battle against wider climatic adaptation of cereal rust pathogens

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Climate fluctuations in the last couple of decades have been challenging for crop production in many areas of the world. Rust diseases of wheat, caused by Puccinia spp., are known to cause severe yield losses worldwide. Wheat breeders have continuously been breeding for rust resistance under changing temperature regimes. Multilocation trials by breeding entities throughout the world represent a good example of selection of wheat genotypes against various biotic and abiotic stresses. In the last two decades, the stripe rust pathogen adapted to relatively higher temperature regimes and has spread to wheat growing regions that were non-conducive for its development. Similarly, the stem rust pathogen evolved to produce pathotype Ug99 that was virulent on the most widely deployed gene Sr31 in commercial wheat cultivars worldwide and was adapted to low temperature conditions in Africa. The Nobel Laureate Borlaug said 'rust never sleeps' and it reiterates that breeding for disease resistance is a continuous journey. Breeding against rust diseases is analogous to successful defence of a country, where army and air force collectively contribute towards safety of the nation. Resistance to rust diseases are controlled by genes that are effective during all stages of plant (all stage resistance; ASR; army) and those that express at the post seedling stages (adult plant resistance; APR; air force). This presentation will cover examples of discovery, characterization and deployment of ASR and APR sources of resistance to rust diseases in wheat using the cutting-edge genomic technologies.

LL 2.1: Taming the Beast-Wheat Blast Disease

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Wheat blast caused by *Magnaporthe oryzae* pathotype *Triticum* (MoT) was first reported in the Parana state of Brazil in 1985 and gradually dispersed to Bolivia (1996), Paraguay (2005) and Argentina (2007). Although blast remained confined to South America for three decades, CIMMYT scientists predicted a serious threat of wheat blast in India, Bangladesh and Ethiopia, due to climate similarities of these countries with South America. The fear came true in 2016 in Bangladesh, when an outbreak of wheat blast appeared in 7 districts in the west and south of Bangladesh, affecting about 15,000-hac wheat area. In the subsequent two years (2017 and 2018), despite the fact that wheat area in Bangladesh was sharply reduced in the epidemic region and disease development conditions were not favorable, wheat blast expanded further and was found in 13 districts including six new ones. This demonstrated the establishment of wheat blast in Bangladesh. As the agro-climatic conditions of a large portion of the wheat producing area of India and Pakistan is similar to Bangladesh, there appears to be a genuine fear that wheat blast may expand to India, Pakistan and other neighboring countries. Strategies to mitigate the impact of wheat blast in South Asia include concept of wheat holiday - stop wheat production for few years, seed treatment, fungicide application in the standing crop, and host resistance. Some of the success and challenges associated with the above strategies to manage wheat blast globally will be presented and discussed.

LL 2.2: Wheat rust research- impact, thrusts and road map to sustained wheat production

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Rusts are very devastating pathogens and are infamous for causing huge losses. Both yellow and black rusts can cause 100% whereas brown rust can cause 50% loss in wheat production. Wheat rusts are free moving pathogens and can spread aerially even across the continents in a short span of time like a wild fire. Introgression of new host resistance is easily overcome by these pathogens by evolving new matching virulences. Wheat rusts could overcome the resistance offered by transgenics even. Evolution of virulences for Lr24, Lr28 and Lr26/Sr31/Yr9 are few of the many examples. Arisal of more virulent forms often leads to the susceptibility of resistant varieties/genes and may result in epidemics as it has been seen in the cases of Ug99 and Yr9 pathotypes in many countries. According to the words of noble laureate Dr. Norman E. Borlaug, rust never sleeps. It is well known that wheat rust is a moving target and wheat Scientists cannot afford to be complacent. Therefore, there will always be a need to track and attack.

Over the years we have now better understanding of wheat rust pathogens, their life cycles, epidemiology, physiologic specialization, host resistance, genomes and molecular basis of host pathogen interaction. Decoding of wheat genome is also an advantage. A wider resistance gene pool including alien sources is available. Use of SAR, ISR, Transcription factors, PR proteins, RNAi, VIGS, Genome editing, Genome wide selection, MAS, Tilling population, and epigenetics are going to be the forefront technologies for managing the wheat rusts in future. Transgenic expression of useful traits such as disease and insect pest resistance, herbicide resistance etc. in crop plants are the best strategies for enhancing crop productivity in cotton, maize, soybean etc have been commercialized till date, yet the area under transgenic crops has increased tremendously in the last decade due to high adoption rate. Over the years, we expect these areas to be explored for managing wheat rusts.

In this environment, ecology and human health conscious society, we will continue to use host resistance intelligently as foremost tool to fight wheat rusts. Fungicidal application will be restricted to eradicate the initial foci of infection and under emergency situations only. A time tested strategy to manage wheat rusts is to identify new pathotypes in initial stages, map the pathotype distribution and have resistance gene/varietal deployment based on pathotype situation. While undertaking varietal deployment, a care is taken to use a blend of all time, adult plant (race specific and non race specific), slow rusting types of resistance and other modern features. However, with years more complex and super races are emerging, therefore, integration of present and modern day tools can provide durable rust resistance.

To combat wheat rusts, diversity for rust resistance at village, area, district, state, zone and national level is the key factor. When most of the wheat growing countries in the world had epidemics of wheat rusts during the last 30 years, India could not only avert the rust pathogens but had linear growth in wheat production and it touches 100 million tonnes. The success of the wheat rust management strategy can be envisaged from the fact that we had no wheat rust epidemics for the last more than 46 years.

OL 2.1: Idtification of marker–trait association for stripe rust resistance in bread wheat

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Stripe (yellow) rust caused by *Puccinia striiformis* f. sp. tritici, is one of the major diseases of wheat in the world. The losses due to this rust can be large and can vary from year to year and region to region. Discovery of novel genes and development of resistant wheat cultivars is the most economical and environmentally acceptable solution in combating wheat stripe rust. So far, nearly 78 genes conferring resistance to stripe rust have been identified. However, only few stripe rust resistance genes like Yr18 and Yr29, associated with durable resistance have been used extensively in breeding program. Information about other novel seedling resistance genes need to be generated for developing resistant wheat cultivars with adequate resistance against new virulent pathotypes of stripe rust. With this aim, seedling tests was conducted in green house at IIWBR, Regional Station, Flowerdale, Shimla in 2017 and 2018 winter seasons to evaluate the response of 158 spring bread wheat germplasm lines to the prevailing races of stripe rust at seedling stage. The genetic profile of the 158 genotypes was assessed using 35K axiom genotyping array and an association mapping was explored to determine marker-trait association. Only 19382 of the SNPs were polymorphic and hence used for association mapping analysis. GWAS was performed using a mixed linear model for identifying significant MTA. In the present study, 1A, 1B, 1D, 2A, 2D, 3A, 3B, 3D, 4A, 4B, 5A, 5B, 5D, 7A, 7B and 7D chromosomes contributed to 2.4 to 7.0% of the total phenotypic variance. SNPs showed association with stripe rust resistance QTLs could be used for marker assisted selection, while identified resistant germplasm lines could be used for developing stripe rust resistant cultivars in future.

OL 2.2: Idtification of long non-coding RNAs in response to leaf rust resistance in wheat

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Long non-coding RNAs (lncRNAs), a subclass of regulatory non coding RNA are non-protein coding transcripts longer than 200 nucleotides. Increasingly evidences suggest that lncRNAs are developmentally regulated and play important roles in development and stress responses of plants through gene regulation. Many promising plant lncRNAs have been identified in several plant species, such as maize, rice, cotton, tomato etc. in response to a series of stresses such as cold, heat, drought, salt and mineral deficiencies but very few lncRNAs have been identified in wheat and there is no study till date elucidating role of lncRNAs for wheat leaf rust disease which causes heavy loss of yield worldwide. Therefore we conducted a study to identify genome wide lncRNA in CSP-44 carrying an adult plant resistance gene, Lr48 at pre-adult (susceptible) and adult plant (resistant) stage under control and inoculated (Uredospore inoculation with *Puccinia triticina* race 77-5) conditions at different time intervals to predict their role in leaf rust resistance. Raw reads obtained from transcriptome sequencing data were processed using standard pipeline to predict the lncRNAs. As a result, total 3048 lncRNAs were predicted on genome wide basis, and out of these 197 were identified to be eTM (endogenous target mimics) by PsRobot tool. Repeat Masker classified predicted lncRNAs into different repetitive elements category as Retroelements, transposons, Small RNA, etc. Among 3048 lncRNAs, 763 were predicted to contain Simple Sequence Repeats (SSRs) by MISA, web server. Genome wide idtification of these lncRNA and their function in response to leaf rust infection would help in elucidation of role of lncRNA during leaf rust infection and to design the strategies to combat the same.

OL 2.3: Idtification of effective sources for spot blotch and stripe rust in barley

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Stripe rust and spot blotch are major biotic constraints in yield maximization in barley. Stripe rust is caused by fungus, *Puccinia striiformis* f. sp. hordei and wide spread in northern hills, foot hills and in the states of Punjab, Haryana and Rajasthan. Spot blotch (*Bipolaris sorokiniana*) is one of the major diseases in north eastern Indo-Gangetic plains having warm and humid climate. The resistant sources for stripe rust are available but the genetic resources for spot blotch are indeed meagre. Therefore, the present investigation was carried out to identify combined sources for stripe rust and spot blotch in barley. The experiments for stripe rust were conducted at Durgapura and Karnal during 2015-16 to 2017-18. While, spot blotch evaluation was carried out for two years at Faizabad and Karnal centres during 2015-16 and 2016-17. The indigenous genotypes namely DWRB127, DWRB128, DWRB136, DWRB137, DWRB143, RD2786 and Dolma showed highly resistance reactions for stripe rust. The exotic genotypes Orosus, Bella Union and Notch^{-2} exhibited resistant reaction for barley stripe rust and also showed spot blotch resistance with double digit scores 25, 36 and 36, respectively. The cross combination Canela/Cheri also showed resistance for barley stripe rust and moderate resistance for spot blotch. The identified genotypes are promising and would be gainfully utilized in future resistance breeding programmes.

PP 2.1: Idtification of stripe rust resistant winter wheat lines and utilization for spring wheat improvement

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In India, stripe or yellow rust of wheat (*Triticum aestivum* L.) caused by *Puccinia striiformis* westend f. sp. *tritici* effects wheat productivity significantly in North Western Plain Zone (NWPZ) of the country. In present investigation, 125 winter wheat lines from UK core collection were screened for yellow rust at ICAR-Indian Institute of Wheat and Barley Research Karnal, Haryana during 2015-16. From the artificial screening against of these 125 lines fifteen lines *viz*., EC721358, EC721396, EC609396, EC721320, EC721323, EC721362, EC721366, EC721374, EC721375, EC721493, EC721377, EC721378, EC721394, EC721397, EC721455 were showing resistance for yellow rust at adult plant stage. These 15 winter wheat lines were subjected to SRT analysis against predominant yellow rust races *viz*., T, 110S119, 238S119, 46S119, P, 111S68, 110S247, 78S84, 79S68, 7S0, 79S4, 6SO, K, 20A and L at ICAR-Indian Institute of Wheat and Barley Research RS Flowerdale Shimla. Infection types (resistant and susceptible) on the rust differentials/ test lines were recorded at 14-16 days after inoculation following modified method of Stakman *et al*., (1962). The infection types (ITs) 3, 3+ produced by pathotypes were considered susceptible, whereas lower ITs ('0', '1', '2' and 'X') were considered resistant (Nayar *et al*., 1997). The results revealed that all the 15 lines had shown resistant reaction (; to 2) against stripe rust races T, 111S68, 110S84, 78S84, 79S68, 7S0, 79S64, 6S0, K, 20A and L. The races 238S119, 110S247 and 110S119 were the most virulent and had shown susceptible response in 9 genotypes. The winter wheat lines EC721323, EC721394 and EC721397 had shown resistant response against all the races. These lines are being utilised in breeding programme as new sources for yellow rust resistance and broadening the genetic base for spring wheats.

PP 2.2: Evaluation of advanced breeding lines of wheat for yield components and rust resistance

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The exploitation of inherent potential of wheat in the form of high yielding resistant varieties is considered an economic viable and environmentally safe alternative to minimize losses in both produce quality and quantity. Changing climatic scenario has led to the evolution of virulent pathotypes of wheat rusts which render wheat varieties susceptible. A total of 153 advanced breeding lines were evaluated under preliminary yield trials (PYTs) for yield and its component traits at ICAR – IIWBR, Karnal during 2017-18. Most of these lines were bred through modified pedigree-bulk method however; some of the lines were direct selections from international nurseries received from CIMMYT, Mexico. For yield evaluation, the lines were planted in a plot of 6 rows of 6 m length and 20 cm apart. The experiment was laid in two replications with all the recommended management practices followed to raise a good crop. Six commercially grown wheat varieties were used as checks. Rust epidemics were created using most prevalent virulent races of yellow rust (46S119 and 110S119) and brown rust (77-5, 77-9 and 104^{-2}) at experimental. Also data was recorded on various agro -morphological traits such as days to heading, plant height, number of tillers, 1000 grains weight etc. The yield ranged from 1658-3672 g/plot with the mean of 2506 g/plot. The yellow rust severity ranged from 0-60S whereas, brown rust severity ranged from 0-40S. Based upon superiority over the checks with respect to yield and acceptable level of disease resistance (score ≤ 10MS) and grain quality, 25 lines were identified for further multi-location evaluation and if found suitable will be entered in varietal release process.

PP 2.3: Validation of molecular markers linked with agronomic traits and yellow rust in wheat and their further utilization in MAS

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Indian wheat breeding programs are constantly improving wheat quality, yield, and disease and pest resistance to maintain and expand domestic and international markets. Most of the Indian wheat varieties are developed by public wheat breeding programs. Each breeding program targets traits most important to its agro-climatic zone. Each zone has different pest and disease problems. Requirements for the agronomic traits of the varieties also vary from one wheat growing zone to another. Molecular markers, with lesser effect of environment and independence of stage and condition for their expression, present attractive option to breeders to improve selection efficiency. In our study 492-wheat genotypes released and cultivated across India were characterized with molecular markers for different agronomic traits based on vernalization and photoperiod sensitivity along with resistance to yellow rust resistant genes. The molecular markers for Vrn-A1 (Tm-60°C), Vrn-B1 (at-60°C),Vrn-D1 (at-65°C), Vrn-B3 (at-57°C), PpdA1 null (at-51°C), Ppd A1a.3 (at58°C), Ppd A1a ½(at-51°C), PpdB1a (A) (at-58°C), Ppd B1a.1 (B) (at-54°C), Ppd B1a (B) (at-60°C), Ppd D1null (at-56°C), PpdD1a (at-59°C), ppd D1a.1 (at-59°C), URIC/LN2-F (at-64°C) for Yr17, barc 8 (at-56°C) for *Yr15*, STS 7/8 (at-46°C) forYr5, SCAR (E51100 with at-56°C) for Yr10, gwm389 (at-51°C) for Yr57) and DArT-STS (Sun106 with at-56°C) for Yr51) were validated and used to characterize the wheat genotypes. These molecular markers are further being used in marker assisted breeding.

PP 2.4: Response of various wheat genotypes in NW Himalayan region against yellow rust disease

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To access the various responses of wheat varieties against yellow rust in NW Himalayan region, 1160 Mexican landraces, 240 Iranian landraces, 30 elite lines and 200 advanced breeding materials were screened along with check Agra local, PBW 343 and HD 2979. These lines were known to possess genes of yellow rust resistantance such as *Yr10, Yr16, Yr 9, Yr18* and *Yr27*. It was observed that 62 genotypes of Mexican landraces, 24 genotypes of Iranian landraces, 13 genotypes of elite lines and 85 genotypes of advanced breeding material gave resistance response to yellow rust. The resistant genotypes of 13 elite line also posses early maturity, higher test weight and yield. Stripe rust resistant genes (*Yr* genes) *viz.,Yr10, Yr15, Yr9, Yr18* and *Yr27* was crossed in all possible combinations and with genotypes PBW 343 and HD 2967. Eight agronomically superior and stripe rust resistant genotypes were selected for genetics of resistance. These were crossed with susceptible cultivars Agra Local/Lehmi, PBW 343 and HD 2967. Additionally, these were crossed among themselves. In all 28 no. Resistant x Resistant and 24 no. Resistant x Susceptible crosses were attempted. The results were found that 50 F1s showed resistant response against yellow rust. The selected lines were separately harvested to develop a new resistant variety of wheat against yellow rust disease in NW Himalayan region.

PP 2.5: Marker assisted pyramiding of rust resistance genes *Yr15* and *Lr57-Yr40* with high grain weight in PBW 550 background

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Wheat production is globally affected by rust diseases and deployment of resistant varieties with single rust resistance gene leads to frequent breakdown of resistance. One of the most effective strategies to incorporate multiple rust resistance genes is by marker assisted gene pyramiding. The aim of present study was to combine high grain weight (HGW) with rust resistance in background of an elite wheat variety PBW550. HGW introgression lines (IL) were derived from repeated backcrossing of PBW550 with HGW line Rye Selection III (BC2F4 PBW550-Rye Selection III) and stable ILs were developed. The HGWILs with thousand grain weight equal to more than 46.0gm were crossed with stripe rust resistant version PBW550+*Yr15* and single F3 plants with HGW and homozygous for *Yr15* were selected. Introgression for HGW was mapped with SSR markers selected at equal distance from the 21 wheat chromosomes. A total of 147 SSR markers were amplified on Rye selection III and PBW550+*Yr15* and 56 polymorphic SSRs were amplified on selected 423 F3 plants. Molecular data was subjected to graphical genotype (GGT 2.0) and introgression was obtained on all the three A, B and D genome chromosomes and with most of the F3 plants having multiple introgressions. Of the 56 polymorphic markers, SSRs from 9 chromosomes (1A, 2A, 4A, 6A, 7A, 1B, 2B, 3B and 2D) showed Rye Sel III specific introgression for HGW in 27 selected F3 plants carrying with *Yr15* also which were further crossed with PBW550 line carrying linked *Lr57-Yr40* genes. Plants with HGW having introgression of *Yr15* and *Lr57-Yr40* in homozygous conditions were selected using SSR and KASP markers, respectively again in F3 generation. Thus stable ILs with HGW and three rust resistance genes have been developed in PBW 550 background which will be evaluated in yield trials.

PP 2.6: Genetic diversity and association studies for seedling and adult plant stripe rust resistance in Indian bread Wheat

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In present study, a panel of more than 500 genotypes comprised of landraces, elite lines, exotic collection, released varieties and genetic stocks for various traits of agronomic importance. Genotyping of the panel was done using 35K Axiom SNP Array followed by quality filtering of markers. Genetic diversity and association analysis were done with 14K highly polymorphic SNP markers with available position information. Phenotyping of the panel was done for seedling resistance with five different races of Puccinia stritiformis (Pst) and also for adult plant resistance (APR). Diversification of resistance was observed in our study panel against stripe rust. In the diversity analysis based on SNP markers, three clusters were observed. The cluster having mostly indigenous genotypes was observed to have genotypes resistant to stripe rust. In association studies, 16 marker trait associations (MTAs) were found for APR, whereas, 12, 15, 13, 21 and 109 MTAs for Pst races *viz.* Yr_46S119, Yr_110S84, Yr_110S119, Yr_238S119, and Yr_T, respectively. In our preliminary studies, these MTAs were found to be significant (log10P ≥ 3), based on stringent evaluation in association analysis. Several genotypes were observed to have strong APR. The identified diverse resistant sources for stripe rust will be proposed to the breeders as crossing block entries for varietal improvement.

PP 2.7: Transcriptome analysis to identify gene and pathways associated with yellow rust resistance in wheat

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Stripe rust caused by *Puccinia striiformis* Westend f. sp. tritici is a devastating pathogen of wheat (*Triticum aestivum* L.) that can cause significant yield losses in almost every part of the world especially cooler areas. To examine the early response to the pathogen in wheat, gene expression alterations, inoculated leaf tissues of virulent and predominant pathotype 46S119at 12 hpi and 48 hpi (hour per inoculation) was measured. RNA-seq has emerged as the technology of choice to quantify gene expression and to provide a standard analysis framework with the packages of Bowtie2, TopHat, Cufflinks and CummeRbund. idtification and annotation of candidate gene will reveal genes directly or indirectly involved in regulation of biological processes, molecular function and DEG's (differentially expressed genes). Further detailed studies on these genes will help us know the expressions of various defence related genes which can be of great significance.

PP 2.8: Evaluation of UK wheat germplasm derived from Paragon\Watkins-Landraces for stripe and leaf rust in India

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Wheat stripe (*Puccinia striiformis* f. sp. tritici) and leaf (Puccinia recondita) rusts are the most important wheat diseases in major wheat growing regions of the world and in India also. A set of wheat germplasm lines derived from Paragon\Watkins-Landraces comprising 242 progenies received from John Innes Centre, UK were screened against stripe rust and leaf rust races at ICAR-IIWBR, Karnal and IIWBR-RS, Dalang Maidan during 2016-17 to identify resistance lines. The experiment was laid in augmented design with susceptible infector rows repeated after every 20 entries. Stripe rust response in 242 lines varied from free to highly susceptible (100S). Out of 242 lines screened, 5 lines were immune (Rust score=0), 81 were resistant (0-10S), 60 were moderately resistant (20S), 94 lines were moderately susceptible (30S-60S) and one line was highly susceptible (>60S). For leaf rust, 34 lines were early maturing and no disease was recorded in them. In 208 lines, normal distribution for leaf rust response was observed. Two lines were identified as immune, 56 lines were resistant, 45 were moderately resistant and 105 lines were moderately susceptible. The behaviour of resistance vs susceptible lines indicated that 3-4 adult plant resistant genes may be acting in additive manner to provide resistance against both the diseases. Resistant lines are being used as donors in crossing block to enrich the active wheat germplasm at IIWBR, Karnal.

PP 2.9: Forecasting stripe (Yellow) rust using molecular tools for sustainable wheat farming

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Stripe rust (yellow rust (Yr) of wheat caused by *Puccinia striiformis* f. sp. tritici (Pst), is one of the most widely devastating wheat disease in the world, especially in areas with cool and moist environments. Monitoring plant health and detecting pathogen early are essential to reduce disease spread and facilitate effective management to overcome stress. Therefore early detection of yellow rust pathogen, a highly susceptible wheat variety, Kharchia, was grown in net house. Leaf samples were infected with different strains of *Puccinia striiformis* f. sp. tritici (Pst). Leaf samples were collected at dierent intervals of post-infection with and without visual symptoms of pathogen and also samples of different pathotypes were collected from field area and genomic DNA was isolated from non-symptomatic and symptomatic leaves. LAMP PCR was performed on leaf samples. A simple and reproducible method was developed which could detect the pathogen at an early stage *i.e.* 3 day of post infection without any visible sign of pathogen attack on the leaf sample.

PP 2.10: Meteorological models for monitoring yellow rust in wheat crop

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An attempt was made to estimate yellow rust (YR) severity in wheat using weather parameters; prior to the occurrence of disease (generally January month) using multiple variables regression technique in SPSS software in US Nagar district of Uttarakhand. The weather variables directly influence and in most of the cases, it has been observed that a specific set of weather conditions prove to be congenial for the outbreak and infestation of YR disease. The models were developed using different combinations of meteorological parameters. Decadal/10 days' average of all meteorological parameters from 1st January to end of January(2005-06 to 2014-15), which is important for yellow rust disease development, was taken into consideration. The first model used only average maximum temperature of 1stdecade of January month and its co-efficient of determination (R2) was 0.47. Model 2 used both maximum temperature of 1st decade of January and maximum relative humidity of 2nd decade (average of maximum relative humidity from 10th January to 20th January) to estimate/forecast the disease impact. The measured disease index ranged from -0.49% to -14.52% and the disease severity estimated by model-1 and 2 ranged between 0.65% to -11.85% and 0.26 to -12.63, respectively. The high value of R2=0.69 (model^{-2}) suggests that meteorological models could prove to be accurate in estimating the disease losses precisely and timely. It was inferred that the model could be used effectively for estimating/forecasting the disease impact on wheat crop well in advance leaving the scope of disease control in the respective season, itself. The severity maps of yellow rust with different degree of severity for the rabi season 2005-06 to 2014-15 have been exported and displayed under the gallery section of web page (http://cropdiseasemonitor.in/).

PP 2.11: Development of Integrated Spray Schedule for the management of Leaf Rust of wheat caused by *Puccinia triticina* Eriks. in Karnataka, India.

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Leaf rust caused by *Puccinia triticina* Eriks.is considered to be the major constraint in the production of wheat in Karnataka. This is mainly due to the cultivation of leaf rust susceptible varieties like Amruth, DWR-162, Kiran etc. Two triazole fungicide *viz*, hexaconazole and propiconazole have been recommended long back for the control of leaf rust. However, their continuous use may pose the problem of development of resistance in leaf rust causal pathogen to these fungicides. Hence, in the present investigation efforts were made to develop an integrated spray schedule involving in vitro and cost effective fungicides, commercially available botanicals, bioagents, ITK's in an integrated approach for the management of leaf rust of wheat.Chlorothalonil at 0.1 percent, hexaconazole at 0.1 percent and hexaconazole 4% + zineb 68% at 0.2 percent were found effective in inhibiting uredospore germination. Similarly, among commercially available botanicals, bioagents and ITK's,nimbicidine at 1.0 percent, Trichoderma harzianum + Bacillus subtilis combination at 1.0 percent and panchagavya at 10.0 percent concentration, respectively were found effective in inhibition of uredospore germination of P. triticina.The spray schedule, hexaconazole @ 0.1 %- hexaconazole @ 0.1% has recorded highest grain yield of 35.38 q ha-1 with highest BC ratio of 2.30 and it was statistically on par with combi product, hexaconazole 4% + zineb 68% WP, hexaconazole 4% + zineb 68% WP 0.2% (35.13 q ha-1 and BC ratio 2.12). In case of spray schedule involving fungicide and non fungicide, hexaconazole 4% + zineb 68% WP 0.2%,panchagavya @ 10.0% rerecorded the grain yield of 33.45 q ha-1 with BC ratio of 2.20 followed by hexaconazole @ 0.1%-panchagavya @ 10.0% which has rerecorded the grain yield of 33.47 q ha-1 with BC ratio of 2.20. Hence, fungicide followed by ITK's found to be the best integrated spray schedule for the management of wheat leaf rust.

PP 2.12: Population dynamics of wheat leaf rust virulences in Karnataka, India

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In Karnataka, wheat is cultivated over an area of 2.0 lakh ha with production of 2.31 lakh tones and productivity of 1318 kg ha-1. Productivity of wheat in Karnataka is much lower compared to many of the north Indian states. This low productivity in Karnataka may be attributed to two reasons, one is that almost 60% of the area is under rainfed cultivation and another is cultivation of leaf rust susceptible genotypes (Amruth, DWR 162, Kiran etc.). Leaf rust (*Puccinia triticina* Eriks.) appears every year in Karnataka and it plays a major role in epidemiology as it serves as a donor of leaf rust inoculum to different parts of the country. Change in the virulence of *P. triticina* reflects the severity of leaf rust in other parts of the country. Hence, it is essential to understand the change in the virulence pattern of *P. triticina* in Karnataka for effective leaf rust resistance breeding in the country. In the present paper, data pertaining to virulence pattern of *P. triticina* in Karnataka over last 10 years (2005-06 to 2015-16) has been analyzed. Over the decade, totally 30 leaf rust races (12, 12-1, 12^{-2}, 12-3, 12-4, 12-5, 12-6, 12-7, 12-8, 12-9, 12A, 77A, 77A-1, 77-1, 77^{2}, 77-3, 77-5, 77-6, 77-7, 77-8, 77-9, 77-10, 77-11, 104^{-2}, 104-3, 104B, 162, 162-1, 162^{-2} and 162A) have been identified. Pathotype group 77 was identified with highest frequency of 40.00 % followed by 12 (36.67 %), 162 (13.33%) and 104 (10.00%). Pathotype 77-5 (36.67%) and 77-9 (23.33%) in 77, 104^{-2} (36.67%) and 104-3 (30.33%) in 104, 12-5 (16.67%) in 12 and 162^{-2} (16.67%) in 162 group appeared in highest frequency.

PP 2.13: Variability among Karnal bunt pathogen of wheat in India

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Karnal bunt (KB) of wheat caused by Neovossia indica (Tilletia indica) was first reported from India by Mitra in 1931. Since then it has been reported in other countries of South Asia (Afghanistan, Pakistan and Nepal) and from other countries of the world including Iran, Iraq, South Africa, Mexico and USA. In India, KB has been mostly severe in the north western plains zone (NWPZ) which provides wheat to the national buffer stock. Pathogenic variation among 17 Tilletia indica isolates was studied by inoculating on wheat varieties, WH 1105, HD 2967, HD 29, HP 1531, WL 711, PBW 502, WL 6975, HD 2009, DDK 1009, RAJ 3765, WH 542, PBW 343 and W 485 during 2014-15 and 2015-16 crop seasons. There was significant variation for Karnal bunt incidence and coefficient of infection with different isolates on different wheat varieties. During 2013-14, 39 monosporidial lines were isolated from single primary sporidia of *T. indica* infected grain of HD 2967. All lines were inoculated on two susceptible wheat genotypes, WL 711 and WH 542. During 2014-15 and 2015-16, twenty two monosporidial lines of T.indica were inoculated in different combinations on susceptible wheat varieties WH 542 and HD 2967. Compatible monosporidial lines which resulted in KB infection on susceptible wheat varieties were identified. Virulent isolates and compatible monosporidial lines identified in present study will help in identifying KB resistant sources for improving resistance status in popular cultivars of wheat.

PP 2.14: Heat shock protein 60 and glyceraldehyde 3-phosphate dehydrogenase act as a potential biomarker for early detection of Karnal bunt of wheat

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Karnal bunt (KB) of wheat, caused by Tilletia indica Mitra, is a vicious disease on wheat as well as an important international quarantined disease. Several genomic studies indicated that heat shock Protein (Hsp) 60 and glyceraldehyde 3-phosphate dehydrogenase (GPD) is found abundant in *T. indica* genome and serve as important virulence factor andfacilitate fungal invasion and colonization inside wheat tissues. Therefore, in this study, attempts were made to develop a diagnostic biomarker based on these genes for rapid and early idtification of *T. indica.* Protein sequences of these virulence related genes were retrieved from genome sequence of *T. indica* and subjected to further sequence and structure based functional annotation using bioinformatic tools. The conserved and variable region specific to KB pathogen was identified and different primer sets were designed and tested to detect DNA polymorphisms between *T. indica* and related species (*Urocystis agropyri, Tilletia foetida and Ustilago segetum tritici).* The primer combination Hsp60F1/Hsp60R1 and GPDF1/GPDR1 amplified a unique DNA fragment of 200 and 243 bp, respectively, in all isolates of *T. indica*, but not in the related pathogens. The detection limit with the primer set Hsp60F1/ Hsp60R1 and GPDF1/GPDR1 was 0.1 ng of DNA. In conclusion, both the primers set distinguished *T. indica* from other related pathogens.

PP 2.15: Idtification of bacterial endophytes with antagonistic potential for combating foliar blight (*Bipolaris sorokiniana*) of wheat

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Endophytes with bio control potential have received great interest as an eco friendly substitute to health hazardous chemicals employed extensively for the management of plant diseases. Bacterial endophytes from wheat cultivars (WB2, UP2950 and HD3272) were assessed for their potential as bio control agents against *Bipolaris sorokiniana* (BS), the causal agent of foliar blight of wheat. A total 78 endophytes were screened using dual culture techniques and examined for the effect on growth, sporulation and antifungal activity under in vitro conditions. Strain WB2-5, UP2950-7 and HD3272-18 significantly reduced the colony diameter of the pathogen. In addition, all these endophytes, reduced significantly the percent spore germination of BS compared to the control by 78%, 72% and 65%, respectively. These strains found non antagonistic to each other in compatibility test. Sensitivity tests to different levels of Vitavax (0- 1%; v:v) showed that these strains have tolerance upto 0.5% of fungicide. Phenotypic and biochemical features, together with 16S rDNA gene sequence similarly comparison with type strains indentifiedWB2-5, UP2950-7 and HD3272-18 strains as *Bacillus subtilis, Bacillus cereus and Bacillus subtilis* subsp. subtilis. From these findings, it can be concluded that these bacterial endophytes have potential in the biological control of foliar blight of wheat, but more greenhouse and field studies are required to confirm in vitro results.

PP 2.16: Spot blotch of barley caused by *Bipolaris sorokiniana* and its management

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The investigation regarding variability and management of *Bipolaris sorokiniana* and the yield loss caused by it was carried out during the year 2016-17 at Kanpur. The disease was reported in all the barley growing areas of Uttar Pradesh with the maximum disease occurrence in Kanpur district with the range of 29.55-48.15%, followed by Farrukhabad ranging from 29.28-45.82%. However, minimum disease was observed in Kannauj district (30.06-40.61%). Cultural and morphological variability of *B. sorokiniana* isolates exhibited that the colonies were effuse grey-white to effuse black and velvety-white mycelial growth with regular to irregular margins. The colour of colonies varied from grey to dark brown and white to light grey. The number of septation in isolates ranged from 3.9 to 6.3 and spore size ranged from 35.07 to 60.53µm in length and 13.20 to 17.60µm in breadth. The shape of the spore was elliptical, slight curved and straight with tapered end. All the isolates (BS1 to BS10) showed excellent growth on PDA while in PCA medium they showed fair growth. On the basis of pathogenic response of *Bipolaris sorokiniana* isolates on different barley genotypes, isolates BS2 and BS9 were categorized as highly virulent, whereas isolates BS7 and BS 10 as least virulent. Isolates BS2, BS3, BS4, BS5, BS6 and BS8 were moderately virulent. One hundred forty three barley genotypes were screened against spot blotch disease under artificially inoculated field conditions. Barley genotypes *viz.* BH1001, BH1003, DWRB157, RD2899, HLB113, KB1425, VLB118 were found resistant, while BH1004, BH1010, BH1011, BH1016, BHS444, BHS448, BHS449, DWRB140, DWRB149, DWRB151, DWRB152, DWRB153, DWRB154, DWRB159, HBL752, HUB242, HUB247, HUB249, HUB251, JB331, RD2946, VLB147, BHS352, BHS400, HLB276, K560, were ranked as moderately resistant against *B. sorokiniana.*

PP 2.17: Evaluation of powdery mildew and yellow rust resistance in advanced breeding material of wheat

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Wheat powdery mildew (PM) caused by *Blumeria graminis* f. sp. *tritici* (Bgt) and yellow rust (*Puccinia striiformis*) are the most important diseases in NHZ and NWPZ of India. Yield losses of upto 100% have been reported by both the diseases. Development of high yielding and disease resistant varieties is a continuous process which requires idtification of resistant donors. In this context, 61 advanced breeding lines of wheat developed at Malan were evaluated at hot spot locations *i.e.* Palampur (2016-17 and 2017-18); Malan and Dhaulakuan (2016-17); Kukumseri (Summer, 2016) and PAU, RS Keylong (2017) against PM and YR. The genotypes were also evaluated at seedling stage (ST) against PM at Malan. None of the genotypes were free and thirteen genotypes *i.e.* AB-67, 73, 102, 104, PW 1066, 1067, 1068, 1076, DW 212, BW 236, VL 892, HS 562 and VL 829 were moderately resistant to PM at ST. Thirty seven genotypes AB-4, 7, 9, 23, 40, 50, 51, 73, 74, 77, 85, 88, 90, 98, 99, 101, 102, 103, 105, 107, 108, 112, PW-1067, 1075, PW 1060, 1061, 1062, 1063, 1074, 1076, BW 235, 236, 241, DW 212, 214, 237 and VL 829 with mean disease severity ≤15% developed AUDPC, rAUDPC and infection rate/day (r) ranging between 241.1-641.6, 27.36-50.77 and 0.02-0.06 unit/day, respectively and were categorized as slow mildewing genotypes. Genotypes AB-7, 8, 22, 36, 40, 43, 50, 51, 60, 67, 77, 78, 82, 88, 90, 99, 104, 107, 108, 113, PW 1060, 1061, 1062, 1067, 1068, 1074, BW 235, 236, 241, DW 216, 218, HS 562 and VL 892 with mean YR severity ≤5 and were highly resistant and 13 genotypes (severity ≤10) were resistant. Five genotypes AB-103, BW 235, 236, DW 212, PW 1074 showed combined resistance to PM and YR.

PP 2.18: Threat assessment of Wheat Blast like disease in West Bengal

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Wheat blast caused by the fungus *Magnaporthe oryzae* pathotype *Triticum* (MoT) can infect many grasses, including rice, wheat, barley, lolium, but specific isolates of *Magnaporthe oryzae* generally infect only a single species; that is, wheat isolates infect only wheat. This disease is an exotic disease mainly occurring in South American continent. First sighted in Brazil in 1985, blast is widespread in South American wheat fields, affecting as much as 3 million hectares in the early 1990s and seriously limiting the potential for wheat cropping on the region's vast savannas. Experts had foretold the possible spread of blast from Latin America to regions of Africa and Asia where conditions are similar. A severe outbreak of blast in key wheat districts of south western Bangladesh in early 2016 has validated that prediction. In 2017 and 2018 this disease also reported from our neighbouring country, Bangladesh. The spread of wheat blast could be devastating to South Asia, which is home to 300 million undernourished people and whose inhabitants consume over 100 million tons of wheat each year. Therefore creation of strict quarantine measures, monitoring, generation of basic knowledge on pathogen, evaluation of wheat varieties and integrated disease management is of much importance to manage the possible threat of this disease. Keeping this view in mind, BCKV conducted three Trap Plot Nursery (12 entries) at different Government Farms confined to Indo-Bangladesh boarder of West Bengal. As per our finding, we could not observe any Wheat Blast Like (WBL) disease on these. In India wheat blast like disease symptoms may be caused under humid and warmer environment due to spot blotch and Fusarium head blight also. During our survey in 2017-18 crop season we could not notice any WBL disease at farmers' fields in any place of West Bengal (six districts– Hoogly, Burdawan, Malda, Birbhum, Howrah and South 24 Paraganas).

PP 2.19: Defensive breeding and preparedness to mitigate wheat blast disease

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Wheat blast, a recently reported disease of wheat from Bangladesh, has the potential for quick spread to Indian parts and thus to safeguard our wheat crop from future threats, continuous survey and surveillance in the Bangladesh bordering region (particularly West Bengal) and defensive breeding efforts were initiated at IIWBR, Karnal in collaboration with research organizations in West Bengal, Bihar, Jharkhand and Assam. This will require change in selection of parental lines, varietal promotion criterion and exercising selection pressure under natural hot spot locations for developing tolerant varieties with wider stability and adaptability. In addition, some preventive measures so as to restrict entry of the disease into the country it was advised to use only certified treated seed of the latest recommended varieties of wheat. The approach of defensive breeding strategies included i) idtification of potential donors based on screening of the Indian genotypes in Bolivia and Bangladesh as well as utilizing promising genotypes, sources possessing Milan/2NS translocations and exotic lines, resulted to potential donors to attempt target crosses, ii) advancing generation of these selected crosses at Off season nursery (Dalang Maidan) for faster the breeding programme, iii) constituting and conducting anticipatory wheat blast screening nursery including potential donors, promising lines and advanced generation breeding material at disease prone locations, iv) conducted regular surveys in bordering districts and creating awareness and interacting with the farmers and other stakeholders including state agriculture officials, v) organizing awareness cum training programme about healthy seed production of wheat in the region, vi) distribution of newly identified blast resistant variety DBW 187 in NEPZ. This approach will not only have preparedness to mitigate threat of wheat blast but will also help in improving productivity, resistance and stability of future wheat genotypes possessing better resilience to changing climate.

PP 2.20: Evaluation of Wheat germplasm for loose smut resistance

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Loose smut (*Ustilagonudatritici*) is the most serious internal seed borne disease of wheat particularly hilly areas of NW Himalayan states of India, wherein seed treatment is rarely practiced due to non availability of chemical as well as organic cultivation. Cool and humid weather favors the disease development by prolonging the flowering period. Under such circumstances disease management through host-plant resistance is the best option available to contain this disease. In the current study, 700 accessions of wheat were evaluated for resistance to loose smut during Rabi 2017-18. These were inoculated during rabi 2016-17. The Go-Go method was followed to inoculate each accession and 3 resistant (VL 639, VW 0919, VW 0948) and 3 susceptible checks (Sonalika, VL 977, VW 1159) were kept. Before anthesis, 5 ears in each accession were dusted with loose smut inoculum to produce sufficient seed for evaluation during 2017-18. Out of 700 accessions, 130 found immune (free of any infection), and 40 accessions showed highly resistant reaction (0.1 to 5 % infection).

PP 2.21: Characterization of symbiont diversity in corn leaf aphid, *Rhopalosiphum maidis* (Fitch) infesting wheat crop through metagenomic approaches

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Symbiotic microorganisms are widespread in nature and can play a major role in the ecology and evolution of animals. Associations among insects and microbes can lead to beneficial or parasitic interactions. Using 16S microbiome profiling sequencing, we compared microbiome diversity and abundance among field collected populations of the corn leaf aphid, *Rhopalosiphum maidis* (Fitch) infesting tolerant wheat variety, HD 2967 and susceptible genotype, A-9-30-1. The number of observed bacterial species was comparatively higher (384) and diverse (alpha diversity: 1.66) in aphid collected from tolerant variety HD 2967 than 359 species and 0.84 alpha diversity in susceptible genotype A-9-30-1. The fungal species associated with aphid collected from HD 2967 was 179 with alpha diversity of 3.35 as compared to 61 species with diversity 2.83in A-9-30-1. Our results suggested that *Buchnera* (relative abundance of 92.1%) and *Pseudomonas* (3.7%) were the major bacteria associated with R. Maidis collected fromA-9-30-1, but in HD 2967, Buchnera was the only abundant species (78.6 %).The major fungal genus associated with aphids were *Filobasidium, Alternaria* and *Cladosporium* with relative abundance of 44.5%,12.5% and 10.4% in aphid collected from susceptible wheat genotype, A-9-30-1.Our results will allow for improved comparative aphid-symbiont research and broaden our understanding of the interactions among insects, endosymbionts and their environments in wheat crop.

PP 2.22: Abundance of aphids and their associated natural enemies on wheat, *Triticum aestivum*

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The abundance of two species of wheat aphid *viz.*, *Rhopalosiphum padi* and *Sitobion avenae* and their different associated natural enemies was studied in Rabi season during 2017-18. The aphid population was recorded during firstweek ofJanuary and reached to their peak (30.40 aphids/shoot) during thirdweek of March. Among natural enemies, seven different species of coccinellid beetles were recorded. *Coccinella septempunctata, Hippodamia variegata* and *Coccinella transversalis* were found to be predominant. Peak population of adults (8.10 beetles/m2) as well as of grubs and pupae of coccinellids were observed during firstweek of April. The peak population of adults (13.00 adults/5 sweeps) and maggots/pupae of six different species of syrphids *viz*, *Episyrphus balteatus, Episyrphus viridaureus, Ischiodon scutellaris, Sphaerophoria sp.* and *Melanostoma* spp. was recordedduring thirdand first week of April, respectively. Lacewing, *Micromus* sp. started appearing on wheat from first week of March and peak population (2.65 adults/5 sweeps) was recorded during thirdweek of March. The peak activity of aphid parasitoid (Diaeretiella sp.) was found during first week of April with 16.60 per cent parasitization. All these natural enemies showed a significant positive correlation with aphid population. Aphids, lacewings and Diaeretiella sp. had positive but non-significant correlation with maximum and minimum temperature whereas, it was negative and non-significant with rainfall and relative humidity. Coccinellids and syrphids showed a significant positive correlation with maximum and minimum temperature.

PP 2.23: Management of termite through broadcasting of insecticides in standing wheat (*Triticum aestivum* L) crop.

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Wheat is most important crop which is grown throughout the country. A number of insect-pest have been found to attack the crop, out of which termite (*Odentoterm isobesus Rambur*) is regular and well established pest of wheat crop. Previously, they were considered as the serious pests of rain fed crop only. But now a days they are commonly seen infesting irrigated crop also. Keeping in view the above facts, field experiment was conducted at the Crop Research Farm Nawabganj, Kanpur under irrigated condition to observe termite infestation on variety K0402 for two consecutive years (2016-17 and 2017-18). Eight insecticides *viz*, Thiamethoxam 25WG (300gm/ha), Imidacloprid 17.8% (400ml/ha), Acephate 50% +Imidacloprid 1.8% (350gm/ha), Fipronil 5 SC (2.5lit ha-1), Imidacloprid 600FS48% (300ml/ha), Clothianidin 50WDG (200gm/ha), Fipronil 40% + Imidacloprid 40WG (1000gm/ha) and Chlorantranilprid 18.5%SC (200ml/ha) were tested. All the treatments with an untreated check were replicated thrice in 5×4 m plot size. Damage of termite was recorded five weeks after germination and finally at heading stage. The seed yield was also recorded at harvesting. Significantly lowest shoot damage at 5 week after germination was recorded 1.23 and 1.18% in Fipronil 40% + Imidacloprid 40WG treated crop in two consecutive years, which was at par with the shoot infestation in other treatments. Effective damage tillers/m row in Fipronil 40% + Imidacloprid 40WG were 1.33% and 1.21% in two consecutive years, while at heading stage, damage effective tillers were 2500 and 2333.33/ha in two consecutive years. At harvesting grain yield /m. row length was found significantly higher in all treatments in comparison to untreated check in both the years. It can be concluded that the shoot damage at 5 weeks after germination and damaged effective tillers at heading stage due to termite was recorded significantly lowest in the crop treated with Fipronil 40% + Imidacloprid 40WG and gave significantly higher grain yield in both the years.

PP 2.24: Seasonal abundance and management of wheat aphid, *Rhopalosiphum maidis* (Fitch.) in north western Himalayas

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Wheat is the most important Rabi season crop in Himachal Pradesh cultivated in 364.2 thousand hectares with production of 608.6 thousand tones. In Mandi district, it is cultivated in 66373 ha with production of 121.2 thousand tones. The crop had generally been free from the ravage of insect pests till recent past, but with changing climate wheat aphids especially, *Rhopalosiphum maidis* (Fitch.) has assumed economic importance and has become regular pest in all major wheat growing areas. Weekly observations on aphid count at RSS Sundernagar revealed that the aphid appeared during second fortnight of February/ first week of March on the crop and its population increased thereafter coinciding with grain development until last week of March. The peak population of aphids/head (56.43) was recorded during third/ fourth week of March and a declining trend in population was observed thereafter. Water pan trap catches in wheat crop also revealed higher catches of aphid during end of March. The population of natural enemies *viz*, lady bird beetle and syrphid fly was also high corresponding to aphid population build up. The temperature had positive and significant impact on aphid population. Among the synthetic insecticides evaluated for the management of wheat aphid, imidacloprid treatment resulted in minimum aphid count/head (0.28), followed closely by acetamiprid (0.80) and thiamethoxam treatment (0.87) after 7 DAS. Owing to minimum aphid population, imidacloprid treatment resulted in highest yield (3782 kg ha-1) followed by thiamethoxam and acetamipride. Among the organic formulations evaluated, Ghaniri (Polygonum) extract (50ml/liter) resulted in minimum aphid count/ head followed by Melia and Eupatorium extract at 7DAS.

PP 2.25: Seasonal incidence of aphid complex, an emerging insect pest of wheat in Hamirpur District of Himachal Pradesh

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Wheat is reported to be attacked by a number of insect pests *viz*, termites, armyworm, shoot fly, brown wheat mite, cutworms and aphids which hamper its production. The pest scenario in wheat has changed over the years and aphids are now emerging as an important insect-pest of wheat in Himachal Pradesh also. Keeping in view the current status of aphid infestation in wheat, studies were conducted on the seasonal incidence of aphid complex in wheat at district Hamirpur, which falls in the low hills of Himachal Pradesh. The study was conducted at three locations of the district *viz*, Dhanpur, Dobbar Kalan and Lag Manwin. The observations on aphid population were recorded at five randomly selected spots from the field at each location. Data was collected from ten randomly selected shoot per plant at weekly intervals starting from December till crop harvest. It was observed that the aphids started appearing during third week of January during both the seasons after which there was a slow increase in their population. The aphid population recorded a drastic increase during third week of March during 2010-11 (13.4 aphid/ shoot) and second week of March during 2011-12 (67.5 aphid/ shoot) which also was the peak aphid population. The aphid population further declined to 6.7 and 38.0 aphid per shoot during last and third week of March during 2010-11 and 2011-12, respectively; thereafter the aphids showed a sudden decline in population along with the maturity of wheat crop.

PP 2.26 *Melolontha virescens* Brenske: An emerging pest of wheat in high hills and dry temperate zone of Himachal Pradesh

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White grubs are highly polyphagous pest both in grub and adult stage and inflict heavy damage on various fruit/ forest trees, their nurseries, vegetables, lawns and field crops. The scarabaeid beetles are most common chafers, whereas larvae are among the most destructive soil pests feeding on roots of various plants. Almost all field crops grown during rainy season are damaged by the white grubs. In Himachal Pradesh, white grubs were reported earlier on forest/ fruit plants and potato; however, no record exists on any white grub damage to wheat until 2010. *Brahmina coriacea* (Hope) and *Holotrichia longipennis Blanchard* were found to be the predominant species of white grubs causing damage to different crops in Himachal Pradesh. Recently, in response to changing climatic conditions, *Melolontha virescens* Brenske was recorded in alarming numbers causing damage to several crops including wheat. In surveys conducted in Himachal Pradesh, *M. Virescens* was found to be fairly common in Chuhar valley and Sangla valley (2268^{-2}588 m amsl) of the state. Few adults were also recorded on light traps at Palampur. In wheat, the damage of *M. Virescens* grubs was recorded in Sangla valley. All underground parts of wheat were susceptible to grub feeding. The symptom of damage was root pruning by grubs showing varying degrees of wilting, yellowing, browning and eventually death of plant. There was appearance of patches of dry and wilted plants in the infested fields. There was browning and drying of leaves, followed by death of the plants. When the plants were uprooted, the roots were found to be totally pruned and the grubs were generally observed in root zone of the plants. In Barot valley, the adults of *M. Virescens* were collected on wheat spikes on first week of July. Although scarab beetles are generally nocturnal in behaviour and come out of soil at dusk, but *M. Virescens* beetles were also recorded on plants during day time. The observations on the biology of *M. Virescens* were recorded under laboratory conditions. After about one week of adult collection from the field, the egg laying was recorded in soil. Eggs hatched within two weeks of laying. In Himachal Pradesh, the pest was found to have two years life cycle. The third instar grubs occupied about 300 days. Full fed third instar grubs move deep into the soil and constructed an earthen cell and overwintering occurred inside these earthen shells. The third instar grubs averaged 55 mm in length and the head capsule width was approximately 8.4 mm. The grubs cause damage mainly in July; therefore the management strategies need to be targeted accordingly to check timely infestation of the pest.

PP 2.27: Eco-friendly management of rice weevil, *Sitophilus oryzae* on stored wheat

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Studies were conducted to evaluate different plant powders as grain protectants against rice weevil, *Sitophilus oryzae* (L.). For this purpose, ten different plant powders prepared from the shade dried leaves (drupes in case of Melia) of *Ageratum conizoides, Murraya koenigii, Ocimum sanctum, Ocimum basilicum, Mentha longifolia, Vitex negundo, Azadirachta indica, Eupatorium adenophorum, Melia azedarach* and *Eucalyptus citriodora* were mixed with the wheat grains (@10g/kg of seeds) of variety HPW^{-2}36. Counted number of weevils were released in each container and observations were recorded on adult mortality, population build-up, extent of damage and per cent germination at regular intervals after their release. The leaf powder of *A. conyzoides* proved to be the best treatment against the weevil which resulted into maximum mean cumulative mortality (96.67%), the lowest monthly average of population increase (18.33) and the least grain damage (12.61%) and weight loss (1.75%) in six months of storage. The next best treatment was the drupe powder of *M. azedarach* followed by *V. negundo* and *O. sanctum*. These treatments did not cause significant reduction in seed germination. *A. conyzoides, M. azedarach* and *O. sanctum* were found effective even after three months of their preparation. The leaf powder of *M. koenigii* resulted into the lowest mean cumulative adult mortality (14.23%), the highest monthly increase in population (132.78), the highest grain damage (47.50%) and weight loss (11.07%)

and the lowest germination (21.67%) after five months of treatment. Among ten plant powders, *A. conyzoides* and *M. azaderach* gave the best results against *S. Oryzae* which can be used as grain protectants for the eco-friendly management of the rice weevil in stored wheat.

Theme 3: Abiotic stress in relation to climate change

KL 3: Field crops breeding for resistance to biotic and abiotic stresses at ICARDA: Achievements and Prospects

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Crop production is highly affected by biotic and abiotic stresses at global level in general and in the Centeral and West Asia and North Africa (CWANA) and Sub Saharan Africa (SSA) regions in particular. Associated to climate change, heat and drought stresses are increasingly important resulting in reduction of photosynthesis, pollen viability, grain number and weight, and hence lowering yield and quality of major cereals and legumes crops. The crop breeding program at ICARDA uses conventional and molecular approaches such as FIGS, mega environments, shuttle breeding, doubled haploids, marker-assisted selection or genomic selection, speed breeding and key location phenotyping to identify sources of resistance, develop elite genotypes with high yield potential and resistance to the major biotic and abiotic stresses. Marker Trait Association (MTA) has been identified for different crops and they are being used in the breeding process. ICARDA distribute yearly more than 1000 of such genotypes to its partners through international nurseries. In the last 5 years alone, more than 100, many of them heat and drought tolerant varieties of ICARDA origin have been released by NARS in the CWANA and SSA regions.

LL 3.1: Mitigating abiotic stress for enhancing wheat productivity

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The major abiotic stresses of wheat in India include high temperature, drought, salinity/alkalinity, waterlogging, mineral deficiency, crop lodging and preharvest sprouting. Although more than 95% of the wheat area sown in India has access to irrigation, major parts face water deficits due to restrictions in the quantity of water availability particularly at critical plant growth stages. The entire wheat area in India experiences heat. The central and peninsular zone experience all through the crop season and significant parts of north-western and north-eastern plains experience terminal heat. About 6.73 million ha land in India is salt affected, 3.77 and 2.96 million ha are covered by sodic and saline soils, respectively. The Indo-Gangetic plains include 2.5 million hectares of sodic soils and 2.2 million hectares affected by seepage water from irrigation canal. Waterlogging adversely affects production in about 4.5 million hectares in irrigated soils of the Indo-Gangetic plains of northern India. The combined effect of salt and waterlogging stresses significantly reduces wheat yield. Preharvest sprouting (PHS) is also of major concern for wheat cultivation in eastern and far- eastern parts of India due to early cessation of rains around maturity time during the month of March. Crop lodging caused by storms and hail is another important factor which severely affects the wheat production. In addition, mineral deficiency is also likely to emerge as a major abiotic constraint in zones under intensive cultivation

The ICAR-IIWBR being a nodal institute for wheat research in India is having various programmes to mitigate these abiotic stress effects on wheat production. In the wheat co-ordination system extensive multilocation testing of the genotypes at various hotspots for different abiotic stresses across India was done. Based on these efforts, various varieties and genetic stocks for different stresses were identified. C 306, Dharwar dry, Hindi 62,NI5439, WCF-12^{-2}08 are tolerant to drought stress where as WH 730, Raj 3765, Halna and DBW 150 are heat tolerant genetic stocks identified and used in wheat breeding programme. The controlled condition screening was also followed for these stresses at ICAR-IIWBR by using precise phenotyping methods and facilities. The precision phenotyping for drought stress is done under rainout shelter (ROS) to identify the real drought-tolerant wheat genotypes. A novel temperature-controlled state of art phenotyping facility (TCPF) has helped in precise classification of heat tolerant and sensitive genotypes.

The micro plot facility have been established at ICAR-IIWBR for salt stress tolerance screening and some of the potential donors for salt stress tolerance includes Kharchia local, K 9423 and KRL 99. The screening for water logging and PHS has been regularly done in breeding programme both under multilocation testing in wheat co-ordination and under controlled condition by providing artificial screening environment. The lines namely Perenjori, BH 1146, Kharchia 65, Krichauff, DBW 39, PBW 343, PBW 636, KRL 268, NW 4018 and Six germplasm lines including 3 bread wheat (EC 383445, PI 376842, AC domain), two durum wheat (EC 362087,EC 201931) and one compactum wheat(CITR 4926) were identified as relatively tolerant to waterlogging and PHS respectively. The HD 2967 and few dwarf varieties were identified as lodging tolerant under controlled conditions. With all these integrated approaches to address multiple abiotic stresses India is able to achieve record wheat production for several years.

LL 3.2: How to adapt durum wheat to climate change: G + GxE against E

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Durum wheat is the tenth most important crop in the World, but its cultivation is mostly limited to harsh, arid, and heat prone marginal lands. Breeding for tolerance to these conditions is often considered the most strategic approach to ensure adaptation, especially when paired with best agronomical practices. The word 'adaptation' summarizes all the research efforts conducted to identify the many traits controlling the mechanisms for withstanding or escaping the traceries of the environment. It can be summarized as "GGE vs E". The durum wheat breeding program of ICARDA has released over 100 varieties in 25 countries since its initial inception in 1982. The strategy is to deploy genetic diversity from the genebank through targeted phenotyping methods in combination with genomic scans to dissect these 'adaptive' traits into simple loc*I*. These loci can then be pyramided via a combination of international field testing, markers assisted selection, genetically-driven crossing schemes, and genomic selection to derive climate-ready cultivars. Here, several examples of this approach are presented and their implications for 'adaptation' are discussed.

LL 3.3: Phenomics to accelerate wheat improvement in agro-ecosystems challenged by abiotic stresses: Focus on unexplored adaptive traits to stabilize yield

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Adaptation of wheat to a wide range of agro-ecologies is evident from the fact that it appears in sub-tropical to temperate agriculture from coast to the hills in diverse type of soils which range from sandy loam to deep black as witnessed in India. However, during domestication, many of the crucial adaptive traits were ignored with enhanced priority to productivity over adaptability. We cannot continue to do so as the genetic gain in wheat obtained through productivity improvement can fail to translate into production-increase in the events of extreme climate variabilities such as high temperature and sub or supra optimal precipitation at critical growth stage. This can be more evident in problematic soils featured by salinity, alkalinity and poor water holding capacity and can make it difficult to rely on mega-environment tailored breeding programs. With increasing realization that future gain in productivity is likely to come in bits and pieces, any efforts to introgression desired traits for abiotic stress tolerance can be effective if plant designs are matched with specific agro-ecologies with greater precision and speed. Abiotic stress traits will have to be the integral component of such designer plant types oriented for climate resilience. Thus trait-based breeding is the need of the hour which can be met through genome aided complementation of conventional breeding approach. However, this approach depends on While genomics has become robust enough to meet these demands there has been no matching progress in generating phenotypic data at a level desired for idtification of genes and QTLs with high power of predictions. Hence, characterization of plant responses has now assumed high throughput mode with interventions of image based tools and automation in recently emerged area of science called phenomics. These image based tools allow noninvasive quantification of crop growth, leaf senescence, morphological changes when cameras with visible range of wavelength are employed. It is possible to monitor tissue water content, photosystem health, and canopy temperature dynamics through NIR, chlorophyll fluorescence and infrared imaging systems. Further it has been clearly shown that it is possible to employ CT techniques to observe root dynamics without disturbing the soil and metabolite changes through hyperspectral imaging. Surrogate traits provided by these phenomics tools can effectively differentiate the genotypes for potential adaptive traits in plants. Thus they have potential to accelerate trait idtification and trait phenotyping for facilitating detection of genes relevant to abiotic stress tolerance. However, it is essential to optimize the methods for evolving phenotyping solutions targeted for particular crop and agro-ecological situations. With optimized methods not only the mapping population aimed at genes and markers but also germplasm collected and preserved in germplasm bank can be screened for potential donors for desired traits. Such efforts for hunting genes of relevance to abiotic stress tolerance can begin with small set of mini core or core set of genotypes representing huge collection. This needs inter-institutional and meaningful multidisciplinary approach involving crop scientists and even computational biologist which is possible with advances in these areas of science.

OL 3.1: QTL mapping and gene action studies in bread wheat under rainfed condition

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Wheat is one of the major important food and nutrition sources across the globe. Almost 20% area in India is rainfed and another 66% is under partial irrigation thus these are prone to drought. Six generation model in the cross MACS 6272 (drought tolerant) x UP 2828 (drought sensitive) was used to study the gene action and composite interval mapping (CIM) was used for the QTL detection during 2014-16. Eight physiological traits were studied under rainfed conditions. The scaling tests showed significance of either one or more scales in the traits under study except for relative water content (RWC). Canopy temperature (CT) was governed by significantly negative and positive additive x additive [i] and dominance x dominance [l] epistatic interactions, respectively. Dominance gene effect [h] and all digenic epistatic interactions were significant for SPAD trait. Grain filling period (GFP) was governed by significant additive x additive [i] and additive x dominance [j] epistatic interactions. Grain weight (GW) showed significant additive and dominance gene effects, as well as negatively significant additive x dominance [j] epistatic interaction. The complexity in the inheritance of grain yield per plant and harvest index was evident as these traits were governed by duplicate gene action (along with SPAD) with significant dominance gene effect [h] and epistatic additive x additive [i] and dominance x dominance [l] interaction. Thus, grain yield and harvest index needs patience on breeder part and one has to wait for selection in later generation. The rest of the traits except relative water content (RWC) were having significant epistatic interactions and thus their improvement needs selection to be exercised in later generations of segregation. Composite interval mapping detected 25 QTLs with LOD scores ranging from 3.3 to 9.1. Nine QTLs out of these twenty-five are within 50 cM distance from the closest marker. The identified QTLs from composite interval mapping were associated with canopy temperature, SPAD value, NDVI and GW, and the chromosomal locations were also identified. The findings of the study could be useful in wheat breeding programme

OL 3.2: Exploring heat stress responsive microRNAs and their targets in developing seeds of wheat using small RNA and degradome profiling

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High temperatures during grain filling stage directly affect the metabolism, growth duration and grain filling rates, as well as quality, grain maturity, and hence overall yield of wheat. During heat stress, miRNAs act as significant regulatory factors in controlling gene expression by repressing translation or promoting degradation of the target mRNA. In this study, 36 wheat genotypes were evaluated for heat tolerance under controlled and stress conditions for two consecutive years at ICAR-IIWBR. On the basis of precision phenotyping, Raj 3765 (heat tolerant) and HUW 510 (heat susceptible) were chosen for miRNA studies. Four small RNA libraries were prepared from developing seeds at 10 days after anthesis from the two genotypes grown in normal and heat stress conditions. High-throughput sequencing and its analysis revealed 76 conserved miRNAs mostly belonging to MIR156, MIR159b, MIR160, MIR398 families and 80 novel miRNAs. To gain an insight of the functions of the novel miRNAs identified, the putative targets of these miRNAs were predicted. Gene Ontology and KEGG pathway enrichment analyses of the expressed miRNAs indicated their involvement in signal transduction (e.g. MAPK cascade), carbohydrate transport and metabolism, chaperone binding, reactive oxygen species (ROS), metabolic process (e.g. hydrogen peroxide catabolism), hormone-mediated signaling pathways (e.g. auxin, abscisic acid- activated signaling pathways) and transcription factors (e.g., MYB, ZFP, MYC, bZIP). Through degradome sequencing, the targets of miRNAs, degradation sites and cleavage products were identified. The cleaved targets of various miRNAs were found to correspond to transcripts involved in seed development (cell division, cell size, seed maturation) and heat stress responses. These observations indicate the miRNA driven regulation of gene expression and how these miRNAs influence the regulatory pathways involved in wheat's heat stress response during seed developing stage.

OL 3.3: Dissection of salt tolerance in wheat: Mainstreaming soil sodicity and residual alkalinity in irrigation water for agricultural sustainability

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To unravel the adaptation of salt tolerant wheat variety KRL 210 (CSSRI bred), a total of 126 demonstrations were conducted in farmers' participatory mode under predominant rice-wheat system in salt affected agro ecosystems representing marginal to high soil sodicity and RSC waters. In technology validation trials, ruling variety of wheat was taken as control (farmer's practice, HD 2967) and salt tolerant wheat variety KRL 210 was taken as new technology. To reduce the experimental error, technology validation trials were categorized into six groups accordingly to stress intensity, such as soil pH2<8.0, 8.0-8.5, 8.50- 8.75, 8.75- 9.00, 9.00- 9.25 and >9.25 and RSC <3, 3-4, 4-5, 5-6, 6-7 and >7 meq/l. Cumulative average gains elucidate 4.4% increase in grain yields was observed with salt tolerant wheat variety KRL 210 in comparison to HD 2967. Under normal conditions (pH2<8.0), HD 2967 attained significantly higher grain yield (5.4 t ha-1)in comparison to KRL 210 (5.29 t ha-1). Although non-significant differences was observed in both the varieties at marginal sodicity and poor quality irrigation water (upto soil pH2~8.5 and RSC~4 meq/l).However at increasing sodicity stress (beyond soil pH2>8.5) and deteriorating irrigation water quality (RSC>4 meq/l), grain yield superiority of KRL 210 was observed with each incremental gradient in comparison to HD 2967. Confidence of interval (CI) of regression coefficient for sodicity stress (soil pH) indicated lesser yield reduction (750-960 kg ha-1) with KRL 210 compared to 940-1260 kg ha-1/unit in HD 2967 for each unit increase in soil pH. Similarly, confidence of interval for RSC water indicated yield reduction of 330-490 kg ha-1/unit for KRL 210 against the yield reduction of 470-670 kg ha-1/unit in HD 2967. It is interesting to note that sodicity (soil pH) has more profound effect in terms of yield penalty in comparison to residual alkalinity in irrigation water (RSC). In conclusion, problematic sodic soils having soil pH2>8.5 irrigated with high RSC waters (RSC>4.0 meq/l) may be set as critical limit for choosing salt tolerant wheat variety KRL 210 over the traditional ones and can be recommended as an important biological reclamation strategy to counter the yield reduction in wheat under sodic ecosystems.

PP 3.1: *In silico* approaches for development of miRNA-SSRs for use in targeting heat tolerance in wheat

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Wheat is one of the most commonly grown cereal grain worldwide. High and stable yields are the most important target for wheat breeding. Due to increase in average global temperature, abiotic stress such as heat stress has become one of the major limiting factors in wheat production especially at the reproductive and early grain filling stages. Heat stress leads to damaging cellular structures, altering various metabolic pathways, relating to membrane thermo stability, photosynthesis and starch synthesis. Since it is a polygenic trait, difficult to quantify and is regulated by different molecular mechanisms. MiRNAs are non-coding RNAs which are highly conserved and regulate gene expression. These are involved in various biological processes, metabolic pathways and their networks. MiRNA SSRs (micro-RNA simple sequence repeats), a new class of molecular markers, are functional markers that could be used for marker assisted breeding. Although several wheat SSR markers are available now, challenge remains to identify the trait-specific miRNA-SSRs which can be used in wheat breeding. In order to identify heat responsive-miRNA SSRs in wheat, twelve heat responsive miRNA of wheat were selected from data available in public domain and sequences containing miRNA were retrieved. Further, these sequences were used for SSR mining using default parameters and tri-nucleotide repeats (GGA) were found to be predominant. Only seven primer pairs were designed from SSR flanking regions with BatchPrimer3 server. The parameters were set as follows, length range= 18-23 nucleotides with 21 as optimum, PCR product size range = 100-400 bp, optimum annealing temperature = 55°C, and GC content 40-60% with 50% as optimum. The designed SSR primers were validated using in silico PCR. Only six miRNA-SSRs were validated in wheat genome with the help of in silico PCR (primerdigital.com/fastpcr.html). Experiments are in progress to use these MiRNA-SSR markers in molecular analysis of selected wheat genotypes. This would pave the way for tagging heat tolerance trait and accelerating wheat improvement program after genetic diversity assessment of wheat cultivars/ germplasm.

PP 3.2: Genotype specific profiling of rhizosphere metagenome and physico-chemical properties related to heat tolerance in bread wheat

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In India wheat is a major cereal crop grown across different climatic zones. Among different species of wheat, bread wheat (*Triticum aestivum*) constitutes nearly 95 % of the India's total production. However, it is prone to fluctuations in temperature during anthesis and maturaty stages. The present study was aimed at studying variations in the rhizospheric parameters of the heat tolerant and sensitive genotypes grown under irrigated conditions at Karnal. The parameters studied were total rhizosphere microbiome, carbohydrate active enzymes, physico-chemical properties, root exudates profiles and plant growth promoting rhizobacterial (PGPR) population at booting and anthesis stages. Rhizospheric soil samples were drawn from field conditions and temperature controlled phenotypic facility in triplicate at both stages of bread wheat varieties HD 2967(sensitive) and WH 730 (tolerant). The rhizospheric soils, loosely and tightly bound to the roots were processed for metagenomic analysis and physico-chemical properties. The values of pH, electrical conductivity, sodium, magnesium, bicarbonate and chloride increased from booting to anthesis stage in heat tolerant genotype WH 730 compared to sensitive genotype HD 2967. The PGPRs population also increased several folds during anthesis stage in tolerant genotype. Amongst root exudates, D-xylose and citric acid were absent in tolerant genotype at booting stage, while D-Galactose and L-Arabinose were absent at anthesis stage. In metagenomic analysis, bacteria belonging to *Azovibrio* genus and Pedosphaerales group were exclusively present in the rhizosphere of tolerant genotype at booting stage. However, at anthesis stage bacteria from *Nocardioidaceae* family and *Flavisolibacter* genus were exclusively present. At both stages, bacteria from few specific genus and family dominated in rhizosphere of the tolerant genotype than the sensitive genotype. CAZy analysis was also performed, which showed nearly one and a half fold higher OTU values in sensitive genotype at booting stage, which shifted to nearly two folds higher in tolerant genotype at anthesis stage.

PP 3.3: Heat Susceptible Index: Major selection criteria for idtification of heat tolerance donors towards development of climate resilient cultivars in wheat

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Heat stress is one of the major limiting factors in wheat production and quality of produce. It is expected to rise under present scenario of climate change. It influences growth and development especially anthesis, and accelerates the grain growth rates resulting in shortened grain filling duration, is responsible for decline in wheat production in many environments worldwide. The objective of the study was to identify the heat tolerant and susceptible genotypes among 27-wheat genotypes. Heat Susceptible Index (HSI) was calculated from diverse parentages for estimation of yield reduction based on differences in yield traits between the stressed and control to use it as selection criterion for heat tolerance in two consecutive years. The phenotypic and genotypic correlation was carried out by single-marker linear regression approach in order to confirm the association between the SSR markers and the phenotypic traits *viz.*, grain filling duration (GFD), grain weight (GW), thousand grain weight (TGW) and grain growth rate (GGR). The HSI of GW, GGR, TGW and GFD explained up to 34.98, 28.50, 27.30 and 24.30 % additive phenotypic variance in the first year respectively whereas, 26.14, 10.87, 17.37 and 16.67 % in the second year respectively of study for heat tolerance using data individually pooled from two consecutive years. Based on reduction percentage under stress conditions and HSI for TGW, genotypes NW 1014, HS 277, K 7903, K 9107, AKW 1071, RAJ 3765 and DBW 17 were found tolerant during both the years. Molecular Markers indicated high level of polymorphism, and significant marker traits association was found for GW, TGW and GGR. This study validates the use of these yield attributing traits for measuring heat tolerance and hence, can be targeted for future studies. Use of such genotypes in breeding programs towards the development of heat tolerant varieties will be helpful in minimizing the losses due to heat stress.

PP 3.4: Heat Susceptibility Index and Correlation Analysis in Bread Wheat

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The P1, P2, F1, F2, BC1 and BC2 were developed from 5 parental genotypes of wheat *viz,* DBW 14 (heat tolerant), NP 846 (heat and drought tolerant), PBN 51 (heat and drought tolerant) and WH147 and RAJ4014 (heat susceptible for late sown). The F1's of all the crosses were susceptible bearing S value of > 1.0 and the F2's segregated in tolerant as well as susceptible level for all the four characters used in the heat susceptible index. The BC1 and BC2 were examined on the basis of heat susceptible index and biological yield. The heat susceptible index for biological yield revealed that biomass was affected when temperature rises from +4.5 to 6.8 0C. The high yield tolerant parents in their respective crosses performed better in the segregating material whereas S was either <0.5 (heat tolerant) or 1.0 < S > 0.5 (moderately tolerant). Based on heat susceptibility index DBW 14, NP 846 and PBN 51 were identified as heat tolerant and RAJ 4014 and WH 147 were observed as heat susceptible lines for late planting. Reduction in number of tillers per plant decreased grain yield per plant. High yielding genotypes responded in a way to escape from the heat stress at terminal stage by their genetic makeup while the low yielding crosses behaved by reducing the heading period. Selection for short duration genotypes would be effective in the breeding material generated from the crossing of low x high yielding parents, while the crosses with high x low yielding parents might throw the segregating genotypes for delayed leaf senescence. Correlation analysis depicted favourable association of higher x lower yielding crosses under late sown condition.

However, lower x higher yielding crosses were found to be associated with quantitative and physiological traits under timely sown condition.

PP 3.5: Mitigation of heat stress through application of chemicals in Wheat (*Triticum aestivum* L.)

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Wheat is grown in India under sub-tropical environment during mild winter. The crop gets exposed to higher ambient temperature of the summer as well as hot spells at the time of grain filling which cause significant reduction in productivity. Terminal heat stress is an important constraint during wheat production. This can be managed by applying different chemicals, so an experiment was conducted with an objective to study the effect of these applications on growth and yield of wheat. In light of this a field experiments on "Mitigation of heat stress through application of chemicals in Wheat (*Triticum aestivum* L.)" was conducted at the Research Farm, Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (MS, India) during rabi seasons of 2016-17 and 2017-18. The study involved twenty-one treatment combinations comprising of three sowing dates in main plot (*i.e.* 25th November, 15th December and 5th January) and seven chemical treatments in subplot *i.e.* Glycine betaine (600 ppm), Salicylic acid (400 ppm), Salicylic acid (800 ppm), Ascorbic acid (10 ppm) + Citric acid (1.3%), α- tecopherol (150 ppm), KCL 1% and control (no spray) which were evaluated in factorial randomized block design with three replications. Among the different dates of sowing, 25thNovwas found significant for all the morphological, physiological and biochemical parameters except the cell membrane thermos-stability (% heat injury). Foliar application of different chemicals had significant effect to mitigate the heat stress. As compared to recommended sowing date, Optimum yields (39.52q ha-1) were recorded under late sown condition besides, more test weight (38.24g) and less stomatal frequency (55.57). Among foliar applications of chemicals, the treatment Ascorbic acid 10 ppm + citric acid 1.3%, had significant effect on grain yield (46.60q ha-1). Other treatments like, salicylic acid 400ppm; Tsalicylic acid 800ppmand Glycine betaine also recorded appreciable yields (39.01 q ha-1, (36.97 q ha-1 and 34.88 q ha-1, respectively). Foliar application of above treatments in late sown condition also improved the yield as compared to control. Ascrobic acid 10ppm + citric acid 1.3% followed by salicylic acid and glycine betaine were found to be the best chemicals to mitigate the heat stress in wheat crop.

PP 3.6: AMMI and GGE Biplot analysis of Indian Durums under terminal heat stress

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In India, Durum wheat is cultivated in more than one million hectares in central and peninsular regions, where the effect of heat stress is prominent especially during the grain filling period affecting the crop yield drastically. To evaluate the stability and performance of durum wheat under late sown conditions, a field study was conducted for three seasons *i.e.*, 2012-2013 to 2013-2014 at ICAR-IARI, Regional Station, Indore (Madhya Pradesh) India, involving 102 durum wheat genotypes at two sowing dates *i.e.*, late sowing (7th December) and very late sowing (25th December) every year. Sowing was done in two rows of 2.5 m length each with a row to row spacing of 18 cm in RBD in three replications. The stability performance analysed using AMMI biplots and Biplot analysis have showed that both AMMI and GGE bi plot analysis genotypes ranked HI 8498,MACS 9, N 59 RAJ 6516 as most stable genotypes for grain yield, similarly MACS 3125, WH 896 were identified as high yield genotypes but suitable for specific conditions under late heat stress. HI 8550, HI 8653, Mandsour Local, NI 5759 were found to be best stable genotypes for high number of tillers under all the environments; for stable low canopy temperature under pre anthesis stage both model explains that the genotypes Line 1172, MACS 2694, MACS 306, MPO 1215 having low canopy temperature and were highly stable for all the environments. GGE and AMMI biplot ranked GW 1139, GW 1170, GW 1209, N 59 as best stable genotypes for 1000 grain weight. This study showed that the genotypes tolerant to post-anthesis high temperature stress and short duration can be best suited to the late sown conditions of India increasing the scope for durum wheat production under late sown and terminal heat stress conditions in India.

PP 3.7: Evaluation of bread wheat genotypes for heat stress tolerance

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Genetic resources enable plant breeders to create novel plant gene combinations and select crop varieties suited to needs of diverse agricultural system especially in changing climatic condition. In the present study 300 test entries of aestivum wheat with 3 checks () were evaluated in an augmented design in timely sown and very late sown condition ecology representing non stress and stress environments. These genotypes comprised of international nurseries (CIMMYT and ICARDA) lines, synthetic lines, advance breeding lines, exotic lines, Ug99 resistant lines and released varieties. Heat susceptibility index and reduction percentage was estimated for non stress and stress condition. The adjusted treatment effects were significant for all the agronomic traits except spikelets per spike; whereas adjusted block effects were found non significant indicating homogeneity of blocks in both the condition. Mean squares due to controls vs varieties were found significant for all the traits under evaluation indicating test entries significantly differ from the controls. Under timely sown condition on an average of 10 blocks, GW 451 was the best check and out of 300 only six genotypes surpassed the best check, whereas in heat stress condition GW11 was the best check and under this condition only eight genotypes surpass the best check for grain yield. Only three principle components had Eigen values above unity and as such were considered. The latent roots ranged from 1.69 for first PC to 0.45 for Sixth PC. The first component explained 28.22 % of variation followed by PC2 (20.35 %) and PC3 (17.33 %). Promising genotypes showing low Heat Susceptibility Index (HSI) and per cent reduction were identified from studied material could be a potential source of donor parent in breeding programme aimed at heat tolerance.

PP 3.8: Evaluation of LOK 1× HUW 468 RILs population of wheat for terminal heat stress using grain size parameters

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Seed shape and size are the most important among agronomic traits because they affect seed yield and market price. To promote genetic analysis and selection for seed size and shape in plant breeding, an efficient, reliable, high-throughput seed phenotyping methods are required. "GrainScan" a high throughput image based software tool was used in our study for evaluation of wheat RILs population (LOK1 × HUW 468). 151 RILs including parents were sown under two conditions *i.e.*, timely (20th Nov) and late (20th Dec) during 2017-18 and harvested seeds of each line were analyzed using GrainScan software that gave result of different grain size parameters like grain area, grain perimeter, grain length and grain width. Heat susceptibility indices (HSI) was calculated for each grain traits using both sowing condition and their results being used for screening genotypes against terminal heat tolerance. In our study, ANOVA of HSI of 4 traits showed highly significant variation for genotypes confirmed a wide variation among RILs population. The RILs were categorized on the basis of HSI values as, <0.0 (negative value indicating better trait performance in late sown condition, highly resistant), 0.0 to 0.25 (resistant), 0.25 to 0.5 (moderately resistant), 0.5 to 0.75 (moderately susceptible), 0.75 to 1.00 (susceptible) and >1.00 (highly susceptible). A significant number of genotypes was recorded as HSI value <0.05 for 4 grain traits, on this basis 63, 65, 64 and 72 lines were found to be tolerant for seed area, seed perimeter, seed length and seed width respectively. Out of these lines, 36 genotypes were common and found to be tolerant lines for all grain traits. Therefore, estimation for HSI of grain size parameters could be effective way for evaluation of wheat lines against terminal heat stress and may subsequently be utilize in breeding program for heat tolerance.

PP 3.9: DNA methylation patterns in wheat cultivars with contrasting response under drought stress

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DNA methylation is heritable epigenetic mechanisms regulating gene expression in plants in response to environmental conditions in which the activity of DNA segment change without changing sequence. Drought stress is responsible for changes at morpho-physiological, biochemical and molecular traits in plants. In this study, methylation patterns under the drought stress in two contrasting wheat genotypes were assessed using methylation-sensitive amplified polymorphism (MSAP). Sixteen wheat genotypes were evaluated for drought under controlled and stress conditions. Out of these, we selected two contrasting wheat genotypes for methylation studies and results revealed that demethylation was higher in C306 genotypes (drought-tolerant genotype) as compared to HUW468 (drought-sensitive genotype). A total of 535 and 295 reproducible amplified fragments were generated in root and leave samples, respectively. A high percentage of polymorphic bands resulted after comparison of different MSAP pattern between tolerant and susceptible wheat genotypes for root and leaf samples at booting, anthesis, heading and tillering stages. Moreover, a different number of contrasting allele were found between drought tolerant and susceptible genotypes at heading stage (9), tillering (7), anthesis (4) and booting (3), respectively. Only 1/3rd of the total contrasting loci were found in leaves as compared to roots. Therefore, DNA methylation might play an immense role in morphophysiological and biochemical changes that occur in roots to make a plant tolerant to drought stress. Additionally, a few sites with stable DNA methylation differences were identified between drought-tolerant and drought-sensitive cultivars, thus providing genotype-specific epigenetic markers. These results not only provide data on differences in DNA methylation changes but also contribute to dissection of molecular mechanisms of drought response and tolerance in wheat.

PP3.10: Uncovering drought responsive microRNA in root tissues of contrasting wheat genotypes using high throughput sequencing

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Drought stress is a major environmental constraint contributing to disastrous impacts on plant growth, yields and the quality of the produce. MicroRNAs change the regulation of gene expression at either transcriptional or post transcriptional level, which controls the molecular signaling pathways of the plant's response to drought. In this study, 16 wheat genotypes were phenotyped for drought tolerance under stress and controlled conditions at ICAR-IIWBR, out of which NI5439 (drought tolerant) and WL711 (drought susceptible) were selected for miRNA studies. Four small RNA libraries (two from each genotypes) were constructed from the root tissues. High throughput sequencing result revealed a total of 349 precursor miRNA sequences, 59 conserved miRNAs and 243 mature novel miRNAs. Most of the miRNAs belonged to MIR9662, MIR159, MIR9653 and MIR9664 families. Differential expression of the wheat miRNAs in tolerant and sensitive wheat cultivars implied that miRNA regulation is different between the tolerant and susceptible wheat cultivars under water deficiency. GO and KEGG pathway enrichment analysis indicated relevant biological processes. GO analysis showed a majority of the miRNAs involved in response to stimulus, catalytic activity and transporter activity. The KEGG analysis indicated many targets involved in metabolic pathways, including plant hormone signal transduction (ABA signaling, auxin response pathway), ABC transporters, photosynthesis and drought-related transcription factors such as AP2, EREBP, MYB, WRKY, ERF,GAMYB, HD-Zip III, and NAC. These identified candidate novel and conserved miRNAs from the present investigation reveal important information about the regulatory mechanisms underlying plant resistance to drought stress in wheat.

PP 3.11: Comparative rhizosphere metagenome and physico-chemical profiles associated with contrasting genotypes of bread wheat under rain-fed conditions

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Wheat is one of the major cereal crop of the world grown in almost all continents. Among the crucial inputs, water is one, which is going to decide the future production statistics. Thus under present study, rhizospheric microbiome, carbohydrate active enzymes, physico-chemical properties, root exudate profiles and the Plant Growth Promoting Rhizobacterial (PGPR) population of drought tolerant and sensitive genotypes were studied at booting and anthesis stages. Wheat (*Triticum aestivum*) varieties HUW 468 and C306 grown under rain-fed conditions were used in the study. The drawn samples were divided in to loosely bound and tightly bound to the roots and were processed for metagenomic analysis and physico-chemical properties in triplicate. The values of electrical conductivity, sodium, bicarbonate and manganese increased from booting to anthesis stage in drought tolerant genotype C306. The population of majority of the PGPRs also increased several fold during anthesis stage in tolerant genotype C 306. Amongst root exudates, D-xylose, D-fructose and citric acid were absent in tolerant genotype, while these were present in sensitive genotype. In metagenomic analysis bacteria belonging to *Haliangiaceae* and *Sinobacteraceae* family, while of *Sphingomonas* and *Agrobacterium* genus were exclusively present in the rhizosphere of drought tolerant genotype. Enhanced proportion of *Streptomyces, Flavisolibacter and Xanthomonadaceae* was also recorded. Slightly varied spectrum was recorded during booting stage, means the class of bacteria varied at different growth stages and were decided by the genotype. At booting stage *Pseudomonas, Flavobacterium,* Gemmatimonadales were exclusively present while *Agrobacterium, Streptomyces, Kaistobacter and Nocardioidaceae* were in higher proportions. CAZy analysis was also performed where a shift in OTU values from booting to anthesis stage was noticed for six classes of carbohydrate active enzymes. At booting stage it was nearly three times higher in sensitive genotype, which changed to slightly higher in tolerant genotype at anthesis stage.

PP 3.12: Application of phenomics to assess intra-spike variation in grain size in wheat (*Triticum aestivum* L.) exposed to soil moisture stress

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Reduction in grain weight is one of the responses when crops like wheat are subjected to drought. This reduction varies across the length of the spike. We hypothesized that the genetic variability with respect to intra-spike variation in grain size can be one of the opportunity to improve grain weight per spike and hence to improve the productivity of wheat. However, this task is tedious as size of each grain has to be measured in a large set of germplasm or breeding lines. Hence we explored phenomics approach involving image based tools to assess the intra-spike variation in grain size. Ten genotypes varying in their spike morphology and grown in varying soil moisture stress environment at the time of grain development were used to determine the genetic variation in grain morphology. Each grain was separated from the rachis of each of the three spikes for each genotype under each treatment. Images were acquired with Samsung Galaxy J2 Cell Phone with maximum care to retain the exact distance between the camera and the object placed on dark background. An open source software Imagej was used to analyse the number of grains per spike and the size of each grain at different locations within the spike. The image based parameters like area, the number of objects in each image, length and width could explain the actual number of grains per spike, width and length of grains in selected genotypes. The method developed could differentiate sensitive and tolerant genotypes with respect to their capacity to retain grain size even under soil moisture conditions relative to plants grown with sufficient soil moisture. The results proved that it is possible to quantify intra-spike genetic variation in grain size in wheat by employing image based phenomics approach. We demonstrated it by using images acquired by mobile phone and open source software for image analysis.

PP 3.13: Idtification of moisture stress tolerant wheat genotypes using physiological indices

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Moisture stress being temporally and spatially heterogeneous is highly unpredictable and a major concern for crop productivity in arid and semi-arid regions of the world. In India also, it is one of the major constraints for achieving potential wheat yields across various wheat growing zones. The situation is further worsened by increased frequency of weather extremes and unpredictable rainfall due to climate change. For sustaining productivity, the ability of wheat genotypes to perform fairly well under variable moisture stress is an important trait. Several drought stress indices *viz.* stress tolerance (TOL), stress susceptibility index (SSI) and stress tolerance index (STI) have been suggested and have proved to be robust in identifying the tolerant high yielding genotypes under moisture stress conditions. The study was conducted for two consecutive years in split plot design replicated thrice with irrigation in main plots (80% and 60% of CPE) and thirty genotypes () in sub plots to identify moisture stress tolerant wheat genotypes with desirable yield and WUE. Relatively smaller TOL and SSI values suggest better stress tolerance, whereas, it is reverse in case of ST*I*. Out of thirty, ten genotypes produced optimum yield in the range of 5099 kg ha-1 (IBWSN-1278) to 4730 kg ha-1 (UAS269\HD2819\\24thSAWSN-3192) under 80% CPE with water use efficiency of more than 1.54 kg/m3. Significant positive correlation between yield and STI was obtained with the highest value for highest yielding genotype IBWSN-1278 (1.581) whereas it was 1.157 for UAS269\HD2819\\24thSAWSN-3192 having 10th rank. In contrast, the genotypes with 1st (IBWSN-1278) and 2nd rank (DBW-166) in terms of yield recorded -0.772 and -0.351 SSI, respectively. The lowest TOL values were recorded for IBWSN-1278 ($^{-2}$.480).

PP 3.14: Genetic studies for grain yield and some agro-morphological traits in bread wheat (*Triticum aestivum* L.) under moisture stress conditions

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Twenty-five diverse wheat genotypes varying in adaptability and drought tolerance were evaluated under irrigated (E1) and drought-stress (E2) environments with the objectives to characterize variation in their response to drought stress and to work out drought resistance indices for identifying selection criteria. Analysis of variance revealed that mean squares due to genotypes were highly significant for all the characters except grain weight per spike under both the environments. Grain yield, peduncle length and plant height exhibited high heritability coupled with high genetic advance under E2, while high heritability coupled with moderate genetic advance was exhibited for grains per spike, grain weight per spike, thousand-grain weight, biological yield, harvest index and grain filling period. High PCV, GCV, heritability and genetic advance was obtained only for flag leaf area under E2. Correlation analysis indicated that grain yield had a significant positive correlation with spike length, effective tillers per plant, grains per spike, grain weight per spike, biological yield, harvest index and flag leaf area under both the environments. Besides, grain yield had significant negative correlation with drought susceptibility index ('S') and significant positive correlation with peduncle length, plant height, seedling height and drought response index ('DRI') only under E2. Path coefficient analysis revealed that biological yield followed by harvest index had high positive direct effects on grain yield under both environments. Also most of the traits exhibited high indirect effects via biological yield and harvest index under both the environments. Biological yield and harvest index appeared to be the important characters for selecting high yielding genotypes under both conditions. On the basis of low drought susceptibility index 'S' and high 'DRI' values, wheat genotypes *viz.*, NI 5439, C 306, kanku, NIAW 1415, NIAW 1594, HPW 349, WH 1021 and HS 507 were found to be moisture stress tolerant.

PP 3.15: Utilization of shuttle breeding approach for the development of drought tolerant genotypes

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The climate change is being considered as major bottleneck in production of food crops in the country. Water scarcity coupled with early and late heat stress is a common climatic feature of the wheat crop grown in central and peninsular India which affects crop growth at different stages of development. Targeting development of specific breeding lines is a promising methodology to cope with such abiotic stresses. Shuttle breeding, devised by NE Borlaug, is a promising approach to develop stress tolerant genotypes. A research programme on breeding wheat genotypes for warmer areas was initiated with integration of shuttle breeding approach with cooperation of wheat research centres of central and peninsular India. In this, the target specific crosses were made at IIWBR, Karnal and segregating populations were planted at the cooperating centres where selections were made in location specific environments. The selected materials were shuttled between Karnal and the cooperating centres in alternate filial generations for screening under high productive as well as stress environments. The resultant advanced lines were evaluated under timely sown irrigated (IR) as well as restricted irrigation (RIR) conditions and the data were recorded for yield and its component traits and physiological parameters. The yield data under irrigated and restricted irrigation were utilized for estimating various drought tolerance indices. During 2017-18, a total of 120 advance lines along with 8 check varieties were evaluated for yield and physiological traits under IR and RIR conditions and based on drought tolerance indices, 14 genotypes were found promising. Among these 14 entries, five were contributed to the IIWBR station trial-4 for RIR condition and ten entries were contributed to the Drought Tolerance Screening Nursery (DTSN) during 2018-19 crop season. The better performance of these genotypes for various drought tolerance indices indicated adaptability of these entries to varied stress environments which was attributed to the shuttle breeding approach. These entries may be further utilized in wheat improvement.

PP 3.16: Effect of salinity treatments on germination and early seedling vigour in wheat (*Triticum aestivum* L.) genotypes

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Four genotypes of wheat (*Triticum aestivum* L.) RSP 561, Raj 3765, WH 1080 and C306 were subjected to salinity treatment using NaCl at concentration of 0 M, 0.01M, 0.05M, 0.1M, 0.5M and 1M to study its effect on germination and early seedling vigour. The experiment was conducted under laboratory conditions by growing the seeds in petri dishes with different salt concentration. Data on germination parameters *viz.*, germination percentage, recovery test and root length were recorded. Early seedling vigour at 20 days after sowing was recorded in terms of seedling growth, chlorophyll content, root/shoot length, root/shoot biomass and salt tolerance. A general trend of decline in percent germination with increase in NaCl concentration was recorded for all the genotypes under study. Days to germination also increased for all genotypes at all concentrations of treatments indicating the inhibitory role of NaCl in the biochemical pathway of germination. The genotype C 306 appeared to be the most tolerant while WH 1080 was the most sensitive to NaCl during germination. The genotype RSP 561 was the most tolerant in terms of early seeding vigour and growth. The increase in NaCl concentrations decreased the shoot/root length and biomass of all the wheat genotypes. The response of all genotypes to salinity stress followed similar pattern indicating non differential mechanism of salinity tolerance across genotypes till germination. The intensity of stress varied with the genotypes and those which responded poorly at germination stage showed better response at seedling growth stages.

PP 3.17: Bread wheat germplasm screening for alkalinity tolerance under field condition

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In India among all the crops, wheat suffered the highest production loss of around 4.60 million tonnes due to salt stress. Every year, India loses ~ 3.60 million tonnes of wheat production from 3.77 Mha of sodic area, which accounted monetary loss of rupees 4996 crores. These problems of soil sodicity can be managed in two ways either change the growing environment or through development of salt tolerant cultivars. Although development of cultivars depends on the genetic resources, unfortunately very few salt tolerant donors *i.e.* Kharchia and its derivatives (KRL 3-4, KRL 99 and KRL 19) are available. Keeping in mind these views; a screening trial consisting of 1513 indigenous/exotic accessions was conducted under alkaline field condition (pH 9.1 to 9.6) during 2015-16 at CSSRI, Karnal. The plant materials (100 seeds per entry) were sown in 1 row of 2 meter length with 30 cm apart in a non- replicated trial (ARCBD) with seventeen blocks each having 90 accessions and five standard checks (KRL 3-4, Kharchia 65, C 306, RAJ 3765 and HD 2967) were repeated in every block randomly. Simple univariate methods and analysis of variance were used to examine the variation within the set of gene pool. Wide variation was observed for the genotypes based on the studied traits. Based on the statistical analysis 25 indigenous/exotic germplasm (IC405226, IC443722, IC279230, IC572928, IC547592, IC260876, IC531920, IC531998, IC554661, IC47550, IC416168, IC535493, IC335683 IC47797, IC524304, IC336648, IC138600, IC540908, EC463441, EC556485, EC415831, EC463434, EC574784, EC479375 and EC566309) showed yield potential (>Adjusted Mean+2.576SD), better that the best check KRL 3-4. These can be used as potential donors for developing alkalinity tolerant cultivars. These lines can also be used for idtification of salt tolerance gene using allele mining tools and their deployment for the development of salt tolerant bread wheat cultivars.

PP 3.18: Characterizing the plasticity of wheat seeds under terminal heat stress

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Wheat, one of the staple food grain crops, provides maximum share of the carbohydrate and calories in the diet. Terminal heat stress which is one of the major problems in wheat growth and yield. Here, we analyse the effect of elevated temperature during pollination and grain filling on starch filing, packaging and quality of seeds of wheat cultivars HD 3086 and HD 2967. We observed significant variations in the size of harvested seeds in both the varieties under heat stress; the seed size in case of HD 2967 was bigger as compared to HD 3086 under terminal heat as compared to control. The seeds in wheat cv. HD 2967 showed non plasticity, as compared to cv. HD 3086. Total starch and amylose content decreased in both the cv. under heat stress; percent decrease was observed maximum in HD2967 (7.7%) as compared to HD 3086(6.5%) under terminal heat .we observed increase in the total amylolytic activity in both the cultivars under stress (HD 2967: 4.8 sp. activity and HD 3086: 4.9 sp. activity) as compared to control (HD 2967: 3.9 and HD 3086: 4.0) .The plasticity of seed was measured in terms of total antioxidant potential. The TAC was observed maximum in seeds of HD 3086(9.5Mm/g) as compared to HD 2967(7.3Mm/g). The thermo tolerance capacity of HD 2967 was observed better at all the stages (pollination and grain filling) as compared to HD 3086. There is a need to further characterize the regulatory network associated with defence and nutritional traits of seeds in order to enhance the quantity as well as quality of wheat grains.

PP 3.19: Mitogen activated protein kinase gene(s): signaling molecule triggering the defence network of wheat under heat stress

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Wheat (*Triticum aestivum* L.), one of the most important and ancient cereal crops grown across the world. It provides 55% carbohydrate and 20% of the calorie in the diet. Although, adapted to a wide range of agro-climatic regions,wheat is sensitive to heat stress (HS), especially during critical stages drastically reducing the quantity and quality of grains. Under the present era of climate change, plants have evolved an inbuilt defense mechanism to combat abiotic stresses including signaling pathways among which Mitogen activated protein kinase (MAPK) cascade is one of the major players. Here, we identified 64 novel transcripts from wheat showing homology with MAPKs using de novo transcriptomic sequencing approach. Based on the digital fold expression, transcript_1494 was targeted for the cloning. RT-PCR amplification showed amplicon of ~1.3 kb which was further cloned and sequenced by Sangers di-deoxy method. The nucleotide sequence was submitted to NCBI GenBank (acc. no. KT835664.1). BLASTn search showed maximum homology with transcript of *Hordeum vulgare* (acc. No. AK353742). BLASTp analysis showed maximum homology with MAPK protein in *Zea mays* (accession. no. NP_001167676.1). ORF analysis showed the presence of 369 amino acid. Conserved domain search showed the presence of Serine/Threonine type kinase (STK) domain in the sequence. Transcript profiling of MAPK showed many fold increase in the expression in response to HS. Stage specific expression analysis showed abundance of transcript during early-ripe, as compared to milky-ripe stage under HS. Expression was observed maximum in thermotolerant cvs. (HD3059 and Halna) compared with thermosensitive (HD2329 and PBW550) under differential HS. Heterologous expression of MAPK in BL21 strain of *E.coli* resulted in protein of ~40.5kDa on Polyacrylamide gel. The activity assay of MAPK and characterization of phosphorylation site will help us to use this potential protein as sensors of HS in wheat. The candidate MAPK genes can also be used as marker for the wheat breeding program in order to develop "climate-smart" crop.

Theme 4: Resource optimization for enhanced productivity

KL 4: Climate Smart Agriculture in Intensive Wheat Based Systems of South Asia

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South Asia, home to about 1.7 billion people, over 30 per cent of whom are still living in poverty, faces a major challenge in achieving rapid economic growth and Sustainable Development Goals (SDGs) under mounting challenges of natural resource degradation, escalating inputs cost, volatile markets and risks associated with global climate change. During past half century; in process of achieving multi-fold increase in crop production in the region, inefficient use and inappropriate management of non-climate production resources (water, energy, agro-chemicals) have vastly impacted the quality of the natural resources and also contributed to climatic variability affecting farming adversely. The natural resources in South Asia are severely stressed due to population, economic and political pressures and can potentially add to adversity of climatic risks, making a large number of people in the region vulnerable to climate change. Increasing climatic variability affects most of the biological, physical and chemical processes that drive productivity of agricultural systems.

With no scope left for horizontal expansion of farming; we need to produce 70% more food to feed the projected population by 2050. Nonetheless, having high risks of climate change induced extreme weather events, the crop yields in the region are predicted to decrease from 10 to 40% by 2050 with risks of crop failure in several highly vulnerable areas. Increase in mean temperature, increased variability both in temperature and rainfall patterns, changes in water availability, shift in growing season, rising frequency of extreme events such as terminal heat, floods, storms, droughts, sea level rise, salinization and perturbations in ecosystems have already affected the livelihood of millions of people. Studies show that there would be at least 10% increase in irrigation water demand in arid and semi-arid region of Asia with a 1^{o}C rise in temperature. Thus, climate change could result in the increased demand for irrigation water, further aggravating resource scarcity. Moreover, climate change on the one hand, can intensify the degradation process of natural resources which are central to meet the increased food demand, while on the other hand, changing land use pattern, natural resource degradation (especially land and water), urbanization and increasing pollution could affect the ecosystem in this region directly and also indirectly through their impacts on climatic variables. For example, about 51% of the Indo-Gangetic Plains of South Asia may become unsuitable for wheat crop, a major food security crop of region, due to increased heat-stress by 2050. Therefore, adaptation to climate change is no longer an option, but a compulsion to minimize the loss due to adverse impacts of climate change and reduce vulnerability. Moreover, while maintaining a steady pace of development, the region would also need to reduce its environmental footprint from agriculture.

Considering these multiple challenges, agricultural technologies that promote sustainable intensification and adapting to emerging climatic variability yet mitigating GHG emissions are scientific research and development priorities in the region. There are a wide range of agricultural practices that have the potential to increase adaptive capacity of wheat based systems, reduce GHG emissions or enhance carbon storage yet increasing food production. In our presentation, based on several years of strategic and applied research, we will share the scalable evidence on climate smart agriculture practices (CSAPs) for a sustainable wheat farming future in South Asia.

LL 4.1: Wheat productivity enhancement through climate smart practices

Yadvinder Singh

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Agriculture production in India must be increased to meet food demand for a growing population which is likely to be 1.6 billion by 2050. The projections for wheat demand and supply by 2030 are 128.8 and 114.6 MT respectively, with a gap of 14.2 MT. Furthermore, a shift in consumption from rice to wheat is taking place even in the traditionally rice-eating states of India. To me*et al.* the food and nutritional requirements of the growing population, the nation will have to increase its current levels of food production with higher emphasis on better natural resources (soil, water and environment) management, achieving technological breakthroughs and addressing climatic and environmental concerns. The agricultural production systems in Green Revolution lands of NW India may be closer to productivity limits by following improved agricultural strategy. The region is now showing serious and growing threats to the sustainability of the yields. Future increase in food grains production in India are becoming more difficult due to unpredictable climates characterized by extreme weather events, and degrading soil health and water resources. The '4‰ Initiative[1]: soils for food security and climate,' launched in Paris, aims to show that food security and combating climate change are complementary and to ensure that agriculture provides solutions to climate change, and to build up organic matter in soils. This will have wide-ranging benefits in farming systems: increasing crop productivity and soil health and enhancing the sequestering carbon for climate change mitigation. Improved climate smart agricultural practices need to be developed and adopted to improve the agricultural yields by 20% and offset emissions by 15% of CO_2eq. The climate smart technologies such as conservation agriculture (CA), smart nutrient and water management are needed to increase wheat productivity with minimal environmental foot prints. These practices can also deliver co-benefits in the form of reduced greenhouse gas emissions, increased water conservation and enhanced yields and soil health. Several studies show benefits of climate smart practices in terms yield increases, sequestering soil carbon although the magnitude and variability of results varies by specific practice and agro-climatic conditions. Research is in progress to develop technologies of adapting to climate change, increasing wheat yields and mitigating greenhouse gas emissions. More research is needed to identify key cross-cutting practices such as the use of leguminous crops, CA, water management (e,g. drip irrigation), site specific nutrient management, genotype x environment x management interactions and climatic adaptation and mitigation practices for sustainable wheat yields and improved soil health.

LL 4.2: Resource Optimization For Enhanced Wheat Productivity

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In the realm of food crops in the world, wheat (*Triticum aestivum* L.) occupies the number one position. It is foremost among cereals and is a main source of carbohydrates and protein for both human beings and animals; contains starch (60-90%), protein (11-16.5%), fat (1.5-2%), inorganic ions (1.2-2%) and vitamins (B-complex and vitamin E). India is the second largest producer of wheat after China with annual production of 98.51 million tonnes and productivity of 3.2 t ha-1 during 2015-16. Considering its growing demand for consumption and trade due to burgeoning population, the target for wheat in India is projected around 140 million tonnes by 2050. Several inherent problems that co-exist with conventional wheat production system are imbalanced fertilization, soil salinity and alkalinity problems, weed shift and resistance, ground water depletion, soil compaction and structural damage, declining soil health, terminal heat stress in wheat, etc. This has led to fatigued natural resource base and a plateau in wheat productivity, thus threatening the sustainability of wheat production in recent years.

Resource conservation and resource optimization strategies will help to overcome the production constraints and achieve sustainability in wheat production. Wheat sowing with Turbo happy seeder under residue laden fields leads to reduced soil disturbance, timely sowing of wheat (prevents terminal heat stress), addition of organic matter to soil, reduced incidence of the herbicide resistant weed *Phalaris minor* and carbon sequestration. Moreover, replacement of older varieties with improved cultivars should be done for bringing second green revolution in eastern India. Development of biofortified, disease resistant and restricted irrigation conditions varieties should be given priority to reduce the adverse effects of climate change and water shortage. Adoption of Laser Land Levelling, micro irrigation and mulch helps in water savings, thus, efficiently using each drop of water. Raising wheat under FIRBS (furrow irrigated raised bed system) helps in saving water, reducing lodging and increasing productivity. Nutrient management via 4R nutrient stewardship, precision tools like LCC, SPAD, Green seeker, balanced fertilization, foliar fertilization of micronutrients (biofortification), INM helps in increasing efficiency of nutrients by reducing losses and reduction in nitrous oxide emissions. Besides, crop diversification by including green manure crops, legumes enriches the soil by increasing organic matter content of the soil. Adoption of legume crops has been found to improve physical health of soil as well as 25% saving of N application. Diversification of the existing system with rice-wheat-green gram, rice-wheat-cowpea and rice-vegetable pea-wheat crop sequence results in higher wheat equivalent yield and more profitability than rice-wheat system alone. Again, planting of wheat in standing cotton result in timely wheat sowing and better yield. Thus, sustainable agriculture must be a broad-based effort, which will help in sustainable productivity and production of wheat resulting in secure, equitable, sufficient and stable flow of both food and ecosystem services for the 7.7 billion people to inhabit the Earth.

LL 4.3: Wheat productivity enhancement through climate smart practices

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Due to the adoption of high-yielding varieties, chemical fertilizer, pesticides, irrigation and mechanization since the green revolution the agricultural production in India has considerably increased. But nowadays sustaining the achievements of the green revolution is become challenging because of negative environmental issues, such as groundwater depletion, soil fertility degradation and chemical runoff resulting from resource-intensive agriculture. Increasing climatic variabilities exert further pressure on the sustainability of the existing production system of crop in general and wheat in particular. But under such circumstances the climate smart agriculture technologies will helps in the mitigation from the adverse effect of climate change on the productivity of wheat. Climate smart agriculture practices sustainably increases productivity, enhances resilience (adaptation), reduces/removes greenhouse gases (mitigation) where possible. There are number of climate smart technologies have been formulated for enhancing wheat productivity without affecting the environment. Conservation agriculture (CA) is one of them. It advocated the zero tillage with need based residue retention on the soil surface followed by sensible crop rotation.

Management of soil fertility and organic matter, and improvement of the efficiency of nutrient inputs, enable more to be produced with proportionally less fertilizers is the goal of CA. It also saves on energy use in farming and reduces emissions from the burning of crop residues. Moreover it helps in sequestering carbon in soil. Due to avoidance of tillage it minimizes occurrence of net losses of carbon dioxide by microbial respiration and oxidation of the soil organic matter and builds soil structure and bio-pores through soil biota and roots. Retaining residue on the surface of soil also provides a substrate for soil-inhabiting microorganisms which helps to improve and maintain water and nutrients in the soil. What production with CA also advocate rotations and crop associations that include legumes are capable of hosting nitrogen-fixing bacteria in their roots, which contributes to optimum plant growth without increased greenhouse gas emissions induced by fertilizer's production.

LL 4.4: Optimization of resources for sustainable wheat productivity and enhanced profitability

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Agriculture till recent past was focused on achieving food security through increased area under high yielding varieties, expansion of area under irrigation and increased use of external inputs like chemical fertilizers and pesticides. In India, the indiscriminate use, or rather misuse, of water for irrigation and nitrogen especially under rice-wheat cropping system, has led to the groundwater pollution as well as depletion of ground water resources. The intensive tillage is another issue of concern adversely affecting the soil health. It leads to depleting soil organic carbon status, decreasing soil fertility and reduced factor productivity. If we continue to misuse inputs especially nitrogen and exploit the natural soil and water resources at the current level, productivity and sustainability are bound to suffer. Therefore, to achieve sustainable higher wheat productivity as well as profitability, efforts must be focused on reversing the trend in natural resource degradation by adopting efficient resource conservation technologies.

Generally, fields are not properly levelled leading to poor performance of the crops, because, part of area suffers due to water stress and part due to excess of water leading to reduced productivity. Precision land leveling is a precursor resource optimization option for increased inputs use efficiency coupled with more area under the crop due to reduced area under bunds and channels leading to higher productivity. Hence, adoption of laser land levelling will help produce more crop per drop. Conservation Agriculture is much more than just reducing the mechanical tillage. In addition to saving on cost involved in intensive tillage, the surface residue retention has multifarious benefits. It protects the soil from the physical impact of rain and wind, stabilizes soil moisture and temperature in the surface layers, provide favourable habitat for a number of organisms, from larger insects down to soil borne fungi and bacteria and helps improve the organic carbon status of soil. Adopting zero tillage saves more than Rs 3000 per hectare thereby increasing the profit margin of the farmers. Moreover, fertilizer application especially top dressing of urea just before irrigation helps improve the yield by about 4% over the recommended practice of urea application 2-5 days after irrigation. Use of NDVI sensor for need based nitrogen application saves 15-20% nitrogen without any reduction in productivity of wheat as well as rice crop. The water applied at each irrigation was marginally lower in zero tillage whereas water saving was substantial in bed planting compared to conventional tillage. The total water saving compared to conventional tillage was about 2.5 per cent lower in zero tillage and about 20 per cent in FIRB system of wheat cultivation. Leaving crop residues at soil surface *i.e.* conservation agriculture can help save one irrigation which would be more than 15% water saving. The micro-irrigation practices (sprinkler and drip) can save more than 20% water compared to conventional flood irrigation practice. The evolution of multiple herbicide resistance in *Phalaris minor* and development of herbicide resistance in other weeds like *Rumex dentatus*, Polypogon and *Avena ludoviciana* is another serious threat to wheat production and to tackle these issues effective weed management practices need to be evolved. Hence, to achieve the higher productivity and profitability, adoption of multipronged strategy of using improved varieties, balanced fertilization, appropriate irrigation and weed management practices is a must.

OL 4.1: Sustaining wheat productivity by management of herbicide resistant weeds

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Weed infestation is a major problem limiting production and productivity of wheat. Further, the evolution of herbicide resistance in weeds has made their management difficult. In India, the populations of three grassy weeds namely Littleseed canarygrass (*Phalaris minor*); wild oat (*Avena ludoviciana*) and Rabbitfoot grass (*Polypogon monspeliensis*) and two broadleaved weeds (*Rumex dentatus* and *Chenopodium album*) have evolved herbicide resistance. Among these *P. minor* is more serious problem and has evolved multiple herbicide resistance to three modes of action (Photosynthesis at photosystem-II site A, ACCase and ALS inhibitor). Some of the resistant populations exhibited GR50 values for clodinafop and sulfosulfuron >20 times greater than that of the most susceptible population. Whereas, wild oat has evolved resistance against ACCase and ALS inhibitor herbicides. *P. monspeliensis* has also evolved resistance against ALS inhibitor herbicides (sulfosulfuron, mesosulfuron and pyroxsulam). Also, two broad-leaved weeds, *R. dentatus* and *C. album* have evolved resistance against ALS inhibitors.Management strategies must be developed against herbicide resistant populations. Many farmers in northern India are facing significant wheat yield reductions due to herbicide resistance. One important aspect for resistance management is early detection and to identify the effective alternative herbicides. Multiple herbicide resistant *P. minor* populations are sensitive to pendimethalin, flumioxazin, flufenacet, pyroxasulfone and metribuzin. Pyroxasulfone and flufenacet were also found effective for control of herbicide resistant *P. monspeliensis* and wild oat. Whereas, ALS herbicide resistant C. album and *R. dentatus* were sensitive to pendimethalin, 2,4-D and carfentrazone. However, for long term effective herbicide resistance management, alternative herbicides should be integrated with non-chemical methods consisting of crop rotation, adjustment in sowing time and method, competitive cultivar, higher seed rate, closer spacing and straw mulching. The adoption of zero tillage with residue retention besides reducing the weed infestation also helps in improving the profitability.

OL 4.2: Carbon sequestration through Agro-forestry system and its impact on adoption and sustainable farming

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Carbon sequestration is the process of carbon capture and the long-term storage of atmospheric carbon dioxide. Agro-forestry systems can contribute to stabilising and improving the yield of annual crops *i.e.* wheat along with carbon sequestration in tree. The paper has examined the carbon sequestration and crop potential of the prevailing agro-forestry system in Udham Singh Nagar district. Two block of Udham Singh Nagar were selected for study purposes in which two spacing were followed by sample farmers *i.e.* 6m x 5m and 5m x 4m. SHODOR method was used to determine the carbon sequestration rate from both the spacing. The result indicated that carbon sequestration in agro-forestry with spacing 6m x 5m is 37.87 qtl/ha in comparison to spacing 5m x 4m *i.e.* 39.75 qtl/ha. This shows that carbon sequestering potential in spacing 5m x4m was more in comparison to 7m x 3m. Wheat is common crop that is taken in both the spacing *i.e.* 6m x 5m and 5m x 4m. CACP method is used to compute the yield potential of wheat along with tree in the agroforestry system .For both the spacing it is found to be 28 qt ha-1 and 30qt ha-1 respectively. The study observed that the adopter farmer's income has increased considerably. This study has suggested that policy support in terms of promotion of agro-forestry system is government should provide carbon credit to the farmers for encouragement of adopting agro-forestry system.

PP 4.1: Effect of tillage in rice-wheat system on the productivity of rice and wheat crops

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The intensive tillage is reported to be responsible for the soil health deterioration in the North Western Indian Plains especially under the rice-wheat system wherein wet tillage for puddling is being practised to grow the rice crop. The intensive wet tillage leads to deterioration of soil structure in addition to development of hard pan at a depth of 25-30 cm in the soil profile. A long term field experiment was conducted at the research farm of the ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India to evaluate the effect of tillage options in rice-wheat system on crop productivity. The treatments comprised of three tillage options in rice (Zero tillage transplanted; Dry rotary followed by ponding of water and transplanting; and Wet rotary *i.e.* puddling using rotary tiller and transplanting) superimposed on which were three tillage options (Zero tillage, Conventional tillage and Rotary tillage) in wheat. The results showed that the wheat productivity was not significantly affected by tillage either in rice or in wheat. Over the years, marginally higher wheat yield was recorded in rotary tillage but the differences were not statistically significant. However, due to single pass sowing using zero and rotary till drills, saving on tillage cost made these technologies profitable. In case of rice crop, the tillage in wheat had non-significant effect but the tillage in rice especially zero tillage transplanting had an adverse effect on rice productivity. The yield attributes except thousand grain weight were adversely affected leading to lower rice productivity in zero tillage transplanting whereas similar yield was recorded in dry rotary and wet rotary indicating that puddling (Wet tillage) may not be required and dry field preparation followed by ponding of water and transplanting may be a better option to avoid the destruction of soil structure by wet tillage for puddling.

PP 4.2: Effect of different rice establishment methods on productivity of zero tillage wheat at different nitrogen levels

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Rice-wheat is one of the most important cropping systems of our country which meets the food and energy requirement of our population. With increasing emphasis being given on various resource conservation agriculture practices, particularly direct dry seeding in rice, it has become important to study the effect of these technologies on the subsequent crops. Keeping this in mind the present investigation was conducted for two years during 2013 – 14 to 2014 - 15 at Rice and Wheat Research Centre, Malan to evaluate the effect of different rice seeding methods on the performance of zero tilled wheat raised with different nitrogen levels. The treatments consisted of three rice establishment methods during summer (kharif) *viz.*, puddle transplanted rice (PTR), zero tilled transplanted rice (ZTTR) and dry direct seeded rice after conventional tillage (DDSR) and four nitrogen levels in zero tilled wheat during winter (rabi) (0 kg N / ha^{-1}, 75 kg N / ha^{-1}, 150 kg N / ha^{-1} and LCC based nitrogen application) were tested in strip plot design with three replicationsPooled data showed that the rice establishment methods had no significant influence on the performance of wheat raised under zero tillage conditions. However the nitrogen levels had a significant influence on the productivity of wheat crop with significantly highest grain yield recorded with the application of 150 kg N / ha^{-1} though it was at par with the treatment in which nitrogen was top dressed on the basis of LCC. Significantly lowest yield was recorded when no nitrogen was applied to the wheat crop. On the basis of the results so obtained it can be concluded that the rice established methods have no influence on the yield of subsequent wheat crop though the nitrogen application in wheat significantly influenced the grain yield

PP 4.3: Performance of wheat genotypes under different dates of sowing

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Wheat has a prominent position among cereals. Among the various factors responsible for low yield of wheat crop in the country, sowing time and varietal selection are of primary importance. A field experiment was conducted at research farm of Regional Research Station, Gurdaspur, Punjab to study the performance of nine wheat genotypes under normal, late and very late sowing conditions. The experiment was laid out in a split plot design during rabi season of 2017-18 with three replications. Treatments consisted of three sowing dates of sowing *i.e.* normal (11.11.2017), late (11.12.2017) and very late sown (01.01.2018) in main plots and nine wheat varieties *viz.* HD3226, PBW752, PBW757, HD3059, DBW71, DBW173, HD 3086, WH1105 and WR544 in the sub plots. Performance of different genotypes was judged on the basis of yield and yield attributing characters. Yield attributing characters like, ear-heads per square meter, grains per ear-head and thousand grain weight differed significantly in all the genotypes under different sowing dates. All genotypes recorded the highest yield under normal date of sowing as compared to late and very late sowing conditions. On average basis, normal sowing recorded 15.9 and 52 % higher grain yield than late and very late sowing conditions, respectively. Among genotypes, PBW757 ranked the first with mean yield of 45.75 q ha-1 and was at par with DBW 173 and HD3059. The highest yield in PBW757 was due to production of maximum grains per ear-head. The genotype PBW752 recorded the lowest yield.

PP 4.4: Agronomic and physiological assessment of advance wheat lines under early planting conditions

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The time of sowing is an important factor influencing the grain yield of crops. Sowing wheat (*Triticum aestivum* L.) at the right time is one of the most important means of maximising grain yield. With the aim to assess the hypothesis that early sowing of wheat cultivars with suitable maturity would increase wheat yield, thirty wheat advance breeding lines were sown during last week of October in randomized block design with three replications during rabi season of 2014-15 at ICAR-IIWBR farm Karnal. The data were recorded on germination percent, early vigour, days to heading, plant height, tillers per meter, ear length, lodging, grain yield, NDVI values at tillering stage, stem elongation stage, booting stage and inflorescence emergence stage as per the standard procedures and protocols. High coefficient of variation was observed for lodging % (48.7%), grain yield (16.5%), early vigour (13.8%), ear length (13.5%), tillers per meter (13.3%) and agronomic score (11.2%). The analysis of variation revealed that significant differences among genotypes were present for days to heading, plant height, tillers per meter, NDVI values recorded at pre flowering stages, grain yield and thousand grains weight. Principal Component Analysis (PCA) showed that the first four components accounted for 69.9% of total variation. The major contributing traits for diversity in first principal component were NDVI values recorded at vegetative stages, however in the second principal component grain yield, agronomic score and days to heading contributed maximum towards diversity. The cluster analysis classified the thirty genotypes in to three major clusters. The genotype by trait analysis showed that under early planting conditions high grain yield was associated with the agronomic score, plant height and thousand grains weight. The plant height and lodging vectors were at 1800 with the grain yield and had caused opposite ranking of the tested genotypes.

PP 4.5: Effect of different altitudes and different dates of sowing on yield of wheat

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Wheat is geographically grown from below sea level near the Dead Sea and in the Imperial Valley of California to as high as 5000 m altitude of Tibet. In India, it is grown from sea level to elevations of 4000 m in the Himalayas. The climate of high altitudinal regions differ greatly from that of lower or mid altitudes even at the same latitude. Climatic condition at a given location is not only governed by its altitude but other physiographic characteristics also play a significant role. The response of different varieties of wheat crop is different at different altitudes due to variable thermal regime. The solar radiation and availability of soil moisture and prevailing winds and sunny sites are other important factors which affect the phenology, growth and yield of wheat crop. Therefore, the present study was conducted to explore the yield potential of different varieties at four different altitudes and widely varying weather conditions prevalent in the state of Himachal Pradesh during rabi season of 2016-17 at four research farm of CSK HPKV, Palampur (1291m), RWRC Malan (1109m), HAREC, Bajaura (1074m) and HAREC, Dhaulakuan (411m). The experiment was laid out in factorial RBD design using three replications at each location. The experiment consisted of 12 treatment combinations of three dates of sowing and four varieties. For grain and straw yield, Bajaura was found to be the most suitable location. 25th October and 25th November sowings being at par with each other were significantly higher than 25th December sowing at all the locations. The reduction in grain yield per 100 m increase in altitude was found to be highest between Malan and Palampur

(1.45 to 3.67 q ha^{-1}) followed by Dhaulakuan and Bajaura (0.28 to 0.77 q ha^{-1}) and Dhaulakuan and Malan (< 0.5 q ha^{-1}) in all the dates.

PP 4.6: Effect of different Composts on the performance of wheat

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The use of organic manures has assumed greater significance in the present set up of agriculture due to increasing awareness about chemical free farming. A field experiment was conducted during rabi season 2017-18 in the department of Organic Agriculture and Natural Farming at CSKHPKV, Palampur, India with an objective to study the effect of different composts and their time of application on its performance in wheat. Nine treatments consisting of different composts (Vermicompost 10 t ha^{-1}, Nadep 15 t ha^{-1}, Himcompost 7t ha^{-1}, Ghan jeevamrit 0.25 t ha^{-1} + Vermicompost 5 t ha^{-1}, applied at two intervals one at sowing and another at one month after sowing) along with absolute control were tested in the field. All these composts were solid compost having base material cow dung, cow urine and biomass. Whereas, in vermicompost vermiculture was used, in ghanjeevamrit gram flour and jaggery was added and in himcompost different nutrient additives were added in addition to base material. The wheat plant height, biological yield and grain yields were statistically different from control. In terms of seed yield , the highest productivity was recorded in the vermicompost treatment applied at sowing, which was statistically at par with Himcompost applied at sowing and vermicompost treatment applied at one month after sowing followed by Himcompost applied at one month after sowing, Nadep applied at sowing, Nadep applied one month after sowing, Ghan jeevamrit + Vermicompost treatment applied at sowing and one month after sowing and lowest value was found in absolute control. The application of vermicompost at sowing, Himcompost at sowing and vermicompost applied one month after sowing treatments resulted in 85.8, 64.5 and 66.6% higher seed yield, respectively over the control.

PP 4.7: Effect of integrated nutrient management on productivity of wheat

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A fixed plot field experiment was conducted at the Research Farm of the Indian Institute of Wheat and Barley Research, Karnal, Haryana for three consecutive years during 2012-13 to 2014-15 to study the effect of integrated nutrient management on productivity of wheat. The treatments were Recommended NPK, NPK+Farm Yard Manure (FYM) @15 t ha^{-1}, recommended N only, recommended P only, recommended K only, NPK+GM and absolute control (no organic or chemical fertilizers). The major nutrients were supplied through chemical fertilizers and organic sources were FYM and green manuring. The recommended doses of chemical fertilizers were 150 kg N, 60 kg P_2O_5 and 40 kg K_2O ha^{-1}. Full dose of phosphorus, potash and 1/3rd nitrogen were applied as basal and the remaining 2/3rd nitrogen was applied in two equal splits just before first and second irrigation *i.e.* 21-25 and 40-45 days. Wheat variety DPW 621-50 was grown at 20cm row spacing during second week of November every year. All the recommended package of practices prescribed for wheat crop were followed. The soil of the experimental field was sandy loam having low organic carbon content, low available nitrogen, medium available phosphorus and potassium. The results of three year study revealed that on pooled basis, the highest productivity (52.71 q ha^{-1}) was recorded in treatment where all the recommended major nutrients along with 15 t ha FYM were applied followed by the treatment in which all the recommended major nutrients as well as green manuring was done and recommended NPK. These treatments were at par to each other but were significantly superior to the other treatments. Even nitrogen alone gave significantly higher yield as compared to the treatments where only phosphorus, potassium or no nutrient (absolute control) was applied indicating the importance of nitrogenous fertilizers for wheat production.

PP 4.8: Effect of site specific nutrient management in wheat in rice-wheat cropping system in mid hill region of Himachal Pradesh

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Rice-wheat is one of the most important cropping system on which food security of the nation depends. With the prevalent scenario in which emphasis is being given on the resource conservation technologies, it has become imperative to develop technologies that are specific to the particular field or particular set of resources. For achieving this the present investigation was conducted for a period of two years from Rabi (wheat) season of 2015-16 through Kharif (rice) season of 2017 at the experimental farm of CSK HPKV, Rice and Wheat Research Centre, Malan. The experiment consisted of 10 treatments combinations comprising five nutrient management practices in wheat *i.e.* recommended fertilizer dose(120:60:30 kg ha^{-1} NPK) with top dressing of nitrogen after irrigation; recommended fertilizer dose with top dressing of nitrogen before irrigation; fertilizer dose as recommended by software Nutrient Expert – Wheat (125:45:78 kg ha^{-1} NPK) with top dressing of nitrogen before irrigation, Nutrient Expert – Wheat guided fertilizer dose (70% nitrogen recommended by software and rest with green seeker technology) with top dressing of nitrogen before irrigation and N-rich plot which received 150% of recommended nitrogen with top dressing of nitrogen before irrigation and two tillage options *i.e.* conventional tillage and zero tillage tested in strip plot design, replicated three times. The soil of the experimental field was silty clay loam in texture, acidic in reaction, medium in available N, high in available P and medium in available K. Results revealed that tillage options had no significant effect on grain yield of wheat. Nutrient management practices had significant effect on yield of wheat with significantly higher yield recorded in N-rich plot in which 150% of recommended nitrogen was added. The wheat yield achieved with application of fertilizer dose recommended by software Nutrient Expert – Wheat for a target yield of 55 q ha^{-1} was considerably lower than the targeted yield indicating the need to improve the software. Top dressing of nitrogen after irrigation gave better result than top dressing of nitrogen before irrigation though the differences were not significant.

PP 4.9: Effect of irrigation schedules and nitrogen levels on the grain yield and nitrogen use efficiency of wheat under submountainous region of Punjab

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To maximize wheat productivity, nutrient and water management are two important key inputs. A field experiment was designed to investigate the effects of irrigation and nitrogen (N) application rates on grain yield of wheat. The experiment followed a completely randomized split-plot design with two different irrigation schedules, IW/CPE ratio of 0.9 and based on irrigation at critical stages *i.e.* crown root initiation, tillering, jointing, flowering and grain formation of wheat crop in the main-plots and four N levels of 0, 60, 120 and 180 kg N ha^{-1}as split-plots. The pooled data of two years showed that scheduling of irrigation to wheat at 0.9 IW/CPE ratio not only brought at par grain yields with irrigation scheduled at critical stages, but also savedone irrigation. Results of the study further revealed that nitrogen fertilization increased the yield of wheat linearly and was maximum at 180 kg nitrogen per hectare. However, nitrogen use efficiency (NUE) in terms of agronomic efficiency (AE) and recovery efficiency (RE) decreased with the increase in the nitrogen level. AE varied from 21.9 to 56.9 kg kg^{-1} in different treatments of irrigation and nitrogen levels. Almost similar trend was observed in recovery efficiency (RE) in all the treatment combinations. The values of RE varied from 39.7 to 88%.

PP 4.10: Effect of continuous fertilization and amendments on nutrient contents and wheat yield in Western Himalayas

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The major share of the food production (85%) in Himachal Pradesh comes from maize and wheat. In Himachal Pradesh, the continuous use of suboptimal doses of nutrients in cereal-based cropping systems has led to severe depletion of nutrient reserves in soil, causing multiple nutrient deficiencies and threatening the sustainability of crop production and quality. Since raising the productivity of wheat is indispensable for the transformation of agricultural scenario in Himachal Pradesh, so a field experiment was conducted at the Research farm of the Department of Soil Science, CSKHPKV Palampur in ongoing long term fertilization trial during rabi (2014-2015) to study the effect of continuous fertilization and amendments on wheat yield and NPKS content in grain and straw. Experiment consists of sub-optimal, optimal and super optimal doses of fertilizers with FYM and lime as amendment in two treatments and one treatment was without sulphur and one with zinc. The FYM amended plot resulted in highest grain (32.3 q ha^{-1}) and straw (57.56 q ha^{-1}) yield which was statistically comparable with lime amended plot. The plot without S resulted in about 40 percent reduction in grain yield. Continuous application of urea resulted in no yield due to toxic levels of hydrogen and aluminium ions. The contents of nitrogen, phosphorus, potassium and sulphur were significantly higher in FYM amended plots and their values were 1.79, 0.45, 0.45 and 0.34 % in wheat grain and 0.63, 0.09, 0.82 and 0.02 % in wheat straw, respectively. To sustain the crop productivity and quality integration of organic sources with recommended doses of fertilizers is must. In acidic soils lime can replace the FYM up to certain level. Sulphur should also be recommended with nitrogen, phosphorus and potassium to achieve higher yields.

PP 4.11: Assessment of the quality of wheat as affected by continuous application of fertilizers and amendments in an acid Alfisol

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Wheat is an important staple food of about one third of the world's population and contributes 70-90% of protein consumed in developing countries. The quality of wheat products such as bread, biscuit, cake etc. governed by optimized grain protein content and other quality constituents. So to assess the quality and productivity of wheat a field experiment was conducted at the Research farm of the Department of Soil Science, CSKHPKV Palampur in an ongoing long term fertilization trial during rabi (2016-2017). Experiment consisted of sub-optimal, optimal and super optimal doses of fertilizers with FYM and lime as amendment in two treatments and one treatment was without sulphur and one with zinc. Parameters like crude protein, gluten, moisture, ash, fat, fibre, carbohydrate and nutrient content were selected to assess the quality of the wheat. The highest grain (28.22 q ha^{-1}) and straw (46.66 q ha^{-1}) yields were obtained in the plot where integration of FYM was done with recommended dose of fertilizers, which was statistically comparable with lime amended plots. FYM amended treatment enhanced all the quality parameters significantly as compared to control and that are; crude protein (10.10%), gluten (28.0 %), ash (1.72%), fat (1.80%), fibre (1.87%) and carbohydrate (76.27%). The phosphorus, calcium, magnesium and iron contents in wheat grain were also significantly higher in the FYM amended treatment as compared to control. Continuous cropping without fertilization for the last 45 years led to decline in crop quality as well as crop productivity.Thus, it can be concluded that integration of FYM with fertilizers has sustained the productivity and quality of wheat and lime can be a good option to substitute the FYM in acid soils.

PP 4.12: Effect of different need based nitrogen management techniques and tillage options in wheat on nitrogen use efficiency and economics returns in North-Western Himalaya

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Nitrogen (N) fertilizer represents a significant cost for the grower and the excessive use may lead to environmental contamination. In order to economise nitrogen use in wheat, different precision agriculture tools can be employed for better results. One of such techniques is the use of Green seeker which may improve nitrogen use efficiency. Keeping this in consideration, a field experiment was conducted in rabi seasons of 2014-15 and 2016-17 in silty loam soils under irrigated conditions. The highest grain yield (42.83 q ha-1), gross returns, net returns and benefit cost (B:C) ratio were recorded with the application of higher dose of N (180 kg N / ha^{-1}) in three equal splits, though, this treatment recorded the lowest agronomic nitrogen use efficiency (23.79 kg/ kg N). It has been observed that among the precision techniques the use of Green Seeker can save on an average 22.0 kg N ha^{-1} as compared to Nutrient Expert (NE) and 17 kg N ha^{-1} over the State recommendation to obtain statistically similar grain yield. Grain yields recorded with the application of recommended dose of fertilizer with nitrogen top dressing done either before or after the irrigation were at par with the yield obtained with the fertilizer doses as guided by the software Nutrient Expert- Wheat + Green seeker. Also the yields obtained with the Nutrient Expert-wheat recommendation were considerably lower than the target yield of 5.0 t ha^{-1} is the indicative of the need to modify the software. Among the tillage practices, zero tillage recorded statistically similar grain yield (36.20 q ha^{-1}) compared to conventional tillage grain yield (39.38 q ha^{-1}). However, the highest benefit cost ratio (Rs. 2.61) was obtained with zero tillage practice compared to conventional tillage (Rs. 2.51). It has been concluded that for better agronomic nitrogen use efficiency (35.56 kg/ kg N), the use of precision agriculture tool Green Seeker is the best for sustainable wheat production in North-Western Himalayan region.

PP 4.13: Enhancing nitrogen use efficiency in wheat using Leaf Colour Chart

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Application of nitrogenous fertilizers has played a major role in enhancing global wheat production. However a large part of the applied nitrogen is lost through various means like leaching, volatilization and runoff making it imperative for researchers to develop technologies that can increase the use efficiency of applied nitrogen by synchronizing the application with its actual utilization by the plant. Leaf Colour Chart (LCC) is one such technology which can increase the nitrogen use efficiency. A field experiment was carried out during the winter seasons (rabi) of 2015-16 and 2016-17 at the experimental farm of CSKHPKV, Rice and Wheat Research Centre, Malan to evaluate the efficacy of this technology for different wheat varieties. The treatments consisted of three varieties (HPW 349, VL 907 and HS 507) in main plot and seven nitrogen management practices in sub plot, replicated thrice in split plot design. The seven nitrogen management practices included no nitrogen, 150 kg N / ha^{-1}, N management through LCC in which 35 / 25 kg N / ha^{-1}, 45 / 35 kg N / ha^{-1} and 55 / 45 kg N / ha^{-1} was to be applied at the time of second top dressing, if the LCC $<$ 4 / LCC $\geq$ 4, respectively, nitrogen management through Green Seeker and nitrogen rich plot in which 225 kg N /

ha^{-1} was applied. In this trial the LCC readings at the time of second top dressing was higher than 4 and hence 25, 35 and 45 kg N / ha was applied at the time of second top dressing in the three LCC treatments. Significantly highest grain yield of wheat was recorded with the application of 45 kg N / ha at second top dressing through the use of LCC. The highest value of agronomic efficiency of applied nitrogen was recorded when Green Seeker was used for quantifying nitrogen need of the crop whereas use of LCC also gave higher values of agronomic efficiency as compared to the blanket application of 150 kg N / ha. Amongst the varieties, HPW 349 gave significantly highest yield though it was at par with HS 507. The results so obtained indicated the need to popularize these technologies for better utilization of the applied nitrogen.

PP 4.14: Yield maximization in wheat through fertilizer management and plant growth regulators

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Wheat is the most widely grown crop in the world and provides 20% of the daily protein and energy for the global population. It is also the second most important food crop after rice in Indiaand is a staple food for large part of Indian population. With the ever increasing population and near stagnant area it has become imperative to maximize the productivity of this crop so as to meet the increasing demand. Balanced use of fertilizer and use of growth regulators are the two approaches that can be used for maximize the wheat productivity. Keeping these points in mind, a field investigation was carried out at Rice and Wheat Research Centre, Malan during winter seasons (rabi) of 2016 – 17 and 2017 - 18 to study the effect of growth regulators and fertilizer levels on growth and yield of wheat. The treatments consisted of four fertilizers levels (control; 100 % of recommended NPK, 12:60:30; 150% of recommended NPK and 150% of recommended NPK + 15 t FYM / ha) in main plot and four growth regulator treatments (two sprays each of water, chlormequat chloride @ 0.2 %, tebuconazole @ 0.1 % and chlormequat chloride + tebuconazole at first node and flag leaf stage) in sub plot were tested in split plot design with three replications. Significantly highest wheat yield was recorded with the application of 150% of recommended NPK + 15 t FYM / ha followed by 150% of recommended NPK, recommended NPK and control in that order, each treatment differing significantly from one another. Application of growth regulators significantly lowered the plant height with maximum reduction recorded with the application of chlormequat chloride. However, growth regulators also increased the grain yield of wheat over check though the increase was significant only with the application of tebuconazole (0.1%) alone. Application of chlormequat chloride through increased the grain yield over check (water application) but the increase was not significant.

PP 4.15: Differential response of wheat genotypes in organic and inorganic input conditions

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Adverse effects of conventional agriculture on the environment and human health have spurred the growth of organic farming systems. The major challenge of organic farming systems is to maintain high yields and excellent quality utilizing farming practices that have acceptable environmental impacts. Despite the potential environmental benefits of organic farming, the question must be addressed of whether organic agricultural systems are capable of producing enough food to feed the world's population today and in future. Several yield trial comparisons between organic and conventional farming systems have shown significantly lower yields for organic systems in certain crops like wheat, maize and rice compared to the higher yields in certain other crops like pulses and millets. The crop yield comparisons depend on the crop in question. Organic agriculture primarily rely on modern cultivars that have been selected by plant breeders under conventional systems that may not accurately represent the conditions present in organic farming. For this reason, these studies may be biased toward finding higher yields in a conventional agriculture. Keeping this in view present investigation was conducted using 24 genotypes of wheat which include 18 improved cultivars, 2 local collections (HPWO-4, HPWO-5) and one landrace (kanku) under two environments *i.e.* organic and inorganic (chemical input) conditions. The experiment was conducted at the experimental farm of Department of Organic Agriculture, CSKHPKV, Palampur, during winter 2017^{-2}018. Under conventional high input system 4 genotypes *viz*; HPW-365, HPW-962, HPW^{-2}36 and HPWO-5 were significantly superior among all the genotypes for grain yield whereas under organic input system, HPW-957, HPW-365, HPWO-5, HPWO-4 and HPW-973 were found significantly superior among all . Out of the best ten genotypes for yield among all in both the systems, only 4 genotypes *viz*; HPWO-5 ,HPW-957, HPW-962 and PW-1054 were common, indicating broad non-system specific adaptation and the potential of high yields across systems. The genotype HPWO-4 which ranked at number 4 under organic input was the lowest yielder under conventional input system. On the other hand, PW-1083 ranking 7th in conventional system was among the lowest yielders under organic system. Hence, the results indicate that genotypes vary in their yields under different environments and yield evaluations must be done to identify specific genotypes for organic environment to get good yields.

PP 4.16: Efficacy of new herbicides for broad-leaved weed control in wheat under mid hill conditions of Himachal Pradesh

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A field experiment was conducted at Rice and Wheat Research Centre, Malan, Himachal Pradesh during 2016-17 and 2017-18 to evaluate the efficacy of new herbicides halauxifen -methyl ester + florasulam for controlling broad-leaved weeds in wheat. The experiment was conducted in randomized complete block design replicated three times and consisted of 12 treatments. The treatments werehalauxifen methyl ester + florasulam + polyglycol surfactant 12.76 g+750 ml ha^{-1}, metsulfuron methyl + surfactant 4g + 625 ml ha^{-1}, carfentrazone 20 g ha^{-1}, 2,4 - D Na salt 500 g ha^{-1} and 2,4 - D ethyl ester 500 g ha^{-1} and their combinations at reduced doses with carfentrazone 20 g ha^{-1} along with weed free and weedy check for comparison. All the herbicide treatments provided significant control of weeds causing significant reduction in density of target weed flora and also significantly improved the grain yield in comparison with weedy check. The highest weed control efficiency {81.81 and 78.04% at 30 DAA (Days after herbicide application) and 71.56 and 69.80 % at 60 DAA during 2016-17 and 2017-18, respectively} and maximum grain yield of 45.18 and 46.04 q ha^{-1} with 38.21 and 40.75% increase in grain yield over weedy check were recorded during 2016-17 and 2017-18, respectively where halauxifen methyl + florasulam + carfentrazone + surfactant were applied together. This herbicide combination was found comparable with weed free treatment during both years of study. The weed population and grain yield in weedy check were 154.7 and 152.3 weeds m2 at 60 DAA and 32.69 and 32.71 q ha^{-1} in 2016-17 and 2017-18, respectively. No crop injury was observed in any of the herbicide treatments. Among the herbicides used alone halauxifen methyl ester + florasulam + surfactant produced the highest grain yields (44.53 and 45.59 q ha^{-1}, during 2016-17 and 2017-18, respectively) and increase over weedy check was 36.21 and 39.38%, during first and second year respectively. In light of the results, it is concluded that halauxifen methyl ester + florasulam + surfactant and in combination with carfentrazone were the most effective treatments for achieving a desirable weed control and increasing grain yield of wheat in irrigated conditions of mid hills of Himachal Pradesh.

PP 4.17: Herbicides for control of broadleaved weeds in wheat

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Wheat is the second most important staple food after rice crop worldwide and in Indiaits production increased from 11.0 million tons during 1960-61 to 99.70 million metric tons during 2017-18. Weeds account for about one third of total losses caused by all pests. Weeds not only reduce the yield but also make the harvesting operation difficult. Therefore, for sustaining food grain production to feed ever- increasing population and ensuring food security, effective weed management is very essential. Experiment was carried out during rabi season of 2016-17 and 2017-18 under All India Co-ordinated Wheat and Barley Improvement Project, at BTC, College of Agriculture and Research Station Sarkanda , Bilaspur, Chhattisgarh. The eleven weed control treatment combinations *i.e.* (i) Halauxifen - methyl ester + florasulam 40.85% WG at 12.76 ga.i ha^{-1} + surfactant (ii) Metsulfuron methyl 20 WG at 4.0 ga.i ha^{-1} + surfactant iii) Carfentrazone 40DF at 20 ga.i *ha*$^{-1}$ iv) 2,4-D Na 80 WP 500 ga.*i* ha^{-1} v) 2,4-D E 38 EC 500 ga.i *ha*$^{-1}$ vi) Metsulfuron+carfentrazone + surfactant at 4+20 ga.*i* ha^{-1} vii) 2,4-D Na + Carfentrazone at 400 + 20 ga.i *ha*$^{-1}$ viii) 2,4-D E + Carfentrazone at 400 + 20 ga.i *ha*$^{-1}$ ix) Halauxifen methyl + florasulam+ carfentrazone + surfactant at 10.21 + 20 g a.*i.* ha^{-1} + 750 ml x) Weedy check and xi) Weed free were replicated thrice. Broadleaved herbicides were applied at 30-35 days after sowing. A blanket dose of clodinafop 60 g was applied about 5 days before or after the broad leaf herbicide application to control grassy weeds. The highest grain yield was obtained under weed free situations during both the year of experiment (45.98 and 50.41 q ha^{-1}). Among herbicidal weed control treatments, post emergence application of metsulfuron + Carfentrazone + S, produced higher yield (44.95 and 47.32 q ha^{-1}) and was at par with halauxifen + florasulam + carfentrazone + S (44.56 and 47.18 q ha^{-1}) during both the year of experiment. Almost similar trained was observed for straw yield. Gain in yield was due to better weed control as a result higher number of earheads/ sq.m and 1000 grains weight. These treatments also reduced weed number and dry weight to great extent as compared to other treatments.

PP 4.18: Effect of continuous and rotational use of herbicides in rice –wheat cropping system on weeds and productivity of wheat under north-western Himalayan region

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Rice-wheat is the major cropping system covering about 11 million hectare area of the country. This cropping system not only has a major share in Indian food security but farmer's economic security as well. However, weeds are one among the major bottlenecks reducing the crop yields up to 35%. Usage of herbicides is the main option in managing weeds in these crops. Nine weed control treatments consisting of continuous and rotational use of herbicides were evaluated in rice - wheat cropping system at Palampur from 2000 till 2018 for wheat yield. During rabi 2000, *Phalaris minor*, *Avena ludoviciana*, Vicia sativa, Anagallis arvensis and Coronopus didymus were dominant weeds. Population density of all these weeds decreased in later years. Coronopus didymus was not observed after 2009-10. After 3-4 years, Poa, Lolium and Ranunculus were appeared. Poa and Lolium had alarming proportion in the later years while Ranunculus disappeared after 2-3 years. From 2005-06, Polygonum and Alopecurus were the new invaders. In the later years, Trifolium, Stellaria, Lathyrus, Plantago and Daucus carota had little infestation in the experimental field. Yield of wheat was higher during the middle years followed by latter and former years. All weed control treatments were superior to farmers' practice in increasing wheat grain yield. Rotational use of herbicides both in rice and wheat [Cyhalofop butyl 90 g ha^{-1} fb 2,4-DEE 1.0 kg ha^{-1},/ Butachlor 1.5 kg ha^{-1} fb 2,4-DEE 1.0 kg ha^{-1} and clodinafop / isoproturon fb 2, 4-D in wheat] along with either 100% fertilizer alone or a part of N substitution through Lantana leaves in rice resulted in significantly higher wheat grain yield over other treatments. Incorporation of Lantana to rice with rotational use of herbicides in both crops had the highest sustainable wheat yield index (0.743).

PP 4.19: Effect of conservation tillage on weed flora in wheat in the maize-wheat cropping system

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Global warming leads to the concurrence of a number of abiotic and biotic stresses, thus affecting agricultural productivity and ecosystem. Occurance of abiotic stresses can alter plant–pest interactions by enhancing host plant susceptibility to pathogenic organisms and insectsas well as by reducing competitive ability with weeds. The field experiment was undertaken in order to study the effect of conservation tillage and weed management treatments on weed dynamics variation and yield under mid hill conditions of Himachal Pradesh. Experiment consist of fifteen treatment combinations of five tillage methods *viz.* CT-CT, CT-ZT, ZT-ZT, ZT-ZTR and ZTR-ZTR (CT, conventional tillage; ZT, zero tillage and ZTR, conservation agriculture) and 3 weed management methods *viz.* H-H, IWM-IWM and HW-HW; (H, herbicide; IWM, integrated weed management; HW, hand weeding) in maize-wheat cropping sequence. During 2015-16, invasion of *Phalaris minor* (7%), *Avena fatua* (23%), *Lolium temulentum* (19%), *Vicia sativa* (20%), *Coronopus didymus* (15%) and *Anagallis arvensis* (16%) was recorded in wheat. There were drastic changes in weed flora in wheat during 2016-17, *Erodium cicutarium* (38%), *Euphorbia helioscopia* (17%) and *Oxalis corniculata* (17%) were the new weeds emerge due to change in climatic scenarios. Tillage and weed management treatments brought about significant variation in the count and dry weight of weeds associated with wheat crop during 2015-16. ZTR-ZTR remaining at par with CT-CT and CT-ZT resulted in significantly higher wheat grain equivalent yield over other tillage treatments. IWM-IWM gave 37.2 and 56.6% higher wheat grain equivalent yield over H-H and HW-HW, respectively. Among all treatment combinations, ZTR+IWM-ZTR+IWM (conservation tillage along with integrated weed management in both crops of maize-wheat rotation) was found comparable to CT+IWM-CT + IWM (conventional tillage with integrated weed management) in influencing wheat grain equivalent. Thus conservation tillage with integrated weed management can be an viable option to address the issues of global warming and its aggravated problem of weed menace.

PP 4.20: Mutation in the acetolactate synthase (ALS) gene endowing resistance to ALS-inhibiting herbicide in *Phalaris minor* populations

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Littleseed canary grass (*Phalaris minor* Retz.) is the most common and predominant weed of wheat under rice-wheat cropping system in the North-Western Indian Plains. Moderate infestation of *P. minor* alone can cause 15^{-2}0% reduction in grain yield of wheat. This weed has evolved herbicide resistance across three modes of action: photosynthesis at the photosystem II site A, acetyl-CoA carboxylase (ACCase), and acetolactate synthase (ALS) inhibition. Herbicides of the ALS group are highly vulnerable to resistance evolution and occupy first position in resistance development worldwide. Acetolactate synthase is the first enzyme in the pathway for biosynthesis of branched-chain essential amino acids valine, leucine and isoleucine. In most of the resistance cases in weeds, the target-site based mechanism can occur by point mutations in the gene resulting in amino acid changes in a target enzyme, which prevents or reduces herbicide binding. The *P. minor* populations collected from farmers' fields having a history of poor or no control with sulfosulfuron were evaluated under pot conditions against sulfosulfuron (0, 12.5 and 25 g ha^{-1})along with two known susceptible populations to identify the resistant and susceptible populations for molecular studies. The populations exhibiting almost complete kill at 12.5 g ha^{-1} were taken as susceptible. To identify the molecular basis for resistance, the partial ALS gene from seven resistant and two susceptible populations were sequenced by amplifying ALS gene using the primers designed based on homologous regions of ALS sequences from *Alopecurus myosuroides* and *Lolium multiforum.* The sequence analysis revealed that four of resistant populations were heterozygous at amino acid position 197 and susceptible biotypes were homozygous at this position.Based on the sequence analysis results for the mutation site, allele-specific PCR was designed to further characterize resistant and susceptible populations. This is the first report from India about sulfosulfuron resistance being conferred by specific ALS point mutations at amino acid position 197 in *P. minor*.

PP 4.21: Evaluation of new timely sown wheat genotypes under restricted irrigation conditions of west Bengal

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Water availability during critical growth phase is pivotal to realize full yield potential of a crop. If irrigation water availability is resptricted then idtification of suitable genotypes is of prime importance. A field experiment was conducted during the winter (rabi) season of 2016-17 and 2017-18, under the aegis of Bidhan Chandra Krishi Viswavidyalaya at AB block farm, Kalyan*I*. The experiment was carried out in split plot design with three irrigation levels {no irrigation, one irrigation (CRI stage) and two irrigations (CRI and boot stage)} in main plots and six cultivars (HI 1612, HD 2888, C 306, K 8027, HD 3171 and K 1317) in sub-plots. Full dose of NPK (90:60:40) was applied as basal in no irrigation treatment and 1/3rd nitrogen, full phosphorus (60 kg P_2O_5 ha^{-1}) and potash (40 kg K_2O ha^{-1}) was applied at the time of sowing and remaining N was top dressed at 1st node stage in other two main plots. Weed control measures were followed as per the recommended practice. The normalized seed rate used was 100 kg ha^{-1}. Wheat genotypes were sown in lines at 23 cm spacing (9 rows at 23 cm spacing). All necessary intercultural operations were followed as per recommended practice. The performance of various genotype were evaluated under restricted irrigation conditions on the basis of pooled data analysis of two years. Number of earheads and grains per earhead was highest registered with the two number of irrigation and showed parity with one irrigation level. With various genotypes highest earhead count observed was with HD 2888(mention the number) and was at par with all other treatments except HD 3171. Grains per earhead failed to produced any statistical difference with various subplot treatments, however this was more with the HI 1612 and followed by HD 3171 and C 306. Under main plot treatments, highest grain yield observed with two irrigation (24.94 q ha^{-1}) and was significantly better to other treatments. This was followed by one irrigation application (21.58 q ha^{-1}). Increasing number of irrigations successively gave significantly higher grain yield. One and two irrigation application gave 37.43 and 56.91 % higher grain yield, respectively than no irrigation. All the yield attributing parameters were increased as the number of irrigation increased. So, the yield increase was due to cumulative effect of all the yield attributing parameters. Amongst various genotype, the highest grain yield was observed with the cultivar C 306 (23.04 q ha^{-1}) and was at par with all the genotypes except HD 2888 (17.76 q ha^{-1}), which gave the lowest yield. Yield of cultivars HI 1612 ranked fourth and was at par with best yielder cultivar (C 306).

PP 4.22: Prospective of dual purpose wheat in North Western Indian Himalayas

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The North Western Indian Himalayan region encompasses states of Jammu and Kashmir, Himachal Pradesh, Shivaliks of Punjab and Uttarakhand. Food as well as livestock feed security is of utmost importancein the region due to poor socio-economic conditions of farmers. Region faces shortage of green fodder which goes up to 60% during winter months. The most subsistence farmers cannot spare their small land holdings forfodder production at the cost of main food crops. Wheat is the main rabi (winter) season crop in the region. Under this situation dual purpose wheat (fodder cum grain) can be an answer. Spring wheat does not respond well to such management and its grain yield is adversely affected. Typical exotic winter wheat also does not perform well under these conditions due to their long vernalisation period, lodging, disease susceptibility and poor regeneration after fodder cut. However, facultative wheat *i.e.* neither spring nor winter wheat; with intermediate vernalisation and photoperiods may be the most suitable for such situations. Three years testing of wheat variety VL-829 for dual purpose under sub-temperate conditions of Palampur, HP, (India) with same management inputs in fodder cut and no cut systems resulted in green forage yield of 6.6 t ha^{-1} to 11.88 t ha^{-1} with fodder cuts at 70 days after sowing (DAS) to 90 DAS and grain yield of 4.44 t ha^{-1} to 2.31 t ha^{-1} against grain yield of 4.01 t ha^{-1} in no fodder cut system. Fodder cut at 70 DAS resulted in better grain yield, straw yield, economic returns and overall productivity in terms of forage equivalent yield with the same inputs as in grain crop indicating better resource use efficiency of dual purpose wheat. Therefore, facultative type dual purpose wheat varieties can represent a unique and economically important resource, ensuring fodder and food security in the region.

PP 4.23: Level of resource use and technical efficiency in Indian wheat production - A case of Bihar

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Yield and production plateau is a serious concern owing to inefficient use of resources and input services. Increasing the crop output is possible primarily through enhancing the productivity that could be achieved by optimal use of resources. In the milieu, an attempt has been made to analyse the existing level of resource use, quantify the yield gaps and estimate the technical efficiency in wheat production. Data on crop production particulars were collected from 200 randomly selected respondents in 2018 across two districts of Bihar *viz.*, Muzzafarpur and Vaishali through a structured pre-tested interview schedule. Tabular, percentage, and graphical analyses were used for arriving meaningful conclusions. Data Envelopment Analysis (DEA) were performed to estimate the technical efficiency of resource use in wheat production. Findings indicated that the Yield Gap-I *i.*e., experimental yield – farmer's potential yield was negative and highest in Muzzafarpur (-9.39q ha^{-1}-16.53%). Inter alia, yield gaps arise due to difference in management practices adopted by the farmers. However, Yield Gap-II (farmer potential – average farmer) was positive in both the districts. Analysis of resource use pattern indicated that there exists significant difference in the use of resources across farm households in two districts. Seeds were used more than the recommended dose, whereas, nutrients (NPK) were either over used or under used. DEA showed that wheat producers are technically efficient by 74.28% indicating around 26% of additional output can be produced with optimal use of input bundle (seeds, fertilizer, irrigation, plant protection chemicals and manure/bio-fertlizers). Further, it was found that a majority of the farmers (58consisting of 29%) fall under 61-70% efficiency. Around 32 farmers (16%) were technically inefficient by 47% indicating ample scope for yield enhancement. Overall, the study advocates for optimizing the resource use, especially seeds and fertilizer for ensuring incremental production.

Theme5: Changing food habits and value addition for quality improvement

KL 5: Potential of biofortified wheat to alleviate hidden hunger

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Biofortification, the process of breeding nutrients into food crops, provides a sustainable, cost-effective strategy for delivering micronutrients to rural households in developing countries. Biofortification is now being well recognized as a potential intervention along with fortification and supplementation to address hidden hunger, caused by micronutrient deficiency. In fact, more than 190 biofortified crop varieties have been released in 30 countries across the globe, where > 33 million people are already consuming biofortified food.

In India, nearly 40% of children under 5 years old are physically stunted and markedly vulnerable to common infections, like diarrhea and pneumonia. When not corrected prior to the second year of life, stunting may become irreversible, gravely impairing individual and societal development. Indian diets are limited in zinc-rich animal foods, and include an abundance of grains and legumes which inhibit zinc and iron absorption. Access to commercially fortified foods and zinc supplements are also limited in Indian resource-poor settings. Realizing the role of wheat to address zinc deficiency, Indian wheat breeders are working in collaboration with CIMMYT and HarvestPlus to enhance zinc concentration.In fact, two zinc rich conventionally-bred wheat varieties have already been released for the NWPZ by IIWBR and PAU, with more nutrient-dense varieties in the breeding pipelines in ICAR institutes and several SAUs. Efficacy studies in India have shown that children under 5 years who ate foods prepared with whole wheat enriched with zinc, spent significantly fewer days sick with pneumonia and vomiting. And mothers who consumed it spent fewer days with fever. These positive health outcomes, as well as recent successes in delivery, provide evidence that biofortification is a promising strategy for combating hidden hunger.

LL 5.1: A decade of progress on genetic enhancement and development of climate resilient biofortified wheat with enhanced micronutrients concentration

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Wheat provides approximately 30% of the total calories of more than 4 billion people in developing countries, and is the major staple in South Asia. Poor quality diets, dominated by food staples, are often deficient in minerals and vitamins, however, wheat serves as major source of protein and vitamins B and E and micronutrients such as iron (Fe) and zinc (Zn) to the resource poor families. Traditional breeding of wheat cultivars with higher levels of Zn and Fe in wheat grain could potentially eliminate micronutrient malnutrition problems worldwide. Wheat grows in diverse environments and geographies and has a high potential to be bred to provide productive cultivars that are attractive to farmers and consumers, including for their nutritional properties. The international maize and wheat improvement center (CIMMYT) has successfully developed and deployed competitive high zinc wheat cultivars in the target regions of South Asia with an additional 30-40% higher Zn. The biofortifcation breeding of wheat is an excellent example of the effective use of both adapted and exotic genetic resources in crop improvement where high Zn QTLs from progenitor species such as *Triticum* spelta, *T. dicoccon* based synthetic hexaploids and landraces were successfully introgressed. High Zn donors were crossed with elite wheat germplasm that had high yield potential and good agronomic traits, such as disease resistance and drought tolerance and better processing quality. Marker-assisted selection for the desired QTL alleles of key progenitor QTLs for Fe and Zn can accelerate fast-track development of competitive high Zn wheat varieties. The competitive high zinc wheat lines with better tolerance to drought and heat stress developed at CIMMYT-Mexico tested across target environments through public and private sector partners led to the release of more than eight biofortified wheat cultivars in South Asia. Faster dissemination of biofortified wheat cultivars for farmer's adoption has been achieved through seed distribution through community-based PVS approach and other seed producers as well as startup national seed companies to help accelerate multiplication and commercialization in rural areas with limited market access. Nutritional studies have shown that Zn biofortified wheat is an efficient source of Zn and consumption of biofortified wheat has demonstrated to improve overall health of deficient young children in India who consumed foods with Zn enriched wheat showed number of days they spend sick with pneumonia and vomiting significantly reduced.

LL 5.2: Improving nutritional quality of wheat: challenges and progress

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Wheat is an important cereal crop which contributes significantly in food and nutritional security of human population. The distribution of nutrients within the wheat kernel is typical of many cereals. The germ is rich in vitamins B and E, high quality protein, unsaturated fats, minerals, and carbohydrates while the bran consists mostly of the insoluble carbohydrates such as cellulose, protein, traces of B vitamins and minerals and anti-nutritional factors such as phytic acid. The endosperm is the largest part of the grain and consists mainly of starch and protein, and trace amounts of vitamins and minerals. Though, it contains significant quantities of protein, carbohydrate, fats, minerals, antioxidants and vitamins required for human health, there are problems with respect to their bioavailability leading to "hidden hunger". The consequences of hidden hunger in terms of mortality, impaired physical and cognitive development, and eye problems are of staggering magnitudes. Existing micronutrient interventions such as pharmaceutical supplementation or industrial fortification are effective yet have their limitations, particularly in rural settings. These limitations can be overcome through the production of new food crops with higher micronutrient densities, an approach often referred to as "biofortification". Therefore, enhancing wheat micronutrient density and their bioavailability for humans and monogastric animals could lead to both improved human health, reduced pollution and more sustainable agriculture. Recently there have been concerns of CD toxicity of wheat gluten in human beings. In addition, there is need to improve wheat for diabetic persons. Recently we have generated information about micronutrient content, level of anti-nutritional factors, and variability in the amount of CD toxic epitopes in wheat germplasm. Large variations have been identified in Fe and Zn content in wheat germplasm which is the important source of improving micronutrient content in high yielding backgrounds. Enhanced genetic variability in different nutritional quality traits have also been generated in high yielding backgrounds using EMS mutagenesis during 2008-09 crop season. 800 mutant lines in the background of PBW 502 were advanced into higher generations and evaluated for phytase and phytic acid levels during 2014-15, 2015-16, 2016-2017 and 2017-18. Low phytic acid and high phytase level mutants have been developed. This is the first report of evaluating large germplasm of wheat for both phytase and phytic acid levels and also the development of high phytase and low phytic acid lines through mutation breeding. Development of micronutrient-rich wheat grains using Biofortification tools can substantially reduce micronutrient deficiencies. Both genetic and agronomic improvement in wheat Fe and Zn content can lead to improved health of human beings. Progress made and future perspectives in both genetic and agronomic strategies for improvement of wheat nutritional quality will be discussed.

OL 5.1: "Indian durum wheat" - potential for pasta industry and to enhance farmers' income

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In India, an estimated 1.5 to 2.0 million tonnes of durum wheat is produced annually. Dry and hot environment of central and peninsular parts of India *viz.*, Madhya Pradesh, Gujarat, Maharashtra, Karnataka and Southern Rajasthan are suitable for durum cultivation. Best quality durum wheat with excellent appearance, good hectolitre weight, high protein and less yellow berry incidences predominantly produced in the Malwa plateau of Madhya Pradesh due to longer grain filling period and short vegetative growth in the region. Its grain density, combined with high protein content (>12.5%), low yellow berry incidence(<10%) and high ß-carotene content(>7.0 ppm)and gluten strength, make durum the wheat of choice for producing premium semolina, which is being used in making Indian recipes *viz.*, rava-dosa/macaroni/noodles/snack foods etc. With the rising demand for speciality foods like pasta in India and other countries, the market for durum wheat is growing at an exponential rate. Intensive research and development efforts made by Regional Research Station, Indore of ICAR-Indian Agricultural Research Institute brought the durum wheat back into cultivation in Central India with very high yield potential. With intensive popularization of newly evolved high yielding and rust resistant durum varieties *viz.*, HI 8627, HI 8663, HI 8713, HI 8737 and HI 8759etc., with a yield potential of more than 50 q/h awith at least 4 to 5 quintals grain yield advantage over bread wheat; and their "low-cost cultivation technology", durum wheat production in Madhya Pradesh improved significantly leading to the declaration of the state as 'Agri-Export Zone (AEZ)' for durum wheat also. The pasta industries are looking for more hectolitre weight and hardness to have better extraction rate (~ 68-72%), high protein (~13%), less black tip and dark crease, freedom from yellow berry and Karnal bunt for good finishing of pasta products. Compared to bread wheat, higher heat tolerance of durums ensures higher yields with lesser irrigation. Modern durum varieties are generally resistant to currently prevalent bread wheat virulent rust pathotypes, and thus, have been contributing to arrest the spread of wheat rusts in the country. Thus, it is an ideal wheat to be grown in Central and Peninsular parts of the country for improving the farmers' income, and for ensuring food and nutritional security, increasing employment opportunities through fast food industry and sustainability. An awareness campaign is, therefore, urgently required for the growers, traders and consumers about the importance of durum wheat as high economical crop and for use as health food.

OL 5.2: Amylase-Trypsin inhibitors: An important anti-nutritional factor causing intestinal inflammatory disorders of gastrointestinal tract

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Wheat intolerance is an emerging issue for a considerable population in the world which cause gastrointestinal problem when wheat products are consumed. Though wheat seed is a rich storehouse of nutrition, it contains some anti-nutritional factors causing negative responses to some genetically indisposed people. The negative responses include non-celiac wheat sensitivity (NCWS) caused by amylase-trypsin inhibitors (ATIs) and fructans, Irritable Bowel Syndrome (IBS) also caused by fructans, celiac disease (CD) caused by gluten and ATIs, Bakers asthma caused by serine peptidase inhibitors (serpins), lipid transfer proteins (LTPs), ATIs and gluten. ATIs are one of the recently known molecules which not only inhibit digestive enzymes but also aggravate other wheat intolerance problems. Amylase/trypsin inhibitors (ATIs) the non gluten proteins present in wheat, barley and rye strongly induce innate immune responses. They actually work as plant defence system, inhibiting animal enzymes to digest starch and glycogen present in grains making them as natural pesticides for plants. ATI may exist as Wheat Monomeric Amylase Inhibitors (WMAI. *e.g.* 0.28, molecular wt. 12kDa), non-covalently linked Wheat Dimeric Amylase Inhibitors (WDA*i.e.g.* 0.19, 0.51, molecular wt. 24kDa) and Wheat Tetrameric Amylase Inhibitors (WTAI.*e.g.* CM1, CM2, CM3, CM16, CMX2, CMX1/3, molecular wt. 60kDa). It has also been reported that the quantity of ATIs is different in different wheat genotypes. Characterization of different ATIs in wheat during grain development is essential for further manipulating them. In our study we have cloned, sequenced and in silico analysed the prominent ATIs from a popular hexaploid wheat variety HD3086. Expression pattern of these genes are studied during grain development not only in bread wheat but also in durum wheat and their diploid progenitors. Other than the basis studies, we are working towards development of a high through method to screen low ATI containing genotypes. This in combination with low immunogenic gluten in wheat will help in stepping forward towards tackling CD problem.

OL 5.3: Comparative performance of Indian barley varieties with respect to malt quality

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Malt quality is a very complex trait and is affected by large number of factors. Therefore, breeding for a variety combining yield, biotic/abiotic stress tolerance and desired quality parameters is a very challenging task. The systematic malt barley breeding programme started in India in early nineties and several barley varieties have been released since then. However, before that several varieties not specifically bred for malt purpose were also found to possess certain desirable characteristic from malting quality perspective. Varietal breeding is a continuous process to achieve improvement over existing genotypes and, therefore,a study was planned to evaluate malting quality of nineteen genotypes grown under similar environment and cultural practices to see their comparative performance with respect to different quality traits. The crop was grown during 2015-16 rabi season at ICAR-IIWBR, Karnal farms under timely sown conditions.The bold grains were micro-malted and then grain and malt parameters were analyzed. Genotypes were identified with individual parameters for good malting quality. The highest test weight of 70 kg/hl was achieved in Alpha 93, while the bold grain percentage was maximum in DWRB 92 (95.4 %). Husk content was lowest in Alpha 93 (9.2 % dwb), protein content in DWRUB 64 (8.6 % dwb) and beta glucan content in Amber (2.9% dwb). The grain beta amylase activity was highest in Alpha 93 (24.2 betamyl units/g^{-1}). The malt friability was maximum in Alpha 93 (77 %), hot water extract in DWRB 101 (84.3 % fgdwb) and diastatic power in Amber (115.5 oL). Beta amylase activity in malt was maximum in RS 6 (29.1 betamul units/g). This preliminary information on different malting quality parameters could be useful for malt barley improvement programme and basic studies in future.

PP 5.1: Evaluation of durum wheat genotypes for yield and quality traits

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India is one of the leading durum producing countries in the world. In India, durum wheat is preferred over bread wheat in making a number of traditional recipes like daliya, laddu, churma, sevaiyan, suji-halwa etc. Durum wheat is an economically important crop because of its unique characteristics and end products. The kathiagehoon which is also called as durum wheat, was the predominant wheat species grown in central India, particularly in the Malwa plateau in Madhya Pradesh, parts of Gujarat, southern Rajasthan and Bundelkhand region of Uttar Pradesh until 1950s. Subsequently, the area under durum cultivation continually declined due to limited yield potential of the local durum varieties. It is further complicated due to exposure of durum growing areas for climate change. The quality of durum wheat is highly correlated with the quality of its end products. Therefore, it is imperative to develop new breeding materials and/or genotypes/ cultivars which have high yield potential with good quality adapted to fluctuating climatic conditions by hybridization among diverse sources of valuable genes for yield and quality traits. In the present study, a set of 50 advance wheat genotypes including two checks (HI 8713 and AKDW 4883)were used for the study of different yield and quality traits. The experiment was conducted in a RCBD design with two replications during 2017-18. Each genotype was planted in a six rows plot of four meter length with spacing of 23 cm between rows and 10 cm between plants within rows. Observations were recorded for plant height, spike length, tillers per meter, protein content, moisture contents, beta-carotene, iron, zinc and grain yield. Out of 50 durum wheat genotypes, 15 genotypes were found to be better as compared to the checks for yield and quality traits. The genotypes having unique sources of valuable genes for various yield and quality traits were thus identified and are being used in the breeding program.

PP 5.2: Exploring Indian wheat genotypes for less Celiac disease toxic epitopes

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Celiac disease (CD) is an autoimmune intestinal chronic disorder caused by an intolerance to gluten proteins (gliadins and glutenins) of wheat, barley and rye. CD mainly results in small-intestinal mucosal injuries and nutrient malabsorption in susceptible individuals. CD occurs at a prevalence of around 1% of population worldwide. In India, the prevalence of CD is more in north, north-western and central parts as compared to other regions in the country. CD toxicity is mainly caused by the presence of glutenin and proline rich specific epitopes in gluten protein. The idtification and/or breeding of wheat cultivars naturally deficient in CD toxic epitopes is very appealing. A study was initiated in which 80 wheat varieties representing last 100 years were evaluated for the concentration of CD toxic epitopes. Indirect ELISA protocol was standardized using Gliadin peptide antibody 4F3 specific to a CD toxic epitopes. The results were further verified by western blotting. Although there are varietal differences, there was no significant change in the average level of CD toxic epitopes in wheat varieties released in India during last sixty years. But, the level of epitopes was comparatively lower in the varieties released before 1960. Wheat and barley genotypes with less content of CD toxic epitopes can be identified. The identified genotypes can be used in breeding in reducing CD toxic epitopes in high yielding varieties. This will bring less CD toxic wheat products in food chain with consequences of reduced celiac disease.

PP 5.3: Novel sources of variation in grain Zn concentration identified in wild wheat species of *Agropyron, Aegilops, Secale, Thinopyrum, Triticum, Elymus genera and their derivatives*

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Micronutrient deficiencies, particularly, zinc (Zn), are widespread globally and affect human health. Wheat is an important source of dietary Zn in many developing countries. Domestication of wheat has narrowed the grain Zn concentration in modern wheat. Therefore, the aim of this study was to evaluate a panel of 225 wild accessions, and derivatives for grain Zn concentration and the grain ionome. Ear samples of 225 wild accessions were provided by the Nottingham/BBSRC Wheat Research Centre (WRC), hand threshed to get the five grains per accession. Experiments were conducted under controlled glasshouse conditions to grow the 17 amphidiploids, five wheat cultivars and 13 wild wheat species in 2014-15 and 2015-16. Grain samples were analysed for mineral composition traits using inductively coupled plasma-mass spectrometry (ICP-MS). The mean grain Zn concentration of 225 wild accessions varied from 47.4 to 178.4 mg kg-1. The mean grain Zn concentration of 17 amphidiploids varied from 67 to 223 mg kg^{-1}, averaged across years. Amphidiploids showed up to 2.5-fold greater grain Zn concentration than wheat parents. There were no relationships between flag leaf Zn and grain Zn concentrations. However, grain Zn and iron (Fe) concentration were positively correlated. Wild wheat species, for example, Amblyopyrum muticum, Aegilops speltoides, Aegilops umbellulata and Aegilops comosa and their derived amphidiploids could be useful sources of variation to increase the grain Zn concentration in breeding programmes. Further work is needed to look at relative size of endosperm and grain Zn concentration in different fraction of grain.

PP 5.4: Application of Iron and Zinc spray for enhancing micronutrient content in wheat

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Wheat is widely grown cereal crop occupying around 17% of the world's total cultivated land and a staple crop for 35 % of world's population. Wheat like other staple cereals contains low levels of Iron (Fe), Zinc (Zn) and other micronutrients. End use and industrial quality of wheat depends mainly on the chemical composition of wheat grain. As a measure to enhance micronutrient content of wheat grains, an experiment was conducted on a set of 12 wheat genotypes including recently released varieties and some promising advanced lines developed at ICAR – IIWBR, Karnal during 2017-18. The genotypes included DBW14, DBW16, CBW38, DPW621-50, DBW90, WB2, DBW173, DBW223, DBW237, DBW256, DBW258 and DBW259. The spray of Fe and ZN was made at two different stages, i.e. pre anthesis (flowering) and post anthesis (grain filling). The treatments included foliar sprays of 125 ppm Fe + Zn and 250 ppm Fe + Zn individually and in combination at pre-anthesis and post-anthesis stages. Data was recorded on days to heading, plant height, number of tillers per meter, spike length, number of grains per spike, 1000 grains weight and yield per plot. The grain samples from each plot were used to analyze Fe and Zn content. The results indicated that the spray of both Fe and Zn led to enhanced content of these elements in the wheat grains. Among the genotypes DBW16 and DBW 90 were highly responsive to Zn accumulation and upto 30 per cent higher Zinc content was estimated than the control plots.

PP 5.5: Transcriptomic response of *Triticum aestivum* L. to Fe/Zn starvation identifies key transporter genes

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In the recent past, knowledge of molecular mechanism of Fe/Zn transport in wheat was lacking at genome level, however, availability of wheat genome in public domain has fastened the research to identify the genes involved during Fe/Zn transport. Here, we conducted transcriptome analysis of four extreme Fe/Zn rich (Sonora-64, Vinata (N-8223), PAU 1660) and deficient wheat genotypes (DBW-17). Sequencing analysis of sand culture grown one month old wheat seedlings showed a total of 415.03 million (150x2) reads. Read assembly depicted 176891, 178525, 218802 and 209227 transcripts respectively in above mentioned wheat genotypes. About ~62.81% of transcripts were functionally annotated. Amongst them, ~1.96% heme binding, ~3.4% zinc ion binding and ~3.8% metal ion binding transcripts were found. Nevertheless, further analysis of the data enabled to the idtification of 28 key transcripts involved in Fe/Zn uptake and translocation. The qPCR and heat map analysis showed varying degree of expression of the transcripts across the genotypes with maximum in PAU1660 followed by Sonoara 64, Vinata and DBW 17. Thus, in this investigation, we identified repertoire of genes associated with high Fe/Zn in hexaploid wheat. The identified genes could be exploited as a proof of concept for further validation in mapping population and subsequent utilization in MAS for increased Fe/Zn content.

PP 5.6: Molecular characterization of high protein quality pyramided lines derived from cultivated wheat varieties

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Grain protein concentration (GPC) of hexaploid wheat is one of the important factors that determine the end-product quality, as well as playing a pivotal role in human nutrition. Pyramided wheat lines were developed by crossing two cultivated wheat varieties UP 2338 and UP 2382 as recurrent parents with different donors and these pyramided lines were than screened for different desirable traits like high grain protein content, rust resistance and high glutenin content. SSR markers were used for foreground selection to screen one twenty-two pyramided lines for traits like high grain protein content, rust resistance and high glutenin content. SSR markers used in present investigation for foreground selection were Xucw108 (high grain protein content), Dx5a and Dx5 (high glutenin content) and for leaf rust resistance Wmc221 (Lr19), SCS1302 (Lr24), Xgwm273 (Lr15) were used. The results of marker analysis revealed that there were five lines that shows maximum number of desirable traits like high grain protein content, high glutenin content and rust resistance genes like Lr19 and Lr15.

PP 5.7: Effect of delayed sowing on wheat grain quality

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Wheat is a highly adapted crop and grows in varied latitudes and longitudes around the world. The performance of the crop in terms of yield and grain quality, however, is affected by several climatic factors such as soil moisture, fertility, temperature and photoperiod. The effect of changes in these physical factors on the grain quality has been studied earlier also,but now-a-days it has assumed more importance than ever in view of the climatic change. In this study, sixteen wheat genotypes were grown in a randomized complete block design on two sowing dates ~ 30 days apart. Yield, plant height and days to flowering along with nine end-use quality and three nutritional quality traits were examined. The genotypes showed significant interactions with the date of sowing for all the 15 traits studied. In the later sowing, the yield and plant height uniformly reduced in all the genotypes whereas, the days to flowering either reduced or remained the same in different genotypes. Thousand kernel weight, test weight(hectolitre weight) and flour recovery was significantly reduced whereas, the traits namely, grain hardness index, protein content, sedimentation value and grain Zn concentration increased significantly with delay in sowing.

PP 5.8: Assessment of genetic variability and diversity for grain nutrients and yield contributing characters in bread wheat

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Thirty genotypes of bread wheat were studied for generating requisite information on nature and magnitude of genetic variability and diversity for designing a breeding programme. The experiment was conducted at Agricultural Research Station, Niphad, MS, during rabi season 2016-17 and laid out in a randomized complete block design with three replications. The data were recorded on 50 per cent heading, days to maturity, coleoptiles length, plant height, number of productive tillers per running meter, number of grains per spike, thousand grain weight and grain yield per meter while, phytic acid, protein, Fe and Zn content of grains was estimated in the laboratory. Analysis of variance revealed significant differences among the genotypes for all the characters under study. Estimates of Phytic acid content of genotypes ranged from 4.88 mg kg^{-1} to 11.36 mg kg^{-1} with mean content of 7.369 mg kg^{-1} while, the values for protein content ranged from 9.73 % to 13.53 % with mean protein content of 11.433 %. The estimates of Fe and Zn content of grain ranged from 29.87 mg kg^{-1} to 44.93 mg kg^{-1} with mean content of 40.010 mg kg^{-1} and 19.8 mg kg^{-1} to 35.47 mg kg^{-1} with mean content of 29.839 mg kg^{-1}, respectively. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for grain yield per meter followed by Phytic acid content. All the characters under exhibited exhibited higher estimates of heritability in broad sense while, protein content exhibited lowest estimate of heritability. High heritability estimates coupled with higher estimates of Genetic advance as per cent of mean were observed for Grain yield per running meter, Phytic acid content of grains, number of productive tillers per meter, Zn content of grains, Coleoptile length and number of grains per spike indicating that these characters were under the control of additive gene action and improvement in these characters

PP 5.9: Marker assisted backcross breeding for improving malt quality in Indian barley varieties

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Barley is one of the important commercial crops due to demand of barley malt in beer and food industry. Breeding malt barley varieties gained momentum in 1990s and good number of two row malt barley varieties have been released under AICRP on Wheat and Barley. These barley cultivars have yield comparable to six row varieties and offered good malt quality for commercial purpose. Beverage industries favour exotic barley lines due to their desirable low beta glucan content for barley malt. Taking this into consideration, we have started marker assisted backcross breeding (MABB) efforts to further refine the β-glucan content in Indian barley cultivars to fulfil demand of Indian breweries and promote barley cultivation in India. Prominent barley cultivars like DWRB101 and RD2849 from north-western production zone were used as recipients for incorporation of low beta glucan QTLs using a marker-assisted backcross (MAB) breeding approach. Two exotic lines, SLOOP SAWL3167 and SLOOP VICVB 9953, identified for low β-glucan content were used as donor parents. Four cross combinations *viz.* DWRB101/SLOOP SAWL3167, DWRB101/ SLOOP VICVB 9953, RD2849/ SLOOP SAWL3167 and RD2849/ SLOOP VICVB 9953 were made at Karnal during 2015-17 and backcrosses were developed. Both foreground and background selection were done using gene specific and SSR markers in each cross combination along with biochemical estimation of β-glucan content using EBC enzymatic method in backcross populations. QTL- HvCSFl6 located on 7H is found as prominent QTL controlling β-glucan content in contrasting parental lines used in this study. Gene based marker HvCSFI-6 (7H) and STS marker Brz (7H) were selected for foreground selection of beta glucan trait in parents and segregating backcross lines. Based on the study, we are targeting to improve content of β-glucan at lower side in prominent Indian malt barley cultivars to address industrial demand of malt barley.

PP 5.10: Formulations for preparation of cake from blends containing different proportions of wheat and rice bean flours

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The study was undertaken with the objective to formulate and evaluate nutritional characteristics of cake prepared from blends containing different proportions of wheat and rice bean flours. Cake is form of sweet dessert that is typically baked from low protein wheat flour and preferred and consumed by a large segment of population of different age groups. The nutritional profile of cake improved with the utilization of rice bean which is under-utilized pulse especially in the Himalayan region. The blends of refined wheat flour and rice bean flour in different ratios (100:0, 75:25, 50:50, 25:75 and 0:100) were standardized. The cake prepared from different blends was analyzed for nutritional profile and sensory characteristics. The protein, fat, fibre and ash contents of cake prepared from refined wheat flour (100%) were 10.65, 24.46, 3.39 and 1.94 per cent, respectively. The addition of rice bean flour in different proportions improved the nutritional profile of the cake. The acceptability of the cake in terms of colour, flavour, taste and texture was assessed on nine point hedonic scale and mean values for these parameters of cake prepared from refined wheat flour (100%) were 7.80, 7.75, 7.78 and 7.57 respectively which decreased slightly with the addition of rice bean flour but the scores were in the acceptable range. The overall acceptability of cake prepared from refined wheat flour (100%) was higher as compared to cake prepared from blends containing different proportions of rice bean flour. Further the values of colour, flavour, taste and texture slightly decreased with storage intervals but the changes were with in the acceptable range. From the results it has been observed that the standardized formulations have industrial application and can be boosted for preparation of cake on commercial lines with added advantages for nutritional improvement and consumer's acceptability.

PP 5.11: Estimation of nutritional profile of selected pseudo-cereals along with phenolic content and anti-oxidant activity

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Millets are the staple food items in the dietary of many people in many of underdeveloped countries. These are not only rich in macro-nutrients but are also dense in micro-nutrients. Whole millets are a source of several functional ingredients and their consumption is essential for a healthy lifestyle. Some millets are still underutilized despite their rich nutritional profile. Whole flours of locally procured pearl millet, finger millet, sorghum and oat flour were studied for their proximate composition, crude fibre and dietary fibre(DF) composition and compared with oat flour. Protein content was found to be 14.71, 12.11, 11.25 and 7.45 in descending order in oat, pearl millet, sorghum and finger millet respectively. Whereas, values for fat was estimated as 2.05, 2.67, 4.94 and 4.96 in finger millet , sorghum, oat and pearl millet respectively in a ascending order. In terms of dietary fibre composition, NDF (neutral detergent fibre) was high (11.29g/100g) in sorghum than other millets and ADF (acid detergent fibre) is high (5.81g/100g) in finger millet. Study revealed that pearl millet had highest total phenolic contents (TPC) of 1.14mg/g and also good antioxidant profile amongst the crops studied. This signifies their superior nutritional quality and suitability for functional food use.

PP 5.12: Nutritional diversity: characterizing the starch metabolism in developing endosperm of different genotypes of wheat

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Wheat is the second most important staple food grain crop after rice, consumed by 65% of the population in India and is likely to increase further due to changes in food habits. Heat stress is a major abiotic stresses limiting crop production. It reduces wheat growth by affecting the various physiological and biochemical processes. Wheat is highly sensitive to heat stress (HS) especially during the critical stages like pollination and grain-filling. HS causes denaturation/ aggregation of key enzymes involved in starch biosynthesis pathway affecting the quality and quantity of the grains. Here, we analyze the nutritional quality parameters of starch in developing endosperm and harvested seeds in four contrasting wheat cultivars - HD2932, HD2985, Raj3765 and C306. We used different biochemical markers like activity assay of Total amylase and alpha amylase, total starch content, amylose and amylopectin accumulation, etc. The specific activity of total amylase in harvested seeds was observed maximum in C 306 (2.6 U/mg^{-1} protein), and minimum in Raj3765 (2.0U/mg^{-1} protein). The percent starch content in harvested seeds was observed maximum in HD2932 and minimum in C306 while amylose content was observed maximum in HD2985 as compared to the other three cultivars. All varieties were performed well but the best performer is HD2932 in terms of high starch content and low amylase activity. Gel-based proteomic analysis also showed very good banding pattern in HD2932. There is a need to correlate the biochemical marker with the nutritional quality of cultivars under different locations in order to use it as best performer.

Theme 6: Impact of climate change on adoption and sustainable production

KL 6: Conservation agriculture for enhancing wheat productivity in the context of climate change

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Conventional agricultural systems are characterized by repeated tillage operations, monocropping or fixed crop rotations, clean cultivation, greater dependence on chemical fertilizers and other agro-chemicals, and flood irrigation in most areas. Adoption of these so called modern cultivation practices coupled with introduction of dwarf-statured high-yielding varieties of wheat led to increased productivity and also profitability during the first two decades of green revolution. Subsequently, the production costs started increasing due to high energy requirements for tillage, fertilizer, ground water and others. Further, there were reports of degradation of natural resources of soil, water and environment. It is believed that these practices are not climate resilient and sustainable in the long run; and therefore, there is a need to reorient crop production practices for achieving higher productivity while ensuring ecological sustainability in the context of climate change.

Conservation agriculture (CA) is an ecosystem approach based on the practical application of locally-adapted three interlinked principles: (i) continuous no or minimum mechanical soil disturbance (no-till seeding/planting and weeding, and minimum soil disturbance with all other farm operations including harvesting); (ii) permanent maintenance of soil much cover (crop biomass, stubble and cover crops); and (iii) diversification of cropping system (economically, environmentally and socially adapted rotations and/or sequences and/or associations involving annuals and perennials, including legumes and cover crops), along with other complementary good agricultural production and land management practices. These production systems are considered to be more innovative, knowledge-intensive and resource-use efficient, climate-resilient, and thus help in overcoming the problems associated with conventional agricultural systems.

Rice-wheat is the major cropping system in the north-western plain zone covering Punjab, Haryana and western Uttar Pradesh. Combine harvesting of north crops is quite common and the resultant crop residue left in the field is often burnt. This has caused serious environmental problems as it pollutes the environment and also affects soil health. Considering this, efforts were made to develop tillage and residue management options since 1990s. Initially ZT wheat after transplanted rice was promoted using a specially-designed ZT seed-cum-fertilizer drill.

This technology became quite popular in some areas as it saved time, labour and cost. The area under ZT wheat reached around 3 M ha in the first decade of this century but stagnated or even decreased in some areas thereafter. Burning of residue has now become rampant. To check this new generation farm machinery including combine harvester with super straw management system (SMS), happy seeder, roto-till drill, bailer, shredder etc. have been introduced.

No major effort was made in central India to develop and promote CA until the Directorate of Weed Research at Jabalpur initiated a flagship programme in 2012. Results of the last 5 years period have shown wonders as evident from timely sowing of crops (by June-end for rainy-season crops, October-end for mustard and chickpea, mid-November for wheat, and March-end for greengram and blackgram); increase in cropping intensity from <150% in 2012 to 300% in 2016; large savings in diesel cost, machinery repair and irrigation water; increased productivity (>10 t ha-1/year) and profitability; and improvement in soil health. This technology has proved to be climate-resilient as it avoided burning of crop residues, puddling for rice transplanting, and ensured C-sequestration through residue recycling and zero-till cultivation.

CA-based practices have been found to be climate resilient owing to timely sowing of crops, reduction in diesel burning for ploughing, recycling of crop residues in situ and avoiding burning, decreased use of chemical fertilizers and agro-chemicals in the long-run, less oxidation of soil organic matter and greater C-sequestration, modification of hydro-thermal regime in the soil profile, moderation of temperature within the crop canopy and minimizing adverse effects of terminal heat stress in crops like wheat. All these benefits accrue despite lower cost of cultivation, higher crop productivity, improved soil fertility and cleaner environment. However, there are still some apprehensions and myths about CA primarily due to ignorance, lack of experience, and faulty application of all the principles and associated practices in a holistic manner. There is a need for large scale demonstrations and adoption of these technologies in diverse environments for deriving full benefits of enhanced productivity, profitability and sustainability in the context of climate change.

LL 6.1: Impact of climate change on adoption and sustainable production

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Climate change impacts on agriculture are being witnessed all over the world, but countries like India are more vulnerable in view of the huge population dependent on agriculture, excessive pressure on natural resources, and poor coping mechanisms. The challenges are manifested in different ways like global warming. Significant negative impacts on crops, livestock, poultry, and fishery have been projected with medium term and long-term climate change. To address these challenges, there is a need of coordinated efforts at national and global level to understand them and devise suitable strategies on the basis of vulnerability of natural and socio-economic systems in different areas. Enhancing the resilience of agricultural production to climate change, therefore, is critical for ensuring food and nutritional security for all, particularly the resource poor small and marginal farmers.

In the context of climate variability, farmers need to adapt quickly to increasing frequency of drought, flood and other extreme events to stabilize crop yields and farm income. Over the years, the National Agricultural Research System has developed an array of practices and technologies to foster stability in agriculture production against the onslaught of seasonal variations. ICAR launched the National Initiative on Climate Resilient Agriculture (NICRA) to undertake strategic research on adaptation and mitigation and also to demonstrate climate resilient technologies at farmers' fields. The Technology Demonstration Component (TDC) of NICRA project is aimed at enhancing the resilience and adaptive capacity of farmers to cope with the increasing climate variability in different agro-ecosystems spread across 121 climatically vulnerable districts and implemented by Krishi Vigyan Kendras (KVKs).

The villages selected under NICRA are vulnerable to different stresses such as drought, cyclone, flood, heat/cold wave, seawater intrusion etc. Appropriate climate resilient interventions were tailored for each village in consultation with farming community along with village extension workers, rather than following a "blanket recommendation" approach. Institutional interventions including establishment of Village Climate Risk Management Committee (VCRMC), CHCs for farm implements, seed banks for access to improved crop cultivars, and fodder banks were promoted through collective action to build resilience among communities. Capacity building by extensive participatory demonstrations of location-specific agricultural practices, trainings, and exposure visits helped farmers gain access to knowledge and gave confidence to cope with adverse weather conditions.

Location-specific integrated action plans including demonstration of resilient technologies, management practices, and institutional and policy interventions have shown promising results at several locations. Case studies of different villages have demonstrated significant enhancement of system productivity and livelihoods, and adaptation to weather aberrations with mitigation of co-benefits. Some of the successful technologies and practices that promoted resilience to climatic stresses are being mainstreamed in many national and state government programs for their up scaling in applicable domains. Irrigation is influenced by climate and need to be taken up as an adaptive measure as, there is an expected increase in the irrigation probability. The developed CRVs have become model villages for gradual expansion horizontally in the cluster of villages and bring the element of resilience in overall Indian agriculture.

The dual benefits envisaged in the strategy of NICRA in India, is to improve and sustain the country's food security by adapting agriculture sector to weather aberrations and extreme climatic events along with environmental services in terms of reducing GHG emission. Enhance funding for promotion of strategic technologies and encourage the expansion of credit policies for implementation of irrigation technologies for sustainable food production.

LL 6.2: Sustainability is crucial to guard wheat productivity enhancement in the era of climate change

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Yield sustainability in wheat is imperative for strategic planning required to ensure food security in India; especially when the acreage is huge, production environments are diverse and the climate keeps changing. Progress made through genetic improvement often gets impaired by the yield loss occurring due to climate change and poor sustainability. This study aims to mark foot prints of global environmental change in wheat productivity and realize extent of this un-harvested yield under Indian conditions. To register impact of climate change, average per year mean yield of the released and pre-released wheat varieties tested under irrigated condition in the national wheat improvement programme for the past 25 years was examined. Regression analysis was applied to gauge growth in wheat productivity under ten different production environments representing two production conditions i.e. timely-sown and late-sown, in five mega zones of the country. Although yield gain between the start and closing five-year periods was quite substantial, coefficient of determination was low in some environments reflecting possibility of climate interference in harnessing progress made in varietal development. Impact of climatic variations was different in each production environment and the yield flux also varied. This was further substantiated by the productivity trend observed in some long-term varieties when their $16^{-2}0$ year performance was examined at fixed test sites. At a time when global warming is perceived as a big threat, trend in wheat productivity was even positive in certain parts of India. Polynomial trend in yield growth was examined to monitor climate induced yield deviations and goodness of fit supported such changes in five out of ten production environments. To learn more about yield sustainability in the present scenario, six years data of four leading varieties was statistically examined at twelve fixed locations in three major zones under both production conditions. Various shades of year effect i.e. positive/ negative or even non-significant were observed and each production environment expressed different sustainable yield index. Irrespective of year effect, year x location interaction emerged as the second most powerful source of variation in every production environment. Predominance of year-location interaction abets uncertainty, the most important fall out of global environmental change. Consequently, significant difference in variance and deviations in yield sustainability index were noticed even when mean yield of two years or locations was statistically similar. It illustrates that hidden impact of global warming can still be there even when average productivity shows no major deviation. Although sites with higher mean yield ensure higher production, the variable locations can be useful in screening materials for climate resilience. In every production environment, there were varieties showing similar productivity level but different sustainable yield index. Study indicates that some adjustment in crop phenology can be useful in developing wheat varieties which can withstand climate variations and express enhanced yield sustainability. To ensure high wheat production in India, it is pertinent therefore to select conditions and the genotypes which help in sustaining productivity.

OL 6.1: Farmers' perception on climate change and adoption practices in Indian wheat production

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Climate change is a serious concern affecting wheat production prospects, which potentially undermine the household food security, socio-economic development and sustainability. In the milieu, an attempt has been made to document the perception of farmers on climate change as well as the extent of adaptation strategies practiced at wheat farms along with the associated constraints in adoption. Data on socio-economic profile, production, awareness on climate change, adaptation practices and constraints were collected during 2016-17 through a pre-tested interview schedule from a randomly selected 500 wheat producers across five states *viz*., Haryana, Madhya Pradesh, Bihar, Himachal Pradesh and Maharashtra, each falling under one pre-classified wheat production zones. Conventional tools *viz*., tabular, percentage, scoring and graphical analyses were performed for arriving meaningful conclusions. Findings indicated that the perception of sample farmers on climatic variables over the past 30 years matched with the climatology i.e., long-term trend. Frequency analysis alerted that a majority (56.6%) of the farmers have not changed their wheat varieties despite climate change belief barring Haryana wherein, 54% seed replacement was noticed which is attributed to the higher literacy level and progressive nature of farmers. The survey reported that wheat area has not changed much among farm households. Further, it was perceived that wheat yield has increased over a period of time with no change in the straw yield. Barring a few adoption practices like application of organic manures, new varieties, crop insurance and irrigation management, the awareness on rest of the strategies is very low among the wheat producers, since every technology/technique is rooted with certain socio-economic constraints in adoption like higher cost, limited availability and/or lack of skill. The study recommends for upscaling and outscaling of validated region-specific participatory climate-smart farming practices and/or adaptation strategies like conservation agriculture practices for ensuring sustainable wheat production in the long-run.

OL 6.2: Simulating impact of climate change on late sown wheat production in Himachal Pradesh

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Wheat {*Triticum aestivum* (L.) emend. Fiori and Paol.} is the staple food of millions of Indians, particularly in the North India. Wheat production is affected by climate change, i.e. increase in temperature, CO_2 content and rainfall variability. Optimum sowing window is one of the adaptation measures to offset the changing climatic conditions. The study examined the impact of changing climatic conditions on wheat crop using crop simulation model. The InfoCrop model was validated using the historical data generated by the research trials at Palampur (Himachal Pradesh). The site falls in sub-humid and sub-temperate type of climate and is located at longitude 720 30'' E, and 320 20'' N latitude with an elevation of 1290 m amsl. The model was run for 20 years from 1989 to 2008 for Palampur weather station. The results indicated that sowing of wheat done on 30th November found to be the best planting window, followed by 15th December, whereas, the sowing done on 30th December resulted in lowest yield. The elevated levels of CO_2 resulted in an increase in wheat yield as compared to 370 ppm. Magnitude of increase yield under 50 ppm elevated level resulted 3.6 to 4.0% whereas, under 100 ppm yield increased to the tune of 1.7 to 7.5%. The 10^{0}C and 20^{0}C elevated levels of temperature coupled with 50 ppm level of CO_2 increased the yield by 23.0 to 69.7 % and 39.5 to 123.5 %. Further increase of 100 ppm CO_2 also increased the yield to the tune of 27.9 to 76.1% and 46.4 to 133 % under irrigated conditions with 10^{O}C and 20^{O}C elevated levels of temperature, respectively. The 10^{O}C rise in temperature coupled with 50 ppm higher level of CO_2 advanced the maturity of the crop by 4 to 5 days whereas, 20^{O}C rise in temperature coupled with 50 ppm CO_2 level advanced the maturity by 7 to 8 days. On further increase of CO_2 to 100 ppm level showed similar number of days in advancing the maturity period.

PP **6.1: Potential benefits of zero tillage demonstration in wheat production in India**

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Sustainable wheat production against climate change and shrinking productive resources is a daunting task and priority policy problem. National Agricultural Policy has strong orientation towards sustainable agriculture and hence popular conservation agriculture technologies like zero tillage is widely recommended particularly in the intensive rice-wheat cropping areas. In the background, the paper describes the potential benefits of zero tillage demonstrations in India. Data pertains to the period from 2013-14 to 2017-18. Two sample 't' test assuming unequal variances was employed to statistically test the significant difference in yield for zero tillage vis-à-vis conventional tillage followed by cost-benefit analysis to estimate the level of profitability. During the period from 2013-14 to 2017-18, 160 demonstrations ranging from 0.4 to 1 hectare on zero tillage method of sowing of wheat in India were conducted. Demonstrations registered an average yield ranging from 41.34 to 45.97 q ha^{-1} under zero tillage against 39.09 to 44.17 q ha^{-1} under conventional tillage. A significant difference in the yield level at 10% level of probability was noticed between zero and conventional tillage. Apart from additional yield, the demonstration helped in cost reduction especially on field preparation. The operational cost under zero tillage was estimated at INR 28753 per hectare against the conventional tillage at INR 31198 per hectare. Around 8.50% of the operational costs were saved using zero tillage which helped to reap an additional profit of INR 5493 per hectare over conventional tillage. On an average, with adoption of zero tillage, a farmer would get INR 2.93 per rupee of investment which is higher than the conventional tillage by 13.13%. Also, incremental benefits were observed like time saving in land preparation, reduced soil tillage, less weed flora, less irrigation water requirement, resistant to lodging and reduction in fertilizer usage which altogether will reduce the operational costs in comparison to conventional tillage. Owing to multiple benefits of the technology, the study recommends, up scaling and out scaling of the technology in other suitable areas for sustainable wheat production.

PP 6.2: Idtification of short duration high yielding wheat lines suitable for irrigated late sown conditions

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Late sown wheat is prone to terminal heat stress due to high temperature during grain filling stage. The terminal heat at grain filling stage adversely affects wheat yield and quality. For ameliorating these problems, the short duration wheat genotypes having plasticity for sowing period, and tolerance to terminal heat stress are recommended. Short Duration Screening Nursery (SDSN) of AICRP on Wheat and Barley, is one such initiative to identify such genotypes which are exposed to heat stress by planting them late. Three wheat genotypes namely RWP2013-09 (pedigree HD 2985/DBW 31), RWP2013-10 (pedigree HD 2984/DBW 36) and RWP2014-18 (pedigree DBW22/DBW 30) have been developed at IIWBR, Karnal following modified pedigree bulk method. These genotypes were identified after four years of evaluation in SDSN (2014-15- 2017-18) at multiple locations in augmented design using six checks namely DBW14, DBW71, Sonalika, NIAW 34, HD2932 and WR544. All the three genotypes were superior in yield and earliness than the checks during entire period of evaluation. RWP 2013-09 had significantly higher yield compared to all the checks with average mean yield of 487 g/plot and 437 g/plot in multi-location testing in NWPZ. RWP 2013-09 is a short duration genotype with days to heading of 78 which is at par with best check and matures in 119 days after sowing on an average. In Peninsular Zone, RWP 2013-10 showed significantly higher yield compared to all the checks with a three year average mean yield of 437 g/plot. Its days to heading are at par with best check and it matures in 100 days after sowing on an average. RWP 2014-18 had significantly higher yield compared to all the checks with a three year average mean yield of 330 g/plot in NHZ. The genotypes RWP 2013-9, RWP2013-10 and RWP2014-18 would be very useful as parents and donors in developing short duration and high yielding wheat varieties.

PP 6.3: Physiological studies in wheat under the regime of climate change

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Increase in atmospheric CO_2 and temperature are two most important drivers involved in climate change and likely to have significant effects on crops. So far, most of the studies conducted on climate change have been focussed on individual climate change factor. However, how these factors in combination would impact crop production, is not clear. Hence, attempts have been made to study effect of elevated CO_2 and temperature individually and in combination on wheat. Present study was conducted in wheat at ICAR-DWR, Jabalpur in open top chambers. After emergence, plants were subjected to long-term exposure to elevated CO_2 (550 ± 50 ppm), elevated temperature (ambient + 2^oC) and combination of these two (elevated CO_2 + elevated temperature). Morpho-physiological, phenological, biochemical parameters, gene expression and activity of soil enzymes were recorded periodically. In general, enrichment of atmospheric CO_2 had a positive effect on overall growth of wheat, however, elevated temperature alone or in combination of elevated CO_2 had adverse effect on phenology of wheat crop. Treatment-specific regulation as well as induction of new iso-forms of enzymes involved in antioxidant defence in response to elevated CO_2 and elevated temperature and combination of these two was evident. Elevated CO_2 and temperature also influenced the activity of soil enzymes (FDA hydrolysis, dehydrogenase and urease) in rhizosphere of wheat. It can be inferred that rise in atmospheric CO_2 alone would benefit wheat crop in terms of grain yield while elevated temperature alone would adversely affect grain yield. However, elevated CO_2 counteracted adverse effect of high temperature on grain yield to considerable extent.

PP 6.4: Android Mobile Application: JAU JANKARI

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Jau Jankari is an android application developed by the Indian Institute of Wheat and Barley Research (ICAR-IIWBR). It is developed in Hindi language for the maximum benefit of farmer community. Farmers can take full advantage of their barley crop using the information provided in this app. It provides information on different aspects of crop production, selection of suitable area specific varieties, seed treatment, use of fertilizer, seed rate, harvesting and storage. This app not only includes crop advisory, frequently asked questions ,barley health benefits and home uses but also the current crop rates in the market, current weather along with videos for barley uses. Interaction between farmers and experts is made possible through Consult Experts and Feedback options of this mobile app. This app is developed using android platform version 3.0.1 during 2017-18 and is freely available on Google play store. It can be downloaded through the following link: https://play.google.com/store/apps/details?id=berley.agriculture.barley. The front end of the app is designed in a way to make it farmer friendly and it has options like advanced varieties, crop management, disease and pest management, fertilizer and weed management, barley lab facilities, barley use videos, current market rates of crop, current weather details, barley literature,

PP 6.5: GxE interaction estimation by BLUP's for wheat coordinated system

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Conventionally linear model approach with ordinary least squares estimation procedures is used in wheat breeding trials. As the distribution of error term in breeding program experiments is often more complex as that of in standard linear models analysis, an alternate is required. Best linear unbiased predictor (BLUP), as a technique for predicting random effects proved numerous applications in field experimentations to estimate fixed and random effects of genotypes, environments and interaction effects. This improves per se performance of prediction procedure as compared to the ordinary least squares approach. Mixed models had been utilized as alternative analytical approaches to overcome limitations of the fixed analytical approach. The mixed model prediction of untested crosses relies on the genetic relationship between tested and untested crosses. Mixed linear model approaches may circumvent the problems of fixed ANOVA methods for combining information from different trials and incorporating genetic correlations by treating genotype effects as random variables. Multi environment wheat trials data under irrigated conditions of NWPZ from 2013 to 2018 had been utilized to produce BLUP's by REML and SAS software's to highlight improvement in wheat production of the zone. Average yield of best five performing genotypes increased from 53.3 q ha^{-1} to 56.7 q ha^{-1}.