

P001

Utilization of F₁ monosomics for genetic analyses involving awn expression in crosses of tetraploid and hexaploid wheats

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To identify the chromosomes carrying the genes for awn development 14 monosomic lines of Chinese Spring were crossed as female with two accessions of *Triticum turgidum* var. *dicoccoides*. Various awn expressions were found in crosses involving chromosomes 1A, 3A, 4A, 5A, 1B, 2B, 3B, 5B, 6B and 7B. All monosomic F₁ plants had awns approximately 1-3 cm in length with exceptions in 2A, 7A (Td1055) and 4B which were different from the expression of sister disomic F₁ plants. The occurrence of fully awned in crosses involving chromosomes 4A and 6B was expected because of the known awn inhibitors *Hd* and *B2* and awn-producing *al* in CS. Their appearance in crosses involving 1A, 5A, 6A, 2B, 5B, and 7B was not expected on the basis of published information. Therefore it is assumed in *T. dicoccoides* that these chromosomes may carry other recessive awn-promoting allele which effects the production of short awns.

P002

Genetic diversity and population structure analysis among Indian bread wheat cultivars

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Understanding genetic diversity and a research project on association mapping in wheat is under way in our laboratory. As a first step towards this goal, we carried out genetic diversity and structure analyses in a collection of 134 Indian wheat cultivars that were released over a period of ~100 years (1910 to 2006). For this purpose, we used a set of 42 SSR markers, one each from each arm of 21 individual chromosomes. The above 42 SSRs had a total of 257 alleles, which included 71 (27.6%) rare alleles occurring at a frequency of <5%. The number of alleles per locus ranged from 1 to 13 indicating considerable genetic diversity in the cultivars studied. The cultivars formed two groups, one with 31 cultivars released during pre-green revolution period and the other with 103 cultivars released during post-green revolution period. The average number of alleles/locus in the cultivars from post-green revolution period was relatively higher (5.29 vs 4.76 alleles/locus), but genetic diversity did not differ (0.63, 0.62), indicating that green revolution did not lead to any loss of genetic diversity. Further, analysis of molecular variance (AMOVA) showed that the proportion of the variance among cultivars within groups accounted for 94.4%, but between the groups only 5.6% of the overall molecular variance. The model-based *Structure* analysis identified a total of 10 sub-populations including two sub-populations, from pre-green revolution cultivars, and the remaining eight from post-green revolution cultivars.

P003

Revisiting old landraces of wheat for stem rust resistance

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Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is of major concern due to the emergence of a new pathotype, Ug99, in Uganda. Eight hundred and thirty eight accessions from 33 countries were screened for stem rust response under field conditions for three years. Seedling stem rust responses

against three predominant Australian pathotypes were also studied. Multipathotype testing of 140 accessions producing low stem rust response (≤ 5 on a 1-9 scale) under field conditions revealed the presence of *Sr2*, *Sr6*, *Sr8a*, *Sr8b*, *Sr9g*, *Sr12*, *Sr17* and *Sr30* either singly or in various combinations. Eighteen accessions possessed uncharacterized seedling resistance gene(s). The presence of *Sr2* in 18.9% of entries was identified using the closely linked molecular marker. On the basis of field tests (rust response ≤ 7), greenhouse screening (lacking major genes) and marker data (lacking *Sr2*), putatively new sources of adult plant stem rust resistance were identified.

P004

Wheat genome resources for bread wheat

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The elucidation of genetic factors controlling complex traits in wheat will assist in more accurate breeding selections and assist to increase production and quality attributes. However, to date the genetic resources have provided insufficient resolution to enable fine mapping down to the sub centimorgan level whilst providing a resource for mapping a large number of traits and therefore the resources required, on a per trait basis, have been large. The computational and statistical resources are now sufficient to map QTL in complex backgrounds and utilise a much larger diversity of germplasm. In order to address a number of challenges posed by wheat gene-mapping, such as background specific effects, epistasis, population sub-structure and environmental influences we have developed two large multi-parent recombinant inbred lines involving four and eight founders respectively. By increasing the number of founders we are able to exploit the genetic and phenotypic diversity available in current breeding material from around the world. The controlled breeding design alleviates difficulties often encountered in association mapping such as population structure. Increasing the number of rounds of meioses increases the resolution available and therefore increases the efficiency of gene identification. Due to the large number of RILs in these populations (1500 and 5000) we will also be able to better understand the environmental influences on a range of traits without the constraints imposed by traditional approaches. The large number of RILs also provides a mechanism to conduct hierarchical phenotyping for expensive to measure traits. These resources will provide the research community with a focal point for research across a range of applications.

P005

***Aegilops tauschii*: A valuable source for Karnal Bunt resistance**

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Karnal bunt (KB) of wheat caused by *Tilletia indica* adversely affects international wheat trade and the movement of germplasm due to quarantine restrictions. The genetic base of cultivated wheats for Karnal bunt resistance is extremely narrow to achieve the required zero tolerance. The wild germplasm of wheat, however, represent a rich and still unexploited source for KB resistance. Here we report the evaluation of *Aegilops tauschii* germplasm for KB resistance, identification of resistance sources and transfer of resistance to *T. aestivum*. A collection of 183 accessions of *Ae. tauschii*, were screened under artificial inoculation with a mixture of nine KB isolates for 2-3 years in a specially designed screen house. Twenty-two accessions of *Ae. tauschii* were found to be highly resistant whereas 10 were moderately resistant. For transferring KB resistance to hexaploid wheat, a synthetic amphiploid between a KB resistant *Ae. tauschii* accession (#3743) and KB susceptible *T. durum* cultivar was crossed with KB susceptible elite wheat cultivar. Homozygous introgression lines (ILs) derived from this cross were evaluated extensively for KB resistance under field as well as screen

house conditions for four years(2004-2007). Mean KB incidence in KB resistant ILs ranged from 0-1.2% compared to 10.7% in the recipient parent and 30% in a highly susceptible cultivar. Molecular characterization and graphical genotyping of the ILs using 60 D-genome specific polymorphic markers detected introgressions of *Ae. tauschii* specific alleles on chromosomes 1D, 2D, 4D and 6D. The number of introgressed segments, however, varied from line to line. The work for further tagging and marker assisted pyramiding of the introgressed resistance in elite wheat cultivars is in progress.

P006

A new method for detection of induced mutations in wheat

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As more and more plant genome sequence become available, reverse genetics is proven to be useful and feasible in plants to explore gene function and identify desired mutations for breeding. TILLING (Targeting Induced Local Lesions IN Genomes) is a reverse genetics tool that combines traditional chemical mutagenesis methods and high-throughput PCR based mutation detection techniques to yield an allelic series of point mutations in a gene of interest. Wheat is a hexaploid crop with a large and complex genome. It has much less genome sequence information than *Arabidopsis* and rice. It is sometimes difficult to design allele-specific PCR primers in a much conserved region (high homology between three homoeologous genes) or in a gene lacking intron information. Here we describe a new mutation detection method which combines High Resolution Melting (HRM) and sequencing analyses using Mutation Surveyor software. The method is sensitive enough to detect a heterozygous SNP in a PCR amplicon containing 3 homoeologous gene fragments. Therefore it can be used for screening three homoeologous genes simultaneously, especially in a conserved functional domain or some EST sequences. This method can also be used for SNP marker development and eco-TILLING.

P007

Winter wheat landraces and obsolete cultivars - possible donors of characters for breeding

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Two sets of winter wheat landraces and obsolete cultivars (122 in set I. and 101 in set II.) and two modern check cultivars were studied in three- years field experiments. Increased spike productivity in modern cultivars could be assigned mainly to increased number of grains in spikelet and increased HI, whereas TGW has slight effect. Old cultivars proved higher crude protein content. It was difficult to characterize the cultivars according to the country of origin, however, earliness and lower spike productivity were characteristic for South-East origin. Spike productivity characters, except of TGW, were in negative correlation with crude protein content in grain. Regression analyses confirmed that main controlling character for the spike productivity was number of kernels in spikelet while effects of TGW was about half-size. Potentially valuable donors of grain quality, earliness, winter hardiness and longer grain filling period were identified and characterized. High crude protein content (up to 18%) was found in cvs. Bergland, Ukrajinka, Sippbachzeller, Innichen Nr. 25001 and Barbu du Finistère); cvs. Visperterminen 640 E, Hatvan, Szekacz 1242, Berchtesgardener Vogel, Ble du Lot and Barbu du Finistere were early. In the both sets HMW *Glu* -subunits were identified and 70 selected lines with defined alleles were multiplied and studied in three-year field experiments. Besides important agronomical and quality characters also content and structure of protein were studied. In general, high crude protein was linked to glutenins and gliadins fractions; differences in globulin and especially albumin content were much lower. Among this set 12 lines showed crude protein content 18% - 18,8 % (when gluten index and Zeleny test varied from 29 to 68 and 29 to 46 respectively). Using PCR

(SSR) analysis high-protein lines could be divided into several genetically distant groups. High values of all quality characters proved lines gained from cultivars Mindeszentpusztai (HUN), Szekacz 19 (HUN), Bartweizen linie a (AUT), Viglasska cervenoklasa (CZE) and some others.

P008

Rust resistance genes in *Triticum speltoides* var. *ligustica* accessions

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Distantly related or uncultivated relatives of wheat have long provided an abundant source of new resistance genes. For example, two stem rust resistance genes, namely, *Sr32* and *Sr39*, have previously been transferred to wheat from *Triticum (Aegilops) speltoides* by other workers. We screened five accessions of *Triticum speltoides* (Tausch) Gren. ex K. Richt. subsp. *ligustica* (Savign.) Chennav., namely, AEG357-4, AEG363-5, AEG818-4, AEG874-60 and AEG2106-38 for resistance to stem, leaf and stripe (yellow) rusts. High levels of resistance to all three diseases were observed after inoculation with pathotypes predominant in Australia. All five accessions were crossed with the Australian cultivar 'Angas' as the male parent and viable F1 seeds produced from AEG357-4 and AEG874-60 plants. F1 plants from each of these two crosses were treated with colchicine and backcrossed up to four times with cv. Angas and later with cv. Westonia. Alien chromosome addition lines were selected which carried either single or multiple *T. speltoides* chromosomes using representative RFLP probes previously mapped by others to each of the seven Triticeae homoeologous chromosome groups. Stem rust resistance in plants derived from crosses with *T. speltoides* AEG357-4 was associated with the markers specific for the 2S chromosome using probes BCD111, ABG358 and ABC454. RFLP markers showed distinct polymorphisms from 2S chromosomes carrying other known stem rust resistance genes from *T. speltoides*, namely, chromosome 2S#1 (*Sr32*) and chromosome 2S#2 (*Sr39*). The stem rust resistance gene from *T. speltoides* AEG357-4 has been tentatively named *Sr2S#3*.

P009

Population structure and linkage disequilibrium in wild emmer wheat (*Triticum dicoccoides*) based on EST-SSR

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Wild emmer wheat (*Triticum dicoccoides*) is the tetraploid progenitor of cultivated wheats and contains two genomes and 28 chromosomes ($2n=4x=28$; genome AABB). It is fully compatible with the tetraploid (AABB) durum wheat and can be crossed with the hexaploid ($2n=6x=42$; AABBDD) bread wheat (*T. aestivum* L.). Wild emmer offers a valuable source of allelic variation for various economically important traits including drought resistance, grain protein and mineral concentrations. This study analysed population structure and linkage disequilibrium (LD) among 150 wild emmer wheat accessions, representing a sample of the collection maintained by the Australian Winter Cereals collection. Twenty-one EST-SSR loci, selected because of homology to genes of known function, were used to generate molecular profile of the wild emmer accessions, and allowed comparison with

those of 10 durum wheat used as controls. We used several methods to estimate population structure and the genome-wide LD, including STRUCTURE 2.2, BAPS 5.1, and traditional F_{ST} analysis. Results showed population was highly structured along eco-geographical lines, and significant correlation with various climatic and soil factors suggests that natural selection caused adaptive genetic differentiation. Implications on current efforts to create new synthetic hexaploids will be discussed.

P010

DNA polymorphism in wild emmer wheat (*Triticum Dicoccoides*) using barley expressed sequence tag-derived microsatellite markers

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Molecular markers that target the transcribed region of the genome are often transferable among related species, because gene sequences remain highly conserved during evolution. The recent increase in the availability of expressed sequence tag (EST) data has facilitated the development of microsatellite or simple sequence repeat (SSR) markers in a number of plant species groups, including cereals. As these SSRs are derived from ESTs/genes (EST-SSRs), they exhibit a higher potential for transfer through cross-amplification in related species than SSR markers generated from genomic DNA libraries. In this study, we examined the ability of microsatellite primers from barley cDNA sequences to amplify polymorphic fragments between 160 accessions of wild emmer (*Triticum dicoccoides*) and 10 durum wheat lines used as controls. Out of 20 primers tested, 14 (70%) showed amplification of products, with number of alleles per locus ranging from two to five. Our results demonstrate transferability of barley EST markers to wild wheat, facilitating the study of synteny conservation, and co-linearity between the related genomes. Our long-term goal is to determine the utility of gene-based markers as a tool for gene discovery and efficient use of wild emmer to broaden genetic diversity in bread wheat.

P011

Enhanced fusarium head blight resistance in bread wheat and durum by alien introgressions

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Fusarium head blight has become a devastating disease of cereals in temperate- climate regions of the world. We have been searching for unique resistance genes in alien species with which to augment existing FHB resistance. Thus far we have incorporated into bread wheat, FHB resistance found in *T.monococcum* (AA), *Ae. speltoides* (BB), *T.timopheevi* (AG), *Ae. cylindrica* (CD) and *T.miguschovae* (AGD). Minimal linkage drag has accompanied the transfer of the resistance. Additional resistance has now been found in *Hordeum californicum* and its transfer into bread wheat has been initiated. In the meantime, molecular markers are being developed to be used to pyramid the various sources of resistance and incorporate them into contemporary cultivars. Chromosome7E from *Th.elongatum* has excellent FHB resistance. Microarray analysis has been conducted on this line to determine the function of the resistance gene(s). Alien sources of resistance for durum FHB improvement have been found in *T.carthlicum* (AB), *T. miguschovae* (AGD), *Tritordeum* (ABH) and

Th.elongatum amphiploids (ABE). The *T. carthlicum* resistance has recently been mapped to chromosome 6B. The range of DON levels in *Tritordeum* derivatives was 0.6-11.3 ppm, where the level in cultivar Strongfield was 14.1 ppm, in field plots in 2006. Attempts are underway to incorporate the resistance from the E genome into durum wheat. Disomic addition lines (2n=30) with resistance have now been isolated.

P012

Genetic variation of Triticeae species for improvement of end product quality of wheat

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Wild species of wheat are useful source of genetic variation for crop improvement. They have been utilized for improving the tolerance of wheat to different biotic and abiotic stresses. However, their potential for wheat quality has not been much investigated. In this study, we used 177 disomic addition lines belonging to 17 wild species of wheat. These lines were screened initially by polyacrylamide gel electrophoresis for identification of addition lines carrying seed storage proteins like high-molecular-weight glutenin subunits (HMW-GSs), low-molecular-weight glutenin subunits (LMW-GSs) and gliadins from wild species. The loci of HMW-GSs, LMW-GSs and gliadins were observed on homoeologous group 1 chromosomes of wild species of wheat. Several new alleles of HMW-GSs were identified and named. Dough strength of addition lines was evaluated for 3 consecutive years and 11 addition lines with strong dough were selected. Rheological parameters of 6 addition lines revealed better quality for bread-making. Among these selected addition lines, *Agropyron intermedium* proteins showed best rheological characteristics followed by *Hordeum chilense*, *Ag. elongatum* and rye (*Secale cereale*). Cloning and sequencing of HMW-GS genes of wild species from selected addition lines showed great diversity among these genes. Wild species whose HMW-GSs gene aligned with those of D-genome of wheat showed much better quality characteristics. Substitution lines of chromosome 1D that eventually appeared from addition lines showed very bad characteristic for bread-making quality. Chromosome 1D carries important genes related to bread-making quality. Thus, substitution of chromosome 1D by alien chromosome is not desirable and must be taken care while transferring genes from wild species of wheat.

P013

Germplasm enhancement in bread wheat targeting quality characteristics

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The synthetic hexaploid approach was used to introgress a novel high molecular weight glutenin subunit (HMW GS) gene (12.4¹) into bread wheat. Tetraploid wheat *T. turgidum* cv Langdon was crossed with *T. tauschii* accession AUS24092. Immature embryos were rescued and placed onto B5 regeneration media. Hybrid F₁ plants were treated with colchicine. Synthetic hexaploid L/24092 was isolated and used for further crossing and backcrossing programs. Bread wheat cvs Baxter, Sunvale, Sunlin, and Sunbri were crossed with synthetic hexaploid L/24092. Doubled haploid lines were produced using F₁ seeds and phenotyped for the presence of the HMW GS Dy12.4¹ protein, using SDS-PAGE of total proteins under reducing conditions. The doubled haploid lines were divided into 17 groups with different combinations of HMW GS, with and without the HMW GS (Dy12.4¹) protein for functional studies.

P014

Estimate of genetic parameters of grain yield and some agronomic traits in durum wheat using diallel crosses

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The aim of this study was to estimate of general combining ability (GCA) of the parents, specific combining ability (SCA) of hybrids progeny, heritability, heterotic patterns and genetic correlations, of grain yield and some agronomic traits considered for the development of high yielding cultivars. A complete diallel crosses set obtained of seven genotypes durum wheat were sown in randomized complete block design in 2006. The results indicated significant differences among the parents for GCA of grain yield and all 17 studied agronomic traits. The SCA were significant for all the traits with the exception of biological yield, flag leaf area, spike length, seed filling duration, days to heading and days to maturity. Reciprocal mean squares were significant for the traits except spike length and days to heading. The ratios of the mean square indicated that both of additive and non additive gene effects were important in genetic control of almost of the traits in these crosses. Narrow-sense heritability was medium to high (59–70%) for grain number per main spike and day to heading but low to medium (5.8–37%) for tiller number, plant height, harvest index and plant grain yield. Among the parents Preion-1, Dipper-6 and Srn/Vic were the best general combiners for grain yield per plant, Preion-1 for 1000-grain weight and Preion-1, Dipper-6 for harvest index. The best specific crosses for grain yield were Preion-1 × PI40098 and Preion-1 × Ajaia/.../Gan. The best cross combinations, in general, involved at least one parent with high or average GCA effect for a particular trait. Base on mid-parent values, Preion-1 × Lound-6 showed the highest hetrois for grain yield per plant (36%) between the crosses. Grain weight per main spike was the strongest genetic correlated with grain yield and the main trait at stepwise regression for explain grain yield variation. Result of biplot analysis of the data for almost of traits was the same as result of conventional methods.

P015

Coleoptile length studies in semi-dwarf wheat (*Triticum aestivum* L.) with different dwarfing genes

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Eleven genotypes (seven varieties and four lines) were studied for coleoptile length. The genotypes having *Rht₁*, *Rht₂*, *Rht₁Rht₂*, *Rht₈Rht₉* and *rht* were compared for their coleoptile length under controlled environmental conditions. The results suggested that traditional tall variety C-591 (*rht*) had the longest coleoptile than the remaining varieties and genotypes. The subsequent genotypes which had longer coleoptile length were Chinese Spring (*rht*) and Rht8-01 (*Rht₈*). The varieties Mara (*Rht₈Rht₉*), Sarsabz (*Rht₁*) and Soghat-90 (*Rht₂*) were not significantly different. The line Rht8-02 carries *Rht₈* dwarfing genes was not significantly different than the Yeccora (*Rht₁Rht₂*) variety a double dwarf. These results suggest that probably the dwarfing genes do not affect the coleoptile length. The genetic background may affect the coleoptile length of individual varieties.

P016

Communication strategies for delivery of the benefits of cooperative research in the CIMMYT suite of projects

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As Australia's major food crops are not native to this country, the international centres provide valuable sources of genetic diversity. Under the sMTA of the ITPGRFA, users of imported germplasm are obliged to return information to the providers, and to fulfil benefit-sharing requirements. This requires a system for tracking distribution and collecting and communicating results. A group of Australian-based projects supported by GRDC (the CIMMYT Suite of Projects) facilitates access to and use of CIMMYT germplasm by Australian wheat breeding programs. These projects span scientific exchange, quarantine of selected material and international nurseries, coordinated increase, trial, phenotyping and genotyping. They also include the International Adaptation Trial and projects for evaluation of synthetic hexaploids and sources of root disease resistance, which have all provided valuable data to assist selection of material suited to Australian conditions, with appropriate tolerances and resistances. The central communication and database development projects ensure that both Australian breeders and CIMMYT staff have rapid access to this data, to inform their decisions. Collaboratively with the IRRI/CIMMYT informatics laboratory, an ICIS module has been developed, capable of handling high-throughput genotyping data to integrate with the existing genealogy, phenotype and pedigree modules of ICIS. The user-friendly, web-accessible front-end means that users do not need specific knowledge of ICIS to extract data for analysis in their preferred software. The ICIS back-end provides high-performance functionality, and as ICIS-based systems are used by both CIMMYT and ICARDA, clean data transfer with the Australian hub is thus facilitated. Examples from selected case studies illustrating the benefits delivered through this cooperative framework will be presented.

P017

Transferring of the biological nitrification inhibition (BNI) character from *Leymus racemosus* to wheat

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Biological nitrification inhibition (BNI) is a character that may result in a reduction of emissions of nitrous oxide (N₂O), a green house gas that has more than 300 times the warming power of CO₂, as well as other forms of N which are lost to the environment. The BNI character has not been found in the three major crops; wheat, rice and maize. However, *Leymus racemosus*, alien species of wheat, has shown high BNI capacity. One of *L. racemosus* chromosome addition lines of wheat, Lr#n chromosome addition line, expressed about 80% of BNI character of *L. racemosus*, showing that BNI can be transferred into a wheat background. Two other addition lines showed higher levels of BNI than the parental wheat line. To introduce the BNI character into wheat cultivars, two translocation lines of Lr#n chromosome have been produced.

P018 and P019

Papers withdrawn

P020

Genetic and genomic dissection of powdery mildew resistance genes derived from wild emmer (*Triticum dicoccoides*)

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Wild relatives are important germplasm for improving yield, quality, resistance to biotic and abiotic stresses of modern crop cultivars. Powdery mildew, caused by *Blumeria graminis* f. sp. *tritici*, is one of the most important fungal disease of wheat (*Triticum aestivum* L.) worldwide. The wild emmer wheat, *T. dicoccoides* ($2n = 4x = 28$; genome AABB), is considered the progenitor of cultivated tetraploid and hexaploid wheats. Wild emmer wheat was found to be highly tolerance to stress and resistance to pathogens, including powdery mildew, stripe rust, leaf rust, and stem rust, as well as highly yield potential for wheat improvement. Several powdery mildew resistance genes derived from wild emmer accessions have been tagged by molecular approach and transferred into common wheat background. Among them, *Pm30* originated from C20 has been assigned on 5BS. Several accessions of wild emmer, including G-275-M, G-722-M, and G-757-M, also contain *Pm30* or its alleles. One dominant resistance gene *mlG-680-M* and one recessive resistance gene *mlG-303-1M* were mapped on the chromosome end of 2BS. Another dominant resistance gene *mlG-573-1* has been mapped on chromosome arm 2BL. Dominant mildew resistance genes were also found on 7AL in G-797-M, TZ-74, Z-115, 2AL in G-168-1-2-6M, G-584-M and 3A in TZ-2. SSR, EST-SSR, EST-SNP, SSCP, AFLP and RGA markers are being employed to develop more tightly linked DNA markers to these powdery mildew resistance genes. Rice and Brachypodium genome sequences are used to construct fine genetic maps surrounding the target genes. Candidate NBS-LRR genes are being isolated from the wild emmer using map based cloning approach. Fine genetic and genomic dissection of these powdery mildew resistance genes will shed light on the molecular evolution of powdery mildew resistance genes in wild emmer.

P021

Development of a multi-parental (four-way cross) mapping population for QTL discovery in durum wheat

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Durum wheat is widely grown in Italy, one of the leading countries in durum and pasta production. DiSTA (University of Bologna) and Società Produttori Sementi have assembled a recombinant inbred mapping population (of ca. 380 lines) developed from a balanced four-way cross. Parental cultivars were Neodur, Claudio, Colosseo and Rascon, characterized by different quality parameters and resistance to powdery mildew, leaf rust and *Fusarium* head blight. This resource should allow for a more efficient analysis of the genetics of complex traits such as yield, adaptation to diverse environment, quality and response to wheat fungal diseases with respect to the use of traditional biparental mapping populations. Further, the identification of epistatic interaction effects should be facilitated. As part of the European project "BioExploit Food CT 2005-513959", a genetic map is being generated by Keygene N.V. based on AFLP[®] markers (Keygene N.V.) and anchoring SSR markers (DiSTA) using the single segregating four-way individuals. This preliminary map is being integrated with anchoring SSR markers and further AFLP markers. At Keygene, SNP polymorphisms specific for the four parental cultivars are being identified using the novel Keygene CRoPS[™] Marker Technology (Complexity Reduction of Polymorphic Sequence) assisted by high-throughput

sequencing developed by 454 Life Sciences. This map will provide the possibility to assess the effect of multiple alleles at single QTLs and to investigate their interactions.

P022

Assessing wheat genetic diversity using quality traits, amplified fragment length polymorphisms, simple sequence repeats and proteome analysis

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The genetic diversity among 10 Iranian bread wheat (*Triticum aestivum*) genotypes was analysed using 12 quality traits, 320 amplified fragment length polymorphisms (AFLP) polymorphic fragments, 491 simple sequence repeats (SSR) alleles and 294 proteome markers. The results revealed that the genotypes differed for quality traits, AFLP, SSR and proteome markers. The average genetic diversity based on quality traits (0.684 with a range of 0.266–0.997) was higher than AFLP (0.502 with a range of 0.328–0.717), SSR (0.503 with a range of 0.409–0.595) and proteome (0.464 with a range of 0.264–0.870) markers. Although there were apparent similarities between the groupings of particular genotypes, the overall correspondence between the distance matrices appeared to be rather low. In this study, the cluster analysis based on AFLP data showed the closest agreement with genotypes' regions of origin or pedigree information. In addition to the genetic diversity assessment, specific proteins with known function were detected uniquely for the studied genotypes. Our results suggest that the classification based on quality traits and genotypic markers of these wheat genotypes will be useful for wheat breeders to plan crosses for positive traits.

P023

B- and C-type low molecular weight glutenin subunits in tetraploid wheat germplasm

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The B and C-type low molecular weight glutenin subunits (LMW-GSs) are structural components of the gluten proteins affecting the viscoelastic properties of dough. They are encoded by genes at *Glu-3*, *Gli-1* and *Gli-2* loci on the short arms of the chromosome groups 1 and 6. In tetraploid wheats these subunits have been much less well-characterized than other gluten protein components. In order to study the role of specific polypeptides and corresponding genes, as those included in the B and C glutenin fractions and to evaluate the effects produced by the loss of specific proteins on the functional properties of flour and semolina, total proteins extracted from different varieties and lines of tetraploid wheats, have been analysed by one- and two-dimensional electrophoresis (1DE, 2DE), chromatographic techniques (RP-HPLC) and polymerase chain reaction (PCR) using specific primers. In particular gliadin and glutenin fractions present in tetraploid wheats *T. dicoccoides*, *T. turanicum*, *T. polonicum*, *T. carthlicum* and a durum wheat line carrying a 1BL.1RS translocation, have been evaluated in order to identify genotypes with different allelic variants at *Gli-1/Glu-3* loci. Preliminary identification of B- and C-type LMW-GS has been carried out submitting to fractionated precipitation, with hydro-alcoholic extracts, the LMW-GSs from tetraploid wheat germplasm. The fractions enriched of B and C-type LMW-GSs have been subsequently separated by 1DE and the patterns/alleles of the corresponding B- and C-types have been represented in a diagram. The same fractions have been submitted to 2DE, to discriminate the true B-type from the C-type LMW-GSs and, when possible, to assign each identified subunit to their encoding genes. Preliminary results of PCR analyses will be also reported. The genetic variability of these LMW-GS groups, including known

alleles quality associated, characterized by different techniques, well define the potential of novel germplasm for the improvement of wheat quality.

P024

Identification of R gene genotypes in Japanese wheat cultivars

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Red grain colour of wheat has been well known to be associated with the development of seed dormancy and affects flour brightness due to the contamination of red pigment in milling process. Recently, Himi and Noda (2005) reported that the red grain colour gene (*R*) of wheat was a Myb-type transcription factor and its recessive alleles showed altered sequences. In this study, we attempted to identify the genotype of *R* gene in 160 Japanese cultivars. DNA was extracted from 2-week old seedlings, using modified CTAB method. PCR conditions were the same as those used by Himi and Noda (2005). Expected PCR products of *R-B1* and *R-D1* were detected by primer sets for *R-B1* and *R-D1*. However, in *R-A1*, unexpected PCR products were observed in a white-grained wheat strain. Thus, there was some variation in the sequence of *R-A1* locus. The *R* genotypes of the strains examined were in accord with their seed coat colour except for a strain with new allele of *R-A1*. The frequency of *R-B1b* (*b*, dominant allele) and *R-D1b* identified in Japanese cultivars was 61.4% and 64.6%, respectively. While, the frequency of *R-A1b* was 86.6% and significantly higher than the frequencies of *R-B1b* and *R-D1b*. Japanese cultivars with two and three dominant *R* genes were 47.2% and 33.1%, respectively. The cultivar with only one *R* gene was 11%. Japanese cultivars, which are grown in wet condition, have been bred to acquire the sprout resistance. These results suggest that the number of *R* gene might be associated with the level of seed dormancy. In this study, we could identify the genotypes of *R* genes with the PCR method based on the sequence data of *R* genes. In future, we might use the *R* genes to breed strains with the higher level of seed dormancy.

Eiko Himi and Kazuhiro Noda. *Euphytica* 143:239-242. (2005)

P025

Occurrence of hetero-branching of spike in bread wheat (*T. aestivum* L.)

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Two hexaploid wheat varieties crossed in normal (WH147 X PBN51) and reciprocal (PBN51 X WH147) fashion and generation developed up to F₂ population. These six generations planted in a complete family block design with 3 replication at Crop Research Centre, GBPUA&T, Pantnagar (India). It was observed that both parent have normal spike, while hetero-branching of spike with fine and clear double spike segregate in the F₂ population in both normal and reciprocal crosses. Even no evidence reported in other generation. Variability for spike morphology reported only in timely sown environment while same set was planted after one month to study the heat stress and no even minute variability was found in late sown experiment for branch spike. It is assumed that the character may be low heritable and threshold that controlled by one or more recessive genes. The minimum and maximum mean temperature during timely sown at heading was 6.90 °C and 22.79 °C while it was 8.39 °C and 24.09 °C for late sown condition.

Keywords: Variability, spike morphology, Double spike, low heritable and bread wheat

P026

Using single morphological and RAPD molecular markers to screen for quantitative traits in an F₂ segregating generation of wheat (*Triticum aestivum* L.)

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An F₂ population derived from crosses between variety Faisalabad and line FM36 was used in the present study at Sharekord University, Iran in 2005. Random Amplification of Polymorphic DNA analysis (RAPD) revealed that among 30 primers tested, 8 primers indicated polymorphism in F₂ individuals and only two primers (OPM35 and OPG12) indicated polymorphism in both the two parents and the F₂ population. The F₂ individuals were classified into 2 groups based on presence or absence of the bands amplified by the primers which showed polymorphism in parents and F₂ and based on two qualitative traits (including hairy glumes and growth habit at the early stages), separately. The results obtained by comparing the means using t-test revealed that subpopulations classified by the presence or absence of the polymorphic band amplified using OPM35 were significantly different for heading date. On the other hand, subpopulations classified by presence or absence of bands amplified using OPG12 were significantly different for days to maturity. No significant difference was found between the subpopulations formed by presence or absence of the bands of the either primers for grain weight. Classifying the F₂ individuals based on the form of growth at the early stages resulted to 2 subpopulations one having erect and the other rosette form of growth. These two subpopulations were significantly different for grain weight, days to heading and days to maturity. Conversely, 2 subpopulations identified by having or lacking hairy glumes were significantly different for none of the traits. Correlation coefficient analysis indicated that hairy glume, OPG12 and OPM35 were correlated with none of the other characters. On the other hand, rosette shape was significantly correlated with grain weight, days to heading, days to maturity and harvest index. In addition, grain weight per plant correlated positively to Harvest Index (HI) and negatively to Days to Heading (DH).

P027

Maternal lineages in polyploid wheat species inferred from organeller DNA fingerprinting

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The genus *Triticum* consists of a polyploid series and is classified into four groups, einkorn (genome constitution: AA, 2n=14), emmer (AABB, 2n=28), timopheevi (AAGG, 2n=28), and common wheat (AABBDD, 2n=42). Polyploid species in *Triticum* and its closely related genus *Aegilops* originated through the allopolyploidization process, i.e., interspecific hybridization and subsequent chromosome doubling. The A genomes of both tetraploid and hexaploid wheat originated from einkorn wheat. The origin of B and G genomes has been debated; however recent studies of nuclear and organellar DNAs provided molecular clues supporting the hypothesis that *Ae. speltoides* was the donor for both B and G genomes. Common wheat (*T. aestivum*) originated through allopolyploidization between domesticated emmer wheat and *Ae. tauschii* (DD, 2n=14). Therefore, in addition to the polyploidization, domestication of wild wheat was a key step in the evolution of agriculturally important species in *Triticum*. Furthermore, it is also accepted that the plasmon of the common wheat originated from the B genome donor species and inherited through wild and domesticated emmer wheat. To elucidate the origin of domesticated wheat species, from the view point of maternal lineage,

we have been studying the molecular variation of organellar DNA using microsatellite DNA fingerprinting. Here, we will report the following: (1) intraspecific variation of chloroplast DNA (ctDNA) in hulled and free-threshing emmer wheat, (2) ctDNA variation in common wheat in Southeast Asia and Europe; (3) ctDNA variation in wild and domesticated timopheevi wheat, and 4) molecular variation in mitochondrial DNA in *Ae. speltoides*. Using these results we discuss the genetic diversity and evolution of polyploid wheat species in *Triticum*.

P028

Genetic diversity of hexaploid wheat and three *Aegilops* species using microsatellite markers

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In this study a set of 21 simple microsatellite primers were used to determine genetic relationship of the D-genome among 52 accessions of *T. aestivum* (AABBDD), *Ae. tauschii* (D¹D¹), *Ae. cylindrica* (CCD^cD^c) and *Ae. crassa* (MMD^{cr1}D^{cr1}), collected from 13 different sites in Iran. A total of 273 alleles were detected across all four species and the number of alleles per microsatellite marker varied from 3 to 27. The highest genetic diversity occurred in *Ae. tauschii* followed by *Ae. crassa*, and the genetic distance was the smallest between *Ae. tauschii* and *Ae. cylindrica*. Cluster analysis classified four species in three groups, locating *Ae. tauschii* and *Ae. cylindrica* in the same cluster using the UPGMA method. It appeared that different genotypes of *Ae. tauschii* could involve in the evolution of polyploid species. A high level of variation and also the highest number of unique alleles were observed within *Ae. crassa* accessions, indicating this species as a great potential source of novel genes for bread wheat improvement.

P029

Amplification profiles of the SSR markers in cultivars of hexaploid wheat and their relatives

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The National Bioresource Project-WHEAT (NBRP-WHEAT), launched by the Japanese government in 2002, is aimed to maintain and distribute seed stocks and DNA clones of "Wheat". NBRP-WHEAT (<http://www.nbrp.jp>) is to continue its second term starting in 2007. Additionally to its primary roles in handling seed stocks and DNA clones, the second-term NBRP-WHEAT features the collection and characterization of DNA markers, which will make the seed stocks of NBRP-KOMUGI more valuable for molecular works on isolation and characterization of genes in wheat. We started to survey amplification profiles of the publically available SSR markers (*barc*, *cfa*, *cfb*, *cfe*, *cft*, *gdm*, *gwm*, *hbg*, *hbe*, *hbd*, *wmc*, and STM markers) in cultivars of hexaploid wheat and their relatives. The lines to be tested includes; eight *Aegilops* species with representative diploid genomes, *Triticum monococcum*, *T. boeoticum*, *T. urartu*, *T. durum*, *T. spelta* and 31 hexaploid wheat accessions. We also take samples of *Hordeum vulgare*, *H. spontaneum*, and *Secale cereale* as outgroup species. The PCR products using template DNA from these lines are separated on a capillary-electrophoresis machine (eGene, Qiagen) and the amplification profiles are documented as chromatograph of fluorescence intensity and pseudo-electrophoretic-patterns. As pilot experiments, we tested 304 markers on 12 lines thus far and established the methodology for stable amplification of SSRs and reproducible separation of PCR

fragments. We will present up-to-date data of our survey and discuss polymorphism rates and phylogenetic relationships among the accessions tested.

P030

Characterization of seedling and adult-plant resistance to stem rust race Ug99 in Iranian bread wheat landraces

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Wheat stem rust, caused by *Puccinia graminis* Pers. f. sp. *tritici* Eriks and Henn. (*Pgt*) was the most feared and devastating disease of wheat worldwide in the 1950's. *Pgt* has been observed occasionally on local wheat cultivars, there were no significant outbreaks of the disease. New stem rust pathotypes identified in Uganda in 1999 (Ug99) has altered the quite period of stem rust. Ug99 has defeated an important number of effective resistance genes including *Sr6*, *7a*, *7b*, *9a*, *9b*, *10*, *11*, *12*, *16*, *17*, *31*, and *Wld-1* that were wide spread in commercial cultivars worldwide. Wheat production in Iran and neighbouring countries where resistance to stem rust relies mostly on *Sr31*, is considered under potential risk to Ug99. In 2006, 2154 Iranian bread wheat landraces (*Triticum aestivum*) were tested at seedling stage using an avirulent pathotypes of *Puccinia graminis* f. sp. *tritici* (*Pgt*) pathotypes (pt). The tested accessions were classified into two groups based on the seedling infection types (IT). Eighty-eight accessions were scored resistant (IT's 0; to 1⁺) to the avirulent *Pgt* pt for *Sr31*. Resistant accessions were evaluated in Kenya under artificial field inoculation with Ug99 that is known for virulence on stem rust resistance gene *Sr31*. Field data showed that among the accessions tested in Kenya, 22 were resistant showing field response of 5R to 20MSS. Among the selected resistant lines, 19 accessions were seedling tested against two virulent *Pgt* pts for *Sr31* that were detected in Iran in 2007, five accessions had low seedling infection types and adult plant resistance. The resistant accessions among Iranian wheat landraces can be potentially used in breeding program as sources of resistance to Ug99

P031

Identification of multiple root disease resistant wheat germplasm against Cereal Nematodes and Dryland Root Rot and their validation in regions of economic importance

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Several species of Cyst Cyst Nematode (CCN-*Heterodera*), Root Lesion (RLN-*Pratylenchus*) nematode and the dryland Crown Rot (CR-*Fusarium*) are known economic biotic constraints to rainfed wheat production systems globally. These often occur together as a soil complex, and effective control can be achieved through host resistance to one or more of these pathogens. Fifty seven wheat germplasm were identified globally with resistance to one or more of these pathogens. These were compiled and distributed by CIMMYT to more than 24 partners globally, with 14 of these in Australia and 10 overseas. The material was screened under replicated greenhouse or field conditions against their local pathogen of importance. The known molecular disease resistant markers were screened across these lines. The data has indicated that more than 25% of the lines express multiple root disease resistance. The published genes for CCN were effective but had variable

reaction depending on the country, and several of the synthetic hexaploids from CIMMYT were found to provide new sources of CCN resistance in several countries. CR resistant sources were validated, with several of these offering resistance to the related foliar pathogen Fusarium Head Scab (*F. graminearum*). Molecular markers for CCN, RLN and CR revealed confirmation of known resistant chromosomal regions, in addition to the identification of other germplasm with same regions, or potentially new regions. The most useful sources and effective sources of multiple root disease resistance have been identified and confirmed for Australia and other global locations which should serve as valuable sources for breeding programs.

P032

Assessment of the genetic variation in Ethiopian germplasm of durum wheat from region with contrasting environment and water stress

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Ethiopian durum wheat germplasm provide useful breeding traits, including disease resistance, environmental stability, drought and low temperature stress tolerance. We analyzed a collection of 234 durum wheat genotypes belonging to nine populations from 3 Ethiopian regions (Tigray, Gonder and Shewa) that are distinguished for their climatic conditions. This gene pool was analysed by 28 SSRs markers randomly chosen one for each chromosome arm in order to define: a) population structure, b) the assessment of genetic variation, c) the relationships between and within populations, d) the presence of rare or unique genotypes. The results of this study allow us to get information on the genetic structure of the analyzed populations evaluating the percent of polymorphism (P), number of alleles (A), number of polymorphic allele per locus (Ap), the expected (He) and the observed heterozygosity (Ho). The level of polymorphism is very high and quite homogeneous among the populations underlining the great diversity existing in Ethiopian germplasm. The great variation within population is probably also due to the high level of out-crossing, as result of cold temperatures during seed setting, demonstrated also by the presence of heterozygotes. The presence and frequency of rare or unique alleles, help us to evidence the existence of particular genetic configurations tied to extreme conditions. Our results provide useful information for an identification of more favorable genetic equipment to tolerate adverse conditions, contributing to safeguard and to evaluate the available germplasm in order to assist wheat breeders in developing of new promising genotypes.

P033

Assessment of genetic diversity in European emmer wheat populations

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The cultivation of emmer wheat (*Triticum turgidum* L. *spp. dicoccum* Schrank ex Schübler) has been reevaluated in the '90s for its healthy characteristics; this has determined an increase of its cultivation. A total of 38 emmer wheat accessions, collected around Europe, were evaluated employing both agromorphological characteristics and molecular markers. The agronomic traits evaluated were: vernalization response, winter hardiness, date of heading and flowering, lodging, plant height at harvest and resistances against powdery mildew, leaf rust and yellow rust. Quality control was also performed measuring the protein content, gluten quality and quantity, and a baking test was executed. The assessment of genetic variability was carried out at the molecular level utilizing 6 SSR, 6 EST-SSR and 6 ISSR primers for a total of 107 loci. The protein content for both winter and spring emmer was considerably influenced by environment and genotype. Nearly all spring emmer accessions

showed resistance to powdery mildew. Measurement of wet gluten content revealed high values. The molecular analysis showed a great genetic distance between the evaluated material; the expected heterozygosity and the variance between accessions were consistent, indicating an equal distribution of the alleles and the presence of great differences in the analysed material. The molecular markers employed were capable to discriminate the country of origin, even if some miss-classification was present. Finally, no defined clusters were obtained considering winter versus spring accessions.

P034

Characteristics of biochemical markers and quality parameters using whole wheat flours in Korean wheat cultivars and lines

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To investigate the application of biochemical markers and small-sample methods using whole-wheat flours for screening in early generation in Korean wheat breeding system, 74 Korean wheats, including cultivar, local breeding lines and experimental lines, were analyzed. Seed storage protein and amylose contents of grains were evaluated. Biochemical markers, including granule bound starch synthase (GBSS), high molecular weight glutenin subunits (HMW-GS) and friabilin were also evaluated by using one-dimensional sodium dodecyl sulfate-polyacrylamide gel electrophoresis with a single kernel. The small-sample methods, including modified SDS-sedimentation test (MST), micro-alkaline water retention capacity (AWRC) and whole-wheat flour swelling volume (WSV) were also tested in this study. Protein content, MST and AWRC was 11.0-15.8%, 2.7-26.2 ml and 71.9-109.7%, respectively. Apparent and total amylose content and WSV was 20.6-25.0%, 26.1-32.4% and 9.0-16.9ml, respectively. There were highly significant correlations between MST and AWRC ($r = 0.592$, $P < 0.001$), but Korean wheats showed no significant difference in protein content, amylose content and small-sample methods. In the biochemical markers, Korean wheats contained all three GBSS encoded by *Wx* loci, except for Suwon 252. Korean wheats showed the high frequency (58.1%) of 1Dx2.2 + 1Dy12 subunits of HMW-GS. Friabilin band was present in 46 lines (62.2%) and absent in 28 lines (37.8%). Friabilin-absence lines showed the higher MST (14.9 ml) and AWRC (92.1%) value than friabilin-presence lines (8.5 ml and 82.4%, respectively).

P035

Puroindolines polymorphism and kernel texture in einkorn (*Triticum monococcum*)

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Puroindolines A (PinA) and B (PinB), the tryptophan-rich proteins controlling grain hardness in wheat, appeared as two pairs of 13KDa polypeptides in the Acid-PAGE (A-PAGE) and two dimensional A-PAGE X SDS-PAGE patterns of starch-granule proteins from bread wheat (*Triticum aestivum*). Puroindolines occurred at higher amounts on the surface of starch granules of soft bread wheat ($5 < SKCS < 45$) as compared with those from hard bread wheat ($50 < SKCS < 90$). In *Triticum monococcum*, a diploid wheat with genome AA ($2n=2x=14$), the *Pina-A^{m1}* and the *Pinb-A^{m1}* genes coding for PinA and PinB respectively, were found to be closely linked in the distal region of the short arm of chromosome 5A and showed a high degree of similarity (>94%) with their *T.aestivum* counterpart. All the accessions of *T. monococcum* analysed so far exhibited an extra-soft grain texture, the mean SKCS value being 5 but with a SKCS index ranging between -35 and +38. The A-PAGE patterns of starch-granule proteins of 113 *T. monococcum* accessions contained four strong bands with reduced mobilities compared to their counterparts in common wheat, as confirmed in A-PAGE X SDS-PAGE analyses. The band with the minor mobility in A-PAGE reacted strongly with an

antiserum specific for PinA from common wheat. Fourteen accessions showing contrasting A-PAGE pattern were investigated in order to identify puroindoline alleles that might be responsible for the different mobility and the variability of kernel texture. Finally isolation and characterization of chemically induced mutations at pins loci was undertaken to develop einkorn lines with hard kernel which turned out to be of superior bread making quality. In addition an harder kernel texture might increase the germination of seeds in the naked einkorn genotypes we have developed.

P036

Genetic and monosomic analysis of spike speltoidy introgressed into bread wheat from *Aegilops speltoides* Tausch

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Spelta type of spike found in some hexaploid wheats (AABBDD, 2n=42) is a complex of morphological traits characterizing with glumes keeledness, rachis toughness, low spike density and poor threshing. As considered nowadays it is controlled with the locus *q* located in 5AL chromosome. The aim of the work was to investigate the possibility of existence of homoeologous gene for speltoid spike in the bread wheat line with introgression from *Aegilops speltoides* Tausch. Genetic analysis with the use of genotypes carrying the known locus *q* in 5AL chromosome, *T. spelta* and substitution line Chinese Spring/*T. spelta* 5A showed the additive interaction in F₁ for such spike characteristics as length and number of spikelets. In F₂ positive and negative transgressions for all spike traits were observed comparing to the parental forms. Monosomic analysis with the use of mono 5A lines of bread wheat cultivars Saratovskaya 29 and Diamant 2 confirmed the introgression into 5A chromosome. The effect of introgression on milling parameters was detected. Interaction of the new gene with bread wheat genotype will be discussed.

P037

Genetic diversity and genetic analysis of the trait “leaf hairiness” in bread wheat

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Leaf hairiness in wild and cultivated cereals is known to play an important role in adaptation of plants under droughty environment. This character is widely spread among the best old and modern commercial cultivars of common wheat in droughty environment of Siberia, Kazakhstan and Volga region. In addition, a role of hairiness in the control of insect pests has also been supposed. The inheritance of this complex quantitative trait is poorly studied and the diversity of the trait in wheat has not been described yet. In this work, the different types of leaf hairiness with known and unknown genetic control will be presented found among bread wheat cultivars and lines with introgression from wild relatives. The results of genetic investigations of the trait will be showed.

P038

Genetic control of biosynthesis of soluble isoforms of lipoxygenase in bread wheat grain

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Lipoxygenase (linoleat: oxygen oxydoreductase EC 1.13.12, LOX) is a poly-functional enzyme widely investigated in the world. It is known about existence of many LOX isoforms both bonded to cell membranes and soluble. The biochemistry and genetic control of LOX isoenzymes are still insufficiently investigated in bread wheat comparing to the other cereals. The structural genes for LOX biosynthesis is known to be located on chromosomes of 4 and 5 homoeological groups. Using the wheat intervarietal substitution lines Saratovskaya 29/Janetzki Probat (S29/JP) with the recipient and the donor having the contrasting levels of LOX activity it has been shown, that chromosomes of different homoelogenous groups participate in control of this character. It may be concluded, that the regulator genes affect the functional LOX activity along with the structural genes. During three-years investigations of soluble lipoxygenase activity in grain of substitution lines S29/JP involving chromosomes of 4 and 5 homeologous groups it was found the most significant influence of substitution for chromosomes 4A and 4D on the trait. The data of LOX measurement in the recombinant inbred lines of ITMI population within two years have allowed mapping two lipoxygenase QTL. One main locus on a chromosome 4B corresponds to a known structural LOX gene. The second minor QTL for the first time was mapped on the long arm of chromosome 7B. Positions of the both loci found coincide with LOX structural genes of barley on chromosomes 4H and 7H. Probably, the soluble isoenzymes coded by these genes are identical in wheat and barley and are introduced from the one common ancestor.

P039

Evaluation of spelt germplasm for polyphenol oxidase activity and aluminium resistance

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Spelt, *Triticum aestivum* ssp *spelta* L. is one of the oldest cereals of the modern world. It is becoming a valuable crop for consumers and wheat improvement programs due to its high protein content, resistance to several diseases and suitability for speciality products such as bread, pastry and noodles. In order to test its suitability for cultivation on acid soils and to make speciality products, we evaluated 125 spelt accessions, collected from various parts of the world for resistance to aluminium, and for low polyphenol oxidase activity (PPO). PPO activity for genotypes ranged from 0.11 to 0.71 and could be separated into two distinct categories. Twenty-seven accessions exhibited low PPO activity (not significantly different to the check cultivar Arrivato). Visual ratings were positively correlated with optical density, indicating that both methods are suitable for measuring PPO activity in spelt kernels. After measuring PPO activity, the same kernels were further used for evaluation for aluminium (Al) resistance using a nutrient solution culture method. The haematoxylin staining test of root tips revealed that 37 accessions were resistant to Al. Molecular analyses using SSR and DArT markers showed that these spelt accessions are diverse. Functional gene markers associated with loci conditioning Al resistance gene (*TaALMT1*) and PPO activity (*XPPO-2A*) in bread wheat confirmed their association with target phenotypes within spelt accessions.

P040

Evaluation of Iranian bread wheats by storage proteins "gliadins"

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All current and old bread wheat cultivars in Iran were characterized for gliadins using acid polyacrylamide gel electrophoresis (A-PAGE). The results showed an extensive polymorphism ($H = 0.82$ in gliadin patterns). A total of 26 band patterns including 13, 8, and 5 different mobility bands were identified, in the zones of ω -, $\beta+\gamma$ -, and α - gliadins respectively. There were a few patterns specific to each region and some were common among all the regions. Genetic variations were observed in gliadins patterns of cultivars grown in different regions in Iran. Individual cultivars showed unique fingerprinting for its gliadin patterns. The ideogram showed larger variation in ω - and $\gamma+\beta$ - gliadins than in α -gliadins. Genetic variability and extensive polymorphism found in *T. aestivum* cvs at *Gli-1* and *Gli-2* loci could be due to the results of single mutations in the gliadin encoding loci, lack of expression of gliadin genes and intralocus recombination. This results may provide complementary information for maintaining genetic diversity, towards improving the quality and end use products of Iranian wheat.

P041

Identification of HMW subunits in Iranian landrace wheat by using STS-PCR method

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Since quality in hexaploid wheat (*Triticum aestivum* L. em Thell.) is a very complex trait which is responsible for the elasticity and cohesiveness (strength) of dough, it is an important determinant of breadmaking quality. Good or poor wheat breadmaking quality is associated with two allelic pairs at the *Glu-D1* complex locus designated *1Dx5-1Dy10* and *1Dx2-1Dy12* respectively. Probing these sub units have been conducted by SDS-PAGE method before. In this study we have reported the development of an alternative screening method based on glutenin genes themselves using the polymerase chain reaction (PCR). This easy, quick and non-destructive PCR-based approach is an efficient alternative to standard procedures for selecting bread-wheat genotypes with good breadmaking characteristics. After adjusting the approach on some well-known Iranian hexaploid cultivars we analyzed some of lines of gene bank. In the next step, DNA samples of the lines were extracted, Using specified primers for *1Dx5-1Dy10* and *1Dx2-1Dy12* pair of alleles, The PCR analysis was done. The results confirm the efficiency of this method for selection the cultivars and lines with the high quality of breadmaking. Results of STS-PCR and SDS-PAGE were compared and found high accordance in majority of observations. The reason of observation of some differences in results derived from PCR and SDS-PAGE could be for the existence of biotype within cultivars or mixing of seeds or the lack of suitable movement (based on molecular weight) in SDS-PAGE method.

P042

Molecular evaluation of genetic diversity using gliadin alleles in Iranian landrace wheat *triticum aestivum* L.

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73 Iranian landrace wheats were characterized by acid-PAGE (A-PAGE) analysis of gliadins. Extensive polymorphism ($H=0.821$) in gliadin pattern was observed in the Iranian landrace wheat analysis of gliadin electrophoretic (A-PAGE) patterns made it possible to identify 52 alleles at six *Gli-1* and *Gli-2* loci (from 6 to 11 per locus) and 73 gliadin genotypes in Iranian landrace bread wheat which from 9 province of century (Tropical and subtropical) were collected. Considered four new alleles were observed among the landrace varieties, which were recognized by Metakovsky and Branlard (1998). The genetic diversity of Iranian landrace wheats was found to be high ($H=0.726$). Genetic distances between Iranian landrace wheat and common Iranian wheat were analyzed. The considerable differentiation of landrace wheat genotypes from different countries and Iranian common wheat might be caused by breeders' personal preferences and by hidden natural selection specific to each local environment. In Iranian landrace wheats, genetic variation in the Tropic/Cold habit of the landraces studied. In order to investigation the gliadin band pattern of landrace varieties and population, banding patterns each of population and varieties were determinate. At zone-wise genetic diversity index was highest in cold ($H=0.71$) followed by tropical region ($H=0.708$). Landraces from Cold region exhibited the largest genetic distance from landraces grown in other zone, this landrace placed in one main group excepted one province (Ardabil) that made a separate group. Some gliadin alleles were probably associated with cold resistance. The frequency of alleles, *Gli-A2r* and *Gli-D2g* was significantly higher, and alleles *Gli-A1a*, *Gli-B2c* and *Gli-D2m* significantly lower landraces with the highest cold resistance.

P043

Characterization of *Elymus humidus* as a candidate for genetic resource of wheat water tolerance

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One of the most serious problems for wheat breeding in monsoon area, like as Japan, is water or moisture stress. In spite of its importance, the breeding of water tolerant wheat has not well been advanced due to the lacking of genetic resources in cultivated wheat and closely related wild species. As a breakthrough of it, we focus wild Triticeae species indigenous to Japan. Among them, *Elymus humidus* (Japanese vernacular name 'MIZUTAKAMOJI') is the most notable candidate for the genetic resource because of its high level of adaptation to paddy field. However, its characteristics, for example genetic diversity, physiological traits and possibility to produce hybrids with wheat, are not revealed. In this study, we tried to clarify its genetic diversity and water adaptation mechanism. Furthermore, intergeneric crossing were performed to introduce its water tolerance to wheat. Based on the results, genetic and physiological characteristics of *E. humidus* and its application to wheat breeding are discussed.

P044

Triticum monococcum: A source of novel genes for improving several traits in hexaploid wheat

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The diploid 'A' genome progenitor gene pool of wheat, comprising three closely related species *T. monococcum* ssp *monococcum* (*T. monococcum*), *T. monococcum* ssp *aegilopoides* (*T. boeoticum*) and *T. urartu*, harbours useful genes for many economically important traits, including resistance to diseases and micronutrient content. Their genomes share considerable homology with the A genomes of cultivated tetraploid and hexaploid wheat enabling the transfer of desirable alleles from the 'non-progenitor' A genome chromosomes into their 'cultivated' homologues without any significant linkage drag. A spring type *T. monococcum* acc. pau14087 has maintained a high level of resistance to stripe rust, leaf rust, cereal cyst nematode, Karnal bunt and powdery mildew. Using a RIL population generated from a cross of *T. boeoticum* acc. Pau5088 with *T. monococcum* acc. pau14087, a linkage map with 179 loci was generated. This population showed segregation for stripe rust, leaf rust, cereal cyst nematode, Karnal bunt, powdery mildew, evolutionary traits like two grains vs one grain per spikelet, and grain iron and zinc content. Using QTL analysis, genes for stripe rust resistance were mapped on 2A^m and 5A^m, cereal cyst nematode resistance on 1A^m and 2A^m; evolutionary trait like single vs two grains per spikelet on 1A^m and 4A^m and high grain iron content on 2A^m and 7A^m and high grain zinc content on 7A^m in diploid species. Putatively novel leaf rust, stripe rust, cereal cyst nematode, Karnal bunt and powdery mildew resistance genes from *T. monococcum* and *T. boeoticum* have been transferred to hexaploid wheat cultivars PBW343, WL711 and C306 without any apparent linkage drag. Leaf rust resistance genes transferred from *T. monococcum* are being mapped in hexaploid wheat background.

P045

Inheritance of adult plant resistance to leaf and stripe rust in four European winter wheat cultivars

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On the basis of multipathotype tests and field observations, it was predicted that four European winter wheats (Armada, Mec, Pegaso and Lona) possessed uncharacterized adult plant resistance (APR) to leaf rust pathogen *Puccinia triticina* (*Pt*). Cultivars Mec and Pegaso showed additional APR to stripe rust pathogen *Puccinia striiformis tritici* (*Pst*). To understand inheritance of APR in these varieties, doubled haploid populations (Mec/Avocet S, 162 lines; Pegaso/Avocet S, 300 lines) or F3 populations (Armada/Cunderdin-sib, 100 lines; Lona/Cunderdin-sib, 65 lines) were developed and tested in field. Genetic studies implied a digenic inheritance of APR to both leaf and stripe rust in the population Mec/Avocet S, and a trigenic inheritance for both leaf and stripe rust resistance in the population Pegaso/Avocet S. APR to leaf rust in Armada showed digenic inheritance, whereas variety Lona showed inheritance of three dominant genes. Application of molecular markers showed that all lacked APR genes *Lr34* or *Lr46*. It is likely that APR(s) in these varieties are currently uncharacterized and hence attempts have been initiated to locate and map these genes by molecular markers for their efficient utilization in breeding.

P046

Utilizing diverse gene pool from synthetic hexaploids for improving bread wheat (*Triticum aestivum* L)

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Bread Wheat (*Triticum aestivum* L) is the most widely cultivated and consumed cereal crop globally. India recorded the highest wheat production of 76.37 million tones during 1999-2000 however, since then production figures of wheat are hovering around 70 million tones or so and thus not maintaining the pace with population growth of the country, which is a matter of concern. Therefore, wheat researchers will not only have to maintain the present growth rate in wheat productivity but also need

to accelerate the pace in productivity per year to achieve 109 million tones of wheat grain by the year 2020. In India, all possible and feasible efforts are being attempted for creating and harnessing the genetic diversity and trait specific variability for economic traits particularly yield attributes. A set of 90 synthetic hexaploid wheats (AABBDD) that were obtained from CIMMYT, Mexico was evaluated in augmented design for yield contributing traits, quality attributes and biotic and abiotic stresses. It was observed that most of the synthetic hexaploid lines showed more tillers per meter square, ear length and better grain size as compared to best available aestivum (PBW 343) and durum (HI 8498) checks, respectively. Besides, a number of synthetics showed superiority for quality and tolerance to various biotic and abiotic stresses. The breeding lines have been developed through intercrossing synthetics and agronomically superior wheat varieties. A number of lines selected from the segregating populations showed great promise with respect to multiple diseases (leaf rust, karnal bunt and spot blotch) resistance, tolerance to heat stress and some quality attributes namely protein content, sedimentation value and grain hardness. However, the material developed showed some undesirable traits like hard threshability, longer duration and red grains. To overcome these problems, 2-3 doses of backcrosses with agronomic parents were given. The present paper highlights the potentials of synthetics and their role in development of model wheat genotypes.

P047

Grain yield improvement through increased assimilates and efficient partitioning of photosynthates in Bread Wheat (*Triticum aestivum* L)

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Wheat is one of the most important cereal crop grown throughout the world. India now ranks second in terms of total wheat production in the world. For the last five years the total wheat production in the country is stagnated. While the consumption of wheat has increased in India during the last two decades it becomes necessary to keep growth of annual wheat production with that of ever increasing population. One of the ways to break this yield plateau is to develop physiologically and morphologically efficient plant types that will have more photosynthate and better sink capacity. Buitre based long spike wheat genotypes are characterized by visually impressive sink and source capacity. Attempts have been made during the last two decades to exploit this genetic resource through further hybridisation with advance lines. Though, many physiological disorders have been cited as major constraints in improving grain yield utilizing these genotypes. These are very susceptible to rusts, leaf blight; have less tillering capacity, poor grain filling & development and are also prone to lodging. An investigation was carried out to assess the intra-spike assimilate variability in selected long spike genotypes to inculcate genetic and physiological explanations for poor grain filling & development. Perceptible variability in distribution of assimilate within the spike was recorded. The increase in number of grains in spike was associated with reduction in individual grain weight in general which was more conspicuous in distal part of the spike. This is not due to the competition for assimilates or poor translocation efficiency. Genotypes with more biomass accumulation were found to support better grain growth even at distal part of the spike. In the present paper, it has been demonstrated that increased biomass achieved by agronomic practices or genetic manipulations may enable long spike genotypes to yield more grains with desired grain size and weight, thereby increasing the per unit productivity and production of wheat.

P048

Evaluation and utilization of *Aegilops* germplasm for biofortification of wheat for high grain iron and zinc content

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Grains of 70 accessions of seven *Aegilops* species with non-progenitor S, U and M genomes along with 15 semi-dwarf bread and durum wheat cultivars, grown over two years at IIT Roorkee, were analyzed for iron and zinc content. The wheat and durum cultivars had very low content and limited variability for iron and zinc content. The *Aegilops* species showed up to 3-4 folds higher grain iron and zinc content than the cultivars. There was significantly high positive correlation between flag leaf iron and zinc content with grain iron ($r=0.82$) and grain zinc ($r=0.92$). Fourteen amphiploids involving *Triticum aestivum* cultivars and different *Aegilops* accessions with high micronutrient content were synthesized. The fertile amphiploids with bold grains had high grain iron and zinc content equivalent to those of the *Aegilops* parents. Putative amphiploids generated through meiotic restitution in F₁ hybrids between *Triticum durum* and *Ae. longissima* accessions had also two to three folds high grain iron and zinc content in comparison to the parental durum cultivars. The amphiploids are being used to transfer useful variability and development of alien addition and substitution lines in wheat background. The sterile F₁ hybrids between wheat and *Aegilops* species were extensively backcrossed with recurrent wheat cultivars to recover fertile introgression lines (ILs). Some fertile advance backcross ILs were found to have high grain iron and zinc content, confirming the transfer of superior genetic system(s) of the *Aegilops* donors for high micronutrient content. The ILs with high grain iron and zinc content are being characterized by using GISH, FISH and SSR markers.

P049

Comparative assessment of wheat landraces from AWCC, ICARDA and VIR germplasm collections based on the analysis of SSR markers

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About 16,000 bread wheat landraces from three significant gene banks were amalgamated into a virtual collection. Each of the landraces was characterized by collection site coordinates (latitude and longitude). Climatic and edaphic attributes were estimated for each collection site. A core collection of 512 accessions and a drought targeted subset of landraces (from dry environments) of 479 accessions were selected based on all available information. In total 976 bread wheat landraces maintained in AWCC (187 accessions), ICARDA (338) and VIR (451) originating from 675 collection sites from 48 countries worldwide were compared based on the structure of 13 SSR loci mapped on different wheat chromosomes. Cluster analysis of the data was applied for evaluation of genetic diversity within the two subsets of landraces. Four major and six minor clusters were identified on the dendrogram constructed by the analysis of 269 different SSR alleles. Landraces from the same country largely had a tendency for grouping into one of the clusters. For instance, the majority of landraces from Russia and the Ukraine have combined in cluster 1, landraces from Turkey in cluster 2, Afghanistan and Iran in cluster 3, and Kazakhstan in cluster 4. Although there are no remarkable differences in the frequency of SSR alleles, accessions collected in dry areas are seldom in cluster 1 but more common

to cluster 3, where the landraces from countries with dry climates are mainly grouped. Peculiarities of geographical distribution of the different SSR alleles and representation of ones in landraces from the three significant gene banks are discussed.

P050

Two major lineages of *Aegilops tauschii* Coss. revealed by nuclear DNA variation analysis

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Aegilops tauschii Coss. is a diploid wild goat wheat and one of the progenitors of common wheat (*Triticum aestivum* L.). *Ae. tauschii* is widely distributed in Eurasia, ranges from Turkey to China, and shows abundant phenotypic and genetic variation. To study the population structure of *Ae. tauschii*, SSR analysis with 17 primer sets was conducted using total DNAs from 62 *Ae. tauschii* accessions representing the entire species range. An SSR phylogenetic tree based on the Nei's genetic distances showed that there were two major lineages in *Ae. tauschii*. Lineage 1 consisted of accessions from the eastern habitats mainly in Afghanistan and Pakistan. Lineage 2 included ssp. *typica* accessions of the western habitats and all accessions of ssp. *stragulata* accessions. The tree was consistent with the chloroplast DNA haplotype network. Furthermore, we analyzed nucleotide sequences of 10 nuclear genes, namely, *Vrn-1*, *Wcor615*, *Ppd-1*, a *CONSTANS* homolog *TaHd1*, 2 MADS-box genes, *WPI1* and *WPI2*, and 4 abiotic stress-responsive genes encoding CBF/DREB-type transcription factors such as *WCBF2*, *TaCBF2*, *WDREB2* and *WDBF1* using 30 accessions of *Aegilops tauschii*. Based on the nucleotide sequence variations, a phylogenetic tree was constructed for each gene and compared with the SSR phylogenetic tree. The *Vrn-1*, *TaHd1*, *WDREB2* and *WDBF1* sequences were clearly divided into two lineages, consistent with the pattern seen in the SSR-based phylogenetic tree. The *WPI1* sequences were also classified into two lineages, but the grouping pattern was completely different from that of the SSR-based tree. The two-lineage structure was not observed for the rest five genes. Overall, the two-lineage structure seemed to reflect the west-to-east dispersal and diversification history of *Ae. tauschii*.

P051

Is synthetic hexaploid wheat a useful germplasm source for increasing grain size and yield in bread wheat breeding?

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Bread wheat (*Triticum aestivum* L.) evolved from limited hybridisations between *Triticum turgidum* L. (AABB) and *Aegilops tauschii* Coss. (DD), restricting genetic diversity. Modern breeding practices have also contributed to further genetic narrowing within cultivated bread wheat. Human-assisted crossing between the progenitors of bread wheat can be used to create synthetic hexaploid wheat that readily hybridises with bread wheat cultivars, providing additional source of genetic diversity for breeding. Synthetic hexaploid wheats have been reported to be useful for increasing both grain size and grain yield in wheat. The objective of this study was to investigate variation in grain size and yield potential of synthetic-derived material under south-eastern Australian conditions. Twenty seven synthetic hexaploids were individually backcrossed to Yitpi, an elite south-eastern Australian bread wheat, and the progeny were developed into 27 families of 15 to 48 BC₁F_{4;6} lines. These were

evaluated in field experiments using a partially replicated trial design, with data collected on grain size and yield. Mean thousand grain weights of the families were similar to or higher than that of the recurrent parent Yitpi. Mean grain yields of the families were all lower than that of Yitpi. These results indicate that synthetic hexaploids can contribute to increased grain size, but further research and breeding effort is required to understand whether these increases can provide useful contributions to grain yield.

P052

Genetic variation of wheat landraces in Afghanistan

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To characterize wheat landraces collected from Afghanistan, intra- and inter-regional genetic variation were analyzed. The landraces we investigated had been collected during 1955~ 78 and maintained by genebank in Japan, which should be valuable genetic resources. Three experiments were conducted in this study, namely, phenotypic variation analysis, storage protein variation analysis, and genomic AFLP analysis. Results indicated that the genebank collections of Afghan wheat we used are true landraces without contamination of modern varieties or introduction of alien genetic factors. We revealed that some accessions contain good potential for application to modern wheat breeding. The results also indicated that the genetic diversity of Afghan wheat is generally high between regions, but not so much within regions, suggesting a bygone occurrence of genetic bottleneck in the border area between Iran and Afghanistan. The materials we analyzed and the information obtained in this study should be useful as genetic resources for wheat breeding and available for reconstruction of Afghan agriculture and society.

P053

Resistance levels of wheat varieties and breeding lines to Ug99 and effective resistance genes

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Wheat varieties as well as potential breeding lines cultivated or targeted for growing in East Africa and Red Sea regions, were assed for their reaction to Ug99 under field conditions in Kenya and Ethiopia. The levels of resistance among bread wheat varieties grown at the high risk areas has been determined under natural infection at the testing sites in Kenya (Njoro), and Ethiopia (Kulumsa and Debra Zeit) There indication that resistant genotypes could be identified and should be further tested at stem rust hot spots. The field evaluation at Njoro Kenya revealed that the quasi totality of the varieties grown in the areas mentioned above is susceptible to Ug99. Among the Egyptian varieties tested only three accession (2%) showed adequate resistance levels to Ug99. Resistance of wheat varieties from Iran, Pakistan, and Turkey varied from 2 to 16%. Slightly over 5 % and 25% of breeding lines from ICARDA breeding program tested in 2006 and 2007 respectively, showed an adequate level of resistance; The biological trap nursery that include stem rust differentials, and cultivars with known resistance genes to stem rust; planted in Ethiopia, Kenya, and Yemen showed wide virulence spectrum of Ug99. Defeated resistance genes in addition to Sr31 will be discussed. Susceptibility of lead varieties (Seri82, PBW43, and cham8) and differentials (Sr31 (Benno)/6*LMPG) is clear indication of presence of Ug99 and an alarming high level of severity. The

potential impact of stem rust is particularly serious in Yemen, where Ug99 was detected in 2006 and continues to evolve; hence more of known stem rust resistance genes are defeated

P054

Analysis of *Pina* and *Pinb* alleles in the micro-core collections of Chinese wheat germplasm by Eco-Tilling

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Kernel hardness, which has important influence on wheat end use properties, is mainly conditioned by allelic variations of the *Pina-D1* and *Pinb-D1* genes. In this work, the Eco-Tilling approach was optimized to investigate *Pina* and *Pinb* alleles in a subset of the core collections of Chinese wheat germplasm. The great majority of the accessions in this micro-core collection set could be clearly defined as hard or soft wheats based hardness index, from which three *Pina* and eight *Pinb* alleles were found. Generally, more *Pinb* alleles were detected in the accessions coming from the regions that grow winter or a mixture of spring and winter wheats. This is particularly evident for the southwestern winter wheat, Xinjiang winter-spring wheat and Yellow and Huai River Valley winter wheat regions. A novel variant (designated as *Pinb-D1x*) was discovered in one of the 11 accessions from the Xinjiang winter-spring wheat region. Compared to the wild type (WT) allele *Pinb-D1a*, two nucleotide substitutions occurred in the coding region of *Pinb-D1x*, one (at nucleotide position 257) resulting in the replacement of wild type cysteine residue by tyrosine and the other (at nucleotide position 382) creating a premature stop codon. We conclude that Eco-Tilling is an efficient approach for analyzing allelic variations of *Pin* genes in wheat. The implications of our data to understanding the diversity of *Pina* and *Pinb* alleles in wheat and to future molecular breeding of wheat kernel hardness are discussed.