

**P277**

**Construction of SSR linkage map and QTL mapping for spike characters in common wheat RIL population**

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Linkage map with SSR markers are highly useful for further map based approach in wheat. In the present study, Recombinant Inbred Lines (RILs) developed from Chinese Spring/Spelta (*Duhamelianum*) was used for constructing the linkage map with SSR markers selected from so far published data and developed some functional markers. As a cost effective platform, for PCR reactions, home made *Taq* enzymes were used and the PCR products were genotyped mostly in Agarose gel. Out of 363 polymorphic primers between parents, 292 resulted as linked markers in linkage analysis. But after elimination of > 50 cM distanced markers, 253 loci were lingered uniformly in all chromosomes except chromosome 1D. Only one linkage break was occurred in chromosome 5A and no linked markers were found for chromosome 1D. The total map length was 2473.5 cM with average mapping distance of 9.77 cM between the markers. A genome accounts for 949.4 cM with 105 loci, followed by B genome of 837.9 cM with 102 markers, whereas the D genome had 686.2 cM with 46 markers. The functional markers were located as we expected based on parental polymorphism. Because the parents phenotypically varied for prominent spike characters (Q/q), phenotypic data were recorded for spike length (SL), spikelet number (SN) and spike compactness (SC) for QTL analysis. Totally eleven QTLs were detected for three traits. For SL, out of four, two QTLs were located on chromosome 2A contributed by CS (Q). Another two QTLs were found on chromosome 5A contributed by Spelta parent (q). For SN, three out of six QTLs were found on chromosome 2A, two QTL located on 2B and the remaining one located on chromosome 4D. One major QTL for SC was found at chromosome 5A.

**P278**

**Stomatal characteristics, heritability and their relationship to grain yield in a double haploid bread wheat population**

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Assessment of heritability of stomatal characteristics and their relation to grain yield is useful in formulating a breeding strategy and reliable selection in crop improvement especially where water supply is limited. A set of 99 doubled-haploid lines was developed from a cross between two Canadian bread wheat lines ES32 and P8911-G1D3, their parents and 5 Iranian bread varieties were evaluated in a 2-year field study, to ascertain and compare heritability for stomata frequency, size, length, width and area in abaxial and adaxial flag leaf surfaces. Moreover, abaxial/adaxial stomata frequency ratio, grain yield and the correlation between these traits were assessed. The results showed that, there were highly significant differences among doubled haploid lines, the parents and the Iranian varieties for all the considered characters with the exception of abaxial/adaxial stomata frequency ratio. The stomata were significantly ( $P<0.01$ ) more frequent on abaxial surface (ranged from 43.38 to 66.81) than the adaxial surface (ranged from 30.18 to 49.20). Stomatal length means were significantly higher ( $P<0.01$ ) for the lower surface (ranging from 45.52 to 61.46) than the upper surface (ranging from 43.35 to 61.20). The stomatal area followed a similar pattern, where means were significantly higher for the lower surface than upper surface. Broad sense heritabilities were moderate to low for all the traits measured, where stomatal frequency of adaxial surface was highest (36.2%) and abaxial/adaxial stomata frequency ratio was lowest (4.4%). There was a negative

correlation between abaxial stomatal frequency with stomatal length ( $r = -0.59$ ,  $P < 0.01$ ), stomatal area ( $r = -0.49$ ,  $P < 0.01$ ) and stomatal width ( $r = -0.19$ ,  $P < 0.05$ ) and similar relations were observed for adaxial surface stomatal characteristics. Among stomatal characteristics, abaxial surface stomatal width ( $r = 0.22$ ,  $P < 0.01$ ), adaxial stomatal length ( $r = 0.23$ ,  $P < 0.01$ ) and stomatal area ( $r = 0.18$ ,  $P < 0.05$ ) showed significant correlation with grain yield. Stepwise regression appeared also confirm relationship of these stomatal characteristics with grain yield.

**P279**

**Applications and challenges of marker-assisted selection in the Western Australian Wheat Breeding Program**

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Molecular markers are being increasingly used for the deployment of multiple genes for disease, quality and agronomic traits. To cost effectively utilize molecular markers, a communication and management structure between molecular team and breeding team must be established. The needs of each group must be discussed periodically. For the effective use of markers breeders require timely delivered accurate and reliable information. This presentation aims to outline; (1) implementation of molecular markers for the breeders' traits, and (2) discussions about the high-throughput and logistics of marker-assisted selection (MAS) applications in a large breeding program. Molecular marker development and validation is fully integrated with the breeding operations, and activities are focused on the traits that breeders prioritise in the program. As new markers were identified from our work and/or literature these were integrated into marker cassettes formed for different group of traits (i.e. quality, disease) for their effective use in MAS. Based on the traits that are required by the breeding program we have established a trait based map that serve as a guide to breeders in their daily activities including crossing decisions. The program currently has the capacity of using MAS for 42 traits/genes from which more than one marker are used for the quantitative traits. To define the needs of three sub-programs and for the timely delivery of the outputs by the molecular lab, we have developed a simple excel based database (DB). This DB has allowed us to keep track of the requirements of each of the three sub-programs to make sure that the marker laboratory spends its resources equally. Data analysis is one of the limitations of high-throughput marker applications and to overcome this additional analysis tools are being developed.

**P280**

**Designing crossing and selection strategies to combine diagnostic markers and quantitative traits**

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Molecular markers are now in common use, particularly where diagnostic markers (i.e. allele-based functional markers or closely linked markers) exist. Diagnostic markers are now available for more than 20 traits in wheat. Many markers for quantitative trait loci (QTL) have been published for numerous traits in wheat. However, few are actually deployed in breeding. The challenge for wheat breeders is how to implement marker information systems with phenotypic selection in the creation of new parental lines and progeny (target genotypes). For simple procedures and small numbers (<3) of

unlinked genes, population sizes and assays can be calculated from population genetic theory. We required simulation to find an efficient crossing and selection scheme (i.e. low-cost, small population size) to combine nine diagnostic markers donated by three parents. The genes included those for alternative height (*Rht-B1*, *Rht-D1*, *Rht-8*), grain quality (*Glu-B1*, *Glu-A3*), tillering (*tin*) and disease (*Sr2*, *Cre1*, *VPM*). The optimal strategy was a topcross which: (1) used Sunstate (the line with the largest number of favourable alleles) as the final parent in a topcross; (2) selected in the TCF1 (HM14BS × Silverstar+*tin*) for homozygotes for two genes and enrichment (selection for heterozygotes) for three genes; (3) further enrichment in the TCF2; (4) selection for the target genotype in doubled haploid or inbred lines. These results are currently being validated by marker screening and field selection experiments. In the current round of this research, we are combining the selection for diagnostic markers with the selection for QTL related to traits that affect performance under drought, including increased coleoptile length, decreased canopy temperature and increased accumulation of water soluble carbohydrates. A description of the software and methodologies will be presented in the poster.

## **P281**

### **Dynamics of wheat x *Imperata cylindrica* - a new chromosome elimination mediated system for efficient haploid induction in wheat**

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Doubled haploidy breeding serves as a useful tool in wheat improvement by providing instant homozygosity, which leads to fixation of desirable characters of recombinants as well as reduction in the number of generations required to achieve success. Of the various techniques for haploid production in wheat, chromosome elimination has been studied to a great extent. The Molecular Cytogenetics & Tissue Culture Lab of the CSK HP Agricultural University, Palampur, India has taken lead in identifying *Imperata cylindrica* as an efficient alternative pollen source to the existing wheat x maize system for the induction of haploids from the wheat x wheat and triticale x wheat derived hybrids. Intergeneric hybridization between wheat (*Triticum aestivum* L.) and a wild weedy species, *Imperata cylindrica* (2n=20) resulted in the recovery of a high frequency of wheat haploids, which were obtained through the elimination of *I. cylindrica* chromosomes. Cytological evidence for the hybrid origin of the wheat haploids and the process of elimination of *I. cylindrica* chromosomes has been established by utilizing the genomic *in situ* hybridization (GISH) approach. Comparisons based on the efficiency of *I. cylindrica* and maize (*Zea mays*) as pollen sources indicated that *Imperata* - mediated haploid production is more productive and economically viable. Natural coincidence of flowering period of *I. cylindrica* with that of wheat is an advantageous step comparing to maize which requires green house cultivation for this purpose. Besides, the newly developed system is genotype non specific like maize and hence easily crossable with all genotypes of wheat. This innovation has globally opened new vistas for the commercial utilization of the recently developed system for large scale production of doubled haploid lines of wheat to be used directly as improved genotypes or as gene mapping populations.

**P282**

**The International Crop Information System manages geneological, phenotypic and genotypic data in a wheat breeding program**

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The International Crop Information System (ICIS) links pedigrees to phenotypic (agronomic, disease and end-use functionality) and genotypic data that is made easily accessible. The Geneology Management System (GMS) interfaces ‘Central’ public and ‘Local’ private databases which facilitates the global sharing of non-sensitive pedigrees, selection histories and other descriptors in the Central database while interfacing with Local databases which contain the sensitive pedigrees. The Central GMS now contains more than 5.8 million wheat genotypes, and our local GMS has more than 30,000 entries each of durum and hexaploid wheat. The Data Management System (DMS), which has public phenotypic data for 491 nurseries spanning 1969 to 2006, manages the phenotypic and genotypic data and links it to lines in the GMS. A Data Comparison Tool (5.5) provides three queries to either compare two genotypes, to retrieve data by trial, or to retrieve data for a list of genotypes, and outputs the phenotypic and genotypic information to Excel or other formats such as text. We routinely apply ICIS to aid in choice of parents for crossing and for managing and linking the genotypic data from haplotyping, association mapping and marker-development projects.

**P283**

**Breeding desired quality wheat by reverse genetics**

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TILLING (Targeting Induced Local Lesions IN Genomes) was first developed in *Arabidopsis* for studying gene function after the completion of *Arabidopsis* genome sequencing. This reverse genetics tool combines traditional chemical mutagenesis methods with high-throughput mutation detection techniques. It identifies a series of point mutations including knock-out and partial inactivation in a gene of interest. Wheat has a large and complex genome. Its polyploidy nature makes it difficult to identify desirable genetic changes based on phenotypic screening due to redundant copies of genes. Therefore forward genetics is more difficult in wheat than in other diploid plants. Here we show that the reverse genetics method TILLING is suitable in wheat for identifying useful mutants for wheat breeding. Screening of Waxy genes *Wx-A1* and *Wx-D1* in 1,025 EMS-treated M2 plants or 2,200 heads has found 119 mutants including truncation mutations in *Wx-A1* and *Wx-D1*. Due to the null-4A (*Wx-B1*) nature of this population, a waxy wheat has been bred by crossing the two truncation mutants (*Wx-A1-truncation* and *Wx-D1-truncation*). Screening of two puroindoline (*Pin*) genes (a and b) has identified 20 mutants. Some of them showed either harder or softer phenotype when compared to untreated wild-type. As wheat genomics is producing a large amount of information of target genes, many genes of interests can be screened for mutations in this TILLING population and mutants can be used for breeding wheat with desired quality.

**P284**

**Effect of the *Gpc-B1* region from *Triticum turgidum* ssp. *dicoccoides* on grain yield and thousand grain weight**

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We previously cloned the *Gpc-B1* gene and showed that wild emmer (*Triticum turgidum* ssp. *dicoccoides*, DIC hereafter) has a functional copy of this gene, whereas tetraploid and hexaploid commercial wheat varieties have a deletion or a non-functional copy as a result of a frame-shift mutation. The DIC allele accelerates senescence and increases protein, zinc and iron content in the grain relative to the non-functional allele. Here we describe the effect of the introgression of the DIC chromosome 6BS segment including *Gpc-B1* on grain yield, thousand grain weight (TGW) and protein yield (grain yield by grain protein content) in hexaploid and tetraploid wheat. We introgressed the DIC segment into six hexaploid and three durum varieties by six backcross generations and developed sister near isogenic lines (NIL) with and without the DIC segment. In 2006 and 2007, we grew the nine pairs of NILs in three locations in a split-plot design with five replications. The lines were maintained disease-free by applying fungicides when necessary, to avoid the confounding effect of the linked *Yr36* resistance gene. In 2006, durum lines carrying the DIC *Gpc-B1* allele showed average grain yield reductions between 6 and 17% relative to the recurrent parental lines. The same year, GPC durum lines showed an 8% reduction in TGW, explaining part of the decrease in grain yield. In 2007, however, durum lines with the DIC *Gpc-B1* region showed grain yield increases in two of the three locations tested, despite of a consistent reduction in TGW. Hexaploid lines carrying the DIC *Gpc-B1* allele showed non-significantly different grain yields compared to the corresponding recurrent parents in both years. The presence of significant gene by variety interactions indicate that the effect of the *Gpc-B1* region varies across genotypes. In general, grain protein concentration was significantly increased by the presence of the DIC allele, although the magnitude of the increase varied across locations and genetic backgrounds. Total protein yield was strongly affected by the variations in grain yield.

**P285**

**Larger root system increases water – nitrogen uptake and grain yield in bread wheat**

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The effect of root biomass on water – nitrogen (N) absorption, drainage, and grain yield was investigated in bread wheat ‘Pavon 76’ and its 3 1RS translocation lines, namely 1RS.1AL, 1RS.1BL, and 1RS. 1DL. These four isolines were grown at optimum (ON) and low (LN) levels of N solution in a sand-tube experiment in a glasshouse. The translocation lines had larger root biomass than Pavon 76 which confirmed previous studies. Root biomass per plant ranged from 1.563 to 2.566 g in LN and from 2,081 to 3.201 g in ON. Regression of N content in whole plant, in roots, in stems and leaves, and in grain; and grain yield on root biomass across genotypes and N levels was significant. For an increase of 1 g in root biomass per plant, solution uptake increased by 39 ml per day during five consecutive days during early grain filling period. Similarly, N content increased in whole plant by 148 mg, in roots by 8.6 mg, in stems and leaves by 44.0 mg, in grain by 95.4 mg; and grain yield increased by 3.1 g. In contrast, the amount of leachate during the same period was reduced by 32.4 mg per day and the amount of N in leachate was reduced, by 17.5 mg L<sup>-1</sup> in LN and by 13.0 mg L<sup>-1</sup> in ON. These results indicate that a larger root system in wheat may increase grain yield and grain protein content while reducing residual N in drain water, thus decreasing N pollution and increasing sustainability.

**P286**

**Genetics of resistance to sunn pest (*Eurygaster integriceps* Put) in bread wheat**

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Sunn pest *Eurygaster integriceps* Put. (Heteroptera: Scutelleridae) is well known as a serious limiting factor for production of wheat grain with strong gluten in the wide area of the Near and Middle East, Eastern and South Europe and North Africa. To study the genetics of resistance to sunn pest in bread wheat, two resistant and a susceptible lines were crossed to each other as follow: 14×30 and falat×30. Their F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> progenies after being produced were planted along with their parents using a randomized complete block design with three replications. In early seed development stage, six sunn pest (nymph<sup>3</sup>) were introduced in each cage having a wheat plant. After fourty days percent damaged seed along with their genetic characteristics were assessed through generation mean analysis method. Gene effects including mean effect, additive, dominance, epistasis effects of additive \* additive, additive \* dominance and dominance \* dominance were observed. The broad sense heritability for 14×30 and falat×30 were estimated 0.78 and 0.84 while narrow sense heritability were 0.51 and 0.67 respectively.

Keywords: Generation mean analysis, Sunn Pest (*Eurygaster integriceps* Put), wheat (*Triticum aestivum*), Gene effects.

**P287**

**Development of a new source of resistance to *Fusarium* head blight and *Stagonospora nodorum* blotch in spring wheat**

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The objective of this study was to transfer FHB resistance from *Triticum timopheevii* to spring wheat *Triticum aestivum*. Crocus spring wheat was crossed to *T. timopheevii*, PI343447, in the greenhouse in 1999. Crocus is a line with the genetic background of cv. Columbus plus three crossability genes *kr1*, *kr2* and *kr3*. The F<sub>1</sub> plants were backcrossed with Crocus. F<sub>1</sub> plants of Both the cross and the backcross were sprayed with 2, 4 -D (100 ppm) after pollination and embryo rescue techniques were used for enhancing the seed set. A segregating population of 1,500 BCF<sub>1</sub> plants was established and advanced to F<sub>7</sub>, using single seed descent (SSD). One hundred lines were selected from 535 BC<sub>1</sub>F<sub>7</sub> lines, based on plant fertility and agronomic traits, and evaluated for reaction to FHB and *Stagonospora nodorum* blotch in the greenhouse for two seasons. One line, TC 67, had high levels of resistance to FHB, comparable to that of Sumai 3, the most FHB resistant wheat available, based on point inoculation. TC 67 also showed a high level of resistance to *Stagonospora nodorum* blotch at seedling stage in inoculated greenhouse trials. The resistance of TC 67 to FHB was further evaluated in replicated field trials, in comparison with two resistant wheat lines Sumai 3 and HY 644, in a FHB disease nursery in 2003 and 2004. The results showed that TC 67 was significantly better than HY 644 in FHB incidence and severity and it was comparable with Sumai 3 in deoxynivalenol (DON) content in the grain.

**P288**

**Comparison of selecting spring wheat in conventional and organic environments**

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Organic production systems represent a different soil and weed environment that is not considered in conventional wheat breeding programs. There is some evidence suggesting that organic environments are sufficiently different to warrant breeding that specifically targets organic cropping systems. However, comparing selection environments requires breeding lines that are representative of the selection environment but derived from common populations. A project has been initiated, since 2004, where the same populations have been selected in both conventional and organic environments. Bulks are created from the best performing 5-10 progeny of each population and selection environment and then grown in replicated yield tests in both types of production environments to evaluate important agronomic traits. Progeny bulks allow for manageable experiments that emphasize the selection environment rather than a specific genotype. Early assessment of progeny bulks have shown some yield advantage and increased seed size of progeny bulks derived from organic selection when grown in organic growing conditions.

**P289**

**Wheat glume colour controlled by *Rg1* locus is useful as a phenotypic marker to select *Glu-B3* alleles encoding LMW glutenin subunits.**

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Japanese wheat cultivars with *Glu-B3g* allele on 1BS encoding low-molecular-weight (LMW) glutenin subunit often have optimum dough strength as well as higher sensory quality for Japanese white salted noodle (Ikeda *et al.* 2005). Extra-strong wheat cultivars ‘Glenlea’ and ‘KS831957’ have the *Glu-B3g* gene. In order to incorporate efficiently the *Glu-B3g* allele into elite breeding lines, DNA marker-assisted selection (MAS) using markers of *Glu-B3* alleles (D’Ovidio *et al.* 1997, Maruyama-Funatsuki *et al.* 2005, Ikeda *et al.* 2006) is a quite powerful tool in wheat breeding programs. In this research, we studied the effectiveness of ‘glume colour’ controlled by *Rg1* locus on 1BS as a phenotypic marker to select *Glu-B3* alleles. Three kinds of recombinant inbred lines (RILs) of F<sub>4</sub> generation developed in our breeding program, derived from the crosses of ‘Kinuiroha’/‘Kinunonami’, ‘Iwainodaichi’/‘Kinunonami’ and ‘Haruibuki’/‘Minaminokaori’, consist of 147, 64 and 97 RILs, respectively, were used. In each cross, genotypes of *Glu-B3* and *Rg1* loci of the maternal cultivar are both different from those of the paternal cultivar. The genotype of *Glu-B3* locus of each RIL was determined by the band patterns of DNA markers. The genotype of *Rg1* locus of each RIL was determined by observing ‘glume colour’ (red, segregating, white) of each RIL. As a result, quite tight cosegregation between *Glu-B3* and *Rg1* loci was found in all of the three kinds of RILs. From this result, we applied ‘glume colour’ controlled by *Rg1* locus as a phenotypic marker to select *Glu-B3g* allele in the breeding program of AARC and confirmed the tight linkage relationship between the two loci. Finally, we clarified that wheat glume colour controlled by *Rg1* locus on 1BS is quite useful as a phenotypic marker which is more convenient and less laborious than DNA markers to select *Glu-B3* alleles. Using this ‘glume colour marker’, breeders can select elite breeding lines with desirable genotype of *Glu-B3* alleles with accuracy in wheat breeding fields only by observing the ‘glume colour’ of each line/plant without any laborious procedures of MAS using DNA marker(s) in the laboratories.

**P290**

**QTL analysis and marker assisted selection for improvement in grain protein content and pre-harvest sprouting tolerance in bread wheat**

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QTL analyses and marker assisted selection (MAS) were conducted by us for improvement of pre-harvest sprouting tolerance (PHST) and grain protein content (GPC) in bread wheat. A number of QTL that were identified by us for PHST and GPC included both main-effect and epistatic QTL (E-QTL). For PHST, a major PHST QTL (*QPhs.ccsu-3A.1*) on chromosome 3A that was identified by us and explained up to 70% phenotypic variation, and for GPC a major QTL (*GPC-B1*) on chromosome 6B identified at the University of California (Davis) were used for MAS. Introgression of these two QTL into 10 Indian elite wheat cultivars including those carrying one or more *Lr* genes was attempted by us. During backcrossing programme, foreground selection was performed using markers flanking the QTL/*Lr* genes and the whole-genome background selection was performed using SSR and AFLP markers. Selection was exercised for reconstituted BC<sub>3</sub>F<sub>1</sub> plants, which contained the QTL allele for PHST/high GPC as well as the *Lr*-gene(s) and exhibited high genetic similarity (up to 100%) with the recipient parent (RP). Phenotypically, these selected plants exhibited high level of PHS tolerance or increased GPC (up to 1.72% higher than the RP genotypes). The selected plants are being advanced to BC<sub>3</sub>F<sub>2</sub> and progenies homozygous for PHST/GPC QTL with leaf rust resistance in laboratory tests will be evaluated in replicated field trials over environments.

**P291**

**Correlation and regression studies in semi-dwarf spring wheat (*Triticum aestivum* L)**

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Correlation and regression studies were conducted for ten commercial varieties of wheat viz. Z.A.77, Pavon, Sonalika, W.L.711, H.D.2009, Mehran, Pak-70, Tesopaco, Torim and Arz. The plant height had negative and significant correlation with yield per plant in varieties W.L.711 and H.D.2009; however, it was positively correlated in varieties Mehran and Tesopaco. The character number of tillers per plant had positive and significant correlation for yield per plant in all varieties. The varieties viz. Z.A. 77, Pavon, Sonalika, W.L.711, Mehran and Torim had positive and significant correlation for spike length of main spike with yield per plant. The character spikelets per spike had positive and significant correlation in varieties Pavon, Sonalika, Mehran, Tesopaco and Torim for grain yield per plant. All the varieties had positive and significant correlation for number of spikes per plant with grain yield per plant. The varieties Pavon, Sonalika, Mehran and Tesopaco had positive and significant correlation for number of grains per spike with grain yield per plant. All the varieties had exhibited positive and significant correlation for harvest index with grain yield per plant. The results suggested that most probably the characters number of tillers, number of spikes per plant and harvest index are very important characters in semi-dwarf wheat for selection criteria under warm climatic conditions in Pakistan.

**P292**

**Breeding for a changing world and genetic modification of photosynthesis in wheat**

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Genetic modification of wheat photosynthesis for increased yield by application of DNA transformation technologies could be considered as a necessary step to wheat crop improvement in modern breeding. Low efficiently results are known so far. The ultimate objective of our research is to investigate the advances in transformation technologies and thus establish approaches for genetic modification of photo-synthesis in wheat for increasing drought resistance and grain yield up to 30% through introduction of maize genes encoding the C4 photosynthesis enzymes into wheat. Simple natural effective genotype independent method of wheat germ-line transformation by *Agrobacterium* Pipetting into the spikelets of wheat before anthesis has being elaborated. Method uses wheat indirect pollen system contains high quantities of flavonol glycosides which acts as inducers of vir region of the Ti plasmid. Elaborated method is very similar to wheat hand hybridization, economic and dont requires expensive complicated tissue culture step. Using this method allowed us to produce putative transgenic wheat plants expressing two important genes: a maize gene encoded phosphoenolpyruvate carboxylase for enhancing photo-synthetic capacity - (PEPC) and a bean gene encoding zeatin O-glucosyltransfe-rase for enhancing growth (ZOG1). 2-steps antibiotic screening technique has also been revealed, used and patented. Totally have been produced about 5000 trans-genic wheat seeds of 30 genotypes, and have been created number of transgenic wheat plants of T1 T3 generations. High level of the maize C4-specific PEPC gene expression in transgenic wheat plants was determined by assaying the activity of PEPC in leaf protein extract, followed by CO<sub>2</sub> gas-exchange and photorespiration measurements, leaf anatomy investigation, yield structure, PCR, Real-time PCR, Southern blot analyses. Stable wheat transformation in T2 has been confirmed by molecular biological techniques and high grain yield increasing up to 25-50% in transgenic plants in comparison with wild types, especially at adverse conditions.

**P293**

**Interrelationships of important agronomic traits and kernel yield in winter wheat**

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Winter wheat yield is a complex, quantitative trait directly or indirectly influenced by other plant traits. An understanding of the interrelationships between important agronomic traits and yield of winter wheat could help to improve breeding results. The objectives of this paper were to examine correlations between several winter wheat traits and their direct and indirect effects on kernel yield. Research work was conducted during two growing seasons in East Croatia (2005/06 and 2006/07) on 11 winter wheat genotypes. Nine genotypes were advanced breeding lines and two were recognized Croatian cultivars Žitarka and Srpanjka. Six traits were included in investigation: ear number per m<sup>2</sup>, plant height, number of spikelets per ear, number of kernels per ear, 1000 kernel weight and kernel yield. Path-coefficient analysis was used to evaluate relations between examined traits. Positive and significant correlation was found between ear number per m<sup>2</sup> and 1000 kernel weight, ear number per m<sup>2</sup> and kernel yield, number of kernels per ear and kernel weight. Ear number per m<sup>2</sup> was in significant negative correlation with plant height and spikelets number per ear. Number of kernels per ear and ear number per m<sup>2</sup> had significant positive direct effects on 1000 kernel weight and kernel yield, while the spikelets number per ear had negative direct effect on kernel yield.

**P294**

**Effects of testing environments and crop density on winter wheat yield**

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Stability of genotypes across different environments is one of the main goals in winter wheat breeding programs. Attention has been devoted to analysing genotype by environment interactions (GEI) to improve crop breeding success. Usually, strategy for selection of winter wheat is that selection should be made on several locations different in climatic and soil conditions. The objectives of this paper were to examine influence of different testing environments and sowing rates on formation of winter wheat kernel yield and, after the stability analysis, to identify most stabile genotypes and locations. Research work was conducted on 14 winter wheat genotypes and four testing locations in East Croatia. On each location genotypes were sown in two sowing rates – 300 and 600 germinable seeds m<sup>2</sup>. Examined genotypes included recognized cultivars (new and older one) and new breeding lines. Testing locations differs in average amount of rainfalls, average temperature and soil type. Combined analysis of variance showed highly significant ( $p \leq 0.01$ ) influence of genotypes, environments (sowing rate and location) and GEI on kernel yield. AMMI 1 model biplot showed that the most yielding location, in combination with higher sowing rate, was one with the best soil conditions (black soil-chernozem). Higher sowing rate at all locations showed higher yield than lower sowing rate at the same location. Biplot also showed that locations were spread from lower yielding to high yielding. Examined genotypes differed in yield and in stability across environments. Genotype Lucija has the highest yield, but it was unstable and adapted to higher yielding environments. Best combination of high yield and good stability was in recognized cultivar Pipi and breeding line OSK 89/05.

**P295**

**Storage, analysis and communication of information from diverse wheat field trials**

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A procedure for the storage, analysis and communication of results from data generated from diverse field trials without compromising institutional confidentiality is discussed. Australian wheat breeders have been growing CIMMYT lines in their own trials for the past 40 or so years, yet only a small proportion of the trial data has made its way back to CIMMYT or other appropriate Australian research entities for further analysis. This information is important in determining which lines from CIMMYT are best for the Australian environment. In addition, timely feedback from the Australian breeders would be useful for the CIMMYT breeders to make decisions on parents. The field trial data (raw data) or some kind of analysis from the raw data is what is normally distributed for further analysis, making it quite difficult to link this information to other research for comparison. A method which allows breeders to share their data without compromising their own institution's privacy rules and which also allows linking of their results with other breeders' results has been developed. All the information gathered on a group of wheat varieties is called a 'study'. Each 'study' is divided into different data subsets, namely: (a) raw data, (b) intermediate data (entry BLUEs and weights from individual trials), (c) derived data and (d) environment data, but it is not necessary for each study to have all the datasets. In addition the availability of the intermediate data enables the analysis of subsets of the data from within or across studies without raw data. Examples of these across-study analyses are given. We will also show how this information is collated together and can be queried to determine results over a number of years and from different locations.

**P296**

**Single-locus and two-locus QTL analysis to detect main effect and epistatic QTL for grain weight in bread wheat**

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In bread wheat, grain weight (GW) is one of the three most important components of grain yield. For the genome-wide genetic dissection of GW in bread wheat, a framework linkage map consisting of 294 loci (194 SSRs, 96 AFLP and 4 SAMPL) was prepared using intervarietal RIL mapping population derived from Rye Selection111 (RS111 = high GW) × Chinese Spring (CS = low GW). Using the genotypic data and GW data of RILs collected over six environments (3 locations × 2 years), genome-wide single-locus QTL analysis using inclusive composite interval mapping (ICIM) and two-locus QTL analysis using QTL Network were conducted to identify main effect QTL (M-QTL), epistatic QTL (E-QTL). Single-locus QTL analysis identified 11 QTL above threshold LOD values (3.95 to 32.0), which contributed significantly to the phenotypic variation (maximum PV in individual environments varied from 4.37% to 82.0%) for GW. These QTL included four major and stable (explaining >20% PV; available in 50% environments), one each located on chromosomes 1A, 1B, 5A and 6B. The major QTL on chromosome 1B (LOD value =10.7-32.0) explained maximum (26.0-82.0%) PV in individual environments. Two locus QTL analysis resolved a total of 30 QTL, which included three M-QTL (also detected by single-locus analysis) and 27 E-QTL involved in digenic Q × Q interactions; no Q × E and Q × Q × E interactions were detected. However, the level of PV explained by QTL identified through two-locus analysis was relatively low. The four major QTL identified through single-locus analysis can be utilized for marker-assisted selection (MAS) for improvement in GW in bread wheat.

**P297**

**Synthesis of a hexaploid club wheat and analysis about the homoeo-alleles of club gene C**

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The authors synthesized the club type (compact and dense spiked), free-threshing and hexaploid wheat strain (i.e. the synthetic club wheat, genome formula AABBDD) from the self-pollinated progeny of the crossed one between the Transcaucasian endemic macha wheat (*Triticum aestivum* ssp. *macha*, husked and semi fragile spiked, AABBDD) and the tetraploid Persian wheat (*T. turgidum* ssp. *persicum=carthlicum*, free-threshing, and lax spike type, AABB). Macha wheat is a polymorphic crop including different spike types; the macha wheat strain used for the cross above has speltoid and semi-dense spike. However the analysis (Unrau 1950) of the club gene C of the club wheat (*T. aestivum* ssp. *compactum*) demonstrated that the gene located on second homoeologous group chromosome of the D genome (2D chromosome), there are tetraploid (without D genome) club type wheats, husked AABB genome crop of *T. turgidum* ssp. *palaeocolchicum=georgicum*, husked AAGG genome crop of *T. timopheevi* and the ancient Egyptian AABB genome crop of *T. turgidum* ssp. *pyramidale* (free-threshing). These tetraploid club type wheats were considered to be old crops, older than the macaroni wheat (*T. turgidum* ssp. *durum*). In addition, there is ancient hexaploid free-threshing club type wheat distinctive from the club wheat, shot wheat, the ancient Indus Valley semi-dwarf wheat of *T. aestivum* ssp. *sphaerococcum*. The second author considers that the shot wheat is an old free-threshing hexaploid wheat, older than the bread wheat (*T. aestivum* ssp. *aestivum*), originated from the above-mentioned tetraploid (AABB) club type wheats. From these facts and considerations, the A or B genome of the shot wheat should have the homoeo-allele of gene C locating on the 2D chromosome of club wheat. The analysis about the homoeo-alleles of the gene C is

performed between the club wheat and the shot wheat. Also, the analysis is performed between the club wheat and the synthetic club wheat.

**P298**

**Genetic dissection of agronomically important traits in bread wheat (*Triticum aestivum* L.) using a chromosome 3A specific RICL population**

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Wheat feeds most of our nutritional demands, and now is emerging as an attractive alternative to feed our demands for biofuel and energy. In view to satisfy these demands, it is important to understand the balance between grain yield and plant biomass (harvest index). This result is possible only by understanding the genetic/molecular basis of both of these complex traits. We initially identified wheat chromosome 3A as a major determinant of grain yield, plant biomass, and other agronomically important traits including plant height, preharvest sprouting tolerance, earliness *per se*, etc. To dissect these traits to their components, a recombinant inbred chromosome line (RICL) population of 95 individuals was developed by crossing Cheyenne with Cheyenne carrying chromosome 3A from Wichita [CNN×CNN(WI3A)]. The above population was genotyped for 43 chromosome 3A specific markers (including RFLPs and SSRs) and phenotyped for grain yield, root and shoot biomass, plant height, kernel weight, kernel number per spike, tiller number m<sup>-1</sup>, days to flowering, etc. QTL interval mapping using these lines allowed identification of at least one major QTL for each of these traits. Major QTLs identified for grain yield, root and shoot biomass explain 21%, 32% and 42% of the variation, respectively. Rice-wheat synteny was used to identify candidate genes (CGs) underlying these QTLs. Some of the interesting CGs (e.g., *BAS1*, *DOG1*, *GID2*, *ABI8*, *GA3ox2*, *GA2ox5* and *CKX2*) identified through comparative analysis are being tested by virus induced gene silencing (VIGS) and RNAi.