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Responses of spring bread wheat lines for Central and West Asia and North Africa (CWANA) Program to stripe rust disease

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Some foliar diseases such as stripe rust of wheat is important diseases in most wheat growing regions cross the world and in the most parts of Iran. In 2005-06 cropping seasons, 378 line of spring bread wheat lines for Central and West Asia and North Africa (CWANA) Program were tested for resistance to stripe rust at adult plant stage with pathotype (pt.) 6E4A+ in Karaj (North) and Zargan (South) with pt. 166E6A+,Yr27+. The new pt. 166E6A+,Yr27+ is going to be dominant pathotype as a hot race in Iran with virulence on plant with Yr27 gene. In the field, each line was planted in two rows of one-meter length with 30cm distance under artificial inoculation. A susceptible wheat cultivar Bolani was planted as spreader around the nursery and between the rows. Field assessments were based on disease severity according to the modified Cobb's scale (Peterson *et al.*, 1948) and disease reaction (Roelfs, 1978) stripe rust disease. The results showed that among 378 line, 96.8% (366 lines) were resistant to pt. 6E4A+ in Karaj, but in Zargan site 166 lines (44%) were resistant to stripe rust pt. 166E6A+,Yr27. This is confirming that pathogenic variation between regions within large cropping areas can be significant.

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Identification of virulence factors of *Puccinia triticina*, the causal agent of wheat leaf rust in Iran

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Leaf (brown) rust, caused in wheat by the fungus *Puccinia triticina* is an important disease in north, west and south of Iran. Use of resistant cultivar is the best way to control of this disease. Leaf rust is an endemic disease in Iran, which each year is appeared. To find resistant sources to the pathogen and use in the breeding program it is necessary to determine virulence factors of pathogen. In this study 20 isolates of leaf rust agent were collected from different parts of Iran. Spores of each isolate after purification and increasing were inoculated on a set of international standard differentials in the greenhouse. After inoculation seedling plants were placed in an incubation room for 24 h at 18 °C and 100%RH in the dark. Following incubation, plants were moved to greenhouse chambers with 22 to 24 °C. Infection types were recorded 12-16 days after inoculation. The objective was to record reactions when the difference between the susceptible control was at the maximum. Leaf rust infection types were recorded using a sacle described by McIntosh *et al.* (1995). Virulene for the genes *Lr1*, *Lr2c*, *Lr3*, *Lr3ka*, *Lr3bg*, *Lr10*, *Lr11*, *Lr13*, *Lr14b*, *Lr15*, *Lr16*, *Lr18*, *Lr20*, *Lr21*, *Lr24*, *Lr30*, *Lr33* and *Lrb* was detected. All isolates had virulence on plant with *Lr2b*, *Lr11*, *Lr14b*, *Lr16* and *Lr30* genes. No virulence was detected for *Lr2a*, *Lr9*, *Lr14a*, *Lr19*, *Lr23*, *Lr25*, *Lr26*, *Lr28*, *Lr29*, *Lr32*, and *Lr36* gene. Use of these genes with combination of adult plant resistance genes is expected to be a useful method to control of leaf rust disease.

Reference

McIntosh, RA, Wellings, CR, and Park, RF 1995. Wheat Rusts: An Atlas of Resistance Genes. CSIRO, Australia, pp. 200.

P108

Dissection of powdery mildew resistance uncover different resistance types in the *Triticum Turgidum* L. gene pool

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Powdery mildew caused by the biotrophic pathogen, *Blumeria graminis* (DC.) E.O. Speer f. sp. *tritici* Em. Marchal (hereafter *Bgt*), is a foliar wheat disease resulting in severe yield losses worldwide. The continuous threat for breakdown of race-specific resistance to powdery mildew is forcing a consecutive effort to enrich the resistance reservoir. In the current study, a large collection of wheat genotypes, consisting of wild and cultivated wheats, were screened for powdery mildew resistance with a set of 42 *Bgt* isolates from Israel. Two *Triticum Turgidum* L. ssp. lines: G18-16 (*T. dicoccoides*) and Langdon (*T. durum*), found to be resistant to 29 and 3 isolates, respectively, were used to generate a recombinant inbred line mapping population (152 RILs). The RILs were tested for powdery mildew resistance with two *Bgt* isolates: (i) *Bgt*#15, collected from *T. durum* and avirulent on G18-16; (ii) *Bgt*#66, collected from *T. dicoccoides* and generating partial resistance response in Langdon. RIL genetic map was constructed using 310 microsatellite, DArT (Diversity Array Technology) and CAPS (Cleaved Amplified Polymorphic Sequences) markers. The segregation ratio of the RIL population in reaction to *Bgt*#15 showed that the resistance in G18-16 is controlled by a single dominant gene that was mapped to the distal end of chromosome arm 7AL. QTL analysis of the reaction to *Bgt*#66 revealed one major OTL on chromosome arm 1AS (LOD 16) and additional four minor QTLs on chromosomes 1B, 2B, 3A and 7A. Host-pathogen evolutionary aspects and future implementation of powdery mildew resistance in wheat breeding programs are discussed.

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Alien introgression for FHB resistance in wheat - challenges and strategies

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Fusarium head blight (FHB) has become a predominant fungal disease of wheat worldwide. Host resistance has been considered an economically and environmentally efficient means to manage this disease. Progress of breeding for FHB resistance, however, has been limited because of the lack of effective resistance to FHB and the complex inheritance of the partial resistance currently available in wheat. Relatives of wheat have proven to be an invaluable gene reservoir for wheat improvement. We have evaluated over one thousand accessions of wheat relatives at different ploidy levels and wheat-alien species derivatives with varied chromosome constitutions for FHB resistance. Over the last few years, we have introgressed FHB resistance identified from the relatives and derivatives into adapted durum and bread wheat backgrounds using various strategies. To date, we have developed a number of resistant introgression lines that contain minimal alien chromatin and do not have obvious linkage drag. Some of the introgression lines exhibited resistance to other fungal diseases in addition to FHB. We found that the biggest challenge of alien introgression for FHB resistance was its strong epistatic interactions with genetic backgrounds. Selection of proper recipient genotypes, therefore, plays a central role in the success of alien introgression for FHB resistance.

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Molecular mapping and marker-assisted improvement of rust resistance in the Australian wheat germplasm

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Molecular markers make the pyramiding of rust genes possible in adapted elite lines. In this study we report the microsatellite tagging of leaf rust genes *Lr13* and *Lr28* in the Leichardt/WAWHT2071 and Sunland/Arrino populations, respectively. Leichardt and Sunland were the sources of resistance genes for *Lr13* and *Lr28*, respectively. F₂ and F_{2,3} populations were used for microsatellite tagging of the genes. Closely linked SSR markers were identified for *Lr13* and *Lr28* on chromosomes 2BS, 4AL, respectively. Molecular markers for a range of other rust resistance genes (*Lr9*, *Lr19/Sr25*, *Lr24/Sr24*, *Lr34/Yr18*, *Lr46/Yr29*, *Lr47*, *Sr26*, *Sr32*, *Sr33* and *Sr36*) are currently being implemented for variety development and germplasm enhancement.

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Gene discovery in recombinant doubled haploid populations for breeding wheat resistance against aphids

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Russian wheat aphid (RWA) (*Diuraphis noxia*) and greenbug (*Schizaphis graminum*) are two devastating pests of wheat worldwide. In Argentina another new aphid pest, *Sipha maydis*, infesting wheat and barley, appeared in 2002. These aphids provoke severe damage to plant growth and production at the seedling and adult plant stages. RWA and greenbug have evolved several biotypes virulent to most of the resistance genes introduced into wheat cultivars. The fast deployment of resistance genes and the continuous appearance of new biotypes and pests require the assessment of new sources of resistance for breeding plant-defence. Resistance to aphids consists of three mechanisms: antixenosis prevents the insect selection of plant hosts; antibiosis imposes a reduced aphid longevity and fertility; tolerance allows the host to maintain a normal growth rate under infestation. Marker assisted genetic analysis and the use of recombinant doubled haploid (RDH) lines and RILs has allowed the mapping of novel resistance genes for Argentinean populations of aphids. Resistance QTL against greenbug have been mapped onto several chromosomes. Antixenosis QTL were located on chromosomes 1B and 6A of a CS x Synthetic set of RDH. QTL for tolerance and antibiosis have been mapped onto chromosome 7D of the ITMI RIL population, and 7D of a CS x Synthetic set of RDH. Resistance to RWA was accounted for by QTL on different chromosomes. QTL for antixenosis to biotype 2 was located on chromosome 6A and tolerance on the 1D and 7D chromosomes of the CS x Synthetic set of RDH. Most of the QTL for tolerance traits to *S. maydis* were mapped on the homoeologous group 1 and 2 chromosomes. These novel genes could be included in wheat cultivars by marker-assisted selection to enlarge the genetic base of defence against the aphid pests.

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Molecular mapping of leaf rust resistance gene *Lr15* in bread wheat

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Leaf rust caused by *Puccinia triticina* f.sp. tritici is the most widespread and commonly occurring rust on wheat crop. Genetic resistance is the most economical method of reducing losses due to leaf rust. The objective of this study has been to pyramid seedling (*Lr15*) and adult plant resistance (*Lr34*) in the background of NI5439, a genotype adapted to terminal heat tolerance and moisture stress through MAS. To identify DNA markers linked to *Lr15*, F₂ mapping population generated by crossing Thatcher (Tc) x Thatcher *Lr15* was phenotyped by screening it with 162A race of *Puccinia triticina* and single gene governance of the resistance by *Lr15* was confirmed. In all 23 polymorphic SSRs from 2DS were used to analyze the entire population. Based on marker segregation, linkage group was constructed with 19 SSRs at LOD 4.0. The closest flanking markers were Xgwm4562 and Xgwm102 at a distance of 3.1 cM and 9.3 cM, respectively till LOD 9.0. Closely linked markers for *Lr34* gene have already been reported from Dr. Keller's (SWM10) and Dr. Lagudah's laboratory (csLV34). For pyramiding *Lr15* and *Lr34* into NI5439, single and double crosses involving parents Tc *Lr15*, Tc *Lr34* and 90RN2491 were performed. These double cross lines were screened for the presence of *Lr15* and *Lr34*. Only selected lines will be backcrossed with NI5439 to enhance the genetic background of NI5439 using MAS, which will lead to development of improved NI5439 genotype.

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Transferring, mapping, cloning of powdery mildew resistance gene of *Haynaldia villosa* and its utilization in common wheat

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H. villosa is highly resistant to wheat powdery mildew disease. The powdery mildew resistance gene has been transferred from *H.villosa* into common wheat through development of 6VS/6AL translocation line, and has been designated as *Pm21* and mapped in the region of FL0.58 of the short arm of 6V using the alien deletion addition line. Based on the above achievement, we further develop genetic resources for accurate mapping and cloning of *Pm21* gene. To significantly improve the induction frequency of small fragment interstitial translocations, γ -Ray irradiation of the mature female gametes of the 6VS/6AL translocation line was employed with higher dosage. More than 20 new translocations and deletions involved in different regions of the short arm of 6V have been obtained, and *Pm 21* was further mapped in a smaller region by genomic *in situ* hybridization and molecular marker analysis. A microarray analysis using the barley Affymetrix Gene-Chip was conducted to clone candidate genes of *Pm21*. A full length candidate clone has been identified, and its transgenic plants were obtained by shot-gun transformation. The transgenic plants in a powdery mildew susceptible receptor variety Yangmai 158 showed high resistance, indicating good compensate function of the candidate gene. A TAC library of the 6VS/6AL translocation line was screened using a primer designed according to the sequence of the candidate gene, and a positive clone of 30kb and then a subclone of 5kb were selected. The sequence of the exon of the subclone was homologous to the cDNA sequence of the candidate gene. TAC-FISH using the positive clone as probe further proved that this TAC was located in the same region of *Pm21*, i.e. FL0.4-0.6 of the 6VS. The 6VS/6AL translocation line has been used as parents in breeding program and a number of new varieties with

high yield and good disease resistance, such as Nannong 9918, Neimai 8~10 and Shimai14, have been developed and released.

P114

Heritability and number of genes controlling slow-mildewing resistance in wheat cultivar Lumai 21

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Since the slow-mildewing resistance is more durable than hypersensitive resistance, it is very important to apply slow-mildewing in wheat breeding. However, little information is available about the genetics of slow-mildewing resistance in Chinese wheat cultivars. To estimate the number of genes and heritability of slow-mildewing resistant wheat Cultivar Lumai 21, 200 F_{2:3} and F_{2:4} lines from the cross Lumai 21/Jingshuang 16 (susceptible) and their parents were planted at Beijing and Anyang in field condition for disease evaluation. Based on both quantitative and qualitative genetic analyses, the results showed that the resistance in the two populations was governed by at least four genes and broad-sense heritability of resistance was from 0.53 to 0.78. Transgressive segregation indicated that Jingshuang 16 might have contributed one minor gene for resistance. Therefore, slow resistance to powdery mildew in Lumai 21 was controlled by three genes.

P115

A novel leaf rust resistance gene transferred from *Aegilops caudata* L. to *Triticum aestivum* L. maps on chromosome 5D

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Leaf rust and stripe rust are the two most important foliar diseases of wheat worldwide. Host genetic resistance is the most economical and environmentally friendly approach to reduce the losses due to rust diseases in wheat. The germplasm of non-progenitor *Aegilops* species have been found to be an invaluable source for new resistance genes. The transfer and mapping of a new leaf rust resistance gene from *Ae. caudata* L. is reported here. A leaf rust resistant accession PAU #3556 of *Aegilops caudata* was crossed with *T. durum* and an amphiploid synthesized for transferring leaf rust resistance to *T. aestivum* through induced homoeologous pairing. Leaf rust resistant introgression lines (ILs) were developed through backcrossing with a leaf rust susceptible cultivar WL711. An F₂ population derived from one of the introgression lines segregated for a single leaf rust resistance gene at the seedling (208R:78S; $\chi^2=0.79$) and adult plant stage (219R:67S; $\chi^2=0.37$). The testing of F₃ progenies confirmed the transfer of a single gene for leaf rust resistance. Bulk segregant analysis was conducted using 101 polymorphic D-genome specific SSR markers. The SSR markers *Xcfd18*, *Xcfd189*, *Xcfd78* and *Xfd81* detected *Ae. caudata* specific alleles in the parental introgression line and the resistant bulks. All these markers mapped on distal region of 5DS indicated a terminal translocation. Analysis of the F₂ population mapped *Ae. caudata* leaf rust resistance gene on chromosome 5DS with *Xcfd18* as the closest linked marker.

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Gene expression of plant defence pathways using *Lr1* transgenic lines and the Affymetrix wheat chip

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Leaf rust resistance gene *Lr1* was cloned and demonstrated by transformation of the susceptible cultivar Fielder. Transgenic line T₀-938 had a single hemizygote *Lr1* insertion and segregated in subsequent generations. Unlike the majority of R-genes, *Lr1* has a co-dominant gene action, i.e., the heterozygotes exhibit an intermediate level of resistance. A gene expression experiment using T₀-938 derived lines was performed to study the resistance, intermediate and susceptible pathways triggered in the presence of *Lr1* in its homozygous or heterozygous states and in the absence of *Lr1*. The 27-Affymetrix chip experiment comprised 3 independent biological replicates, 3 genotypes (T₄-938-homozygous for *Lr1* (R), T₄-938-sister line without *Lr1* (S) and F₁-938-heterozygous for *Lr1* (I)), and 3 time points (before inoculation, 6h and 24h after inoculation). These lines genetically differed almost exclusively by their *Lr1* gene dosage and provided near perfect isogenic lines for profiling the expression pathways triggered during the compatible and incompatible *Lr1* wheat leaf rust pathosystem. Gene expression was measured by comparison to the expression levels before inoculation. A total of 584 of the 61,127 probe sets were differentially regulated in at least one of the 6 possible genotype X time point comparisons. Only 4 and 8 of these differentially regulated genes showed the same trends in all three genotypes at 6 and 24 hours after inoculation, respectively. The majority of genes differentially expressed in the three genotypes and at the two time points differed, indicating that pathways to resistance and susceptibility were largely not shared. Interestingly, the strict number of differentially regulated genes was 5 to 10 times higher in the intermediate and susceptible reactions as it was in the resistant reaction. Expression profiling analysis across genotypes and time points will be presented.

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Mapping resistance gene to leaf rust in wheat line KSWGRC11 using quantitative bulked segregant analysis and DArT platform

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Leaf rust (*Puccinia triticina* Erks.) is one of the most important foliar diseases of wheat (*Triticum aestivum* L.) worldwide. High genetic variability of the pathogen prompts breeders to stack a few major resistance genes into a single cultivar. In order to manipulate effectively with resistance genes, tightly linked molecular markers with resistance loci are required. Major leaf rust resistance gene *Lr42* identified on chromosome 1D of *T. tauschii* was transferred to common wheat line KSWGRC11 (= Century*3/*T. tauschii* TA2450, *T. tauschii* TA2450) (Kansas State University, Manhattan, KS, USA). Recently, using molecular markers resistance gene *Lr42* was located on chromosome 2D. The objective of our study was to confirm its localization and mapping closely linked molecular markers suitable for marker assisted selection. From cross between German winter wheat cultivar Aristos and KSWGRC11 we produced mapping population comprising 154 F_{2:3} families. Seedlings of the F₂ population and F₃ derived families were evaluated for reaction to leaf rust. Observed segregation ratio indicated for resistance controlled by single dominant gene. Microsatellite markers were used to establish 1DS and 2DS genetic maps, but resistance locus (putative *Lr42*) could not be placed reliably on neither of the two chromosomes. Therefore for mapping resistance locus *de novo*, we decided to apply quantitative bulked segregant analysis based on DArT platform. Results of this approach will be presented on the conference.

P118

Evaluating the resistance to sunn pest (*Eurygaster integriceps* Put) and its relationship with high-molecular-weight glutenin subunit in wheat

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To evaluate the resistance of 50 lines and cultivars to sunn pest an experiment using complete randomized block design with 3 replications was carried out in research farm of Paradise of Agriculture and Natural Science, University of Tehran, at Karaj during 2005-2006. In early seed development stage, six sunn pest were placed in each cage having a wheat plant. After forty days, percent seed damaged along with their morphological characteristics were measured. However, the high-molecular-weight (HMW) glutenin subunit composition of seed storage protein of 50 lines and cultivars of hexaploid wheat (*Triticum aestivum*) have been examined by using sodium dodecyl sulfate polyacrylamide gel electrophoresis system. 14 different alleles were found. There were no significant correlation between percent damaged seed and morphological attributes such as kernel color, coverage of seed by glum and glumel, hairiness of glum, plant height, spike density, awn length, number of tillers, days to ripening, biological yield, grain yield per plant, number of kernel per spike and seed thousand weight. However, a negative significant correlation was observed between sunn pest infestation and peduncle length. Percent damaged seed was highest in line 8 (82%) and Gaspard cv. (75/6%) and the lowest in line 20 (38/8%) and synthetic line 18 (43/5%). Line 20 and synthetic line 18 were considered as resistant, lines 4, 7, 15, 18, 21, 26, 31, Falat cv. as semi-resistant, line 8 and Gaspard cv. as very sensitive and others as sensitive lines and cultivars in terms of percent damaged seed. However, the results showed that 7+9 and 12 alleles had positive significant correlation and 7+8 and 2+12 alleles had negative significant correlation with percent damaged seed. Stepwise regression analysis revealed that the subunits 7+9, 12, 7+8 and 6+8 can justify 58.7% of variation in percent damaged seed.

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Relationship between plant height and *Fusarium* head blight resistance for the QTL on the wheat chromosome 2DS, *QFhs.kibr-2DS*

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The FHB resistance QTL region of wheat chromosome 2DS (*QFhs.kibr-2D*) flanks the reduced height gene *Rht8*, which might influence initial infection of FHB under the field conditions. However, it is suggested the existence of other potential resistance gene(s) within this QTL region beside the primary plant height effect by *Rht8/rht8* alleles on the FHB resistance and DON accumulation. The results of QTL analysis using one doubled haploid lines (DHLs) derived from Sumai3 and Gamanya suggest that MRP (multidrug resistance-associated protein) is a possible candidate for *QFhs.kibr-2D*, which has an additional effect for type II resistance and DON content, and acts independently of *Rht8*. The Gamanya allele for the MRP associated with the QTLs for both type II resistance and low-level DON accumulation, and showed additive effect on the *Fhb1* of Sumai 3. On the other hand, the short culm plant with *Rht8* of Sumai 3 tended to suffer from the severe damage to initial infection, which explained the QTL for FHB field response with epistatic effects on the type II resistance and low level DON accumulation. Relationship between *Rht8* genotype, one of the possible genes controlling plant height among the DHL population, and *QFhs.kibr-2D* was examined by drifting of the QTLs in each group of *Xgwm261* allele, corresponding to the *Rht8* genotype. Influence of the plant height on *QFhs.kibr-2D* was also evaluated in the same manner as the *Rht8* genotype between two culm length

groups of the DHLs. From the results of the MRP analysis and the possible effects of *Rht8*, we postulate that *QFhs.kibr-2D* is a resistance gene complex consisting of morphological traits controlled by *Rht8* for type I resistance and a specific gene(s) to control type II resistance by detoxification of DON, like MRP.

P120

Combining ability of resistance to *Fusarium* crown rot of bread wheat

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Crown Rot (CR) caused predominantly by *Fusarium pseudograminearum* (teleomorph *Gibberella coronicola*) is a major soilborne disease problem in the wheat and barley industries of many countries, including Australia. Genetic resistance is a vital tool for combating CR. Breeding for CR resistance has proven difficult in the past, so the combining ability of nine parent lines of varying crown rot resistance was determined. Of the genotypes studied, two of these (Puseas and Kennedy) are susceptible; the remaining seven (2-49, CPI133814, IRN497, Lang, QT10162, Sunco, and W21MMT70) have a level of partial resistance. Three half-diallel glasshouse experiments were conducted (in 2003, 2004, 2005). All experiments found highly significant general combining ability (GCA), as well as highly significant specific combining ability (SCA). Narrow sense heritability estimates were: 2003 – 0.58; 2004 – 0.71; 2005 – 0.59, however the significant specific combining ability makes this figure less valuable. Across the three experiments, IRN497 and CPI133814 (when present) were the parents with the best GCA for improving resistance. The SCA results were variable between experiments. The three experiments were re-analysed using only the seven parents available in all years. The mean rank across all experiments showed that five of the six better F1 crosses had IRN497 as a parent. The significance of GCA effects, and the different patterns of SCA effects suggests that there are many different genes or gene complexes present in these parental lines for crown rot resistance. There is potential for targeting specific high performing crosses, rather than crossing potentially high performing parents and overlooking the optimal gains available.

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Obtaining genetic resistance to *Fusarium* crown rot in bread wheat

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Crown Rot (CR) caused predominantly by *Fusarium pseudograminearum* (teleomorph *Gibberella coronicola*) is a major soilborne disease problem in many countries, including Australia. This work was designed to shed light on the genetics of CR resistance to assist in CR resistance breeding.

Results from a series of nine parent half-diallel experiments indicated that both general and specific combining ability were significant, and that breeding based on the parental phenotype will not always be the optimal approach.

To better understand the resistance genes, experimentation was conducted using the ‘generation means’ quantitative genetics design, which provides much more detail about each cross combination.

Twenty-nine of the cross combinations were tested in the glasshouse. The majority of the combinations with better crown rot resistance also had a more complex genetic model of resistance. This does not mean improved resistance is unobtainable, as detailed knowledge of the genetics of each

cross enables the optimal combinations to be pursued, with the highest heritability, lowest number of genes, combined with the highest resistance. From this shortlist, those which already contain agronomic advantages can be favoured, as they will increase the speed of release of improved crown rot resistance lines.

The genetics of CR resistance have proven to be complex, and highly dependant on which resistant parent is used, as well as being influenced by gene interactions. The knowledge obtained through this project has enabled a selection of populations to be targeted for their superior ability to transfer high levels of resistance to progeny, coupled with some potential for combined agronomic traits, increasing their usefulness to breeders.

P122

Intragenic recombination between pseudogenes as a source of new disease specificity at a simple resistance locus

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The leaf rust resistance gene *Lr21*, coding for an NBS-LRR protein, was identified from the wild goat grass *Aegilops tauschii* Coss, the species that contributed the D-genome to bread wheat (*Triticum aestivum* L.). Unlike most NBS-LRR type resistance genes that are organized as compound loci, *Lr21* is located at a simple locus. We studied the molecular dynamics of this locus in samples of 25 *Ae. tauschii* accessions and 22 bread wheat cultivars, and discovered at least 13 nonfunctional *lr21* alleles existing as truncated expressing pseudogenes and one functional *Lr21* allele. The *Lr21* specificity arose most likely from two susceptible *lr21* alleles through intragenic recombination between the NBS and LRR domains. The discovery suggests plant resistance genes can be generated from the dead alleles. The birth of *Lr21* provides new understanding as to why plants keep and often transcribe truncated resistance gene analogs.

P123

Stripe rust resistance in soft red winter wheat cultivars and lines

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, has emerged as an important disease of soft red winter wheat in the eastern region of the U.S. Identification of stripe rust resistance sources for the eastern U.S. is extremely important to determine the major and minor *Yr* genes involved. Breeding lines and cultivars from Universities and private companies (713 entries in 2006 and 380 entries in 2007) were evaluated in the field at Plains and Griffin, GA. Plots were inoculated with a local field culture of stripe rust. The races of stripe rust used for inoculation were collected in Georgia, identified and designated as PST 101 and 102 (Dr. X.M. Chen, Pullman, WA). Stripe rust infection type and percent severity data were assessed multiple times at each location. The results indicated that numerous cultivars and lines possess the resistant gene *Yr17* in soft red winter wheat. Other sources of seedling resistance were also identified in PIO26R61, Kinsco, and VA 270. A total of 102 lines from the field nursery were identified as having a level of resistance better than that of 'Pioneer 26R61'.

The first large scale replicated screening of 591 breeding lines for stripe rust was undertaken early in 2007, using growth chambers. Eighty-nine lines were detected with some resistance. Again, the majority of the lines had the resistant gene *Yr17*. From field evaluations and a large seedling screening, a number of lines with adult plant resistance were identified such as GA 951395-3A31, GA 96693-4E16 and PIO26R46. Additional evaluations are proposed to identify other sources of adult plant resistance.

P124

QTLs for resistance to spot blotch of wheat caused by *Bipolaris sorokiniana*

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An intervarietal mapping population in the form of recombinant inbred lines (RILs) developed from a cross between 'Yangmai 6' (Resistant) and 'Sonalika' (Susceptible) was used for identification of QTLs for resistance to spot blotch, an important disease of wheat in the warm humid regions of South Asia. The 139 single seed descent (SSD) derived F₈ lines of 'Yangmai 6' × 'Sonalika' were evaluated for resistance to spot blotch for three years in three replications each year. Joint and/or single year analysis by composite interval mapping (CIM) and LR (likelihood ratio) >10, identified five quantitative trait loci (QTL) on the chromosome 2AL, 2BS, 5BL, 6AL and 6DL associated with spot blotch resistance. These QTLs were designated *Q**Sb**.bhu-2A*, *Q**Sb**.bhu-2B*, *Q**Sb**.bhu-5B*, *Q**Sb**.bhu-6A* and *Q**Sb**.bhu-6D* and explained 77.67% of phenotypic variation in a simultaneous fit. Two QTLs with major effects were consistent over all years. All QTL alleles for resistance were derived from the resistant parent 'Yangmai 6'. QTLs for spot blotch resistance offer the possibility of simultaneous marker-assisted selection for major and minor genes.

P125

Transfer of a new leaf rust resistance genes from diploid *T. monococcum* and *T. boeoticum* to *T. aestivum*

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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 leaf rust. *T. monococcum* acc. pau14078 and *T. boeoticum* acc. pau 5088 are immune to all the leaf rust races at adult plant stage and so is the RIL population generated from the cross these two accessions. At seedling stage these lines were resistant to leaf rust races 77-2, 77-5, and 104-2 but population segregated for resistance against race 104-2. *T. monococcum* and two RILs designated as RIL130 and RIL101 were crossed to susceptible *T. durum* parent, N59. Rust resistance was suppressed in the F₁. Further crossing and backcrossing with hexaploid wheat cultivars WL 711 and PBW 343 led to identification of resistant progenies. One BC₂F₂ population of the cross N59/RIL130//3*PBW343

when tested at seedling stage showed single gene segregation (489R: 142S $\chi^2 = 2.0$). Similarly another BC₂F₂ population of the cross N59/*T. monococcum*//3*WL711 also showed single gene segregation (153R:66S, $\chi^2=3.0$) at seedling stage. Both the populations are cytologically stable with 42 chromosomes indicating a stable leaf rust resistance gene transfer from *T. monococcum* to hexaploid wheat. Bulk segregant analysis of the BC₂F₂ population of the cross N59/*T. monococcum*//3*WL711 with 38 polymorphic SSRs indicated that the seedling resistance gene of *T. monococcum* is located on chromosome 5A. As none of the designated *Lr* genes map on 5A, the gene in question may be a novel one.

P126

Infection of wheat tissues by *Fusarium pseudograminearum*

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Crown rot of wheat is a significant cause of yield losses in many wheat producing countries. In Australia crown rot is predominantly caused by the fungus *Fusarium pseudograminearum* (teleomorph *Gibberella coronicola*). Partial resistance has been identified in a small number of wheat lines, such as 2-49 and Sunco, but the mechanisms of resistance shown by these lines have not been identified. This study aims to identify key growth periods of *F. pseudograminearum* during crown rot development in wheat and compare these periods across partially resistant and susceptible lines in order to determine how the disease progresses and when resistance mechanisms are induced. Extensive field trial comparisons between susceptible and partially resistant host genotypes indicate a much slower spread of the fungus in the younger tissues of resistant individuals. These experiments are based on both visible symptom development and re-isolation of the pathogen from tissues at a distance from the infection site. On the basis of these experiments we hypothesise that *F. pseudograminearum* can proliferate significantly in the host tissue before any disease symptoms are apparent. In experiments currently underway, the increase in fungal load in each inoculated host genotype is being measured using a real time multiplex polymerase chain reaction (PCR) assay, allowing simultaneous detection of both pathogen and host DNA. Fungal DNA levels are being monitored across a range of time points from initial infection up until production of gross disease symptoms and at increasing distances from the infection site. Since current disease rating systems for seedlings and plants in the field rely heavily on browning of leaf sheaths and tiller bases, these investigations will illuminate more clearly the relationship between the extent of fungal infection and the expression of disease symptoms in susceptible cultivars and at the same time give indications of the time-course of resistance expression in partially resistant wheat lines.

P127

Validation of *Fusarium* head blight markers in *Triticum aestivum* breeding populations

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With quantitative disease resistance it is difficult to know which loci of a resistant source are passed onto progeny that are subsequently used as parents in further crossing. Without this knowledge, the

application of markers to non-contributing loci will be wasted. The objective of this study is to assess the Sumai3 loci contributing Fusarium head blight (FHB) resistance in breeding populations which have Sumai3 derived parents. Doubled haploid populations of Infinity/ND3085, Infinity/ND744, and Alsen/Helios crosses were evaluated in FHB nurseries at Carman MB, Ottawa ON and Charlottetown PE in 2007 using a two replicate randomized complete block design of 80 lines per population plus parental checks. Percent incidence and severity of head blight, Fusarium-damaged kernels and DON accumulation were evaluated. DNA markers reported as associated with Sumai3 FHB resistance at different loci were assessed on the parents and lines of each population. Statistical analyses were applied to marker and disease results to determine which loci contributed resistance. Resistance was expressed inconsistently across environments and across parents for particular loci. The results demonstrate the need to validate FHB source resistance loci (Sumai3) to determine which have been passed onto progeny that are subsequently being used as parents (eg. Alsen) for efficient application of marker assisted selection.

P128

Different sets of wheat genes are used in *Dn7*-mediated resistance to feeding by two biotypes of Russian wheat aphid

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Diuraphis noxia (Kurdjumov) (Russian wheat aphid) is an economically significant pest in wheat-growing areas, particularly in the U.S. and South Africa. The interaction between wheat and the Russian wheat aphid is poorly understood. When new biotypes appeared in the U.S. between 2003 and 2006, it became evident that specific interactions exist between resistance loci and aphid biotypes. *Dn7* provides a high level of resistance to eight currently existing biotypes. This study was conducted to determine if the same mechanisms are employed in *Dn7*-mediated resistance to two different biotypes (RWA1 and RWA2). Using wheat Gene chip® arrays, we compared the transcript profiles of near-isogenic lines (Gamtoos-R and Gamtoos-S) that were infested with either RWA1 or RWA2. Non-infested Gamtoos-R and Gamtoos-S were used as controls. The number of differentially expressed genes was higher in both resistant and susceptible plants fed upon by RWA1 compared to those fed upon by RWA2. Common sets of genes in response to both biotypes were involved in basic functions such as carbohydrate metabolism and energy generation. Common genes also included cell wall synthesis enzyme genes, and defense-response or stress-related genes. Many genes that were unique to RWA1 or RWA2 response were transcription factors. The results suggest that while common pathways are involved in *Dn7*-mediated resistance to RWA1 or RWA2 attack, divergent pathways appear to be involved as well. This may be explained by interaction of the same *R* gene product (or intermediate) with different eliciting factors from different biotypes. Silencing of candidate genes identified from microarray experiments using virus-induced gene silencing enabled us to identify genes that play important roles in wheat's defense response to the Russian wheat aphid.

P129

Paper withdrawn

P130

Molecular characterization of a *Triticum timopheevii* introgression in a Wentworth/Lang population

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Coping with wheat in a changing environment – biotic stresses: Poster abstracts

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A significant number of breeding lines and wheat varieties in the North East of Australia are derivatives of the variety Cook and contain a *Triticum timopheevii* introgression on chromosome 2B that conveys the stem rust resistance gene *Sr36*. Interest in deployment of *Sr36* diminished in 1984 when the resistance gene was overcome and Cook became susceptible to stem rust. Studies since then have shown that the *timopheevii* introgression contains a number of desirable loci conditioning resistance to black point, crown rot and powdery mildew as well as quality characteristics such as increased milling yield and increased grain protein. Interest in deployment of *Sr36* has been rekindled as it has been found very effective in combinations with other stem rust resistance genes and provides strong resistance to Ug99 stem rust. Unfortunately this segment also appears to be linked to a slightly lowered grain yield. Although the introgression, estimated to be approximately 40 cM in length, is believed to be inherited as one block, there have been reports of cultivars in which some of these loci have been lost. The aim of this project was to use molecular markers to identify potential breakpoints in the introgression in lines of a Wentworth/Lang population (> 900 BC₁F₂ lines). Results to date have suggested that about 40 lines have shorter segments of the introgression. The next generation of these lines is being tested to verify these results. Identifying lines that contain disease resistance and improved quality without the accompanying yield penalty will be of great value to both Australian wheat breeding programmes and global efforts to combat Ug99 stem rust.

P131

Breeding wheats with enhanced crown rot resistance

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Crown rot (CR), caused by species of *Fusarium*, is the most significant biotic constraint to wheat production in Australia. Since the same *Fusarium* pathogens also cause Fusarium head blight (FHB), our initial approach was to seek sources of CR resistance amongst genotypes with known FHB resistance. This work did not show any correlation between CR and FHB resistance. Subsequently we embarked on a screening of more than 2,200 genotypes of wheats and their close relatives using a high throughput CR bioassay. This showed that genotypes with high levels of CR resistance are available in hexaploids. None of the several hundred tetraploid and diploid genotypes assessed showed high level of CR resistance. Current research is aimed at identifying loci conferring CR resistance from two of the best sources by QTL mapping. Single-seed-descendent populations between resistant sources and elite local varieties are being generated to validate QTL effects and to transfer this resistance into locally adapted varieties. As durum (*T. durum* L.) genotypes are more susceptible than hexaploid wheat (*Triticum aestivum* L.), an additional aim is to transfer CR resistance from hexaploids into durum genotypes via a backcrossing program. Latest results from these projects will be presented.

P132

Identification of chromosomes responsible for crown rot resistance in durum wheat

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Crown rot (CR), caused by *Fusarium* species, is the most serious biotic threat to the Australian wheat industry. Compared with bread or common wheat ($2n=6x=42$), durum wheat ($2n=4x=28$) is more susceptible to this disease. As part of our effort to address the wheat CR problem, we analysed three sets of Langdon-*Triticum dicoccoides* (LDN-DIC) disomic chromosome substitution lines. This analysis found highly significant difference among these lines in their reaction to CR infection. CR reaction is clearly quantitatively inherited as several of the substitution lines in each of the three sets showed altered responses to CR infection, some with improved while others with reduced resistance. Substituting any of the Langdon chromosomes by the three different donors failed to consistently improve CR resistance. The response of a particular line for a given Langdon chromosome varies, depending on the different donor genotypes. This suggests that the three donor genotypes have different genes conferring CR resistance, and that genes conferring super-susceptibility may not exist in durum wheat. Further, the most CR resistant lines are not those with the best resistance to *Fusarium* head blight, confirming that, although can be caused by the same pathogens, these two diseases are controlled by different genes.

P133

Wyalkatchem reselections differentiate the adult plant resistance gene *Yr29* in an Australian wheat background

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The commercial variety Wyalkatchem (Machete/Gu:J2.11S135) is mixed for response to stripe rust. The majority of individuals express partial resistance and reach terminal rust severities of 30-70 percent (moderately susceptible). Preliminary mapping of stripe rust resistance in Wyalkatchem identified the main QTL was linked to Xwmc44 on chromosome 1BL, most likely *Yr29* (M. Hayden pers. comm.). A small percentage of Wyalkatchem individuals lack partial resistance and reach terminal severity of 100 percent (susceptible). Among 60 single plants re-selected at random and evaluated for adult plant resistance to stripe rust in the field, 2 were highly susceptible and were presumed to lack *Yr29*. These two lines, together with another 4 single plant selections and a sample of unselected Wyalkatchem, all expressing normal Wyalkatchem phenotype, were tested with a novel single nucleotide polymorphism CAPS marker. The marker is located at the 1BL locus co-segregating with *Lr46/Yr29/Pm39*. The marker assay clearly distinguished Wyalkatchem re-selections that differed in the stripe rust APR response. These single plant reselected Wyalkatchem individuals provide potential 'near-isogenic' genetic stocks with and without *Yr29*.

P134

The genetics of crown rot resistance in durum wheat (*Triticum durum* L.)

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Crown rot (CR) is the number one biotic constraint threatening the durum wheat (*Triticum durum* L., $2n=4x=28$, AABB) industry in Australia. Existing commercial durum wheat varieties are all highly susceptible to this disease. To identify resistant sources useful for breeding durum wheat varieties with enhanced resistance to CR, we have carried out a large scale screening. The materials tested include some 400 durum wheat and other tetraploid genotypes but none of them showed high enough resistance. Genotypes that showed high levels of CR resistance are all hexaploid ($2n=6x=42$, AABBDD). As genes conferring CR resistance in hexaploid wheat have been found on all of the three wheat genomes A, B and D, we are investigating how these resistance genes from the hexaploid wheat would perform once they are transferred into durum backgrounds. Several backcross populations between CR susceptible durum wheat genotypes and resistant hexaploid wheat genotypes have been generated and are being genetically characterised. We are also investigating whether there are genes in durum wheat conferring CR susceptibility. If chromosome segments harbouring such susceptible genes can be identified, it may be possible to improve CR resistance of durum genotypes by replacing these segments with segments from more resistant genotypes.

P135

Mapping genetic factors for resistance to *Soil-borne cereal mosaic virus* (SBCMV) in durum wheat

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Soil-borne cereal mosaic virus (SBCMV) is a Furovirus transmitted by *Polymyxa graminis* Led. causing an important wheat disease widespread in the main wheat growing areas of the world including Italy. Most of the durum wheat cultivars grown in Italy are susceptible to SBCMV but valuable sources of resistance have been identified in the cultivated durum germplasm (Ratti et al., 2006). To date, however, no specific genetic analyses have been carried out in durum wheat. A recombinant inbred population of 184 lines (RILs) obtained from the cross between the medium-resistant cv. Meridiano and the susceptible cv. Claudio plus a germplasm collection of 164 cultivated durum accessions were characterized in a field experiment carried out in 2007 near Bologna, Italy, under severe and uniform SBCMV infection. The same genotypes have been profiled with SSR and DArT markers. A wide range of disease reaction (as estimated by symptomatology and DAS-ELISA) was observed for both RILs (transgressive segregation) and germplasm accessions. Preliminary results from the mapping population indicate that at least four quantitative trait loci (QTLs) accounted for most of the phenotypic variation observed. A major QTL was associated to *Xwmc243* (distal telomeric region of chromosome arm 2BS), with the favourable allele contributed by Meridiano. The additional favourable QTLs, located in the distal regions of the short and long arms of chromosome group 5 (particularly chr 5A), were contributed by both parents. The QTLs identified in the distal regions of 5AL (*Xwmc524*) and 5BL (*Xbarc243*) could represent the homoeologous copies of the major QTL identified in bread wheat (*Sbm1*). The results from the QTL analysis carried out on the complete genetic map of the mapping population will be presented, together with the results from the association mapping experiment at the relevant QTL regions.

P136

A major genetic factor for durable leaf rust resistance in durum wheat maps in the distal region of chromosome arm 7BL

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The genetic basis of leaf rust (*Puccinia triticina* Eriks.) resistance carried by the durum wheat cultivars Creso and its derivative Colosseo was studied using a recombinant inbred population of 176 lines (RILs) from the cross Colosseo x Lloyd, a set of 62 advanced lines from multiple crosses and a collection of 164 Mediterranean durum wheat accessions. The genetic materials were tested under field conditions and artificial rust inoculation. The RIL population was tested in 2006. The two accession panels were evaluated in 2006 and 2007. The percentage of infected leaf area was evaluated through the disease developmental cycle and the area under disease progress curve (AUDPC) was obtained for each field trial. A major QTL (*QLr.ubo-7B.2*) for leaf rust resistance was identified on the distal region of chr. 7BL with the favourable allele inherited from Colosseo. The QTL showed R^2 equal to 72.9% and LOD peak equal to 44.5 for AUDPC. The presence of this major QTL was validated by a linkage disequilibrium-based test using the two accession panels. The association results confirmed that the QTL is most probably located on the small support interval flanked by SSR markers *Xbarc340.2* and *Xgwm344.2*, with the corresponding AUDPC R^2 values ranging from ca. 10 to ca. 35% across the two panels and years. The SSR-based long-range haplotype homogeneous to cv. Creso is widespread in the cultivated durums adapted to the Mediterranean region and is particularly frequent among the elite accessions bred in Italy and at the ICARDA durum germplasm program.

QLr.ubo-7B.2 maps in a gene-dense region (7BL10-0.78-1.00) known to carry several genes/QTLs in wheat and barley for resistance to rusts and other major cereal fungal diseases.

P137

Molecular marker analysis of *Lr34* in Canada Western Red Spring Wheat cultivars

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The leaf rust resistance gene *Lr34* is an important component of the leaf rust resistance in Canadian wheat cultivars. It has provided effective resistance since it was incorporated into the cultivar Glenlea, registered in 1972. The Canada Western Red Spring (CWRS) wheat class is the predominant wheat class in Canada. The objective of this study was to analyze the molecular marker profiles of a historic collection of CWRS cultivars for microsatellite markers closely linked to *Lr34*. Cultivars released from 1900 to 2004 were included in the collection. These results were compared with genetic analyses of the leaf rust resistance in selected cultivars and with the leaf rust resistance in these cultivars. Laura, registered in 1986, was the first major CWRS cultivar to carry *Lr34*, but since that time it has been incorporated into many of the leading CWRS cultivars. The cultivars Katepwa, AC Barrie, and Superb which were the most popular cultivars in the 1980s, 1990s and 2000s, respectively, all had the susceptible allele at the *Lr34* locus. Even though these cultivars had other genes for leaf rust resistance, they were overcome by the *Puccinia triticina* population and they suffered significant losses due to leaf rust. If *Lr34* had been present in these cultivars the losses would have been minimized. Determining the presence of *Lr34* in CWRS cultivars will help ensure that this important resistance gene is incorporated into future CWRS cultivars.

P138

The inhibitor of *Pm8* in certain 1BL.1RS wheat genotypes

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Pm8 for resistance to powdery mildew is one of the disease response genes carried by the widely used 1BL.1RS chromosome with 1RS derived from Petkus rye. However, *Pm8* when challenged by avirulent *Blumeria graminis tritici* cultures is not expressed in all wheat genetic backgrounds. According to Ren et al. the dominant suppressor of *Pm8* is located in close proximity to the *Gli-A1/Glu-A3* loci on chromosome 1AS. These loci are closely linked with the *Pm3* locus. Different selections of Veery and Bobwhite vary in response to powdery mildew even though they have the 1BL.1RS translocation. F2-derived F5 populations developed from crosses between resistant and susceptible (suppressed) selections of each cultivar segregated for response to powdery mildew and resistance in some segregating lines was recessive (dominant inhibition). These populations were subjected to analysis with functional markers for *Gli-A3* and *Pm3*. We have shown that wheats lacking a *Pm3* powdery mildew response either possessed a functional transcribed allele (e.g. Chinese Spring which lacked a known *Pm3* resistance specificity), a terminated allele, or were null. Our analyses indicate that lines with functional alleles of *Pm3*, including the Chinese Spring allele, show suppression of *Pm8*, which we presume to be an orthologue of *Pm3*. We are developing transient assays to test our prediction that *Pm8* will not function when combined with functional *Pm3* alleles, and also combining the translocation in lines with *Pm3* alleles. We know of no wheat genotype with 1BL.1RS and a named *Pm3* resistance allele.

This work has important implications in understanding the commonly reported phenomenon of resistance gene suppression (or dilution) in wheat wide crosses, as well as the actual genetic basis of suppression. It also raises the issue of functions of different alleles transformed into a single wheat genotype.

P139

Genetic analysis of wheat *Pyrenophora tritici-repentis* interactions

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Tan spot of wheat, caused by the fungus *Pyrenophora tritici-repentis*, is a destructive disease worldwide that can lead to serious losses in quality and quantity of wheat grain production. The fungus induces two distinct symptoms; tan necrosis and extensive chlorosis, on susceptible wheat cultivars. Resistance to tan spot was identified in a wide range of genetically diverse genotypes, including three different species *Triticum aestivum*, *T. spelta*, and *T. turgidum*. The major objectives of this study were to determine the genetic control of resistance to tan spot caused by multiple races of *P. tritici-repentis* in the newly identified sources of resistance. Plants were inoculated at the two-leaf stage under controlled environmental conditions and disease assessment was based on lesion-type rating scale. The segregating generations of each cross were analyzed for the allelism and/or inheritance studies. A single recessive gene controlled resistance to tan necrosis caused by race 1 in both tetraploid and hexaploid resistant genotypes studied. The lack of segregation in the inter- and intra-specific crosses between the resistant tetraploid and hexaploid genotypes indicates that they possess the same genes for resistance to tan necrosis and extensive chlorosis induced by *P. tritici-repentis* race 1. Two independent genes, a single dominant gene for extensive chlorosis in hexaploid wheat and a single recessive gene for tan necrosis in tetraploid wheat, controlled resistance to tan spot induced by race 5. Genetic analysis of inter- and intra-specific crosses among *Triticum* species confirms that wheat-*P. tritici-repentis* host-pathosystem follows the toxin model of gene-for gene hypothesis.

P140

Genome distribution of QTL for Fusarium head blight resistance in European wheat germplasm

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The objective of the present study was to map QTL for combined Type I and Type II resistance against Fusarium head blight (FHB) in European winter wheat germplasm. Four populations of recombinant inbred lines derived from crosses between the more resistant *Rht-D1a* cultivars Apache, History, Romanus and Solitär and the susceptible *Rht-D1b* semi-dwarfs Biscay, Rubens, Pirat and Travix were evaluated in spray-inoculated field trials at five locations over two seasons. Genetic maps covered between 1544 cM and 2187 cM of the wheat genome. All wheat chromosomes were represented by linkage groups. The numbers of markers placed on each map were 293 for Apache/Biscay, 394 for History/Rubens, 287 for Romanus/Pirat, and 242 for Solitär/Travix. Analysing the data with MultiQTL programme, we detected 13, 8, 14 and 18 QTL for FHB severity in Apache/Biscay, History/Rubens, Romanus/Pirat, and Solitär/Travix, respectively. The major QTL with the highest relative substitution effect in each population, reducing FHB severity between 16.3 and 31.5%, was on chromosome 4DS close to *Rht-D1* locus. Even for minor QTL, similar genome

regions were identified in the mapping populations. Alignment with maps from other studies in winter wheat revealed significant overlaps of QTL regions on chromosomes 1AS, 1RS, 1BL, 3Bc, 4DS, 5AL, 6Ac and 7BS. FHB resistance in European germplasm seems to be mediated by the absence of the semi-dwarfing allele and several minor QTL which are not suitable for marker-assisted breeding using current genotyping technologies.

P141

Response of bread and durum wheat and triticale to sunn pest, *Eurygaster integriceps* put.

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Sunn pest (*E.integriceps* put.) is the most important pests of wheat in cereal-producing regions of Iran as well as other countries in Central and West Asia and North Africa (CWANA). The use of resistant cultivars is an effective strategy in Integrated Pest Management (IPM). This research was conducted to identify the genetic response of 20 bread and durum wheat and triticale to Sunn pest. Genotypes including eight bread wheat lines/cultivars, four durum lines, three triticale lines and five synthetic wheat lines were evaluated for resistance to sunn pest under artificial infestation in field condition using RCBD with three replications during two crop session years. Spike injury and grain damage caused by over winter adult insect and their nymph, respectively were measured. Some morpho-physiological traits and quality indices of wheat were recorded. Analysis of variance of spike injury revealed significant differences among genotypes. Cultivars Shiraz and Falat with 13% and 1.8% spike damage were resistant and susceptible genotypes, respectively. Genotypes 12 (durum wheat), 13 (triticale), 14 (triticale), 15 (triticale), 16 (synthetic wheat), 19 (synthetic wheat) and 20 (synthetic wheat) didn't have significant difference with Falat, so they were selected as resistant to adult insects. From this result, was inferred that the most resistant genotypes contain gene(s) from rye (Falat and triticale genotypes) or *Aegilops* (synthetic wheats). Yield losses of Adult insect is refer to reduction of ear per area and grain number in ear, Because pest attack reduced Biomass but has not affect on kernel weight. Based on grain injury caused by nymphs of sunn pest was not significant difference among genotypes. In this study was not observed any correlation between grain injury and morpho-physiological traits studied, Whereas Nymph's feeding from grain led to significantly reduction in Protein%, Zeleny sedimentation volume, Bread volume, Water absorption, Gluten index and Gluten elasticity of genotypes.

P142

Genetic analysis of seedling stripe rust resistance in the Australian wheat cultivar 'Batavia'

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Stripe (yellow) rust caused by *Puccinia striiformis* West. f. sp. *tritici* (*Pst*) poses a major constraint to wheat production in Australia that has been effectively controlled by deploying resistant cultivars. Batavia is an Australian wheat cultivar conferring high levels of seedling and adult-plant resistance to *Pst* pathotypes (pts) in Australia. The aim of this study was to gain an understanding of the genetic basis of seedling resistance in Batavia. Parental cultivars and F1 hybrids of cross Batavia x Avocet S were assessed for seedling resistance against two selected *Pst* races (110 E143 A⁺ and 134 E16 A⁺). Parental cultivars produced seedling infection types of; 1^{=CN} and 3⁺, respectively. F1 plants showed seedling IT of 2⁺³-C. F2 seedling plants were scored on an individual basis and plants were classified into one of four seedling IT groups viz. Resistant type 1 (IT ;1^{=CN}), Resistant type 2 (IT 12^{-C}), Resistant type 3 (2⁺³-C) and homozygous susceptible (IT 3⁺). A genetic model for segregation at two

loci was applied to the F2 data that accounted for the partial dominance of the resistance showed by F1 hybrids. The frequencies of seedling infection types were a good fit to the expected segregation ratio for two genes. The chi-squared value for phenotype response classes showed a good fit to a digenic segregation model. Single gene families segregating for low ITs 12^C and 23^C were identified among the segregating F3 lines. Chi-square analyses of individual F3 lines for each gene displayed a good fit for single gene segregation. The data provide support for the hypothesis that the seedling resistance in Batavia is conferred by two genes. The putative single gene lines obtained from the present study would be valuable stocks for use in marker analysis to determine chromosome location, to test effectiveness of *YrBat1* and *YrBat2* as widely as possible to determine any potential vulnerability to pathogen populations and to combine with APR genes for durable resistance to wheat stripe rust.

P143

Phenotypic and molecular genetic analysis of partially resistant bread wheat cultivars against root lesion nematode (*Pratylenchus thornei*)

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Pratylenchus thornei is globally recognized as an economically damaging biotic constraint in rainfed wheat production systems worldwide. One of the most effective control methods is the use of host resistance, however this requires an understanding of the genetic control of resistance. Using both phenotypic screening and molecular characterisation of a F2 half diallel of three partially resistant sources (Australia GS50A, Iraqi land race AUS4930, and CIMMYT synthetic derivative CROC_1/AE.SQUARROSA (224)//OPATA) (CROC), and two susceptible wheat varieties, Pastor and Janz., *P. thornei* resistance was shown to be polygenic and additive in gene action. AUS4930 was identified as the best general combiner with both susceptible parents, followed by CROC. GS50a has a known resistance region on chromosome 6D. Molecular characterization of the two other resistance sources was explored using wheat microsatellite markers linked to previously identified QTL for resistance to *P. thornei* and *P. neglectus*. Using a BSA approach, resistance loci were identified in the AUS4930 x Pastor population on chromosomes 1B, 2B and like GS50a on 6D, and on chromosomes 1B and 3B in the CROC x Pastor population. These data suggest that there are common resistance loci on chromosomes 1B and 6D, and source-specific resistance loci, such as on chromosomes 2B and 3B. These latter loci offer opportunities for gene pyramiding. Further work is required to determine if the QTLs identified on these chromosomes are the same, or allelic, or linked but different resistance loci to those previously identified, and to determine if these two sources contain other novel resistance loci.

P144

A database of RNA profiles comparing susceptible and resistant wheat infected with *Fusarium graminearum*

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Diseases caused by the fungus *Fusarium graminearum* constitute one of the major problems in cereal crops grown in temperate climates worldwide. Conventional breeding approaches have so far produced limited success in improving the resistance of crops, including wheat, to *F. graminearum*. A genomics approach is being applied to gain a better understanding of the wheat response to this fungus in susceptible and resistant varieties. Microarray hybridization experiments have been conducted using the wheat Affymetrix genome array, comparing mock-inoculated and *Fusarium*-inoculated spikelets from samples collected at 1, 2 and 4 days after inoculation. All profiles are being compiled into a database using the softwares Acuity and Access.

So far, we have obtained the RNA profiles of four groups of wheat plants: 1) the spring wheat varieties Roblin (very susceptible), Wuhan 1 and Nuy Bay (both resistant, from Chinese and Japanese sources of resistance respectively); 2) the spring wheat Chinese Spring (susceptible) and the addition lines 7E and 7ES (both resistant, containing the chromosome 7 from *Thinopyrum elongatum* into Chinese Spring background); 3) the winter wheat Augusta (susceptible) and FHB148 (resistant, derived from Frontana, a Brazilian source of resistance); 4) near isogenic lines, derived from the cross Wuhan 1 x Nuy Bay, that segregate for the QTLs 2D, 3BS and 5A which are associated with *Fusarium* resistance. Preliminary findings of a meta-analysis of the data in the database will be presented.

P145

Development of Fusarium Head Blight (FHB) resistant winter wheat cultivar in crosses with a Brazilian spring wheat, Frontana, as the resistance donor parent

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Fusarium Head Blight (FHB) has become a national problem which continues to cause economic and product quality/safety damage to the Canadian wheat crop. Developing FHB resistant winter wheat cultivar(s) is essential to Canada for a sustained wheat production. All wheat producing regions of Canada are affected by Fusarium. Food/feed safety and sustainability of the overall wheat agri-economy in Canada (and other major wheat producing regions in USA, Asia, Europe and Australia) have been affected and/or impaired by the mycotoxin residues on grains and grain products after Fusarium Head Blight (FHB) infection, caused by *Fusarium graminearum*. Agriculture and Agri-Food Canada (AAFC) successfully developed genetic stocks (FHB 143, FHB 147, FHB 148 and FHB 161) from the crosses between Frontana (Brazilian resistance donor to FHB) and standard commercial cultivars, namely Harus, Augusta and Frederick winter wheat cultivars. Backcrosses to the respective F1's and subsequent selections were conducted to restore plant types and winter wheat growth habits. Utilizing these resistant genetic stocks in crosses with the commercial cultivars, namely Augusta, Casey, Diana and Augusta several thousand Doubled haploids were generated via wheat-maize pollination and embryo rescue techniques. All DH lines were screened for their resistance to FHB in the Fusarium epiphytotic nursery. Selected DH's were evaluated for agronomic, disease and quality parameters. We have made progress at AAFC-ECORC, in cooperation with Hyland Seeds of W.G. Thompson Limited; and developed and released the first Soft Red Winter Wheat in (2001-02), **FT Wonder-** the first

resistant/tolerant to FHB in North America that has lowest DON and visual symptoms. The commercial production has already begun. Subsequently in 2005, AAFC-ECORC has registered the two first FHB resistant/tolerant soft white winter wheat cultivars, **FT-Action** and **Ashley** in Canada (and anywhere in the world) in cooperation with Hyland Seed. The data for the performance of the three cultivars are presented and discussed.

P146

The genetic characterisation of adult plant resistance (APR) to yellow rust in the winter wheat cultivar Claire

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The winter wheat cultivar Claire was released commercially by Nickerson Seeds UK Ltd in 1999. At the time it was given a NIAB rating of 9 for resistance to yellow rust (causal agent *Puccinia striiformis* f. sp. *tritici*). Preliminary analysis shows yellow rust resistance in Claire to be polygenic. A double haploid (DH) population has been constructed between Claire and Lemhi. Lemhi is a American spring wheat which is susceptible to all UK *P. striiformis* f. sp. *tritici* isolates. The construction of a genetic linkage map using SSR, NBS-AFLP, DaRT and AFLP markers has allowed the estimation of the number, chromosomal position and degree of effect of yellow rust resistance QTLs within the DH population. A total of 436 markers have been mapped to date creating a map of 1350cM. Preliminary analysis of the Claire x Lemhi linkage map with phenotypic data collected over 2 years of field tests have identified a number of QTLs associated with APR. QTL loci have been identified on chromosomes 2A, 2B, 2D and 5BL/7BL. To improve the genetic map and facilitate the identification of the genetic effect ESTs in the terminal deletion bin of 2D have been targeted for SNP-marker development and added to the Claire x Lemhi genetic map.

P147

Association mapping of Ug99 resistance in a diverse durum wheat population

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Association mapping (AM) is expected to be a complementary strategy for describing associations between genotype and phenotype in crop plants. Genome-wide AM was performed for UG99 resistance to identify and further dissect genomic regions associated with the resistant. Ninety-three genetically diverse durum cultivars were scored with 245 microsatellite markers and assessed for UG99 resistance at an endemic nursery in Kenya (2007) and in greenhouse studies (2008). Nearly half of the durum wheat accessions evaluated were scored as moderate to highly resistant. The remaining lines were intermediate (n=25), moderately susceptible (n=21) or susceptible (n=10). Marker associations for UG99 were identified on several chromosomes, suggesting multiple resistance genes exist in durum. On chromosome 7A, *Xgwm276* was associated with response to UG99. *Xgwm276* is linked to *Sr22*, which is known to be effective against UG99. Marker associations were also identified on the distal end of 5A; and *Xwmc537* and *Cdul* on 5B were also significant. Although the association on 5B is in a region where *Sr* genes have yet to be identified, this region has been associated with stem rust resistance in hexaploid wheat. An association with LOX gene *Lpx-B1.1* was detected and further validation is a priority as elevated LOX activity may confer resistance, but would result in excessive colour loss in pasta products. Field screening will be repeated in 2008, and those

genomic regions consistently identified as being associated with Ug99 resistance will be the target of detailed validation experiments for use in marker assisted selection.

P148

Perspective on wheat rusts in India

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Indian National Wheat Rust Survey programme has conducted national pathotype surveys for the three rust pathogens since 1930. This facility has served the national wheat programme through a range of activities like identification of new sources of rust resistance, working out the genetic basis of rust resistance and enhancement of genetic resistance. The scope of operation was further expanded in 1980 to include near- isogenic lines, present day cultivars and other commonly used resistance genes/ cultivars in India. It has strengthened the national wheat-breeding programme regularly by providing diverse sources of resistance for introgression. Consequently, susceptible lines were not promoted for release. Special programme was launched upon resurgence of Ug99 in Kenya in 2001. Directorate of Wheat Research identified this threat and through the auspices of ICAR took immediate action by sending 200 lines to Kenya for screening. This timely action helped identification of resistant sources which followed generation of pre- breeding stocks carrying resistance / novel genes (FLW2, FLW6 and FLW8). These sources of resistance were later distributed to wheat workers for their use. This way the steps to address the threat were initiated much before the virulent population threatened the crop. However, present challenges remain as susceptible cultivars like PBW343 occupying 7 million hectares and other mega cultivars like HUW234, HD2189, WH147 and C306 needs to be replaced with resistant cultivars. Thus, this programme has paved the way for a sound and focussed wheat-breeding programme of the country.

P149

Stem rust resistance in South African wheat cultivars

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The appearance and anticipated spread of race TTKS (syn. Ug99) of *Puccinia graminis* f. sp. *tritici* have renewed interest in breeding for durable resistance to stem rust of wheat. Although pathotype surveys have been carried out since 1980, stem rust research has not been a priority in South Africa recently. In an attempt to determine the current status of stem rust resistance, 67 South African (SA) bread wheat cultivars and lines were tested with USA and East African races of *P. graminis* f. sp. *tritici*. Entries were also screened with DNA markers associated with *Sr24* (Sr24#50) and *Sr31* (iag95). *Sr2* DNA marker (STM559N) data were compared with seedling chlorosis (SC) and pseudo-black chaff (PBC) scores to validate the use of the STM559N in SA genotypes. Most cultivars interacted differentially with the races tested. DNA marker analysis confirmed the presence of *Sr31* in seven entries. According to phenotype, *Sr24* was postulated in several entries, but confirmed in less when combined with the marker data. STM559N reliably amplified the correct alleles in most local and control lines. However, in several instances *Sr2*-associated alleles were amplified in presumably non-*Sr2* carrying cultivars. Several genotypes lacking *Sr2* were identified for marker-assisted introgression of this gene. This study emphasized that diversification of resistance sources, and more directed

breeding for stem rust resistance, are needed as few SA wheat entries appear to have a broad-based resistance to stem rust.

P150

Genetic analysis of wheat rust resistance genes segregating in a Kariiega x Avocet S population

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Complete adult plant resistance (APR) to stripe rust of the wheat cultivar Kariiega was previously ascribed to two major quantitative trait loci (QTL) on chromosomes 2B and 7D and three minor QTL. In the present study the Kariiega x Avocet S doubled haploid population was increased from 150 to 254 individuals and the map improved by adding Diversity Array Technology (DArT) markers. Additional field (three scoring dates) and greenhouse phenotypic data for stripe rust were collected. Apart from the major QTL regions detected before, minor QTL were consistently identified. As the disease progressed in the field, the chromosome 2B QTL region increasingly explained more of the phenotypic variance (34.2%, 35.3%, 41%) for host reaction type scores (RT), compared to the 7D QTL region (24%, 33%, 23.7%). For the field leaf area infected score (LAI) both the major QTL regions explained more variance over time. A previously minor QTL on chromosome 4A of Kariiega was consistently detected for LAI (up to 28.9%) and the two early RT (up to 13.8%) scores. QTL analysis also indicated that the 2B QTL region may consist of more than one QTL. In addition we used an accelerated greenhouse scoring method for APR to stripe rust, which detected both major QTL, the 4A QTL and another minor QTL. The greenhouse data was a significant improvement over a previous attempt in a growth chamber which only allowed the detection of some of the field QTL. Using an adult plant screening method and different pathotypes of *Puccinia triticina*, several leaf rust resistance genes have been detected in the mapping population. This study has been valuable in confirming and expanding information on the leaf rust resistance genes and QTL for adult plant resistance to stripe rust in wheat.

P151

Resistance to stem rust race TTKS in wheat relative *Haynaldia villosa*

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Stem rust race TTKS and its derivatives have defeated several important stem rust resistance genes used in wheat, rendering much of the worldwide wheat acreage susceptible. Rapid genetic responses including gene discovery, germplasm development and accelerated breeding efforts are essential components of a global effort to safeguard wheat production. In order to identify additional sources of TTKS resistance, we screened the Wheat Genetic and Genomic Resources Center collection (95 accessions) of *Haynaldia villosa* with North American races of stem rust. All accessions were found to be nearly immune and likely contain novel genes for stem rust resistance. Selected accessions were screened with TTKS and maintained high levels of resistance. Screening of a set of *H. villosa* disomic addition stocks in cultivar Chinese Spring revealed that chromosome 6V harbours one or more stem rust resistance genes, temporarily designated as *SrHv6*. *SrHv6* conferred resistance to all North

American races tested and TTKS. Development of compensating translocation stocks for *SrHv6* and further genetic manipulations to derive useful germplasm are underway.

P152

The occurrence of *Sr31* and *Sr36* stem rust resistance genes in wheat cultivars registered in Hungary in the past 25 years

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Stem rust along with foliar diseases is a harmful pathogen causing strong yield reduction worldwide but resistant cultivars provide efficient way for wheat growers to avoid yield losses. In our study, using molecular markers, 200 wheat cultivars registered in Hungary in the past 25 years were investigated. A significant part of the cultivars carried the 1BL.1RS translocation, the source of *Sr31*, *Lr26*, *Yr9*, *Pm8* genes or the *Triticum timopheevi* introgression with *Sr36* gene. During this period, *Sr36* proved to be the strongest and durable stem rust resistance gene in Hungary. Resistance provided by the *Sr31* was also effective, although in less extent than *Sr36*. Rest of the resistance genes of 1BL.1RS demonstrated less (*Pm8*) or no appropriate (*Lr26* and *Yr9*) level of resistance. It turned out that the introgression of alien chromosome translocations did not increase the variation of stem rust resistance genes in wheat cultivars registered in Hungary, as the use of efficient resistance genes became very bias. Among the two main wheat breeding programs in Hungary, the frequency of *Sr31* resistance gene in cultivars of Martonvasar-institute had reached 90% (use of *Sr36* was marginal). Adversely, in the Szeged-cultivars, *Sr36* reached the frequency of 50%, while *Sr31* was only exception there. The narrowed genetic diversity may increase genetic vulnerability. It might open the door to new races of pathogens, i.e. TTKS (Ug99) for *Sr31*. According to our results, there is an urgent need to incorporate several resistance genes against main diseases into the new wheat cultivars. To accelerate it, marker assisted selection provides new and efficient possibility in wheat breeding programs.

P153

QTL identification in a slow-rusting population reveals complex inheritance patterns of resistance

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Slow-rusting or adult plant resistances are expressed quantitatively and are typically small in genetic effect, thereby requiring multiple genes to provide adequate protection against rust pathogens. These effects are valuable and are generally considered to confer durable resistance. Therefore an understanding of the chromosomal locations of such genes and their biological effects are important in order to ensure they are suitably deployed in elite germplasm. The objective of this research was to identify chromosomal regions that contribute to slow-rusting resistance in an F5 RIL population derived from Attila (PBW343) and Avocet-S. The population was scored for final disease severity in the field in Mexico for leaf rust at Ciudad Obregon, and for stripe rust at Toluca. Partial linkage mapping was used to identify important chromosomal regions that contributed to resistance. Genotypic variation for both rusts was large and repeatable with line-mean heritabilities of 94% for leaf rust resistance and 87% for stripe rust. Three loci, including *Lr46/Yr29* on chromosome 1BL,

were shown to provide resistance to leaf rust whereas six loci with small effects conferred stripe rust resistance, with a seventh locus having an effect only by epistasis. There were significant genotype × environment interactions for stripe rust and this was mainly caused by the incursion of an endemic, *Yr27* avirulent pathotype establishing early infection in 2002. A new slow-rusting QTL was identified on 2BL and this also appeared to have race-specificity.

P154

Genetic map of wheat chromosome 3BS including SV2, an adult plant leaf rust resistance gene

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Leaf rust, incited by the biotrophic fungus *Puccinia triticina*, is one of the most important diseases of wheat worldwide, causing in Argentina annual yield losses of about 5-10%. Some old South American varieties as Sinvalocho MA, Buck Manantial and Pergamino Gaboto show durable resistance and were used as sources of resistance in breeding programs worldwide. Durable leaf rust resistance in Sinvalocho MA would be explained by the combination of adult resistance genes and specific genes expressed at seedling stage. Two genes, SV1 and SV2, expressed at flag leaf stage, were identified previously. The SV2 adult resistance gene was mapped on chromosome 3BS where no adult resistance gene was previously reported. A linkage map of 3BS using an F9 population of 91 recombinant inbred lines (RILs), from the cross Sinvalocho MA and Gamma 6 was constructed. Twenty eight AFLPs markers and 8 SSRs were allocated in an interval of 200cM. In order to develop a fine map of this region, an F2 population of 1200 individuals is being used. At present, microsatellite Xgwm533 maps at 3.4 cM of SV2. Fine mapping is a prerequisite for positional cloning provided that the genetic map is representative of physical distances. The use of resistance genes, particularly from varieties that show durable resistance, may be an outstanding contribution for controlling this disease.

P155

Inheritance and genetic mapping of leaf rust resistance genes in the wheat cultivar Buck Manantial

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The durable resistance to wheat leaf rust caused by *Puccinia triticina* is one of the main objectives in current breeding programmes. The Argentinian wheat cultivar Buck Manantial has durable resistance and has been used as a source of resistance to wheat leaf rust in North America and Eastern Europe. Dyck (1989) determined by genetic analysis the presence of the genes *Lr3*, *13*, *16*, *17* and one unidentified adult plant gene. Our objectives were to determine the number and characterization of resistance genes to wheat leaf rust present in Buck Manantial and also identify molecular markers that can be used in marker assisted selection for these resistance genes. An F8 population of 118 recombinant inbred lines coming from a cross between Buck Manantial and the susceptible genotype Purplestraw was phenotyped with different races of *P.triticina* to characterize and map the resistance genes. A genetic linkage map of 533 AFLP and SSR molecular markers was developed with JoinMap v3.0. We identified and mapped the genes *Lr3* (distal end of 6BL), *Lr16* (distal end of 2BS), *Lr17* (distal end of 2AS) and a gene that we named BMP1 that mapped at 1.3 cM from *Lr16*, suggesting a closely linked gene to *Lr16*. A race was used that identified the *Lr13* gene but failed to show the presence of this gene in the Buck Manantial used in the present study. Further analyses are being carried out to confirm the presence of *Lr13*. The BMP1 showed a high effective resistance to natural infection of wheat leaf rust, as demonstrated in field tests in three different locations during 3 years. The study of traditional wheat varieties of South American origin showing durable resistance to leaf

rust is of great value, as they can provide new sources of resistance to this disease.

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P156

Genetic and phenotypic mapping for leaf rust resistance, *Lr34* in Indian bread wheat population

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India is the second largest producer of wheat in the world with production hovering around 70-75 million tons since 1999-2000. Clearly wheat and its products play an important role in India's economy. Among the three rust diseases of wheat, leaf rust or brown rust caused by *Puccinia triticina* Eriks. is widespread throughout the world and also occurs in all the wheat growing zones of India. The Indian spring bread wheat cultivar 'HD 2189' shows leaf tip necrosis and resistance to leaf rust pathotypes in India since its release in 1980. We studied 128 single seed descent lines of an 'HD2189' × 'Agra Local' F₆ population to identify and map quantitative trait loci (QTLs) for leaf rust resistance. Percentage of leaf area infected and the response to infection were evaluated in two field trials in 2006-07 crop season at Directorate of Wheat Research, Karnal (India) and were transformed to the area under the disease progress curve (AUDPC). One-hundred and twenty eight F₆ lines along with both parental lines were analysed with six polymorphic simple sequence repeats (SSRs) markers (GWM1220, SWM1, SWM5, SWM8, SWM10 & WMC463) and one sequence tagged sites (STS) marker, csLV34. A genetic linkage map based on above markers data was established. The region containing *Lr34* was flanked by XSWM8 (proximal) and XWMC463 (distal) and spanned 68.7 cM in 'HD 2189' × 'Agra Local' population. Marker SWM10 was closely located to *Lr34* in present population. By using composite interval mapping and LOD >4.4, QTL analysis of the linkage group representing chromosome 7DS in the HD 2189 × Agra Local population defined a QTL for leaf rust resistance in the interval XGWM1220 - XSWM10 which accounted for 14.8 % of observed phenotypic variation for leaf rust resistance (AUDPC).

P157

Quantitative disease resistance assessment by real-time PCR

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Disease resistance is predominantly a quantitative character. Genetic factors in host and pathogen, environmental conditions (including agrochemicals) and plant growth stage all affect the expression of resistance. Measuring disease resistance accurately and reproducibly is a key requirement for the introgression of partial resistance genes into breeding lines. Numerous methods of differing complexity, cost and skill requirement with differing levels of reproducibility exist for this task. Here, we test a quantitative polymerase chain reaction (qPCR) protocol to measure fungal biomass, using the wheat-*Stagonospora nodorum* pathosystem as a model. A range of cultivars of differing reported resistance levels were used. We show that fungal biomass taken at 220°C thermal days after inoculation accurately predicted the final grain weight loss. We conclude that a test based on qPCR methods is specific, quantitative, rapid, and objective. Such tests could prove useful and economic tools in the development of robustly resistant crop cultivars.

P158

Genetics of rust resistance in the Australian wheat germplasm

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F₂ and F₃ populations targeting leaf rust resistance genes (*Lr13*, *Lr21* *Lr28*) and stem rust resistance genes (*Sr32* and *Sr33*) were phenotyped for seedling resistance. In populations targeting *Lr13* (Leichardt/WAWHT2071), *Lr21* (Tincurrin+Lr21/EGA2248) and *Lr28* (Sunland/Arrino), parents Leichardt, Tincurrin+Lr21 and Sunland were resistant (R) while parents WAWHT2071, EGA2248 and Arrino were susceptible (S) to leaf rust. F₂ progeny in crosses Leichardt/WAWHT2071 and Sunland/Arrino showed a 3R:1S segregation ratio ($\chi^2 = 0.3$ and 1.3; $P = 0.6$ and 0.25) while F₃ families segregated as 1:2:1 (true breeding R (TR):segregating (seg):true breeding S (TS)) ($\chi^2 = 1.8$ and 1.02; $P = 0.4$ and 0.6) indicating the single dominant nature of *Lr13* and *Lr28*. Interestingly F₂ populations Strzelecki/WAWHT2454 and EGA Gregory/Ajana where the resistant parents Strzelecki and EGA Gregory are known to carry *Lr13* in combination with *Lr23* (ineffective in WA) it appears recessive with a 1R:3S reaction observed in both populations. Population Tincurrin+Lr21/EGA2248 targeting *Lr21* showed a 13R:3S F₂ segregation indicating the presence of one dominant and one recessive independent genes. The hypothesis was confirmed in F₃ where families arising from resistant F₂ plants segregated in a ratio of 7:6 (TR:seg) ($\chi^2 = 0.8$; $P = 0.34$) while families from susceptible F₂ plants were all true breeding susceptible. In populations targeting *Sr32* and *Sr33* parents C77.19/3*77W:549-163658 and *Sr33/2*Shortim//4*Jacup/3* were used as the sources of resistance, respectively, while parents WAWHT2046 and Calingiri were susceptible to stem rust. The F₂ progeny in both crosses segregated into a 3R:1S ratio ($\chi^2 = 0.06$ and 3.3; $P = 0.8$ and 0.07) and the F₃ families showed a segregation of 1:2:1 (TR:seg:TS) ($\chi^2 = 5.5$ and 1.2; $P = 0.06$ and 0.6) indicating the single dominant nature of *Sr32* and *Sr33*. Usefulness of the above populations in mapping studies will also be discussed.

P159

Identification and genetic characterisation of a powdery mildew resistance gene in wheat

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Studies were conducted to determine the inheritance of resistance to powdery mildew (PM) by *Blumeria graminis* f.sp. *tritici* in a resistant (R) CIMMYT line 6HRWSN125 and in the resistant cultivar Meri. Resistance was assessed at the seedling stage in a doubled haploid (DH) population (6HRWSN125/WAWHT2074) and in three Meri-based crosses including Meri/Ajana, Meri/Wyalkatchem and Meri/6HRWSN125. Line WAWHT2074 and cultivars Ajana and Wyalkatchem are susceptible (S) to powdery mildew strains in Western Australia. The DH population showed a segregation ratio not significantly different from 1R:3S ($\chi^2 = 1.5$, $P = 0.22$) indicating complementary gene interaction of two genes for PM resistance. Crosses Meri/Ajana and Meri/Wyalkatchem produced S F₁ progeny and an F₂ segregation ratio of 1R:3S ($\chi^2 = 0.5$ and 3.6, $P = 0.48$ and 0.06), suggesting the presence of a single recessive gene in Meri. The hypothesis was confirmed in the F₃ where a non-random selection of F₃ families was examined for segregation of resistance. F₃ families arising from R F₂ plants were all true breeding R while F₃ families from S F₂ plants either segregated or were true breeding S. The *Pm* locus was mapped in Meri/Ajana and Meri/Wyalkatchem to the proximal region on chromosome 3BS, a region not previously identified to contain *Pm* resistant genes. The cross between the resistant cultivar Meri and the resistant line 6HRWSN125 produced R F₁ progeny. The F₂ progeny segregated in a ratio of 43R:21S ($\chi^2 = 0.8$, $P =$

0.36) which supports the hypotheses of two dominant complementary genes in 6HRWSN125 and one recessive gene in Meri. Presence of different resistant genes in parents 6HRWSN125 and Meri was confirmed in F₃ where F₃ families from R F₂ plants either segregated or were true breeding R while F₃ families from S F₂ plants were all true breeding S.

P160

Postulation for seedling and adult plant rust resistance genes against the three rusts in three CIMMYT nurseries

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One hundred fifty three entries belonging to three CIMMYT nurseries, namely, ASN, SAWSN and HTWYT were screened both under greenhouse and field conditions. These nurseries differed with respect to the presence of 1BL.1RS translocation, with the highest proportion in HTWYT. For non 1BL.1RS group, the genes conferring resistance, either singly or in combination against stripe rust were *Yr6*, *Yr7*, *Yr17*, *Yr27*, *Yr34* and some putatively uncharacterised gene (s). *Lr1*, *Lr3a*, *Lr16*, *Lr23*, *Lr24*, *Lr26*, and *Lr27+31* were present either alone or in various combinations. The occurrence of *Lr24* in ASN and *Lr26* in SAWSN was more pronounced. In the case of stem rust; *Sr8a*, *Sr9g*, *Sr12*, *Sr17*, *Sr24*, *Sr30*, *Sr31*, *Sr36*, *Sr38* and some putatively uncharacterised genes were postulated. Adult plant screening over two years revealed that the three nurseries possessed high levels of resistance against stripe rust and moderate to high levels resistance against stem rust and leaf rust. Molecular marker screening identified the presence of *Lr34* and *Sr2* in 63% and 78% of entries.

P161

***Fusarium* head blight QTL mapping in durum wheat and *Triticum carthlicum* sources of resistance**

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Durum wheat (*Triticum turgidum* L. subsp. *durum* (Desf.) Husn.) is susceptible to *Fusarium graminearum* Schwabe [teleomorph *Gibberella zeae* (Schw.) Petch], causal agent of *Fusarium* head blight (FHB), which reduces grain yield, quality and economic value of the crop. This study was conducted to map quantitative trait loci (QTL) for FHB resistance from two crosses. Doubled haploid (DH) lines were developed from the cross (DH1) ‘Strongfield’ x ‘Blackbird’ (a *Triticum turgidum* subsp. *carthlicum* (Nevski in Kom.) Á.Löve & D.Löve genotype), and the cross (DH2) ‘DT707’ x ‘DT696’ (both advanced Canadian durum breeding lines). Both populations were evaluated in replicated FHB nurseries utilizing artificial inoculations under field conditions. The populations were rated for FHB incidence (Type I resistance) and severity (Type II resistance) and on a 1-9 disease rating scale. The two populations were genotyped with microsatellite markers to construct linkage maps and for QTL mapping. The multiple QTL mapping analyses revealed a QTL peak in DH1 at *cfa2153* on chromosome 1AS (Blackbird as the source of resistance) explaining up to 24% of the phenotypic variation (LOD 5.4) for FHB incidence, up to 15% (LOD 3.1) for FHB severity, and up to 15% (LOD 3.2) for the 1-9 rating scale. This marker is reported to be linked to Hessian fly resistance

genes. In DH2, unlinked markers *gwm156* and *wmc110* on chromosome 5A were significantly linked to FHB incidence, severity and 1-9 scale. Significant QTLs on 5A have been previously reported (in hexaploid wheat). The *cfa2153* locus seems to a good candidate for marker-assisted selection because it is putatively novel and is linked to FHB and Hessian fly resistance.

P162

Durable rust resistance in wheat is effective against multiple pathogens

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Stem rust resistance gene *Sr2* and leaf rust resistance gene *Lr34* provides durable, broad spectrum rust resistance globally. *Sr2* was fine mapped to a small genetic interval on chromosome 3BS in a cross between ‘Chinese Spring’ (*Lr31*) and Chinese Spring with 3B chromosome substitution from ‘Hope’ (*Sr2,Lr27*). Previously, complementary race-specific leaf rust resistance genes *Lr27* and *Lr31* were positioned on 3BS and 4BS, respectively and the presence of *Lr27* was associated with *Sr2* in many cultivars. A high resolution *Sr2* mapping family was derived from over 3000 gametes and scored for *Lr27*. Seedling leaf rust resistance with *Lr27* specificity cosegregated with *Sr2* suggesting that a single gene may confer race specific leaf rust and non-race specific, adult plant stem rust resistance in wheat.

Tight linkage was reported previously between *Lr34* and stripe rust resistance gene *Yr18* and powdery mildew resistance gene *Pm38*. We recently demonstrated that *Lr34* was also tightly linked to adult-plant stem rust resistance using a high resolution mapping family in the ‘Thatcher’ background. Seed of the near-isogenic Thatcher line RL6058 carrying *Lr34* were treated with sodium azide. Twelve mutants susceptible to leaf rust and stripe rust in the field were recovered. These mutants were also susceptible to stem rust and powdery mildew in the adult plant stage. Allelism tests between some of the mutants confirmed that the mutation events occurred at the *Lr34* locus suggesting that a single gene confers resistance to three rust pathogens and powdery mildew. Because several wheat cultivars carrying *Lr34* are susceptible to stem rust, we hypothesise that *Lr34* interacts with unlinked gene(s) to confer stem rust resistance in ‘Thatcher’ and *Sr2* interacts with unlinked *Lr31* to confer leaf rust resistance. The future isolation of *Sr2* and *Lr34* will provide insights into the molecular mechanisms of durable resistance and how it might lead to resistance to multiple pathogens.

P163

Synthetic hexaploid wheats for resistance to root-lesion nematodes

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Root-lesion nematodes (*Pratylenchus thornei* and *P. neglectus*), attack wheat roots, causing inefficient uptake of soil nutrients and water resulting in chlorosis, stunting, and reductions in tillering, biomass, and grain yield. Losses to the Australian grains industry are estimated at above \$100m/annum. Wheats with tolerance to *P. thornei* have been bred (reviewed by Thompson *et al.*, 1997), but they still allow nematodes to multiply in their roots. This paper reviews research to find higher levels of resistance among synthetic hexaploid wheats for incorporation into Australian varieties. Initially, 186 primary synthetics, along with their durum and *Aegilops tauschii* parents were screened for resistance to *P. thornei*. From further screening, five of the most consistently resistant synthetics having both parents resistant and covering a number of *Ae. tauschii* varieties as parents were identified (results recently reported by Thompson, 2008). These five SHs were found to be resistant to *P. neglectus* as well. Based on half diallel studies of these five SHs with one susceptible and one partially resistant bread wheat, general combining ability of the SH parents was found to be more influential than

specific combining ability in the inheritance of *P. thornei* resistance (Zwart *et al.*, 2004a). A molecular map was constructed with SSR and AFLP markers (Zwart *et al.*, 2005) based on a doubled haploid population between the SH with the best general combining ability (CPI133872) and the widely adapted Australian cultivar Janz. QTLs for resistance to *P. thornei* were located on chromosomes 2BS, 6DS and 6DL and for *P. neglectus* on chromosomes 2BS, 4D and 6DS (Zwart *et al.*, 2005; Zwart and Thompson, 2008). Further studies with the ITMI population confirmed QTLs for resistance to *P. thornei* from the synthetic parent on chromosomes 2BS and 6DS (Zwart *et al.*, 2006).

P164

Marker assisted approach for incorporating durable rust resistance in popular Indian wheat cultivars

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Rust diseases are common foliar fungal diseases of wheat in India. A major challenge is to avoid rust epidemics as cultivars remain under constant threat of new virulent races. The most promising long-term control strategy against leaf, stripe and stem rusts, is to breed and deploy cultivars carrying durable resistance. To address this issue, molecular marker approach is being utilized for enhancing rust resistance mainly through identification of durable rust resistance gene and pyramiding of different seedling and adult plant resistance genes. Recent studies have indicated that leaf tip necrosis (LTN) is not a reliable marker for confirming presence of durable rust resistance gene *Lr34* in wheat genotypes. Considering this, wheat genotypes postulated to carry *Lr34* gene by virtue of having LTN were screened with 4 microsatellite markers (*Xgdm1220*, *Xgwm130*, *Xgwm295*, *SWM10*) and one STS marker (*csLV34*) reported to be linked with *Lr34* locus. *SWM10* and *csLV34* were found to be useful markers to know the presence of *Lr34* in breeding lines. Indian wheat genotypes confirmed to possess *Lr34* gene through this study, have been identified which are being recommended for utilization to enhance durable rust resistance in breeding programmes. Gene pyramiding using seedling and adult plant resistance genes through 'simultaneous and step wise transfer' approach was followed using molecular markers reported to be linked with different rust resistance genes such as *Lr24*, *Lr28*, *Lr35*, *Lr37* etc. Their subsequent utilization was made for screening BC₁F₁ and double cross F₁ populations where the chi-square analysis showed no segregation distortion in the marker allele(s). With the emergence of new virulent pathotype, possible menace of stem rust looms large and thus genotypes possessing atleast two stem rust resistant genes effective against *Ug99* were selected. Marker assisted pyramiding/introgression of *Sr24*, *Sr25* and *Sr26* along with durable adult plant resistance genes such as *Sr2* is underway. MAS approach, supported by host-pathogen interaction has been found quite useful for enhancing rust resistance in wheat genotypes.

P165

The physical location of a powdery mildew related gene Hv-S/TPK determined by FISH with a TAC clone in wheat

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Powdery mildew (PM), caused by *Ergsiphe graminis* f. sp. *Tritici*, is one of the most damaging diseases for wheat production worldwide. A locus named as Pm21 on the chromosome arm 6VS of *Haynaldia villosa* L (2n=2x=14, V) confers high level of PM resistance. A TAC library was constructed using a 6VS/6AL translocation line harbouring the Pm21 locus. Screening the TAC library with markers linked to Pm21 identified positive clones. Analysing the selected TAC clones found a serine/threonine kinase gene (or Hv-S/TPK) which, when over-expressed in wheat, showed enhanced resistance to PM. One of the TAC clones harbouring the Hv-S/TPK gene, TAC15, was used in this study to determine the physical location of the gene by fluorescence in situ hybridization. As expected, this TAC clone detected a single locus on chromosome arm 6VS in *Haynaldia villosa*. The FL values of this locus varied between 0.566 to 0.587 when assessed using different genetic stocks including 6V-wheat addition lines, 6V-wheat substitution lines and 6VS-wheat 6AL translocation lines.

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Sources for resistance to Soil-Borne Cereal Mosaic Virus (SBCMV) among cultivated accessions of common wheat and its wild relatives

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SBCMV transmitted by *Polymyxa graminis* caused the great damage in yield of cereals i.e. wheat in particular regions, where the climatic conditions the most suitable for their development. Utilisation of resistant varieties currently is only one environmental friendly sustainable control of this disease. However there are no so many varieties of common wheat with known resistance to that pathogen. In the Eastern Europe SBCMV is quite rare, which may be caused by both resistance of wheat varieties of this region to those pathogens or climatic condition not suitable to SBCMV development, we considered to check the resistance of the set of 60 varieties which were planted in this region during XX century and up to date for both SBCMV and *P. graminis* as well as 75 wild and cultivated relatives of common wheat. It was found out that only 4 varieties were completely resistant to SBCMV and 15 were heterogeneous by this characteristic. The most of tested varieties were susceptible to *P. graminis*, however in 2 cultivars there was detected partial resistance to this root parasite. All resistant varieties were screened by molecular marker of resistant to SBCMV identified for UK varieties Cadenza in order to reveal the new genetic source of resistance to this pathogen; however it was appeared that all resistant Eastern European varieties and those heterogeneous one have the same gene of resistance, located of chromosome 5D *Sbm1*. In order to check the efficiency of utilization of SSR markers closely linked to *Sbm1* gene, by which this gene was mapped to particular region, in MAS for wheat improvement, we performed screened of this resistant and susceptible gene pool, using SSR markers linked to *Sbm1* and related gene caused resistant to SBWMV. It was found the low efficiency of their application only wmc765 appeared to be more effective to the first

screening in breeding population. Among wild accessions resistant one were found out among those carrying *DD*, *MM*, *UU* and *VV* genomes.

P167

QTL mapping of multiple disease resistance traits in a synthetic hexaploid x bread wheat population

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A genetic linkage map based on a cross between the synthetic hexaploid CPI133872 and the Prime Hard Australian bread wheat Janz, was established using 111 F1-derived doubled haploid lines. DArT markers were integrated into an existing framework map of SSR and AFLP markers, to increase marker density, using JoinMap v3.0. The genetic map comprises 382 loci (125 SSR, 16 AFLP, 241 DArT markers) and spans 1536 cM. Five disease resistance traits (two species of root-lesion nematode (*Pratylenchus thornei* and *P. neglectus*), yellow spot (*Pyrenophora tritici-repentis*), stripe rust (*Puccinia striiformis*) and leaf rust (*Puccinia triticina*)) were phenotyped in this population over multiple years and/or locations. Interval QTL mapping analysis using MapQTL v4.0 identified reproducible and significant LOD profiles, stable across years and/or locations for each trait. Three QTL for *P. thornei* resistance (6DS, 6DL and 2BS) explain between 13 and 23 % of the variance each. Three QTL for *P. neglectus* (2BS, 6DS, 4D) explain between 15 and 23 % of the variance each. QTL for yellow spot resistance (5B) explains between 27 and 41% and corresponds to the described yellow spot resistance gene *tsn1*. Additional QTL for yellow spot were detected in single trials only on 3D and 5A. QTL for both stripe and leaf rust mapped to the same location on 7DS and corresponds to the durable, non-specific adult plant resistance genes *Lr34/Yr18*. Additional QTL for stripe rust were detected on 1B and 4B, and QTL for leaf rust on 3D. The synthetic hexaploid parent contributed resistance to *P. thornei*, *P. neglectus*, yellow spot and stripe rust, while the bread wheat parent contributed to resistance to *P. neglectus*, stripe and leaf rust. Markers flanking the QTL peaks were located within 1 to 15 cM of all major QTL detected and are candidates for tagging these resistance genes in MAS.

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Evaluation of genetic diversity of Fusarium Head Blight resistance in European winter wheat

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The levels and distribution of genetic diversity in the existing European winter wheat gene pool and the genetic relationship between exotic sources of FHB resistance and adapted cultivars were studied. Genetic diversity was investigated among 295 European winter wheat cultivars and advanced breeding lines from 8 countries (Belgium, France, Germany, Netherlands, UK, Denmark, Czech Republic, and Switzerland) using 47 wheat SSR markers. Ten additional wheat lines with known resistance to FHB were also included for reference. SSR markers linked to putative QTLs for FHB resistance, as reported in the literature, plus additional SSR markers to give an even distribution throughout the wheat genome were used. Cluster analysis was performed by both genetic distance-based and model-based analysis. In general, the UPGMA-dendrogram showed similar groupings to the model-based analysis. Seven clusters were identified by the model-based method, which did not strictly correspond to country of origin. The level of FHB resistance was evaluated in field trials conducted over multiple

years or locations. The following traits were assessed: % FHB severity, % FHB incidence, % diseased kernels, in spray inoculation trials; and % FHB spread and % wilted tips, in point inoculation trials. Association analysis between SSR markers and the FHB disease traits, taking population structure into account, detected markers significantly associated with FHB-resistant genotypes. Haplotype analysis revealed that the FHB-resistant European wheat lines do not contain the 3BS locus derived from Sumai 3.

P307

Reactions of durum wheats to *Fusarium pseudograminearum* in the Northern grain growing region of Australia

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To identify potential sources of resistance to *Fusarium pseudograminearum* (*Fp*), the causal agent of crown rot, a range of tetraploid germplasm was evaluated for incorporation into the durum-breeding program in the northern grain-growing region of Australia. Annually, Australia produces around 500,000 tonnes of durum wheat, of which 40% is exported. It's estimated that crown rot costs the Australian grains industry \$56 million per year in yield and quality losses. Current durum varieties are highly susceptible to crown rot, with favourable disease conditions causing yield losses up to 50% with losses frequently between 20-30%. Partial resistance has been identified in hexaploid wheats at seedling and adult growth stages. To increase the disease resistance of Australian durum varieties, it is thought that pyramiding these sources with tetraploid resistance sources will capture multigenic resistance traits with loci on the A and B genomes. In Toowoomba, Queensland, seedling evaluations were conducted under glasshouse conditions with leaf-sheath lesioning assessed three weeks after inoculation with *Fp*. Field trials were conducted to assess adult plant resistance, on artificially inoculated black earth soils. Valuable resistance was also identified in diverse origins including *Triticum monococcum*, *T. timopheevii*, *T. turgidum* var. *dicoccum* and *T. turgidum* var. *carthlicum*. Mature plants were assessed for disease incidence and severity by rating the internode lesioning and premature head death, expressed as the number of white or deadheads. Homozygous lines have been produced from hexaploid x tetraploid cross populations, by utilising single plant selection in our crown rot nurseries. These lines show useful levels of resistance whilst retaining important agronomic characteristics, beneficial to durum breeding and the Australian durum industry.