

P055

Genomics goes chromosomal to explore the wheat genome

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Tetraploid durum wheat and hexaploid bread wheat possess the largest genomes among cultivated crops. The genomes expanded during the evolution and speciation due to propagation of DNA repeats and polyploidy and the resulting genome structure makes the development of physical maps and positional gene cloning a daunting task. The complexity of these undertakings can be reduced by dissecting nuclear genomes to smaller parts after employing laser flow cytometry to sort mitotic chromosomes. However, initial experiments with chromosome sorting in wheat were compromised due to small differences in size among the chromosomes. As the cytometry discriminates chromosomes according to relative DNA content, which is related to chromosome size, only chromosome 3B could be sorted from lines with wild-type karyotypes. This problem was resolved by using cytogenetic stocks, which carry telocentric chromosomes and/or isochromosomes, and from which particular chromosome arms can be sorted. DNA of sorted wheat chromosomes is intact and the chromosomes are suitable for a range of applications, including construction of subgenomic BAC libraries and molecular cytogenetic mapping. Other important uses of sorted chromosomes include physical mapping using PCR, high-throughput mapping on DNA arrays, and targeted isolation of molecular markers. For most of these applications, fractions of sorted chromosomes and/or their DNA can be prepared and distributed to other laboratories so that they do not have to develop their own infrastructure for sorting. Thus, the chromosome genomics can be employed in different laboratories across the world. Our work has been supported by the Czech Science Foundation (grant awards 521/06/1723 and 521/07/1573) and Ministry of Education, Youth and Sports of the Czech Republic (grant award LC06004).

P056

Chromosome composition in an F₂ hexaploid x durum cross analyzed by DArT markers and MCFISH

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A major constraint to tetraploid durum wheat production in Australia is widespread susceptibility to crown rot, due to infection by *Fusarium pseudograminearum*. Several sources of partial resistance to this disease are available in hexaploid bread wheats and genetic markers for quantitative trait loci conditioning this resistance have been identified. We are currently attempting to transfer crown rot resistance from these hexaploid sources into susceptible tetraploid wheats. However, knowledge of the fate of D-genome material in hexaploid/tetraploid crosses is incomplete, while the degree of recombination between the A- and B-genomes of the parents in these crosses is also of critical interest. Diversity Array Technology (DArT) markers and multicolour fluorescence *in situ* hybridisation (MCFISH) were employed to investigate parental inheritance in the F₂ progeny from a cross between the hexaploid bread wheat line '2-49' and the tetraploid durum variety 'Bellaroi'. Of the 83 F₂ progeny analyzed with DArT, 82 contained one or more D-genome chromosomes, either complete or partial. The marker profiles indicated that all lines possessed recombined A- and B-genome loci derived from both parents, indicating the absence of parental selfs. The majority of A- and B-genome chromosomes showed a random re-assortment of parental genes. MCFISH analysis was conducted on 28 additional

plants from the same F₂ population. All lines contained varying numbers of D-genome chromosomes, while two plants carried A-D translocations. Investigations of F₃ plants from an independent 2-49/Bellaroi cross indicated that only 16 out of 33 plants still contained D genome material.

P057

Creating Wheat-rye Translocation Lines by Monosomic Addition Line

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An elite wheat line R149 was obtained from the selfed progeny of the monosomic addition lines between common wheat cultivar Mianyang 11 and an inbred rye line “baili”, with obvious phenotypic characters of the parental rye inbred line “baili”, such as disease resistance and the yield advantage. Biochemical assay of high molecular weight (HMW) glutenin subunits showed that R149 had the same subunit pair 5+10 as the parental wheat cv. Mianyang 11, which contributes the most to the baking quality of wheat flour. Sequence analysis and genomic *in situ* hybridization (GISH) further revealed that a small segment of rye chromosome containing the 2085-3265 bp (about 1.1kb) segment of pAWRC.1, centromere-specific repetitive sequence of rye were translocated to the terminal regions of wheat chromosomes in line R149. Furthermore, the fragment of pSc119.1 cloned from R149 had only 86% homology with its original sequence. These results indicated that the reconstruction of translocation chromosomes was concerned not only with simple exchange of chromosomal segments but also with the rearrangement of DNA sequences. Learning about the mechanism of reconstruction of this kind of translocation is helpful to study the organization of chromosome and the control of gene expression. Besides, the use of monosomic addition line is an effective approach to transfer the small segments of alien chromosomes into wheat.

P058

Fine structure mapping of a gene-rich region of wheat carrying *Ph1*, a suppressor of crossing over between homoeologous chromosomes

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The wheat gene-rich region (GRR) ‘5L0.5’ contains many important genes including *Ph1*, the principal regulator of chromosome pairing. Comparative marker analysis identified 32 genes for the GRR controlling important agronomic traits. Detailed characterization of this region was accomplished by first physically localizing 213 wheat group 5L-specific markers using group 5 nulli-tetrasomics, three *Ph1* gene deletion/insertion mutants, and nine terminal deletion lines with their breakpoints around the ‘5L0.5’ region. The *Ph1* gene was localized to a much smaller region within the GRR (*Ph1* gene region). Of the 61 markers that mapped in the four sub-regions of the GRR, nine mapped in the ‘*Ph1* gene region’. High stringency sequence comparison ($e < 1e^{-25}$) of 157 group 5L-specific wheat ESTs identified orthologs for 80% sequences in rice and 71% in *Arabidopsis*. Rice orthologs were present on all rice chromosomes although maximum (34%) were on rice chromosome 9 (R9). No single collinear region was identified in *Arabidopsis* even for a smaller region such as ‘*Ph1* gene region’. Seven of the nine ‘*Ph1* gene region’ markers mapped within a 450kb region on R9 with the same gene order. Detailed domain/motif analysis of the 91 putative genes present in the 450kb region identified 26 candidates for the *Ph1* gene, including genes involved in chromatin reorganization, microtubule attachment, acetyltransferases, methyltransferases, DNA binding, and meiosis/anther specific proteins. Five of these genes shared common domains/motifs with the meiosis specific genes

Zip1, Scp1, Cor1, RAD50, RAD51 and RAD57. Wheat and *Arabidopsis* homologs for these rice genes were identified.

P059

An integrated physical map of 2072 SSRs loci (gSSR and EST-SSRs) in bread wheat

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In bread wheat, as many as ~2,800 genomic SSRs (gSSRs) and ~300 EST-SSRs have been genetically mapped. Of these, only 1,320 gSSRs have been physically mapped. As many as 270 of these mapped gSSRs and an additional set of 275 EST-SSRs (not used earlier for genetic/physical mapping) were physically mapped in our laboratory. This leaves a very large number of genetically mapped/unmapped gSSRs and EST-SSRs that are yet to be physically mapped. We extended our studies further, so that in our laboratory altogether we physically mapped as many as ~1,500 SSR loci (~800 gSSR loci + ~700 EST-SSR loci) involving all the 21 wheat chromosomes. This physical map was integrated with all other available SSR containing physical maps in wheat. In the integrated physical map, a maximum of 776 loci (37.45%) were mapped on B sub-genome followed by D sub-genome with 672 loci (32.43%) and A sub-genome with 624 loci (30.11%). To further enrich the integrated physical map, we plan to map 132 class I gSSRs derived from ~14Mb available genomic sequences belonging to wheat and its relatives (<http://www.tigr.org/tdb/e2k1/tae1/info.shtml>). The SSRs loci assigned to specific chromosome bins in the integrated physical map may be used as anchor points in the BAC contig wheat genome physical map proposed under the auspices of International Wheat Genome Sequencing Consortium (IWGSC). However, in this integrated physical map, the loci mapped within individual chromosome bins cannot be ordered. To overcome this problem, we have initiated radiation hybrid mapping, and initially taken up chromosomes 5B and 7B for further fine mapping.

P060

Attempts to transfer salt- and waterlogging tolerances from Sea barleygrass (*Hordeum marinum* Huds.) to wheat

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Wheat crops are adversely affected by salinity and water logging in areas of southern Australia. Sea barleygrass (*Hordeum marinum*), a wild distant relative of wheat inhabiting salt marshes, has a high degree of tolerance to both salinity and water- logging. The initial aim of our work was to cross *H. marinum* and wheat and to produce the amphiploid from the hybrid. Because of the small anther size, *H. marinum* has to be used as the female parent in crosses to wheat and thus far F1 hybrids with Chinese Spring (CS) wheat and several Australian commercial wheat cultivars followed by amphiploids have been produced. These amphiploids showed improved salt- and waterlogging tolerances than the wheat parents. Since the current amphiploids are all in *H. marinum* cytoplasm, they suffer a loss in fertility due to cytoplasmic male sterility induced by the *H. marinum* cytoplasm. The cytoplasm of selected amphiploids, showing better tolerances, are currently being transferred back to the wheat cytoplasm to restore normal fertility. The aim initially is to develop salt- and waterlogging tolerant feed grain which will allow extended cropping onto mildly affected salt land. Furthermore, in a parallel program, 6 out of the 7 possible disomic addition lines (1H^m, 2H^m, 4H^m, 5H^m, 6H^m and 7H^m) of individual *H. marinum* chromosome to CS wheat have been produced and work is being continued to select disomic addition from the 3H^m monosomic addition to complete the set.

These addition lines are being tested for their salt- and waterlogging tolerances. If any *H. maritimum* chromosomes are found to have a major affect on tolerance, attempts will also be made to recombine these chromosomes with wheat to produce breeding material for bread quality salt-and waterlogging tolerant wheat.

P061

Paper withdrawn

P062

Development of durum wheat (*Triticum turgidum* ssp *durum*) lines with soft kernel texture by chromosome engineering

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Puroindolines a and b (Pins) are claimed to be the principal determinant factor of endosperm texture, which is one of the most important technological characteristics of common wheat kernel. They are encoded by the *Pina-D1* and *Pinb-D1* loci on the short arm of chromosome 5D and, therefore, are absent in durum wheat (*Triticum turgidum* spp. *durum*) cultivars. In order to introduce the *Pina-D1* and *Pinb-D1* loci into durum wheat through allosyndetic recombination, the 5D(5B) substitution line of durum wheat cv. Langdon was crossed with a mutant durum wheat line lacking the *Ph1* locus. Amongst the resulting F₆ progeny, 14 recombinant inbred lines (RILs) homozygous for the presence of the *Pina-D1* and *Pinb-D1* loci were found to have soft kernels, as measured by SKCS system. Eleven RILs were crossed as the male parent with durum wheat cv. Colosseo and 81 F₅ progeny from this cross were analyzed for (i) chromosome structure using SSR analysis, (ii) presence and expression of puroindoline genes and (iii) kernel texture, storage protein composition and technological properties. Two lines homozygous for a 5B chromosome containing a small terminal segment from chromosome 5D exhibited soft kernel texture (SKCS index<40), high flour yield and good gluten quality as determined by alveograph analysis.

P063

Cytogenetics approaches to wheat meiosis

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Many of the most interesting aspects of plant cell biology and development occur in cells deep within tissues of the plant. Examples are male meiosis occurring within the anthers and embryogenesis and endosperm development occurring within the developing seed. We have applied fluorescence *in situ* hybridization (FISH) on three-dimensionally preserved tissue sections derived from intact wheat florets to study meiosis, chromosome organization and the behavior of alien introgressions in the wheat background. The method combines vibratome sectioning with confocal microscopy and allows the visualization of three-dimensionally well-preserved tissues means that cell types can be confidently identified. Thus meiocytes have been clearly identified at all stages of meiosis and have been imaged in the context of their surrounding maternal tissue. We have investigated plant nuclear organisation in wheat, which provide excellent models for studying chromosome behaviour. We have used FISH to localize centromeres, telomeres and sub-telomeric regions, and total genomic DNA has also been used as probe to visualize introgressed chromosomes or chromosome segments in the wheat background. In fact the method combining vibratome sectioning and confocal microscopy provides a reliable tool to answer questions about the nature and timing of recognition events, chromosome associations and control mechanisms prior to and during meiosis in wheat, but also to determine, for

example, how universal meiotic events are in plants over a wide range of genome sizes and taxa. Results from these studies are directly applied to wheat breeding programmes to improve the efficiency on the transfer of desirable traits from related species into wheat.

P064

Rapid and targeted introgression of single genes into popular cultivars using marker-assisted background selection

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Rapid and precise introgression in an identity preserved manner is of prime importance to complement popular crop varieties with yield-protecting or value-adding genes. This will become increasingly important with the availability of additional value-added genes. In the absence of genotypic selection, background identity of the selected plants is uncertain even after six backcrosses. We optimized a marker-assisted background selection (MABS) approach to recover >96% of recurrent parent genome (RPG) in two backcrosses. 'Plabsim' computer simulations by incorporating wheat genome structure information, suggested a four-step method of MABS to be the most efficient. Our main focus for BC₁ was to recover recombinants between the target gene and the closest flanking markers. In addition to recovering double recombinant around the target gene, the focus for BC₂ was to select for the non-carrier chromosomes. For background selection, markers spaced at <20cM and flanking each of the 48 wheat gene-rich regions (GRRs), were selected. This approach was tested to introgress stripe rust resistance gene *Yr15* into cultivar 'Zak' and was compared to a backcrossing method without MABS. Two BC₂F_{2.3} plants carrying ~99% of RPG were recovered by screening 200 plants with 251 selected polymorphic SSR markers. Compared to simulations for 99% RPG recovery, systematic and step-wise elimination of unwanted plants reduced the number of plants approximately by 75%. Field evaluation at 17 locations showed these lines to be either equal or superior to the recurrent parent both for plant morphology, and grain yield and quality.

P065

Transfer of a gene for resistant to stripe rust originated from 6R chromosome of rye into bread wheat

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The chromosome 6R of cultivated rye (*Secale cereale* L.) carries several genes for resistance to biotic and abiotic stresses, which could be used in wheat (*Triticum aestivum* L.) improvement. To make desirable gene accessible in breeding, translocation involved the chromosome, which carried this gene, has been induced by means of using wheat-rye monosomic addition line. Several wheat-rye translocation lines, 98-1054-5, 98-1054-17, 98-1054-15-1 and 98-1054-15-2, were selected from a 6R monosomic addition line, which originated from a high-yield wheat cultivar, Mianyang 11, and an inbred line isolated from "Baili" rye, *Secale cereale* L.. All these wheat-rye translocation lines exhibit high resistance to stripe rust and middle resistance to powdery mildew. The gene for resistance to stripe rust, which originated from the 6R chromosome of Baili rye, represents the resistance against different races of *Puccinia striiformis* f. sp. *tritici*, compared with the genes *Yr9*, *Yr26*, *YrCH19* and *YrCH17*. This new gene was temporarily named *YrBL*. The resistant gene *YrBL* in all these translocation lines related to the awn gene on 6B, indicated that the translocation involved the 6B and

6R chromosomes. These translocation lines exhibited also a number of useful agronomic characters, such as high yield, wide adaptation, more erect and thick leaves, etc.

P066

Genetic mapping of stem rust resistance genes *Sr33* and *Sr45*

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Emergence of a new pathotype, Ug99, of the wheat stem rust pathogen in Uganda has threatened wheat cultivation worldwide. Deployment of genetic resistance in commercial cultivars has been the most economical means to combat such threats. Stem rust resistance genes *Sr33* and *Sr45* were transferred from *Aegilops tauschii* and are located on chromosome 1D in common wheat. These genes showed resistance against predominant pathotypes in Australia and are also effective against Ug99. Recombinant inbred line populations segregating for these genes were tested both under greenhouse and field conditions. Bulk segregant analyses using chromosome 1D located molecular markers identified linked markers. Results on identification and validation of markers closely linked with *Sr33* and *Sr45* will be presented.

P067

Second-generation chromosome-specific BAC resources in wheat

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Bread wheat, a crop with an enormously large genome (~17 Gbp), substantial fraction of repetitive sequences and presence of three homoeologous genomes poses a hard nut to crack for genome researchers. Flow cytometry enables dissecting the complex genome into small parts – chromosomes or chromosome arms. Previously, the flow sorting enabled construction of several subgenomic wheat BAC libraries including a composite library from chromosomes 1D, 4D, 6D, chromosome 3B, and chromosome arms 1BS, 1RS and 3AS. Although being invaluable resources for wheat physical mapping and positional cloning, these libraries had lower insert size (typically 75-85 kb). This was a consequence of a limited amount of DNA obtained after a time-consuming sorting which enabled only one size-selection step. Recently we increased the efficiency of BAC library construction, which made the second size-selection step feasible. The improved protocol was used to construct BAC libraries specific for chromosome arms 3AL, 3DS, 3DL, 7DS and 7DL and to expand libraries from chromosomes 1D, 4D and 6D and from 3B, respectively. The average insert size in these libraries reaches 100 -125 kb. Moreover, the increased efficiency enabled construction of a special type of library – customized library – constructed from a smaller number of chromosomes (~1 million) under less stringent size-selection. Such libraries can be constructed for positional cloning of genes that are not present in cv. Chinese Spring, which is used for development of a physical framework map of wheat.

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P068

Validation of Black Point QTLs in wheat

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Black Point (BP) is a dark discolouration of the embryo end of wheat and barley grains. It can result in reduced grain quality and value and is a significant problem in most Australian wheat growing areas. Estimated losses through downgrading have been as high as \$50 million annually. Quantitative trait loci (QTL) for BP resistance have previously been identified in Sunco and Cascades. The aim of this study was to use a full diallele to validate these QTL and also to determine if two other varieties with increased resistance mirror existing sources of resistance or are potentially novel sources of resistance for BP. The BP resistant lines Lang, Cascades, SW95-50213, and Genaro, and one BP susceptible line, Cunningham were used as parental lines in the full diallele. As both Lang and Sunco are Cook derivatives, Lang was used to validate the Sunco QTL. Marker regression analysis confirmed the QTL on chromosome 2BS in Lang crosses. Genaro and SW95-50213, which are more resistant to BP than Sunco or Cascades, indicated an association between BP resistance and chromosomes 2B and 2A,

respectively. The identification of markers for BP resistance in a number of different resistant sources will facilitate the pyramiding of genes for BP resistance in wheat.

P069

Chromosome-specific behaviour in wheat with alien genetic materials

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Chromosomes belonging to a genome have similar characteristics and behave in concert with each other. The examples are seen in similar C-banding patterns of each chromosome in a genome, instability of a certain genome in interspecific hybrid, and occupation of specific spatial territory in the nuclei of interspecific hybrids. However, some chromosomes act independently, out of harmony with the other chromosomes. Here we introduce three cases of such chromosome-specific behavior. 1) Specific retention of chromosome 2D in hexaploid derivatives of octoploid Triticale: In amphidiploid between hexaploid wheat and rye, the D-genome chromosomes tend to be eliminated. Of 14 independent hexaploid derivatives observed, the chromosome 2D was retained in all lines despite most of the other D-genome chromosomes were eliminated. 2) Specific elimination of the chromosome 1D in homoeologous group-1 alien chromosome addition lines: We analyzed the seed storage proteins of 177 lines of wheat with alien chromosomes of various species. Of these, 25 showed novel protein molecules in addition to those of common wheat. Five lines lacked whole or a part of chromosome 1D. No chromosome changes were observed in the chromosome 1A or 1B. 3) Specific amplification of chromosome 3B by interaction with chromosome 3C: Common wheat cultivar 'Norin 26' carries *Igc1*, a suppressor for the gametocidal gene on chromosome 3C of *Aegilops triuncialis*. In the telosomic mapping of *Igc1*, we observed specific amplification of chromosome 3B. These phenomena indicate that seven chromosomes in a genome do not always behave together in evolution.

P070

Production of *Aegilops cylindrica* with *Ae. caudata* plasmon

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Final aim of the present investigation is to demonstrate the genetic effect of a co-existing alien genome to the plasmon. For this purpose, we are attempting to reconstruct *Aegilops caudata* (2n=14, genome constitution CC) from its genome and plasmon, which have been separated about 60 years ago. The plasmon of *Ae. caudata* accession KU 6-2 was first introduced into a common wheat accession Tve, *Triticum aestivum* var. *erythrospermum* (2n=42, AABBDD), by Kihara (1951). We continued backcrossing this (*caudata*)-Tve with the pollen of normal Tve every year for 52 generations. Here, (*caudata*)-Tve represents an alloplasmic line of Tve having *Ae. caudata* plasmon. We crossed this (*caudata*)-Tve as female to *Ae. caudata* acc. KU 6-2, the same accession of *Ae. caudata* used by Kihara in the initial cross. The F1 hybrid, having genetic constitution of (*caudata*)-ABCD, was produced successfully, but the following backcross with the *caudata* pollen was unsuccessful. For this, the F1 hybrids at tillering stage were treated with colchicine, and the amphidiploid, (*caudata*)-AABBCCDD, was obtained successfully. The plants having 2n = 56 was crossed as female to the same *Ae. caudata* accession with no success. Thus, we crossed those octoploids as female to *Ae. cylindrica* (CCDD, 2n=28) and obtained (*caudata*)-ABCCDD (2n=42) hybrids. We backcrossed these hybrids to the same *Ae. cylindrica* as the pollen parent to obtain (*caudata*)-*Ae. cylindrica* plants. Their characteristics are under investigation in comparison with those of euplasmic *Ae. cylindrica* that is known to have the plasmon of *Ae. squarrosa* (2n=14, DD) (Tsunewaki et al. 1976). The entire breeding scheme and genetic characteristics of all generations will be reported. Our future plan is to

cross the alloplasmic (*caudata*)-*Ae. cylindrica* as female to *Ae. caudata* and backcross the hybrid with the same pollen parent to screen 2n=14 plants that should be the reconstituted *Ae. caudata* from its genome and plasmon separated each other for more than a half century.

P071

Development of *Triticum aestivum*-*Hordeum californicum* alien chromosome lines

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In order to transfer useful genes from *Hordeum californicum* into common wheat, a karyotype based on chromosome C-banding and FISH was established. Different *H. californicum* chromosomes could be distinguished by their unique band pattern and could be identified in the wheat background. Among the BC₂F₄ progenies derived the cross between Chinese spring-*H. californicum* amphiploid and Chinese spring, three disomic (DA2H; DAH₁; DAH₄), three monosomic (MA5H; MAH₁; MAH₄), two telosomic (DtH₄, MtH₄ and one multiple addition lines were identified by morphological, sequential C-banding/FISH, configuration analysis, biochemical and molecular marker analysis. Marker analysis further indicated that chromosome H₃ and H₂ chromosome belong to homoeologous group 2 and 5, respectively. Powdery mildew resistance evaluation indicated that addition lines DAH₁, MAH₁, DAH₄, MAH₄ and the multiple addition lines also showed good powdery mildew resistance, indicating that chromosomes H₁ and H₄ might involved in powdery mildew resistance of *H. californicum*.

P072

Development of a set of stem rust susceptible D-Genome disomic substitutions based on rusty durum

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Stem rust (*Puccinia graminis* Pers.:Pers. f.sp. *tritici* Eriks. and Henn.) is one of the most devastating diseases of wheat (*Triticum aestivum* L.) and durum (*T. turgidum* L. *durum*). Prior to the development of molecular techniques, studies of genes for stem rust resistance genes in wheat were completed using the Chinese Spring (CS) aneuploids. However, few genes were studied in durum because the major set of durum aneuploids, Langdon D-genome disomic substitutions (LDN-DS), had limited use due to the presence of at least three genes for stem rust resistance. Thus, development of a set of stem rust susceptible durum D-genome disomic substitutions would be useful for studies of stem rust resistance in tetraploid wheat. To do this, a breeding process was initiated where the LDN-DS were backcrossed to stem rust susceptible durum line 47-1. In the BC₁ generation, double monosomic plants that were susceptible to three stem rust pathotypes were selected for backcrossing. The stem rust susceptible genotype 'Rusty' became available during this breeding process and backcrossing to 47-1 was discontinued in favour of Rusty. In each cycle, double monosomic plants were selected for backcrossing. After six backcrosses to Rusty were completed for all 14 chromosomes, double monosomic plants were selfed and disomic substitutions were selected and confirmed using molecular markers, endosperm protein markers, and conventional cytogenetic techniques. Ten Rusty-DS lines have thus far been selected, the exceptions being 5D(5A), 4D(4A), 5D(5B), and 6D(6B) DS, which are presently under selection.

P073

Identification of wheat–*Dasypyrum breviaristatum* addition lines with stripe rust resistance using C-banding and genomic in situ hybridization

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The genus *Dasypyrum* (or *Haynaldia*), consisting of two species, *D. villosum* and *D. breviaristatum*, has many agronomically important traits including disease resistance, high protein quality, and drought tolerance and, therefore, is a valuable source for wheat improvement. Recent studies concluded that the genome of diploid *D. breviaristatum* is distantly related to the V genome of *D. villosum*, the symbol V^b was assigned to genome of *D. breviaristatum*. The sequential C-banding and Genomic in situ hybridization (GISH) analysis of wheat - *D. breviaristatum* partial amphiploid TDH-2 indicated that the C-banding karyotype of 7 pair of V^b chromosomes of *D. breviaristatum*, temporarily named V^b1-7, are significantly different from the V genome of *D. villosum*. The progenies from the cross and backcross of TDH-2 with common wheat lines were used to produce the wheat-*Dasypyrum* introgression lines. In addition to the stripe rust resistance screening, the diagnostic marker pDb12H was successfully applied to trace the *Dasypyrum* chromatin in wheat background. Two new wheat-*Dasypyrum* addition lines (2n= 44) immune to strip rust were produced from BC1F6 generation. The chromosome composition of these lines was described by GISH and C-banding methods. The results of genomic in situ hybridization demonstrated that karyotype of the lines included one pair of *Dasypyrum* chromosomes each, and C-banding revealed that lines contained the V^b3 and V^b7 chromosomes from *D. breviaristatum*, respectively. The new wheat-*Dasypyrum* addition lines will be a promising donor to produce stripe rust resistance wheat alien translocation lines for the purpose of wheat breeding.

P074

Transfer of genes controlling of agronomic important traits from artificial hexaploid wheat into common wheat gene pool

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Artificial hexaploid wheat developed by crossing *T. militinae* (A'A'GG) and *Aegilops taushii* (DD) possesses a number of useful traits derived from both of donors of its subgenomes and was used as a “bridge” in transferring particular useful traits into the common wheat gene pool. It was crossed with two common wheat varieties Bezostaya 1 and Kavkaz. The set of introgression lines have been studied for the last ten years in order to reveal lines with useful traits, and decreased number and size of alien introgressions, observe the number and character of introgressions and study the interaction of alien genetic material incorporated in the genome of common wheat. During this study a set of lines was developed with single and multiple translocations and recombinations as well as whole chromosome substitutions. The percent of introgressions in lines from chromosomes of three subgenomes A', G and D was different at 52%, 32% and 94% respectively. Differences were observed as well for introgressions from particular chromosomes and homoeologous groups. Application of morphological, biochemical and SSR markers showed that high grain protein content is linked in lines with 2A' and 2G chromosomes and possible with introgression of 2D, 4 A' and 5D. It has revealed links of particular introgressions with resistance to some pathogens such as powdery mildew and leaf rust as well as other characteristics: grain size, form of ear, hairy leaf and glume and other traits. It was found out that some morphological characteristics which were suppressed in the genome of parental forms and amphidiploid were expressed in genome of introgression lines, for example black glume linked with

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introgression of chromosome 1A'. Such phenomena show the complicated system of introgenome interactions in cultivated and wild wheat relatives.