ITEMS FROM GERMANY

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Molecular linkage map of durum wheat.

A molecular (SSR marker) map of a durum wheat population is under development. The mapping population consists of 114 RILs and was developed at ICARDA be crossing Omrabi 5, a drought-tolerant cultivar, with Belikh 2, a heat- and salt-tolerant cultivar. As a prerequisite for the map construction, the parental screening was carried out with 224 Gatersleben wheat microsatellite (GWM) markers of which 114 were polymorphic between the parents. The B genome revealed a higher polymorphism rate (53%) compared to the A genome (47%). The population genotyping is in progress. In parallel, the lines will be phenotyped for abiotic stress response.

Molecular linkage map of bread wheat.

A new, SSR-based genetic linkage map of bread wheat based on 143 F_2 individuals derived from an intraspecific cross between Gatersleben gene bank accessions TRI 11712 and TRI 105, two winter wheat accessions from Pakistan and Sweden, respectively, was constructed. The parental lines were analyzed with more than 600 SSR primer pairs. Out of 600 SSRs tested for polymorphism, 17 (2.6%) did not show amplification (null) in both the parents. Overall, 350 SSR primer pairs were polymorphic and 272 were applied for population genotyping, which yielded 308 polymorphic loci and 288 of these mapped on 19 linkage groups with a total map length of 2,681 cM. The average of chromosome length was 141 cM and the average number of loci per chromosome 15; an average of one locus per each 9.3 cM on this map. Chromosomes 6D and 4D failed to generate proper maps because of the low amount of detected polymorphism. Less loci were mapped to the D genome (21.5%) compared to those on the A (36.9%) or B (41.6%) genomes. More important, this map contained 66 new loci. The described linkage map could be useful to enrich the consensus bread wheat genetic map by incorporating the 66 new loci.

Stable, across-environment QTL.

The International Triticeae Mapping Initiative (ITMI) RIL population was used to detect QTL underlying key agronomic characters in bread wheat. Trait measurements were taken from five independent field experiments performed in Serbia. Stable, across-environment QTL involved in the determination of heading/flowering time and ear morphology (length)/ grain yield were detected on chromosome arms 2DS and 4AL, respectively. These map locations are consistent with those obtained where the same population has been grown in contrasting geographical sites in Germany or Russia. However, as a result of 'QTL x environment' interactions, not all these QTL are expressed in all environments. Nevertheless, the (pleiotropic) effect on ear morphology (length) appears to be expressed in almost all environments and, so, represents a high value target for wheat improvement.

Anthocyanin pigmentation genes on homoeologous group-7 chromosomes.

Three bread wheat crosses 'Saratovskaya 29/Yanetzkis Probat', 'Chinese Spring–Hope 7B DS)/TRI 2732' and 'Golubka/ Novosibirskaya 67' were used for microsatellite-based mapping of genes determining anthocyanin pigmentation of anthers (*Pan-D1*), culm (*Pc-A1*, *Pc-B1*, and *Pc-D1*), leaf sheaths (*Pls-A1* and *Pls-B1*), and leaf blades (*Plb-A1*, *Plb-B1*,

and *Plb-D1*). The clustering of these genes with previously mapped *Rc-1* genes for red coleoptile on chromosomes 7AS, 7BS, and 7DS was shown. In addition, a set of 37 wheat cultivars and introgression lines was analyzed for presence of anthocyanin pigment on different plant organs. A significant correlation has been found between presence of anthocyanin on coleoptile and culm, coleoptile and leaf blade, coleoptile and anther, and anther and leaf blade.

Anthocyanin pigmentation in durum wheat.

Analyzing the F_2 population of a cross between the two durum wheat IPK genebank accessions, TRI 15744 and TRI 2719, a novel gene was described and mapped in wheat that controls anthocyanin pigmentation of the glume and was designated *Pg* (purple glume). This gene was mapped close to one of the two complementary dominant genes controlling anthocyanin pigmentation of the pericarp (gene *Pp3*) in the centromere region of chromosome 2A, whereas another *Pp* gene (*Pp1*) was mapped on the short arm of chromosome 7B, near the gene *Pc* controlling anthocyanin pigmentation of the culm and co-segregating with *Pls* (purple leaf sheath) and *Plb* (purple leaf blade). On the basis of the mapping results, the *Pp3*, *Pc*, *Pls*, and *Plb* genes of durum wheat were regarded as allelic to the bread wheat *Pp3*, *Pc-B1*, *Pls-B1*, and *Plb-B1* loci, respectively, whereas allelism of *Pp1* of *T. turdigum* subsp. *durum* and *T. aestivum* remains disputed, because this *Pp* gene was mapped in the former on the short arm and in the latter on the long arm of chromosome 7B.

Glume coloration.

An allelism test has confirmed that chromosome 1A genes for red and black glume coloration are allelic. Similarly, we showed that chromosome 1D genes for smokey-grey and red glume coloration also are allelic. Consensus maps of chromosomes 1A and 1D, carrying loci *Rg-A1* and *Rg-D1*, respectively, were derived from the mapping data obtained previously. The gliadin-specific microsatellite marker MW1B002 was mapped to chromosome 1B, 2 cM proximal from gene *Rg-B1*. Co-distribution of red glume coloration with specific alleles of locus MW1B002 was found in Russian, Albanian, Indian, and Nepal bread wheat collections.

Preharvest sprouting / dormancy.

In order to compare QTL data of wheat and rye for preharvest sprouting and dormancy the results from the ITMI population were checked against results from disomic wheat–rye addition lines. For wheat, a major QTL could be found on chromosome 4AL for both traits. In a first test with wheat–rye addition lines, chromosome 7R could be identified for these traits. In replications with wheat (Chinese Spring)–rye (Imperial) and wheat (Chinese Spring)–rye (King II) addition lines of chromosome 7R, 7RS, and 7RL, the important region for preharvest sprouting and dormancy, could be localized on chromosome 7RL, on one hand, and on chromosome 7RS, on the other hand. Looking for homologous regions between wheat and rye chromosome, 7RS has a relationship with chromosome 4 of wheat; chromosome 7RL provides no comparability with the wheat results.

Leaf rust and powdery mildew resistance derived from Aegilops markgrafii.

Introgression lines resistant to either powdery mildew or leaf rust and derived from the cross of the wheat cultivar Alcedo and *Ae. markgrafii* accession S740-69, which are susceptible and resistant to both diseases, respectively, were used in a complex crossing program. The aims were the combination of both resistances in one genotype and the identification of the gene(s), which are responsible for powdery mildew resistance regarding number and location.

The F_2 generations originating from a cross between six powdery mildew-resistant introgression lines with the same leaf rust-resistant line were tested at the seedling stage (Ann Wheat Newslett 54:48 2008) and investigated at adult-plant stage for both diseases. Segregation analyses for the inheritance of powdery mildew resistance resulted in two recessive genes for four of the six F_2 progenies. The remaining two F_2 progenies were characterized by two dominant, resistance genes. The leaf rust resistance was inherited by two dominant genes across all F_2 generations.

Only four of the five F_2 progenies from the cross of different powdery mildew introgression lines with the susceptible wheat cultivar Kanzler were grown in the same experimental field described above. According to the segrega-

tion analyses, the powdery mildew resistance was inherited by at least one dominant gene and some minor factors except for one line with three recessive genes.

Information from monosomic analyses was used to start the localization of the powdery mildew resistance genes within the introgression lines. Chromosomes 1A, 7A, and 6D were identified to have main effects with respect to powdery mildew resistance. Therefore, a total of 42 wheat SSR markers distributed over these three chromosomes were selected to detect polymorphisms between the crossing parents and introgression lines. Between the parental lines, 64% of polymorphism was detected. Depending from the introgression line, 6 to 10 SSR markers were finally suitable to detect DNA fragments from the *Ae. markgrafii* parent.

Septoria tritici blotch resistance from Triticum aestivum subsp. spelta.

A new source of resistance to *Septoria tritici* blotch has been mapped on chromosome 7D of *T. aestivum* subsp. *spelta*. A microsatellite-based genetic map was constructed from a set of 87 DH lines bred from the cross between Chinese Spring and a Chinese Spring-based line carrying chromosome 7D from spelt wheat. Two regions of the chromosome were associated with pathogen isolate-specific QTL expressed at both the seedling and the adult-plant stage. One of these may be allelic to the major resistance gene *Stb4* present in the bread wheat cultivar Tadinia.

Seed longevity.

Germination tests were performed on wheat accessions stored in the cold store of the germ plasm bank of IPK Gatersleben to investigate the intraspecific variability of seed longevity. The material originated from various parts of Asian, European, and American continents. In total, 213 accessions were analyzed consisting of 193 hexaploids, 18 tetraploids, and two diploids. The accessions were harvested in 1974 and stored in glass jars at 0±1°C and 8±2% seed moisture content. Initial germination data were available from 1977. Germination rates were high, having a mean of 87.04 ± 9.04%. The average decreased after 34 years of storage to 56.15 ± 23.03%. There was a clear increase in variation. Although 14 accession showed germination rates < 10%, other accessions kept high germinabilities with 68 > 70% and 24 > 80%. The loss of viability detected was independent from origin, growth type (spring/winter habit), and ploidy level of the germ plasm. Because the accessions investigated come from a seed multiplication performed in the same year (1974), at the same place (experimental fields, IPK Gatersleben), handled the same way during/after harvest (threshing and cleaning), and stored under identical conditions in one and the same cold chamber in glass jars, the differences in germinability discovered in the present study must be due to genetic variation in seed longevity.

Mapping the trait for seed vigor in the D genome.

A QTL analysis was performed with a set of 85 bread wheat lines containing homozygous introgressions of the *Ae. tauschii* D genome to identify chromosome regions associated with seed vigor. To assess seed vigor traits, measurements on a range of the germination characteristics were obtained for germination percentage on first (day 4) and final (day 8), mean germination time, mean germination rate, and the coefficient of germination synchrony. All trait measurements were obtained on the bases of 1-mm root protrusion and normal seedling development in fresh seeds (controls) and in seeds subjected to accelerated ageing (AA). The latter involved seed treatment with high temperature and high humidity to mimic natural ageing after prolonged storage. As an estimate of seed longevity, a seed vigor index was determined for all the traits as a ratio of the AA trait and the control trait values.

A total of 53 significant QTL (LOD > 3.0) were detected in clusters on chromosomes 1D (19), 5D (16), 7D (16), and 2D (2), individually explaining 16 to 37 % of the phenotypic variation. Most of the QTL controlling different vigor traits were located on overlapping regions. In controls, the majority of the QTL (25 out of 29) were identified on chromosomes 7D (16) and 1D (9). Following AA, almost all detected QTL were located on chromosome 5D (7 out of 8). Chromosomes 1D (9 QTL) and 5D (7) harbored all detected QTL for vigor indexes.

A wide region close to the centromere of chromosome 1D contributed to the genetic variation in the germination timing, rate, and synchrony both in controls and the corresponding vigor indexes. A broad region in the 5D long arm involving seven QTL affected the post-AA final germination percentage and the corresponding vigor index. A cluster of

QTL in the proximal part of 7D short arm affected the first count germination percentage, timing, and rate of development of normal seedlings in the controls.

In the controls, the wild donor alleles were associated with earlier germination and more synchronized development of normal seedlings. The wild, donor alleles decreased the germination percentage in both controls and AA, and reduced the vigor indexes.

Spot blotch resistance.

Spot blotch is a destructive disease of wheat in warm and humid wheat growing regions of the world. To identify the QTL for spot blotch resistance, an intervarietal mapping population in the form of RILs was developed from the cross 'Yangmai 6 (a Chinese source of resistance)/Sonalika (a spot blotch susceptible cultivar)'. Using SSR markers, four QTL, designated as *QSb.bhu-2A, QSb.bhu-2B, QSb.bhu-5B*, and *QSb.bhu-6D*, were identified. These QTL together contributed up to 63.1% of phenotypic variation. Two QTL on chromosomes 2B and 5B with major effects were consistent over 3 years. Two additional RI populations ('Ning 8201/Sonalika' and 'Chirya 3/Sonalika') also were investigated for the QTL analysis. Four QTL were identified on the chromosomes 2AS, 2BS, 5BL, and 7DS and explained 61.9% of phenotypic variation in a simultaneous fit. In the third cross ('Chirya 3/Sonalika'), the F_7 and F_8 populations were evaluated for 2 years. The selected chromosomes of this population were analyzed for the presence of QTL, and four were identified on chromosomes 2AS, 2BS, 2DS, and 7DS. The QTL identified in the 'Chirya 3/Sonalika' population explained 34.4% of phenotypic variation in a simultaneous fit. All QTL alleles for reduced disease severity were derived from the respective resistant parent in all mapping population.

Stay-green trait.

The stay-green (SG) trait is delayed senescence. Leaves remain green even after the seed has reached chemical maturity and is considered an important trait that allows a plant to retain their leaves in active photosynthetic states. The parents of the mapping population 'Chirya 3/Sonalika' differed in respect to stay-green trait. Therefore, this population was segregating for the stay-green trait, and we identified a QTL on the short arm of chromosome 1A that explained up to 19% of the phenotypic variation. This population will be analyzed with more microsatellite markers covering all chromosomes to identify more QTL for stay green.

Viviparous-1 gene associated with preharvest sprouting tolerance in European wheat cultivars.

Preharvest sprouting reduces the quality of wheat and the economic value of the grain. In this study, we determined the diversity of *Vp-1B* alleles in 490 accessions of European winter wheat cultivars by using the STS marker *Vp1B3* to provide basic information for the breeder for the production of improved PHS-tolerant cultivars. Four alleles of *Vp-1B* were found in the wheat cultivars tested, three of which (*Vp-1Ba*, *Vp-1Bb*, and *Vp-1Bc*) had previously been identified in Chinese wheat cultivars. The fourth was a new allele that had a 25-bp deletion in the third intron region, compared with the nucleotide sequence of *Vp-1Ba*, and was designated as *Vp-1Bd*. The list of tested cultivars can be found at: http://pgrc.ipk-gatersleben.de/viviparous

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