tained by the following lines in an extremely dry season in 2007: Bc 6322/06 (7,168 kg/ha), Bc 2791/05 (6,316 kg/ha), Bc 6310/06 (5,324 kg/ha), and Bc 1276/99 (4,700 kg/ha), which will all be used in further breeding. Triticale breeding results at the Bc Institute so far include the registered cultivar Bc Goran, the production of which has already spread (Fig. 2 and Table 6, p. 45). Additionally, there has been a considerable interest in this variety also in the neighboring countries of Bosnia and Herzegovina and Slovenia.

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ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG – IPK Correnstraße 3, 06466 Gatersleben, Germany.

A. Börner, O. Dobrovolskaya, E.K. Khlestkina, S. Landjeva, U. Lohwasser, P. Martinek, S. Navakode, M.S. Röder, A. Voylokov, A. Weidner, and K. Zaynali Nezhad.

Spike morphology genes.

Genes determining spike morphology in wheat (multirow spike; MRS) and rye (monstrosum; mo) were studied. Phenotypic analysis revealed segregation ratios of 3 (wild type) : 1 (mutant) in both species. Applying molecular markers, the mutants were mapped in comparable positions on the short arms of chromosomes 2D and 2R of wheat and rye, respectively. The distance to the centromere is about 10 cM. We suggest that the loci are homoeoallelic. Furthermore, it should be noted that a spike morphology gene from a *T. turgidum* supernumerary spikelet stock has been described on the short arm of chromosome 2A at a highly comparable distance from the centromere.

Anthocyanin pigmentation.

Different organs of the plant, including anthers, auricles, coleoptiles, culm, grains, or leaves, can show anthocyanin pigmentation. Anthocyanins are secondary metabolites playing an important role in UV protection of plant tissues. Molecular-mapping studies suggested that two groups of genes for anthocyanin pigmentation exist in wheat. The first group includes genes Rc, Pc, Pan, Plb, and Pls determining anthocyanin pigmentation of coleoptile, culm, anthers, leaf blades, and leaf sheath, respectively. They are closely linked to each other and represent homoeoloci on the short arms of chromosomes 7A, 7B, and 7D, and a putative homoeologous set for the same traits on chromosomes 5A, 4B, and 4D, all corresponding to the probable candidate genes coding for Myb protein homologous to the maize gene C1. The second group includes Pp and Ra, which determine anthocyanin pigmentation of the pericarp and auricles, respectively. These genes do not cluster with the others (and not one to another), no homoeoloci have been found for them yet, and

their gene product remained unknown. Another specific characteristic of the second group of genes may be the complementary effect, not found for the genes of the first group.

Flowering time and protein content on chromosome 7B.

Two related segregating populations were used to detect QTL underlying the vernalization response, the photoperiod response, and grain protein content. The QTL *QVrn.ipk-7B* (vernalization response) was identified in a cross between the single chromosome intervarietal substitution line Chinese Spring–Hope 7B and TRI 2732, a Gatersleben genebank accession. *QVrn.ipk-7B* maps close to the centromere of chromosome arm 7BS and probably is identical to *Vrn5*. The QTL underlying the photoperiod response (*QPpd.ipk-7B*) and grain protein content (*QGpc.ipk-7B*) were identified in a cross between Favorit and Favorit/F26-70 7B. Both are linked and map ~20 cM distal from the centromere on the same chromosome arm. Because of the absence of any correlation between grain protein content and grain size in the segregating population, we concluded that *QGpc.ipk-7B* may be involved in nitrogen uptake and/or translocation.

Post anthesis drought tolerance.

QTL analysis was carried out with a set of 114 RILs from the International Triticeae Mapping Initiative (ITMI) population of 'W7984/Opata 85' to identify genomic regions controlling traits related to post-anthesis drought tolerance of wheat. In two experiments performed in Gatersleben in two consecutive years, the amount stem reserves mobilization was estimated by measuring of changes in the 1,000-grain weight after chemical-desiccation treatment. QTL for stem reserves mobilization (*Srm*) were mapped on chromosomes 2D, 5D, and 7D. Comparing the data with studies on drought tolerance performed previously, QTL for drought tolerance preferentially appeared in homoeologous regions at distal parts of the group 7L chromosomes.

In a second study, Iranian bread wheat accessions including 70 winter and 70 spring genotypes were selected from the genebank of IPK Gatersleben being representatives of wheat grown area in Iran. These accessions were evaluated based on Augmented Randomize Complete Block Design in field experiments at IPK Gatersleben in 2006. Chemical desiccation was applied as simulator to induce post-anthesis drought stress. Morphological characters such as plant height, spike length, spike weight, number of seeds/spike, seed weight/spike, awn length, glume hairiness, seed length, seeds width, days-to-flowering, and 1,000-kernel weight were measured and the stress tolerance index was calculated. Significant differences were found for all morphological characters as well as for the stress tolerance index. In both winter and spring type awn length showed highest amount of coefficient of variation while days to flowering had the lowest of this value. Spring genotypes showed more variation than winter forms for most of the traits. Correlations for 1,000-kernel weights at normal and stress conditions were low in both winter and spring wheat. This confirmed that selection against drought stress can be performed under drought stress conditions only. Genetic diversity of these accessions based on SSR markers, its correlation to morphological characters, and its relationship to geographical distributions are under study.

Osmotic stress response in Rht wheat seedlings.

Sets of near-isogenic *Rht* lines in five varietal backgrounds (April Bearded, Berseé, Maris Huntsman, Maris Widgeon, and Mercia) were subjected to osmotic stress induced by polyethylene glycol (PEG 6000). To assess growth responses, the length of longest root, coleoptile, and longest leaf (shoot) was measured and the root-shoot length ratio and tolerance index were calculated. Seedling growth response to osmotic stress was significantly affected by *Rht* allele, other unidentified genes, determined by the different varietal background, and the stress level. Treatment with increasing concentrations of PEG caused gradual reduction in root and shoot length, but elongation of coleoptile at milder stress, followed by coleoptile length decrease at higher stress level. The general trend observed was that genotypes with longer roots, coleoptile, and shoots, as determined by the *Rht* alleles (*Rht-B1b*, *Rht-D1b*, and their combination) and varietal background (April Bearded and Maris Widgeon), had the highest tolerance index and keep maintaining the highest absolute values under stress, whereas genotypes with lower seedling vigor (*Rht-B1c*, *RhtB1c+RhtD1b*; Berseé and Mercia) were affected in a greater degree.

Aluminum tolerance.

Previous studies on aluminum tolerance exploiting 'Chinese Spring (CS)/Synthetics' single-chromosome substitution lines and based on a nutrient solution culture approach revealed chromosome 3B of CS influences the trait positively. As a consequence, a set of doubled-haploid lines derived from the cross between 'CS/Synthetic 3B//CS' was developed and used for QTL analysis. One locus having a LOD score >7 was detected on the long arm of chromosome 3B, close to the centromere. This QTL accounted for 49% of the phenotypic variation.

Preharvest sprouting / dormancy.

A set of seven, disomic Chinese Spring wheat–Imperial rye addition lines was evaluated for preharvest sprouting and dormancy. For the wheat-rye addition lines, chromosomes 4R and 7R could be identified for the traits preharvest sprouting and dormancy in a first test. For wheat, a major QTL for both traits could be localized on chromosome 4AL in the ITMI population. Comparing homoeologous regions between wheat and rye chromosome arm 7RS is comparable to 4AL.

Disease resistance originating from Ae. markgrafii.

Aegilops species possess a valuable potential of resistance against economically important diseases like powdery mildew, yellow rust and leaf rust. The *Ae. markgrafii* accession S740-69 is characterized by resistance against leaf rust and powdery mildew. The accession was used in different prebreeding programs that resulted in either leaf rust-resistant or powdery mildew-resistant introgression lines, because the resistance genes were located on different chromosomes.

In order to combine both resistances in one genotype, a total of six powdery mildew-resistant introgression lines were crossed with one leaf rust-resistant line. The F_2 generations were tested at the seedling stage on leaf samples for both diseases. Special sets of isolates/races were used for the inoculation. These sets are normally applied for the official resistance tests before releasing a new cultivar. Segregation analyses for the inheritance of powdery mildew resistance resulted in at least one dominant gene and some minor factors for three F_2 families tested. Two families were characterized by one recessive gene and one family by two recessive genes that are responsible for the resistance. With the exception of one family, the leaf rust resistance in the plant material was inherited by two dominant genes. In one family, only two recessive genes for leaf rust resistance were found.

For the detection of the number and location of responsible genes, a total of five resistant introgression lines showing different expression of powdery mildew resistance were crossed with the susceptible wheat cultivar Kanzler. The F_2 generations were tested at the seedling stage against powdery mildew as described above. Segregation analyses for the inheritance of the resistance resulted in one dominant gene and some minor factors with respect to three F_2 families tested and, for the remaining F_2 families, two and three recessive genes.

DNA analyses of the plant material has started to find segments of *Ae. markgrafii* in the wheat background by means of microsatellite markers. The aim is the verification of the leaf rust QTL on chromosome 2AS and the localization of the powdery mildew-resistance genes.

Seed longevity.

Genetic variation in seed germinability, seed vigor and deterioration, and seedling performance after long-term natural ageing was evaluated in 135 *Triticum* species accessions stored for up to 33 and 15 years at 0°C and ambient room temperature (RT), respectively, in the Seed Genebank at IPK, Gatersleben. To assess the effects of storage temperature, seeds of identical accessions stored at 0°C and RT were investigated. Standard germination, electrical conductivity of seed leachate, accelerated ageing, and seedling growth tests were performed. The study revealed a considerable genetic variation in seed vigor and longevity, determined by the genotype, duration, and temperature of storage. After 33 years of storage at 0°C, more than half of the accessions still had high germinability (about 60 %). No clear trend between increasing the conductivity of seed leachate with increasing the duration of storage was established. This trait was shown to be mostly genotype-dependent (R2=0.94). However, the conductivity of seed leachate of 0°C seed lots was lower compared with the RT seed lots (P<0.001). A significant negative correlation was established between conductivity of seed leachate and germinability in five- and seven-year-old accessions, but no correlation was observed between the two traits with seed ageing. Seedling growth traits were significantly affected by the genotype, duration, and temperature of seed storage. Subjecting the he 0°C seed lots to accelerated ageing resulted in deterioration effects comparable to those caused by storage of seeds at RT. In addition, the accelerated ageing tests provided tools to differentiate between higher and lower vigor accessions among the high-germinating ones.

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