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ITEMS FROM HUNGARY

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The wheat season. The third extreme drought in one decade characterized the 2008–09 wheat season. A total lack of rain in April and May accompanied by high temperatures caused early maturing and yield decrease. The national wheat average reached only 3.84 t/ha, which was only slightly better than the 3.6 t/ha harvested in the extra dry year 2007. The quality of wheat harvested was good, with low protein in some regions where fertilizer uptake was prevented by drought.

Breeding.

Z. Bedö, L. Láng, O. Veisz, G. Vida, M. Rakszegi, I. Karsai, K. Mészáros, and S. Bencze.

Breeding. Four winter wheat cultivars were registered in Hungary in 2009.

Mv Menüett (Mv 07-05) is an early maturing cultivar with very good quality, selected from the cross 'F1959W1-2/MV22'. Yield level is slightly higher than that of the existing quality wheats. The cultivar has reliable winterhardiness and good lodging resistance. Dough characteristics are favorable, measured both with Farinograph and Alveograph. The HMW-glutenin composition is 2*, 7*+9, 5+10. Mv Menüett is moderately resistant to powdery mildew and leaf rust and resistant to stem rust.

Mv Karizma (Mv 08-07), an early maturing, facultative wheat with winterhardiness, is similar to the medium frost-tolerant winter wheats, which is sufficient under the average Hungarian conditions. Mv Karizma represents a unique quality type, because it overproduces the Bx7 HWW-glutenin subunit that leads to a very strong dough. The top quality has been inherited from a selected line of the famous wheat cultivars of the 1930s, Bankuti 1201 and the short-strawed cultivar Ukrainka characterized by low protein content but very good dough quality. Mv Karizma has a relatively low protein content and very good baking quality; the dough strength and stability, especially, are excellent. The HMW-glutenin composition is 1, 7*+8, 5+10.

Mv Petrence (Mv 08-06) is a medium-early, dwarf wheat with high yield and good baking quality. Mv Petrence is recommended for intensive production under better than average growing conditions. The short straw and very good lodging resistance allow the use of a high rate of fertilizers thus ensuring yield up to 8–9 t/ha. Mv Petrence is the only awnless Martonvásár wheat.

Mv Kolompos (Mv 10-06) is a midseason cultivar selected from the cross 'Eureka/Mv Vekni'. This wheat belongs to the high protein Martonvásár wheat group characterized by 35–38% wet gluten content, A2–B1 Farinograph quality, high water uptake, and high loaf volume. Mv Kolompos carries the T1B·1R translocation.

Disease resistance studies.

Molecular marker-assisted selection. Molecular MAS is being used to incorporate effective resistance genes (*Lr9*, *Lr24*, *Lr25*, *Lr29*, *Lr35*, *Lr37*, *Pm21*, and *Stb2*) into Martonvásár-bred wheat genotypes. The backcross program has been subsidized by national and international research projects (Bioexploit-EU FP6, NAP-BIO-NEWSEED, and DTR_2007).

Molecular markers were used to detect the presence of the *Lr1* and *Lr10* genes in 72 winter wheat cultivars from Martonvásár (Mv). The *Lr1* gene was found in 15% of the genotypes examined (Mv 17, Mv Irma, Mv Madrigál, Mv Matador, Mv Summa, Mv Magvas, Mv Mezőföld, Mv Tamara, Mv Mazurka, Mv Hombár, and Mv Laura) and the *Lr10* gene in 21% (Mv 13, Mv Matador, Mv Martina, Mv Kucsma, Mv Emese, Mv Palotás, Mv Prizma, Mv Matild, Mv Mambo, Mv Béres, Mv Garmada, Mv Hombár, Mv Gorsium, Mv Kemence, and Mv Laura). Three of the Mv cultivars included in the experiments contained both genes (Mv Matador, Mv Hombár, and Mv Laura). Cultivars carrying the *Lr10* gene proved to be more susceptible than those in which the *Lr1* gene was present. Several wheat cultivars containing the *Lr1* or *Lr10* gene were found to be moderately resistant or moderately susceptible.

Effective *Lr* genes. In an artificially infected nursery, the following *Lr* genes continued to provide effective protection against leaf rust in Martonvásár in 2009: *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr28*, *Lr29*, and *Lr35*; the formerly effective *Lr37* became moderately infected.

Powdery mildew race survey. Powdery mildew isolates collected in the Martonvásár area were used to determine the race composition of the pathogen population, the degree of virulence, and the efficiency of known resistance genes. The races dominant in 2009 (and their frequency) were 76 (55.1%), 51 (28.1%), and 77 (9.7%). The virulence complexity in the pathogen population was calculated as 6.13, which was almost as high than in the previous year.

Abiotic stress resistance studies. In the case of water stress, we found that higher general activities of the antioxidant enzymes might indicate that a genotype had better stress tolerance. More sensitive cultivars had relatively higher increases in the activity due to water withdrawal, but even at their highest levels, the antioxidant enzyme activities were lower than those under normal conditions in genotypes with good resistance. Mv Mambo, which had excellent drought tolerance, had outstandingly high antioxidant enzyme activity levels even under normal soil water conditions.

The size and shape of starch granules developing in the endosperm of wheat grains were altered due to heat stress and drought. Heat stress alone had little effect on the granule size while drought or heat and drought reduced it to a great extent (below 7 μm).

From a group of winter wheats characterized for heat stress tolerance, two cultivars (Mv Magma and Plainsman V) were chosen for creating a biparental mapping population consisting of anther culture derived DH lines and RILs for studying the genetic components of heat stress tolerance. Based on AFLP and SSR polymorphisms, the two parental cultivars proved to be genetically diverse, and they also represent different plant developmental types. The early development of Mv Magma is quicker, but this is followed by a significantly longer intensive stem elongation phase leading to later heading, compared to Plainsman V.

The genetic basis of earliness of the winter wheat cultivar Mv Toborzó and its association with the yield components has been studied with the characterization of the F_2 and the F_3 progenies of its various biparental populations segregating for the insensitivity and sensitivity allele of the *PPD-D1* photoperiod response locus. The allele phase of *PPD-D1*, in a population dependent fashion significantly influenced heading date, plant height, the average number of kernels/spike, and the seed yield but had no effect on the number of reproductive tillers and 1,000-kernel weight.

A set of 24 winter wheat cultivars of diverse geographic origins are involved in a series of controlled growth chamber tests for establishing the effects of suboptimal, optimal, and supraoptimal ambient temperature levels on plant developmental patterns with the purpose of studying the extent of plant developmental variability independent of the vernalization requirement and photoperiod sensitivity.

Climate change studies. Wheat plants grown under elevated atmospheric CO_2 level had higher number of spikes and grains per plant, produced more above-ground biomass and grain yield. Due to water deprival, plants had a substantial drop in the grain yield, especially at the ambient CO_2 level, whereas CO_2 enrichment resulted in much more effective biomass accumulation at high CO_2 than that at the ambient concentration despite water stress. The yield decrease due to a water withdrawal for 7 days was attenuated well by the doubled CO_2 level while the effect of longer drought could only be mitigated to a much lesser extent.

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The detection of intergenomic chromosome rearrangements in irradiated *T. aestivum–Ae. biuncialis* amphiploids by multicolor genomic in situ hybridization. The frequency and pattern of irradiation-induced intergenomic chromosome rearrangements were analyzed in the mutagenized (M_0) and the first selfed (M_1) generations of *T. aestivum–Ae. biuncialis* amphiploids (2n = 70, AABBDDU^{b}U^{b}M^{b}M^b) by multicolor genomic in situ hybridization (mcGISH). mcGISH allowed the simultaneous discrimination of individual *Ae. biuncialis* genomes and wheat chromosomes. Dicentric chromosomes, fragments, and terminal translocations were most frequently induced by γ-irradiation, but centric fusions and internal exchanges also were more abundant in the treated plants than in control amphiploids. Rearrangements involving the U^b genome (U^b-type aberrations) were more frequent than those involving the M^b genome (M^b-type aberrations). This irradiation sensitivity of the U^b chromosomes was attributed to their centromeric or near-centromeric regions, because U^b-type centric fusions were significantly more abundant than M^b-type centric fusions at all irradiation doses. Dicentrics completely disappeared, but centric fusions and translocations were well transmitted from the M_0 to M_1. Identification of specific chromosomes involved in some rearrangements was attempted by sequential fluorescence in situ hybridization with a mix of repeated DNA probes and GISH on the same slide. The irradiated amphiploids formed fewer seeds than untreated plants, but normal levels of fertility were recovered in their offspring. The irradiation-induced wheat–*Ae. biuncialis* intergenomic translocations will facilitate the successful introgression of drought tolerance and other alien traits into bread wheat.

Physical mapping of a T7A·7D translocation in the wheat–*Thinopyrum ponticum* partial amphiploid BE-1 using multicolour genomic in situ hybridization and microsatellite marker analysis. The absence of chromosome 7D in the wheat–*Th. ponticum* partial amphiploid BE-1 was detected previously by mcGISH, sequential FISH (fluorescence in situ hybridization) using repetitive DNA probes, and SSR marker analysis. In the present study, the previous cytogenetic and SSR marker analyses were expanded to include 25 other SSR markers assigned to wheat chromosomes 7A and 7D to confirm the presence of a T7A·7D translocation and to specify its composition. An almost complete chromosome 7A and a short chromosome segment derived from the terminal region of 7DL were detected, confirming the presence of a terminal translocation involving the distal regions of 7AL and 7DL. In both cases, the position of the translocation breakpoint was different from that of known deletion lines. The identification of the T7AL·7DL translocation and its breakpoint position provides a new physical landmark for future physical mapping studies, opening up the possibility of more precise localization of genes or molecular markers within the terminal regions of 7DL and 7AL.

Identification of new winter wheat–winter barley addition lines (6HS and 7H) using FISH and the stability of the whole 'Martonvásári 9 kr1–Igri' addition set. A previous paper reported the development of disomic addition lines (2H, 3H, 4H, and 1HS isochromosomic) from hybrids between the winter wheat Martonvásári 9 *kr1* and the two-rowed winter barley cultivar Igri. We isolated two new additions, 7H disomic and 6HS ditelosomic, using FISH with the repetitive DNA probes Afa-family and HvT01. The identification of the barley chromosomes in the wheat genome was confirmed with simple sequence repeat markers. The morphological characterization of the new addition lines is also discussed. Studies of the genetic stability of the whole set (2H, 3H, 4H, 7H, 1HS iso, and 6HS) of 'Martonvásári 9 *kr1*–Igri' additions revealed that the most stable disomic additions are 2H and 3H and the most unstable line is the 1HS isochromosomic addition.

Detection of the 1RS chromosome arm in Martonvásár wheat genotypes containing T1BL·1RS or T1AL·1RS translocations using SSR and STS markers. Several molecular markers have been reported for the detection of the 1RS chromosome arm. Our aim was to study the reliability and reproducibility of six molecular markers specific to the 1RS rye chromosome (GPI, Bmac213, 5S, IAG95, SCM9, and RMS13) in distinguishing between wheat genotypes with and without the T1BL·1RS or T1AL·1RS translocations. In the course of the analysis, PCR products of the expected size were obtained with all the markers, which were found to give a reliable indication of the presence of the 1RS chromosome arm in the wheat genome.

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Genetic and Physiological Studies.

G. Kocsy, A. Szűcs, I. Vashegyi, and G. Galiba.

Involvement of free amino acids and polyamines in the stress response. The involvement of free amino acids and polyamines in the cold acclimation was studied by comparison of wheat genotypes with different freezing tolerance. The increase in proline content correlated with the level of freezing tolerance. Cold acclimation affected the free amino acid composition and resulted in great changes in the ratio of the amino acids belonging to the aspartate and glutamate family, respectively. Among the polyamines, putrescine and spermidine concentrations exhibited a great cold-induced increase. The effect of cold on free amino acid and polyamine levels is probably not mediated by abscisic acid and is not determined at the transcriptional level. The cold-induced increase in amino acid and polyamine contents may improve stress tolerance due to the direct protection of macromolecules or due to the activation of various signal transduction pathways.

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