Navakode S, Neumann K, Kobiljski B, Lohwasser U, and Börner A. 2014. Genome wide association mapping to identify aluminium tolerance loci in bread wheat. Euphytica 198:401-411.
Nenova V, Kocheva K, Petrov P, Georgiev GI, Karceva T, Börner A, and Landjeva S. 2014. Wheat *Rht-B1* dwarfs exhibit better photosynthetic response to water deficit at seedling stage compared to the wild type. J Agron Crop Sci 200:434-443.
Rolletschek H, Fuchs J, Friedel S, Börner A, Todt H, Jakob P, and Borisjuk L. 2015. A novel noninvasive procedure for high-throughput screening of major seed traits. Plant Biotechnol J 13: 188-199.
Salem KFM, Röder MS, and Börner A. 2015. Assessing genetic diversity of Egyptian hexaploid wheat (*Triticum aestivum* L.) using microsatellite markers. Genet Res Crop Evol 62:377-385.
Sato K, Flavell A, Russell J, Börner A, and Valkoun J. 2014. Genetic diversity and germplasm management - wild barley, landraces, breeding materials. *In:* Biotechnological approaches to barley improvement (Kumlehn J and Stein N, Eds). Series: Biotechnology in agriculture and forestry. Springer-Verlag, Berlin Heidelberg, Germany. 69:21-36.
Schmidt U, Taylor M, Börner A, Lohwasser U, and Volkmar Chr. 2014. Observations on *Haplodiplosis marginata* von Roser (Diptera; Cecidomyiidae) in a winter wheat collection in the region 'Ilseder Börde' in 2012. Mitt Dtsch Ges allg angew Ent 19:255-258.
Shcherban AB, Börner A, and Salina EA. 2014. Effect of *VRN-1* and *PPD-D1* genes on heading time in European bread wheat cultivars. Plant Breed 134:49-55.
Simón MR, Ayala FM, Moreno MV, Lohwasser U, and Börner A. 2015. Mapping QTL for resistance against *Pyrenophora tritici-repentis* in wheat. Cereal Res Commun (in press).
Tikhenko N, Rutten T, Tsvetkova N, Voylokov A, and Börner A. 2015. Hybrid dwarfness in crosses between wheat (*Triticum aestivum* L.) and rye (*Secale cereale* L.): a new look at an old phenomenon. Plant Biol 17:320-326.
Tocho E, Lohwasser U, Börner A, and Castro A. 2014. Mapping and candidate gene identification of loci induced by phytohormones in barley (*Hordeum vulgare* L.). Euphytica 195:397-407.
Witzel K, Matros A, Strickert M, Kaspar S, Peukert M, Mühling KH, Börner A, and Mock H-P. 2014. Proteomic analysis reveals early modulation of terpenoid and phytohormone metabolism in salt tolerant barley. Mol Plant 7:336-355.
Zanke C, Ling J, Plieske J, Kollers S, Ebmeyer E, Argillier O, Stiewe G, Hinze M, Beier S, Ganal MW, and Röder MS. 2014. Genetic architecture of main effect QTL for heading date in European winter wheat. Front Plant Sci 5:217.
Zanke C, Ling J, Plieske J, Kollers S, Ebmeyer E, Argillier O, Stiewe G, Hinze M, Neumann K, Ganal MW, and Röder MS. 2014. Whole genome association mapping of plant height in winter wheat (*Triticum aestivum* L.). PLOS ONE 9:e113287.

ITEMS FROM HUNGARY

AGRICULTURAL INSTITUE
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The Martonvásár Cereal Genebank.

M. Megyeri, G. Linc, P. Mikó, A. Farkas, I. Molnár, L. Láng, C. Kuti, and M. Molnár-Láng.

The main task of the Martonvásár Cereal Genebank is to collect, preserve, and maintain wheat species and genetic reserves from related species, and to make detailed investigation on the quality, agronomic value, and biotic and abiotic resistance of the accessions.

The Martonvásár Cereal Genebank is divided into three main parts: a breeder collection, the genetic stock collection, and a set of wheat wild relatives.

Breeder collection. The largest of the collections, the breeder collection consists of more than 11,500 accessions of breeding stocks, cultivars, and landraces. A majority of the accessions are *Triticum aestivum* (90%)

genotypes, but other cultivated cereals (barley, triticale, and durum wheat) also are represented. The breeder collection is an important part of the cereal breeding program at Martonvásár.

Genetic stock collection. Special attention is given to the high-value genetic stocks (1,000 accessions), such as aneuploid material (nullisomic, monosomic, substitution, and addition series), special mutant stocks, and amphiploids. A majority of the genetic stocks were developed at Martonvásár during the last few decades, e.g., the Rannaya 12 monosomic series, and the other part was collected via international material exchanges. The genetic stock collection is used in basic genetic research and prebreeding activities. The maintenance of genetic stocks often requires cytogenetic control.

Wild wheat relatives. This collection consists of about 1,700 accessions, including a majority of species of *Triticum*, *Aegilops*, *Secale*, *Hordeum*, and perennial species of *Agropyron* and *Elymus*. Many of these accessions possess excellent resistance for biotic and abiotic stresses. They are used mostly in prebreeding work. Several prebreeding programs were started at Martonvásár on the basis of genebank accessions to transfer useful traits of wild relatives in to hexaploid wheat. The *T. monococcum* collection, with more than 300 accessions, is outstanding among the European collections. The *Aegilops* collection has expanded in recent years by collecting 130 new accessions via European expeditions.

The entire genebank collection consists of around 14,000 accessions. The long-term, *ex situ* maintenance of the accessions take place in refrigerated storage (–28°C). The majority of the genebank accessions are stored for medium term at 4°C in a cold room. At the same time, perennial species also are maintained *in situ* in an isolated nursery.

Database management of the genebank uses the *Breeder* software, which was developed at Martonvásár for cereal breeding. Characterization of genebank accessions under field conditions is an important part of our activity. All phenotypic and agronomic data collected during the regeneration and conservation processes are recorded in the *Breeder* database, which also is used to manage seed production, storage, and exchange.

ITEMS FROM INDIA

BHABHA ATOMIC RESEARCH CENTRE
Nuclear Agriculture & Biotechnology Division, Mumbai–400085, India.

Development of a gamma ray-induced mutant line in the wheat cultivar PBW-343 with moderate resistance to wheat stem rust race Ug99.

B.K. Das, Vikas, G. Vishwakarma, and S.G. Bhagwat.

Stem rust is a deleterious disease of wheat. In the recent past, the appearance of virulent races, such as Ug99, have broken many important stem rust resistance genes in wheat and barley. Under the aegis of an IAEA project (INT5150, 'Responding to the Trans-boundary Threat of Wheat Black Stem Rust (Ug99)'), the wheat cultivar PBW-343 was irradiated with gamma rays (250, 300, and 350 Gy). The M_1 was raised at Trombay in 2009–10. The M_2 population was sent to a hot-spot for Ug99 in Kenya in 2011 for screening for resistant mutants. Mutants were identified as moderately resistant (MR) or moderately susceptible (MS). These mutants were carried forward to the M_3 and M_4 generations in Kenya. Seed of one mutant line having an MR reaction were brought back to India, and this mutant line (TWM-97) is being multiplied at our station. Morphological characters were noted and molecular characterization of the mutant line is being carried out. Crosses were made with the parent cultivar for an alleleism study. We are thankful to Drs. P. J. L. Lagoda and T. Moleah (IAEA) for supporting this program and Prof. M. Kinyua (Eldoret, Kenya) for screening for Ug99 resistance.