ITEMS FROM HUNGARY

AGRICULTURAL INSTITUTE, CENTRE FOR AGRICULTURAL RESEARCH, HUNGARIAN ACADEMY OF SCIENCES
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Institute reorganization. As part of the reform of its institute network, the General Assembly of the Hungarian Academy of Sciences voted on 5 December, 2011, to establish a Centre for Agricultural Research (HAS CAR), which came into existence on 1 January, 2012. In the course of the reorganization, the Veterinary Medical Research Institute, the Plant Protection Institute, and the Research Institute for Soil Science and Agricultural Chemistry of the Hungarian Academy of Sciences merged with the Agricultural Research Institute and no longer exist as independent, publicly financed institutions.

The new Centre for Agricultural Research (www.agrar.mta.hu) has its headquarters in Martonvásár (2462 Martonvásár, Brunszvik u. 2), where the Agricultural Institute is located. The other institutes making up the Centre for Agricultural Research are the Institute for Veterinary Medical Research (1143 Budapest, Hungária krt. 21), the Plant Protection Institute (1022 Budapest, Herman Ottó út 15 and 2094 Nagykovácsi, Nagykovácsi út 26–30), and the Institute for Soil Sciences and Agricultural Chemistry (1022 Budapest, Herman Ottó út 15). The latter institute continues to maintain its experimental stations in Őrbottyán (2162 Őrbottyán, Kvassay telep) and Sárhatvan (7019 Sárhatvan, Ötvenkilenc-puszta). These institute addresses also serve as invoice addresses.

The acting Director-General of the Centre for Agricultural Research is Zoltán Bedő (+36-22-569570, bedo.zoltan@agrar.mta.hu), who also is the director of the Agricultural Institute. The Financial Management of the Research Centre is also located in the Martonvásár headquarters. The acting Financial Director is Dr Ágnes Gaál (+36-22-569570, gaal.agnes@agrar.mta.hu).

Tibor Magyar (+36-1-467-4060, magyar.tibor@agrar.mta.hu) has been appointed as the director of the Institute for Veterinary Medical Research, and Levente Kiss (+36-1-4877521, kiss.levente@agrar.mta.hu) as the director of the Plant Protection Institute. He also acts as deputy to the Director-General. The director of the Institute for Soil Sciences and Agricultural Chemistry is Attila Anton (+36-1-2122265, anton.attila@agrar.mta.hu).

As the legal successor of the above research institutes, the Centre for Agricultural Sciences carries out basic and applied research and innovation activities, participates in the dissemination of professional and scientific knowledge in the field of both education and agriculture, and works in coöperation with all social organisations whose activities contribute to the sustainable development of agriculture, the food industry, rural development, and environment protection.

Wheat season. After the extremely wet 2010 (>1,000 mm rain), 2011 proved to be the dryest year in the last several decades (262 mm) compared to the average of 550 mm. Due to the dry conditions, no serious disease epidemics occurred. The national wheat average reached only 4.04 t/ha, which is equal to the average of the last 20 years. The quality of harvested wheat was good with relatively low protein content.

Breeding.

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New releases. Three Martonvásár winter wheat and two winter durum wheat cultivars were registered in Hungary in 2011.

Mv Karéj (Mv 18-08) is an early maturing cultivar with high yield potential and outstanding protein quality. The origin of Mv Karéj is 'F29K4-22211/F30K2/3/MVMA/MV12//F2098W2'. The cultivar has very good winter hardiness and good lodging resistance. Grains are hard red, wet gluten content is 30–31%, farinograph quality A1, farinograph stability is 17–18 min, the alveograph W value is 380–440, and extensograph energy (at 135 min) is 170–180. Mv Karéj is moderately resistant to powdery mildew and leaf rust and moderately susceptible to stem rust.

Mv Lepény (Mv 05-08) is a high-yielding, early maturing, soft red winter wheat. Mv Lepeeny has a very low (20–24%) wet gluten content, low water uptake, and poor farinograph stability, alveograph, and extensograph properties. This cultivar possibly could be used for bisquit or beer production. The winter hardiness is reliable and it is resistant to leaf rust and moderately resistant to powdery mildew, but is susceptible to stem rust races used in artificial inoculation.

Mv Sobri (Mv 23-08) is an early maturing, bread wheat cultivar. Selected from the cross 'MV111-88/F2076//KARL92/3/MVMA/MV8//F2098W2-21/4/UKRAINKA', Mv Sobri is resistant to stem rust and has good field resistance to powdery mildew and leaf rust. The gluten content exceeds 30%; gluten quality is good, but not outstanding.

Mv Pennedur (MvTD33-08) isa high yielding, winterhardy, durum wheat. Selected from the cross 'GKD75/Aisberg//GK Bétadur', this cultivar possesses a good combination of high yellow pigment content and strong gluten, as measured by the gluten index method.

Mv Hundur (MvTD05-08) is a winter durum cultivar with a high wet gluten content. According to the results of the official state trial, the 3-year mean protein content of Mv Hundur was 15.5% and the yellow pigment content was 8.0 mg/kg, which were the highest values in case of both quality characteristics. This cultivar has outstanding vitriousness stability among the winter durum wheats.

Breeding for quality traits. Organoleptic, nutritional, and end-use properties of the breeding lines and populations developed under WP3-6 of the SOLIBAM project were studied in the frame of WP7. This study included 750 wheat, 196 durum, 57 barley, and 72 *T. monococcum* samples. Properties were studied on plants growing at different agro-climatic conditions using different breeding techniques and crop management systems. Nutritional properties, such as antioxidants, protein, and starch or amylose content, were measured to evaluate the health-related effects of the organically bred lines. At the same time, the impact of crop management and breeding (crop rotation, mulching, and irrigation) was studied on the end-use quality (breadmaking and pasta making) of the lines, especially taking into consideration the requirements of the production of special local products.

Breeding of wheat with high dietary fiber content. An exotic, Chinese wheat cultivar, Yumai-34, contains extremely high quantities of water-extractable arabinoxylans in the flour compared to wheat cultivars in commercial use in Europe and other parts of the world today. This property was utilized in a breeding program begun in order to produce wheat cultivars with good adaptability and a high dietary fiber content. The breeding lines produced were analyzed not only for dietary fiber, but also for protein and alkylrezorcinol content, in order to select genotypes having several beneficial properties by taking into consideration a multidimensional matrix affect. The F_4–F_6 generations already had been analyzed and outstanding breeding lines were selected for further study and seed multiplication. Oats has another component of dietary fiber in outstanding quantity related to other cereals, β-glucan. In order to improve the dietary fiber content of oat, the variability of β-glucan content was studied in several winter and spring oat genotypes and outstanding lines were used for breeding purposes. We found that the β-glucan content depended on the year and environmental factors, but did not depend on the seasonal type of the cultivar. This project requires the effective coöperation among different areas, plant breeding, cereal chemistry, quality control, nutrition, technology, and food safety. Clinical studies also were applied to strengthen the authenticity of our results for consumers and for the society.

Genotypes with different arabinoxylan and gluten content were selected, and a 'GxE' experiment was set up. The agronomical, biochemical, rheological, and other breadmaking quality-traits were analyed according to protocols developed previously. Correlations of the biochemical traits and the rheological properties, grain hardness, falling number and waterabsorption were studied. The effect of the genotype and the environment were also determined to those properties.

Forty-two genotypes were selected for this study including old and modern Hungarian wheat cultivars using Glenlea and Bezostaja-1 as controls. The old cultivars, TF-Kompolt, TF-Gyulavári, TF-Tiszatarján, and Szekacs 1055-4-1, contained outstanding quantities of water-extractable arabinoxylane, whereas Mv Suba and Mv Marsall were outstanding from the modern wheat cultivars. HMW- and LMW-glutenin composition and quantities were analyzed by LOC, MALDI, and SE- and RP-HPLC methods. Some of the measurements were made in Australia in collaboration with Ferenc Békés. We found that both the HMW- and the LMW-glutenin alleles significantly affected the Zeleny sedimentation, farinograph dough development time, and stability. Alveographic W and the gluten index were determined mainly by the HMW-glutenins, whereas gluten spread, alveograph P/L, and farinograph dough softening were influenced by the LMW-glutenin content. No correlation between the water absorption, falling number, and the protein allele composition of the cultivars was observed. From the quantitative traits, the unextractable polymeric protein (UPP%) content correlated most significantly with most of the breadmaking quality properties (Zeleny, GI, W, stability, and QN). A new mathematical model will be developed based on this knowledge of the relationship of breadmaking and genetic and biochemical properties. At the same time, a useful tool for breeding practices also will be developed to monitor any selelcted genotypes.

Disease resistance studies.

Fusarium head blight resistance. The 228 RILs of the population of 'Ning8331(resistant)/ Martonvásári 17 (moderately susceptible)', established for studying the genetic background of Fusarium head blight resistance, were screened with 17 AFLP primer combinations. The evaluation of the gel images revealed 366 different types of polymorphism. Together with the 97 polymorphic SSR markers identified earlier, a total number of 463 loci were evaluated with the JoinMap4 software and linkage groups were created.

The QTL mapping of the 'Bánkúti 1201-9086/Mv Magvas' population, developed to analyze the Fusarium head blight resistance of the old Hungarian wheat cultivar Bánkúti 1201, was continued by testing the parental lines with a total of 140 microsatellite markers. The whole population was tested with 33 SSR markers and 24 different AFLP primer combinations. A preliminary linkage map was created with JoinMap 5.0 software using 319 polymorphic markers.

Leaf rust resistance. Genotypes carrying designated leaf rust resistance genes were tested for infection in an artificially inoculated nursery. In 2011, genes *Lr9*, *Lr19*, *Lr25*, *Lr28*, and *Lr29* provided effective protection against leaf rust in Martonvásár. Resistance genes (*Lr9*, *Lr24*, *Lr25*, *Lr29*, *Lr35*, *Lr37*, *Pm21*, and *Stb2* were introduced into wheat cultivars adapted to Hungary. By jointly incorporating several resistance genes (pyramiding), winter wheat genotypes carrying new *Lr* gene combinations were developed.

Stem rust resistance. Among the genotypes carrying designated *Sr* genes, lines with *Sr28*, *Sr30*, or *Sr36* were highly resistant to stem rust and, additionally, some more major resistance genes (A, B, C, and D alleles of *Sr9*, *Sr13*, *Sr18*, *Sr31*, and *Sr33*) provided effective resistance againts the spread of the pathogen.

Powdery mildew virulence survey. Studies on the composition of the wheat powdery mildew population showed that race 77 was present in the highest ratio (47.6%) in 2011, followed by race 76 (40.2%). Race 51, which infected all the cultivars tested for differentiation, appeared in an even lower frequency than in the previous year (3.9%). The virulence complexity of the pathogen population was 5.46, which represented a decline compared to previous years.

Impact of elevated atmospheric CO_2 level on disease resistance. Susceptible wheat varieties were found to become more susceptible to leaf rust and stem rust when grown at doubled atmospheric CO_2 level. Resistant cultivars were, however, unaffected by high CO_2. The severity of Fusarium head blight infection in susceptible wheat cultivars also was enhanced under high CO_2, despite that the establishment of the pathogen was delayed in some cases.

Abiotic stress resistance studies. The role of the biotic and abiotic stresses in the antioxidant enzyme activities of wheat cultivars was determined. Based on the results of phytotron and field studies, we found that the activity of peroxidases was outstandingly high in winter, whereas catalase played a role in mitigating the harmful environmental effects in the early summer. The levels of glutathione reductase, glutathione-S-transferase, and guaiacol peroxidase were found to correlate positively with water shortage.

A preliminary molecular genetic study on 759 wheat cultivars, either bred in Martonvásár or originating from various parts of Europe, was carried out. The allele compositions of the major genes regulating vernalization and day-length sensitivity (*VRN-A1*, *VRN-B1*, *VRN-D1*, and *PPD-D1*) were determined in the test sortiment. Based on the genetic diversity, wheat genotype subgroups with even population structures were established (262 genotypes) and drawn into further thorough field and laboratory analyses. The date of anthesis and the grain yield components were determined in the first field experiment with the subgroups.

A mapping population created with the SSD method was tested with SSR markers of known chromosome localization for the background of heat tolerance. Twenty-nine SSR markers were mapped on 323 lines of the wheat population. We selected 282 lines to investigate DArT to create a molecular marker map of the population.

The water use efficiency (WUE) of small grain cereals was investigated at optimum water supply level and under water withdrawal. We found that the water use of cereals was the highest during heading. The greatest amount of water during the entire vegetation period was used by winter barley, irrespective of the water supply level. The requirement of oats was a little lower, whereas water uptake was considerably less for wheat genotypes. The mean values of WUE (m^3 water/kg grain yield) at normal water supply level and under water stress, respectively, were 0.54 and 0.716 for the wheat cultivars, 0.73 and 1.28 for winter barley, and 1.2 and 2.02 for winter oats.

According to a field experiment on the drought tolerance of a biparental dihaploid genetic population, the plants grown under precipitation shortage, without irrigation, headed significantly earlier than those that received irrigation. Significant decreases in the population in plants receiving no irrigation were found in the mean values for plant height parameters, including the length up to the flag leaf, and to the base and top of the spike, but also in the total number of nodes, length of the last internode, and the number of productive tillers. A considerable reduction in the foliage during the vegetation period also was observed.

A comprehensive tool to manage and analyze phenotypic and molecular breeding data.

In recent years, an information system has been elaborated and constantly improved in Martonvásár, making it possible to handle the 3–4 x 10^6 identifications, observations, measurements, pedigree, and other data generated for a total of nearly 120,000 experimental plots each year. The data were grouped according to subject, leading to different data structures within the data model: (1) breeding databases, which are renewed from one year to the next; (2) a genealogical database; (3) a seed exchange database; and (4) a genebank database.

For the data to be available within the information system, special applications were designed to support various research tasks. These applications are based on the technological description of the task in question. Approximately 50 applications are included in the ‘Breeder’ user interface, providing uniform availability to breeders and other agricultural staff. The uniform framework of the various modules contains menus, submenus, and a quick launch toolbar for the most frequently used program modules such as crossing, selection, or plot design.

When crosses are made, the program automatically creates the new pedigree, selection history, and saves major data related to the various crossing programs in crossing lists.

The selection module records the origin of the genotype (previous year: experiment, plot), number of rows planted, automatically develops selection history, and provides links with variety maintenance and frost and resistance testing. The program automatically records grain weight and it is possible to automatically select genotypes according to previously adjusted scoring values or other previously established conditions.

The plot design module is able to automatically add checks or elaborate experiments of a given size. When the plot order is finalized, the breeder has the option of distinguishing between particular spike types, arranging the lines in order of heading, or grouping related lines within genotypes.

The seed exchange module stores information on all the incoming and outgoing seed lots for Hungarian and foreign breeding programs.

The gene bank module was designed to store data on genetic resources and has links to the breeding and genealogical data.

A uniform pedigree model, capable of creating a unique identification code for each genotype and handling the homonyms and synonyms, is one of the cornerstones of the information system. The pedigree data-handling module automatically assign two identification codes to each pedigree; PID identifies the combination and SID differentiates between sister lines arising from the same crossing combination. The name of each genotype appears only once across the whole system, and genealogical information can be attached from here to the records of individual years or experiments.

No special statistical packages are required for the basic statistical analysis of experiments sown at one or more locations, the statistical evaluation of replicated single-factor and multi-factor experiments was incorporated into the system.

Automated data collection is used for instant and automatic capturing of data and information from various sources and is based on automatic data identification. Automatic data identification is based on barcodes, so a module designed to generate and print barcodes was incorporated into the system. With the help of the module, combining a number of data fields into a single barcode and printing them onto self-adhesive or plastic labels directly from the database is possible.

Later, a separate data structure was introduced to accommodate molecular data elements, such as gene source, primer bank, primer combinations, markers, genes, and alleles, but also data management tools and a standalone software interface to combine both molecular and phenotypic data.

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Department of Plant Genetic Resources and Organic Breeding

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Association between pericentromeric SSR bands and intergenomic translocation breakpoints in natural populations of *Aegilops biuncialis* and *Ae. geniculata*. Repetitive DNA sequences are thought to be involved in the formation of intergenomic translocations, which is an important step in allopolyploid speciation. The allotetraploids *Ae. biuncialis* and *Ae. geniculata*, wild, genetic resources for wheat improvement, are excellent objects to study the role of microsatellite clusters in the formation of intergenomic translocations. The chromosomal localization of (ACG)n and (GAA)n microsatellite sequences in *Ae. biuncialis* and *Ae. geniculata* and their diploid progenitors *Ae. comosa* and *Ae. umbellulata* was investigated by sequential *in situ* hybridization with SSR probes and repeated DNA probes (pSc119.2 Afa family and pTa71) and by dual-color GISH. Thirty-two *Ae. biuncialis* and 19 *Ae. geniculata* accessions were screened by GISH for translocations, which were further identified by FISH and GISH. Single pericentromeric (ACG)n signals were localized on most U- and on some M-genome chromosomes, whereas strong pericentromeric and several intercalary and telomeric (GAA)n sites were observed on the *Aegilops* chromosomes. Three *Ae. biuncialis* accessions carried $T7U^b–7M^b$ reciprocal translocations and one had a $T7U^b–1M^b$ rearrangement, and two *Ae. geniculata* accessions carried $T7U^g–1M^g$ or $T5U^g–5M^g$ translocations. Conspicuous (ACG)n and/or (GAA)n clusters were located near the translocation breakpoints in eight out of the ten translocated chromosomes analyzed, SSR bands and breakpoints being statistically located at the same chromosomal site in six of them. SSR clusters seem to be involved in the formation of intergenomic translocations between the constituent genomes of allopolyploid *Aegilops* species. The (ACG)n and (GAA)n SSR motifs serve as additional chromosome markers for the karyotypic analysis of UM-genome *Aegilops* species.

Chromosome isolation by flow sorting in *Ae. umbellulata* and *Ae. comosa* and their allotetraploid hybrids *Ae. biuncialis* and *Ae. geniculata*. An international cooperation with Jaroslav Doležel (Centre of the Region Haná for Biotechnological and Agricultural Research, Institute of Experimental Botany, Olomouc, Czech Republic) was carried out to study the potential of flow cytometry for chromosome sorting in the wild wheats *Ae. umbellulata* (2n=2x=14, UU) and *Ae. comosa* (2n=2x=14, MM) and in their natural hybrids *Ae. biuncialis* (2n=4x= 28, $U^bU^bM^bM^b$) and *Ae. geniculata* (2n=4x=28, $U^gU^gM^gM^g$). Histograms of fluorescence intensity (flow karyotypes) obtained after the analysis of DAPI-stained chromosomes were characterized and the chromosome content of the four peaks on flow karyotypes was determined for the first time for these *Aegilops* species. Chromosomes sorted onto microscope slides were identified after FISH with probes pSc119.2, Afa repeats, and pTa71. Only chromosome 1U could be discriminated by the peak I on flow karyotypes of *Ae. umbellulata* and *Ae. biuncialis* with the standard karyotype. Microscopic evaluation of the sorted fractions showed that chromosome 1U could be sorted at purity >95%. Remaining chromosomes formed composite peaks and could be sorted only as groups. Distribution of chromosomes among the peaks of flow karyotypes reflected different size modifications for the chromosomes 4U, 1M, 2M, 3M, 4M, and 6M in the *Ae. biuncialis* and *Ae. geniculata*. Twenty-four wheat SSR markers were used to map the U- and M-genome chromosomes by the use of DNA amplified from the sorted chromosome fractions and wheat–*Ae. geniculata* addition lines. Ten SSR markers located unambiguously on the *Aegilops* chromosomes supported the chromosome content of sorted fractions and confirmed the suitability of flow-sorted chromosomes for physical mapping. These SSR markers are suitable tools for the marker-assisted production of wheat–*Aegilops* introgression lines. These results open the way for the construction and sequencing of large-insert, chromosome 1U-specific, DNA libraries in *Ae. umbellulata* and *Ae. biuncialis*, which would greatly promote the targeted isolation of molecular markers and the discovery of novel genes for the wheat improvement.

Characterization of a new T4BS·7HL wheat/barley translocation line using GISH, FISH, and SSR markers and its effect on the β-glucan content of wheat. A spontaneous interspecific Robertsonian translocation was revealed by GISH in the progenies of a monosomic 7H addition line originating from a new wheat/barley, 'Asakaze komugi/Manas' hybrid. FISH with repetitive DNA sequences Afa family, pSc119.2, and pTa71 allowed identification of all wheat chromosomes, including wheat chromosome arm 4BS involved in the translocation. FISH using barley telomere- and centromere-specific repetitive DNA probes (HvT01 and AGGGAG) confirmed that one of the arms of barley chromosome 7H was involved in the translocation. SSR markers specific to the long and short arms of barley chromosome 7H identified the translocated chromosome segment as 7HL. Further analysis of the translocation chromosome clarified the physical position of genetically mapped SSRs within 7H, with a special focus on its centromeric region. The presence of the HvCslF6 gene, responsible for (1,3;1,4)-β-D-glucan production, was revealed in the centromeric region of 7HL. An increased (1,3;1,4)-β-D-glucan level also was detected in the translocation line, demonstrating that the HvCslF6 gene is of potential relevance for the manipulation of wheat (1,3;1,4)-β-D-glucan levels.

Constructing a detailed mcFISH karyotype and studying chromosome polymorphisms of *Elytrigia elongata* E genome using highly repetitive and rDNA sequences. *Elytrigia elongata* (= *Agropyron elongatum*, *Thinopyrum elongatum*, 2n=2x=14, EE) has long been used as a source of various resistance for wheat improvement, and numerous transfers have been made. However, despite heavy use, the species has never enjoyed cytological attention it deserves and no high resolution karyotype exists, perhaps because its chromosomes do not C-band well and the genome is rather symmetrical. As the interest in *E. elongata* for wheat improvement does not appear to abate, and alien transfers are now routinely detected and followed using the techniques of *in situ* probing with labelled DNA, a detailed FISH karyotype of the E genome was generated and verified in several accessions. The karyotype itself was generated using highly repetitive DNA sequences and sequential GISH–mcFISH; chromosome identification was using the complete *E. elongata* disomic chromosome addition series and 11 ditelosomic addition lines in Chinese Spring wheat. The E-genome chromosomes in a wheat background were detected by probing with the total genomic DNA of *E. elongata*, followed by mcFISH with five repetitive DNA probes. Of these, two clones failed to hybridize to the E-genome chromosomes. Based on the successful mcFISH, each complete chromosome and each telocentric studied was unambiguously identified. Validation of the karyotype in four *E. elongata* accessions with different geographical origins showed extensive variation of the probe hybridization patterns but this did not prevent positive chromosome identification. We believe that this karyotype will be useful in quick identification of potential donor chromosomes in wheat improvement programs so that proper alien transfer approaches can be selected and implemented.

Development of synthetic amphiploids based on different *Triticum turgidum* × *T. monococcum* crosses to improve the adaptability of cereals. Cultivated einkorn (*T. monococcum* subsp. *monococcum*) is an excellent source of resistance against several wheat diseases and quality parameters. Semidwarf, einkorn lines with good crossability were identified in order to produce '*T. turgidum* × *T. monococcum'* synthetic amphiploids. Two combinations were used to develop the amphiploids: 'durum × einkorn' and 'emmer × einkorn'.

After the genome duplication of the F_1 seed, highly fertile amphiploids were developed. The A^uBA^m genome structure of the progenies was confirmed by GISH. Lines derived from 'durum × einkorn' and 'emmer × einkorn' crosses were studied for agronomic performance, disease resistance, and genetic variability. Both amphiploid combinations showed excellent resistance against certain wheat diseases (leaf rust and powdery mildew), but not against Fusarium. The durum-based synthetic amphiploid lines showed a higher level of phenotypic diversity. The newly produced '*T. turgidum* × *T. monococcum*' synthetic hexaploids are promising genetic resources for wheat breeding. Selected 'durum × einkorn 'lines are currently used in bread wheat improvement to transfer the useful properties of einkorn into cultivated hexaploid wheat via bridge crosses.

Martonvásár Cereal Gene Bank and Organic Plant Breeding. The Cereal Gene bank activity mainly concentrated on the characterization of the different resistance sources such as *T. monococcum* and *T. timopheevii* accessions, and their possible use in the development of new synthetic amphiploids. New, highly crossable, semidwarf, *T. monococcum* lines have been developed, and crossed with selected *T. turgidum* subsp. *durum* and *T. timopheevii* accessions or selected breeding lines. Triploids were identified in the F_1 generation, and treated with colchicine to double the chromosome number of the interspecific hybrids. Fertile hexaploids were selected in the C_2 generation and multiplied under greenhouse conditions. The new synthetics will be used in wheat-improvement programs and are target of independent breeding line development.

Our organic breeding program is highly focused on the development of new, organic cultivars of alternative or underutilized cereals such as einkorn and emmer. A new, organically bred, einkorn cultivar, **Mv Menket**, was released last year. This is the first semidwarf einkorn cultivar in the market, with elevated yield potential, and excellent resistance against most of the wheat diseases, except Fusarium. Mv Menket is an organic cultivar, because it is highly sensitive against all herbicides used in the Hungarian farming practice, and there is no possibility to use it in traditional agricultural practices.

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ITEMS FROM INDIA

DIRECTORATE OF WHEAT RESEARCH

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A study of floral biology traits in bread wheat.

S.K. Singh and Dharmendra Singh.

Summary. Three floral biology traits, anther length, stigma length, and anther extrusion, were investigated in 92 elite wheat germ plasm lines. A wide range of variability was observed for these floral traits and promising genotypes were identified for their further utilization as parents for hybrid wheat development.

Wheat productivity levels in the present genotypes have reached a saturation level, which limits higher production to meet the targets for food security. Newer, innovative techniques can be promising approaches in order to break yield barriers and, in this regard, hybrid wheat development through exploitation of heterosis may be a potential tool. Wheat production in the Northwest Plains Zone has reached peak yields. Knowledge about the variability and character association between floral characteristics is crucial to identify suitable male or female parental lines for further utilization in hybrid development programs. Our objective was to study the extent of variability present in some wheat genotypes for various floral characters and establish correlations between them.

Materials and methods. A total of 92 elite genotypes maintained by the Hybrid Wheat Programme were used in the study. These entries included elite selections from international nurseries and trials from CIMMYT; genetic stocks;