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Identification and phenotypic description of new wheat – six-rowed, winter barley disomic additions. To increase the allelic variation in wheat–barley introgression lines, new wheat–barley disomic addition lines were developed containing the 2H, 3H, 4H, 6H, and 7H chromosomes of the six-rowed Ukrainian winter barley Manas. This cultivar is agronomically much better adapted to the central European environment than the two-rowed spring barley Betzes previously used. A single 'Asakaze/Manas' wheat × barley hybrid plant was multiplied in vitro and one backcross plant was obtained after pollinating 354 regenerated hybrids with wheat. The addition lines were selected from the self-fertilized seeds of the 16 BC2 plants using genomic in situ hybridization. The addition lines were identified by fluorescence in situ hybridization (FISH) using repetitive DNA probes (HvT01, GAA, pTa71, and Afa family), followed by confirmation with barley SSR markers. The addition lines were grown in the phytotron and in the field, and morphological parameters (plant height, fertility, tillering, and spike characteristics) were measured. The production of the disomic additions will make it possible to incorporate the DNA of six-rowed winter barley into the wheat genome. Addition lines are useful for genetic studies on the traits of six-rowed winter barley and for producing new barley dissection lines.

High-resolution, molecular cytogenetic techniques in plants: pachytene- and fiber-FISH. FISH is the most versatile and accurate molecular cytogenetic technique for determining euchromatic-heterochromatic boundaries and the locations of repetitive and single-copy DNA sequences and of chromosome-specific BAC clones on chromosomes. The combination of cytogenetic and genetic methods yields a high-resolution physical map. FISH allows direct mapping of specific DNA sequences inside the cell (interphase nuclei), along meiotic pachytene chromosomes and isolated chromatin (DNA fibers). The increased sensitivity of the technique, and its ability to detect gene locations provide a powerful research tool for genetic and prebreeding studies. FISH-based, physical mapping plays an important role and is increasingly

used for studies at the cytological level on the chromatin organization that controls gene expression and regulation. The mini-review describes some of the benefits of alternative FISH-based techniques and their application for studying plant chromosomes and genomes.

Karyotypic analysis of *Triticum monococcum* using standard repetitive DNA probes and simple-sequence repeats. *Triticum monococcum* represents an important source of useful genes and alleles that it would be desirable to use in wheat breeding programs. The well-defined landmarks on the A^m chromosomes could accelerate the targeted introgression of *T. monococcum* chromatin into the wheat genome. FISH, using the repetitive DNA probes pSc119.2, the Afa family, and pTa71, showed that the pSc119.2 probe was not suitable for the identification of A^m chromosomes. In contrast, the whole set of A^m chromosomes (especially chromosomes 1, 4, 5, and 7) could be discriminated based on the hybridization pattern of pTa71 and the Afa family. In situ hybridization with microsatellite motifs (GAA, CAG, AAC, and AGG) proved that SSRs represent additional landmarks for the identification of A^m chromosomes. The most promising SSR probes were the GAA and CAG motifs, which clearly discriminated the $6A^m$ chromosome and, when used in combination with the Afa family and pTa71 probes, allowed the whole set of A^m chromosomes to be reliably identified. In conclusion, FISH using the repetitive DNA probes of the Afa family and pTa71, combined with SSR probes, makes it possible to identify the A^m chromosomes of *T. monococcum* and discriminate them from A^u chromosomes in the polyploid wheat background.

Detection of various U and M chromosomes in wheat–*Aegilops biuncialis* hybrids and derivatives using FISH and molecular markers. The aim of the study was to select wheat–*Ae. biuncialis* addition lines with *Ae. biuncialis* chromosomes differing from those that were introgressed into the wheat–*Ae. biuncialis* addition lines produced earlier in Martonvásár, Hungary. During the experiments, new wheat–*Ae. biuncialis* addition lines with chromosomes $2U^b$, $3U^b$, $5U^b$, $6U^b$; $7U^b$, $5M^b$, $6M_b$, and $7M^b$ were selected. The $2U^b$ disomic addition line is relatively stable; 91% of the progenies contain this chromosome pair. The $6M^b$ disomic addition line proved to be dwarf and sterile, but still exists as a monosomic addition line. Progenies analyzed from the $6U^b$ monosomic addition line did not carry the $6U^b$ chromosome. One plant containing the $5U^b$, $3U^b$, and $7U^b$ chromosomes and one plant with chromosomes $5M^b$, $6M^b$, and $7M^b$ showed very low fertility. Each of the plants produced a single seed, but seeds of the parent plants are still available. Line 49/00 carried a submetacentric *Ae. biuncialis* chromosome pair and the chromosome number 44 has been constant for several generations. After FISH, no hybridization site was observed on the *Ae. biuncialis* chromosome pair using the pSc119.2 and Afa family repetitive DNA probes, so it was not possible to identify the *Ae. biuncialis* chromosome pair. However, using wheat SSR markers and the (GAA)n microsatellite DNA probe allowed it to be characterized more accurately. These new lines facilitate gene transfer from *Ae. biuncialis* into cultivated wheat and the selection of U- and M-genome-specific wheat SSR markers.

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ITEMS FROM INDIA

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Molecular breeding, induced mutagenesis, and transcriptome analysis in wheat.

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Deployment of molecular markers for the improvement of some important quality traits and drought tolerance in bread wheat. We are attempting to pyramid one or more QTL/genes for grain quality traits along with the *Lr24* gene for leaf rust resistance into a number of high-yielding Indian wheat cultivars with a view to develop wheat cultivars with improved grain protein content (GPC), leaf rust resistance, and preharvest sprouting tolerance (PHST) using marker-assisted selection (MAS). QTL for grain yield under water stress are also being introgressed into high-yielding Indian wheat cultivars, which are otherwise drought sensitive. The progress made in relation to the above objectives is summarized below.

MAS for grain protein content (GPC) and leaf rust resistance. To introgress two genes, one for high GPC (*Gpc-B1*) and the other for leaf rust resistance (*Lr24*), two high-yielding recipient Indian bread wheat cultivars (Lok1 and HD2967) were crossed with a donor genotype PBW343 (*Gpc-B1+Lr24*). The initial crosses were made at the Research Farm, CCSU, Meerut, during 2009–10 crop season. The two resulting F_1s were grown and backcrossed with the respective recipient genotype in an off-season nursery at the Keylong Research Station during the summer of 2010. Seeds of two BC_1F_1s were planted at Research Farm CCSU, Meerut, during 2010–11. Foreground MAS in the two BC_1F_1s was carried out in two steps; the two BC_1F_1 populations included 938 plants for the recipient parents Lok1 and 1,015 plants for the recipient parent HD2967. These BC_1F_1 plants were screened using a SSR marker (ucw108) specific to the *Gpc-B1* gene for high GPC. As a result, 340 plants involving Lok1 and 149 plants involving HD2967 were selected from the two backcross populations. Foreground selection for leaf rust resistance gene *Lr24* was carried out on the GPC positive plants using SCAR marker SCS73719; 147 BC_1F_1 plants involving Lok1 and 39 BC_1F_1 plants involving HD2967 each carried both the *Gpc-B1* and *Lr24* genes, and were selected for background selection.

For background selection, a set of 127 SSRs were used for plants involving Lok1 and 118 SSRs were used for plants involving HD2967. The SSR markers for background selection were chosen such that these were evenly distributed on all the 21 wheat chromosomes. In this manner, eight BC_1F_1 plants (involving Lok1) with >80% RPG recovery were selected and these plants were backcrossed with the recipient genotype Lok1 again to obtain BC_2F_1 seeds. However, no BC_1F_1 plant involving HD2967 could be selected for further backcrossing, because each of the selected plants contained donor parent allele in homozygous condition for one or more SSR markers. This observation was unexpected and could not be explained without further studies, which we propose to undertake in future.

The BC_2F_1 population involving Lok1 was raised in an off-season nursery at Keylong Research Station during 2011. Foreground selection for *Gpc-B1* and *Lr24* was in a set of 248 BC_2F_1 plants; 43 positive plants with the two genes were selected. Background selection of these 43 plants with the help of SSR markers that were in heterozygous state in BC_1F_1 plants led to the selection of eight plants with >93% RPG recovery, and BC_2F_1 seed was harvested. Eight BC_2F_2 progenies were planted during the 2011–12 crop season at the Research Farm at CCSU, Meerut. Out of 380 BC_2F_2