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Development of a wheat genotype combining the recessive crossability alleles *kr1kr1kr2kr2* and the T1BL·1RS translocation for the rapid enrichment of 1RS with new allelic variation. The main objective of this work was to develop a wheat genotype containing both the recessive crossability alleles (*kr1kr1kr2kr2*), allowing high crossability between 6x wheat and diploid rye, and the T1BL·1RS wheat–rye translocation chromosome. This wheat genotype could be used as a recipient partner in wheat–rye crosses for the effcient introduction of new allelic variation into 1RS in translocation wheats. After crossing the wheat cultivars Mv Magdaléna and Mv Béres, which have the T1BL·1RS translocation involving chromosome arm 1RS from Petkus rye, with the line Mv9 *kr1*, 117 F_2 plants were analyzed for crossability, 10 of which had higher than 50% seed set with rye and, thus, presumably carried the *kr1kr1kr2kr2* alleles. Four of the 10 plants contained the T1BL·1RS translocation in the disomic condition as detected by GISH. The wheat–rye F_1 hybrids produced between these lines and the rye cultivar Kriszta were analyzed in meiosis using GISH. T1BL·1RS/1R chromosome pairing was detected in 62.4% of the pollen mother cells . The use of FISH with the repetitive DNA probes pSc119.2, Afa family, and pTa71, allowed the 1R and T1BL·1RS chromosomes to be identified. The presence of the 1RS arm from Kriszta, besides that of Petkus, was demonstrated in the F_1 hybrids using the rye SSR markers RMS13 and SCM9. In four of the 22 BC_1 progenies analyzed, only Kriszta-specific bands were observed with these markers, although the presence of the T1BL·1RS translocation was detected using GISH. We concluded that recombination occurred between the Petkus and Kriszta 1RS chromosome arms in the translocated chromosome in these plants.

GISH reveals different levels of meiotic pairing with wheat for individual *Ae. biuncialis* chromosomes. The *T. aestivum–Ae. biuncialis* (2n=4x=28; $U^bU^bM^bM^b$) disomic addition lines $2M^b$, $3M^b$, $7M^b$, and $3U^b$ were crossed with the wheat cultivar Chinese Spring *ph1b* mutant genotype in order to induce homoeologous pairing, with the final goal of introgressing *Ae. biuncialis* chromatin into cultivated wheat. Wheat–*Aegilops* homoeologous chromosome pairing was studied in metaphase I of meiosis in the F_1 hybrid lines. Using U and M genomic probes, GISH demonstrated the occurrence of wheat–*Aegilops* homoeologous pairing for chromosomes $2M^b$, $3M^b$, and $3U^b$, but not for $7M^b$. The wheat-*Aegilops* pairing frequency decreased in the following order: $2M^b > 3M^b > 3U^b > 7M^b$, which may reflect differences in

the wheat-*Aegilops* homoeologous relationships between the examined *Aegilops* chromosomes. The selection of wheat–*Aegilops* homoeologous recombinations could be successful in later generations.

Molecular cytogenetic evaluation of chromosome instability in *T. aestivum–S. cereale* disomic addition lines. The genetic stability of wheat–rye (Chinese Spring–Imperial) disomic addition lines was checked using the Feulgen method and FISH. Feulgen staining detected varying proportions of disomic, monosomic, and telosomic plants among the progenies of the disomic addition lines. The greatest stability was observed for the 7R addition line, whereas the most unstable lines were those with 2R and 4R additions. Chromosome rearrangements also were detected using FISH. Based on the specific hybridization patterns of repetitive DNA probes pSc119.2 and (AAC)5, as well as ribosomal DNA probes (5S and 45S), isochromosomes were identified in the progenies of 1R and 4R addition lines. These results draw attention to the importance of continuous cytological checks on basic genetic materials by using FISH, because this method reveals chromosome rearrangements that could not be detected either with the conventional Feulgen staining technique or with molecular markers.

Selection of U and M genome-specific wheat SSR markers using wheat–*Ae. biuncialis* and wheat–*Ae. geniculata* addition lines. Wheat SSR markers specific to the U and M genomes of *Aegilops* species were selected. A total of 108 wheat SSR markers were successfully tested on *Ae. biuncialis* (2n = 4x = 28, $U^bU^bM^bM^b$), on five wheat–*Ae. biuncialis* addition lines ($2M^b$, $3M^b$, $7M^b$, $3U^b$, and $5U^b$) and on a wheat–*Ae. geniculata* ($1U^g$, $2U^g$, $3U^g$, $4U^g$, $5U^g$, $7U^g$, $1M^g$, $2M^g$, $4M^g$, $5M^g$, $6M^g$, and $7M^g$) addition series. Among the markers, 86 (79.6%) were amplified in the *Ae. biuncialis* genome. Compared with wheat, polymorphic bands of various lengths were detected in *Ae. biuncialis* for 35 (32.4%) of the wheat microsatellite markers. Three of these (8.6%) exhibited specific PCR products in wheat–*Ae. biuncialis* or wheat–*Ae. geniculata* addition lines. The primers GWM44 and GDM61 gave specific PCR products in the $2M^b$ and $3M^b$ wheat–Ae. biuncialis addition lines, but not on the $2M^g$ addition line of *Ae. geniculata*. A specific band was observed on the $7U^g$ wheat–*Ae. geniculata* addition line using the BARC184 primer. T hese three markers specific to the U and M genomes are helpful for the identification of $2M^b$, $3M^b$, and $7U^g$ chromosome introgressions into wheat.

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ITEMS FROM INDIA

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Application of Real-Time PCR in marker-assisted selection for stem rust resistance gene Sr24.

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Introduction. Real-Time PCR (RT–PCR) is a technique mainly used to amplify and simultaneously quantify a targeted DNA molecule (Gibson et al. 1996). Currently, four different chemistries, TaqMan® (Applied Biosystems, Foster City, CA, USA); Molecular Beacons (Newark, New Jersey, USA); Scorpions® (Sigma-Aldrich, St. Louis, MO, USA); and SYBR® Green (Life Technologies, Carlsbad, CA, USA), are available for RT-PCR. All of these chemistries allow