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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.

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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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