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Molecular cytogenetic identification of a novel 1AL.1RS translocation line with powdery mildew resistance

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ABSTRACT. A wheat germplasm line 13-2-2 with resistance to powdery mildew was isolated; this line was derived from common wheat cv. W770B and rye, *Secale cereale* L. (2n = 2x = 14, RR). The line was characterized based on cytological, genomic *in situ* hybridization (GISH), sequence-characterized amplified region (SCAR), and simple sequence repeat (SSR) analyses. The mitotic and meiotic investigations showed that the chromosome number and configuration of 13-2-2 were 2n = 42 = 21 II. GISH using rye genomic DNA as a probe detected a pair of R genome chromosome arms with strong hybridization signals in 13-2-2. Three 1RS chromosome-specific SCAR markers amplified 1RS specific bands in line 13-2-2. We screened 320 SSR primer pairs on the long or short arms from seven wheat homoeologous groups in the translocation line and parents. However, only three 1AS primers could not be amplified in line 13-2-2, whereas the others were amplified. Thus, these markers suggested that the line 13-2-2 was 1AL.1RS translocation line. Line 13-2-2 was immune to powdery

mildew after inoculation with *Blumeria graminis* f. sp. *tritici* isolates E05 and E07 during the adult plant stages. In contrast, the maternal parent W770B, Kavkaz with *Pm8*, and Amigo with *Pm17* were heavily infected with spores and had reaction response scores of susceptible. Thus, the new wheat-rye 1AL.1RS translocation line with resistance to powdery mildew could be a new and valuable donor source for wheat improvement. The molecular markers developed in this study might also be useful tools for marker-assisted selection.

Key words: 1AL.1RS translocation line; *Secale cereale* L.; Sequence-characterized amplified region; Simple sequence repeat Genomic *in situ* hybridization; *Triticum aestivum*;

