



Diversity resistance to *Puccinia striiformis* f. sp *Tritici* in rye chromosome arm 1RS expressed in wheat

M.Y. Yang, T.H. Ren, B.J. Yan, Z. Li and Z.L. Ren

Key Laboratory for Plant Genetics and Breeding,
Sichuan Agricultural University, Chengdu, Sichuan, China

Corresponding authors: T.H. Ren / Z.L. Ren
E-mail: renxx@umn.edu / renzllab@sicau.edu.cn

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ABSTRACT. The 1BL.1RS wheat-rye translocation contained in the Russian cultivar Aurora has been the most widespread alien translocation in wheat-breeding programs all over the world. However, following the prevalence of new biotypes of the pathogens, disease-resistance genes in this translocation chromosome have been overcome and consequently they have been eliminated in modern wheat-breeding programs. In this paper, we report on 12 new primary 1BL.1RS translocation lines derived from the crosses of a Chinese high yield wheat cv. Mianyang 11 with three rye cultivars collected from China. GISH, C-banding and PCR techniques using the specific primers for 1BS, 1RS and centromeres of wheat and rye were applied to identify the constitution of chromosomes. The results confirmed that all 1BL.1RS chromosomes in the 12 primary translocation lines contained integrated 1RS chromosome arms. In the resistance analysis using five kinds of *Pst* pathotypes, the 12 primary translocation lines showed diversity resistance to stripe rust, which contained at least five different new genes (alleles), significantly different from the *Yr9* gene coming from Russian wheat cultivar Aurora. The results indicated that the chromosome arm 1RS in the rye population carries abundant yet untapped genes (alleles) for resistance to wheat stripe rust, which

would originate from the neutral diversity in the natural population of rye. It is suggested that creating more primary translocation lines in genome modification will be extremely important to use the diversity of alien R-genes, which was generated by long-term neutral mutation and maintained in the population of alien species.

Key words: *Triticum aestivum*; *Secale cereale*; 1BL.1RS translocation; *Puccinia striiformis* f. sp *Tritici* pathotypes; Diversity of R-genes