

Wheat-rye T2BS·2BL-2RL recombinants conferring resistance to Hessian fly (H21).

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The Hessian fly, *Mayetiola destructor* (Say), is a destructive insect pest of bread wheat *Triticum aestivum* L. worldwide. Although 32 genes conferring resistance to Hessian fly have been identified, only a few of them are still effective. One such highly effective gene is *H21*, which was transferred to wheat from Chaupon rye via a compensating T2BS·2R#2L Robertsonian, whole-arm, wheat-rye translocation. This translocation also has a locus for field resistance to powdery mildew. To broaden the use of T2BS·2R#2L in wheat improvement, we attempted to transfer both resistance loci, via homologous recombination, to a T2BS·2BL-2R#2L chromosome. The *H21* locus was linked closely to the telomere; the powdery mildew locus was distal, but closely linked, to the translocation breakpoint in T2BS·2BL-2R#2L. Recovered short-segment, rye translocation chromosomes confer resistance to Hessian fly; no crossover event in the desirable configuration was recovered to produce a short-segment, wheat-rye translocation with both *H21* and the powdery mildew resistance gene present. The T2BS·2BL-2R#2L recombinant chromosome has been transferred to adapted winter and spring wheat cultivars.

An adult-plant resistance gene to stripe rust is located on chromosome 2AS in the hexaploid wheat cultivar Jagger.

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Stripe rust is one of the most common and persistent wheat diseases worldwide. With the continuous evolution of different pathogen races, new resistance genes are needed to defend against the mutated pathogens. In this study, we report that a major quantitative trait locus (QTL) for stripe rust resistance was located on the short arm of chromosome 2A (*QYr.osu.2A*) in a population of recombinant inbred lines (RILs) generated from a cross between Jagger and 2174, two prominent winter wheat cultivars in the southern Great Plains, USA. *QYr.osu.2A* was mapped when this population was tested at two sites in Washington where stripe rust frequently occurs and in Beijing, PR China, where CYR32 was inoculated on adult plants. *QYr.osu.2A* explained 81 to 85% of the total phenotypic variation in relative area under the disease progress curve (rAUDPC) value, showing its nearly complete resistance against natural field infection of stripe rust on adult plants in Washington. Stripe rust races included PST-100, PST-114, PST-116, and PST-138, which frequently occur in Washington and other regions of the U.S. such as the Great Plains. *QYr.osu.2A* also accounted for 36% of the total phenotypic variation, showing its partial resistance to CYR32, currently one of the predominant Chinese races and virulent to 80% of commercial cultivars and germplasm in China. In addition, a minor QTL was mapped on the long arm of chromosome 5A (*QYr.osu.5A*), explaining 22 to 30% of the total phenotypic variation across years and locations. Jagger carried a resistant allele at both *QYr.osu.2A* and *QYr.osu.5A*, whereas 2174 carried a susceptible allele at both loci. Our findings suggest that the *de novo* resistance gene at *QYr.osu.2A* in Jagger can provide consistent and broad-spectrum, adult-plant protection to stripe rust. Resistance in Jagger has remained effective during the 15 years since its release, and we recommend this source of resistance be used in breeding applications in conjunction with the molecular markers. This study also demonstrated that many resistance genes present in local cultivars and available mapping populations can be identified and characterized when they are tested in diverse geographical areas of wheat worldwide.