Registration of UCRBW98-1 and UCRBW98-2
Wheat Germplasms with Leaf Rust and Greenbug Resistance Genes

Two wheat (Triticum aestivum L.) germplasms with interstitial translocations (UCRBW98-1, Reg. no. GP-594, PI 603918 and UCRBW98-2, Reg. no. GP-595, PI 603919) were developed to transfer genes for resistance to leaf rust (caused by Puccinia triticina Eriks.) and greenbug (Schizaphis graminum Rondani) from chromosome 7S of Triticum speltoides (Tausch) Gren. The origin of chromosome 7S is not clear (1, 3) but likely it originated from a population obtained by irradiation of a hybrid CI15092/T. speltoides///Fletcher///3/5*Centurk with fast neutrons (7). Translocations of segments of 7S to 7A were produced by recombination induced by the ph1b mutation (3). Sears’ (4) strategy was followed to reduce the length of the alien chromosome segments. All manipulations were performed in hard white spring cultivar Pavon F76; a total of eight backcrosses were made to Pavon and the likely pedigree of both lines is CI15092/T. speltoides///Fletcher///3/5*Centurk/4/4*Pavon F76/5/Pavon ph1b/6/3*Pavon F76 where Pavon ph1b is Chinese Spring ph1b /8*Pavon M5B. Plants homozygous for the interstitial translocations were selected by C-banding. Translocations were characterized using molecular markers (1).

The short arm translocation line Pavon T7AS-7S#1S-7A:S7AL designated UCRBW98-1 (PI 603918) carries resistance gene Lr47 for leaf rust. This gene confers resistance to a wide spectrum of leaf rust races including nine that are virulent on resistance genes Lrl and Lr10 present in Pavon F76 (PRT codes: TBT-10, NBB-10, MBR-10, LCG-10, SDJ-10, MBG-10, NDB-10, MCG-10, and TDD-10; (2). The T. speltoides segment present in this translocation is located 2 to 10 cm from the centromere and is 20 to 30 cm long (1).

The long arm translocation line T7AS7AL-7S#1 L-7AL designated UCRBW98-2 (PI 603919) carries gene Gb5 (6) that confers resistance to greenbug biotypes C, E, I, and K but not to biotypes B, F, G, H. This gene is located on an interstitial T. speltoides chromosome segment that is 40 to 50 cm long and is located 18 to 22 cm from the centromere of chromosome 7AL (1).

The interstitial segments of T. speltoides chromosome present in both translocation lines do not recombine with wheat chromosome 7A in the presence of the wild-type Ph1 locus and will be transmitted as single loci. Consequently, Lr47 is completely linked to RFLP markers Xwg834, Xcdo475, Xmwg710, Xabc152, Xabc158, XBrz, and Xabc465, and Gb5 is completely linked to RFLP markers Xpsrl29, Xpsrs4777, Xwgs300, Xabc461, Xwgs420, Xwgs802, and Xpsrs680. Molecular markers can also be used to transfer leaf rust resistance gene Lr10 present in chromosome 1A of the recurrent parent Pavon (5).

Despite these translocation lines may be useful in breeding, no information is currently available on putative yield penalties associated with other genes present in the interstitial segment of T. speltoides (1).

nomenclature for Puccinia recondita f. sp. Triticum aestivum.


Regulation of UCRBW98-1 and UCRBW98-2
Wheat Germplasms with Leaf Rust and Greenbug Resistance Genes

Two wheat (Triticum aestivum L.) germplasms with interstitial translocations (UCRBW98-1, Reg. no. GP-594, PI 603918 and UCRBW98-2, Reg. no. GP-595, PI 603919) were developed to transfer genes for resistance to leaf rust (caused by Puccinia triticina Eriks.) and greenbug (Schizaphis graminum Rondani) from chromosome 7S of Triticum speltoides (Tausch) Gren. The origin of chromosome 7S is not clear (1, 3) but likely it originated from a population obtained by irradiation of a hybrid CI15092/T. speltoides///Fletcher///3/5*Centurk with fast neutrons (7). Translocations of segments of 7S to 7A were produced by recombination induced by the ph1b mutation (3). Sears’ (4) strategy was followed to reduce the length of the alien chromosome segments. All manipulations were performed in hard white spring cultivar Pavon F76; a total of eight backcrosses were made to Pavon and the likely pedigree of both lines is CI15092/T. speltoides///Fletcher///3/5*Centurk/4/4*Pavon F76/5/Pavon ph1b/6/3*Pavon F76 where Pavon ph1b is Chinese Spring ph1b /8*Pavon M5B. Plants homozygous for the interstitial translocations were selected by C-banding. Translocations were characterized using molecular markers (1).

The short arm translocation line Pavon T7AS-7S#1S-7A:S7AL designated UCRBW98-1 (PI 603918) carries resistance gene Lr47 for leaf rust. This gene confers resistance to a wide spectrum of leaf rust races including nine that are virulent on resistance genes Lrl and Lr10 present in Pavon F76 (PRT codes: TBT-10, NBB-10, MBR-10, LCG-10, SDJ-10, MBG-10, NDB-10, MCG-10, and TDD-10; (2). The T. speltoides segment present in this translocation is located 2 to 10 cm from the centromere and is 20 to 30 cm long (1).

The long arm translocation line T7AS7AL-7S#1 L-7AL designated UCRBW98-2 (PI 603919) carries gene Gb5 (6) that confers resistance to greenbug biotypes C, E, I, and K but not to biotypes B, F, G, H. This gene is located on an interstitial T. speltoides chromosome segment that is 40 to 50 cm long and is located 18 to 22 cm from the centromere of chromosome 7AL (1).

The interstitial segments of T. speltoides chromosome present in both translocation lines do not recombine with wheat chromosome 7A in the presence of the wild-type Ph1 locus and will be transmitted as single loci. Consequently, Lr47 is completely linked to RFLP markers Xwg834, Xcdo475, Xmwg710, Xabc152, Xabc158, XBrz, and Xabc465, and Gb5 is completely linked to RFLP markers Xpsrl29, Xpsrs4777, Xwgs300, Xabc461, Xwgs420, Xwgs802, and Xpsrs680. Molecular markers can also be used to transfer leaf rust resistance gene Lr10 present in chromosome 1A of the recurrent parent Pavon (5).

Though these translocation lines may be useful in breeding, no information is currently available on putative yield penalties associated with other genes present in the interstitial segment of T. speltoides (1).

Registration of 10 Wheat Germplasms Resistant to Septoria tritici Leaf Blotch

Ten spring wheat (Triticum aestivum L.) ergmpleasms with greenbug resistance genes were developed by the Crosses program of the International Maize and Wheat Improvement Center (CIMMYT), El Batan, Mexico for improvement Center (CIMMYT), El Batan, Mexico for improvement Center (CIMMYT). The lines were derived from the synthetic hexaploids (SH) (7. T. aestivum/Aegilops tauschii) and were crossed with the S. tritici Roberge ex Desmaz. This fungal disease limits wheat production in high rainfall areas across 10.4 million hectares globally (1). The lines were derived from five Mexican isolates that were virulent on both T. aestivum and T. urticum and the moderately resistant cultivar Bagula.

Segregating generations of the crosses were advanced by the pedigree breeding method. The mean agronomic performance of the crosses and disease scoring data of 10 germplasms over three years of field tests is presented in Table 1. The 10 germplasms are F3 to F5.

Five Mexican isolates that were virulent on both T. aestivum and T. urticum were used to select 10 germplasms twice over three weeks during the tillering stage of the germplasm. The lines were derived from five Mexican isolates that were virulent on both T. aestivum and T. urticum and the moderately resistant cultivar Bagula. Segregating generations of the crosses were advanced by the pedigree breeding method. The mean agronomic performance of the crosses and disease scoring data of 10 germplasms over three years of field tests is presented in Table 1. The 10 germplasms are F3 to F5.

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