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### Title

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### 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) Grén. 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-7AS7AL 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 *Lr1* 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 *Xpsr129*, *Xpsr547*, *Xwg380*, *Xabg461*, *Xwg420*, *Xmwg2062*, and *Xpsr680*. 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 segments of *T. speltoides* chromosome 7S. Small quantities of seed of these lines can be obtained for research and breeding purposes from the corresponding author.

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### Registration of 10 Wheat Germplasms Resistant to *Septoria tritici* Leaf Blotch

Ten spring wheat (*Triticum aestivum* L.) germplasms, CIGM90.248, CIGM90.250.1, CIGM90.250.2, CIGM90.358, CIGM 90.412, CIGM90.483, CIGM91.153, CIGM91.191, CIGM91.248, CIGM92.337, (Table 1) (Reg. no. GP-562 to GP-571; PI 610750 to PI 610759) were developed by the Wide Crosses program of the International Maize and Wheat Improvement Center (CIMMYT), El Batán, Mexico for improved resistance to *Septoria* leaf blotch (caused by *Septoria 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 *S. tritici* resistant synthetic hexaploids (SH) (*T. turgidum*/*Aegilops tauschii*) that were crossed with the *S. tritici* susceptible wheat cultivars Seri M82, Yaco, Borlaug M95, Opata M85, Kauz, Papago M86, and the moderately resistant cultivar Bagula.

Segregating generations of the crosses were advanced by the pedigree breeding method. The mean agronomic performance and disease scoring data of 10 germplasm lines resistant to *Septoria* leaf blotch over three years of field tests is presented in Table 1. The 10 germplasms are F<sub>3</sub> to F<sub>6</sub> derived selections.

Five Mexican isolates that were virulent on both *T. turgidum* and *T. aestivum* germplasms were mixed to inoculate populations twice over three weeks during the tillering stage of the lines and cultivar checks with ULVA (ultra low volume) applications. 'Bobwhite' (resistant check), Kauz and Seri M82 (susceptible checks) were included in the 3-yr *Septoria* leaf blotch evaluations. Ratings for *S. tritici* resistance were based upon leaf damage recorded at water (GS71), milk (GS75), and dough (GS85) growth stages (GS) according to Zadoks et al. (3) using a double digit modified scale (1). All lines had the euploid 2n=6x=42 chromosome number with predominantly normal bivalent meiosis. The disease ratings of each of the 10 germplasms indicated their superior resistance over the three bread wheat cultivars (Pú0.05). In addition, we observed that these germplasms possessed resistance to leaf rust (caused by *Puccinia triticina* Eriks) and stem rust (caused by *Puccinia graminis* Pers.f.sp. *tritici* Eriks. & E. Henn.). All germplasms