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 speltaoides (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. speltaoides/Fletcher’53/5*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 these lines is CI15092/T. speltaoides/Fletcher/3l 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-7S1S7AS7AL 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. speltaoides 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 T7A7S7AS7AL 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. speltaoides 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. speltaoides 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 a single loci. Consequently, Lr47 is completely linked to RFLP markers Xwg384, Xcd475, Xwmg710, Xabc152, Xabc158, XBrz, and Xabc465, and Gb5 is completely linked to RFLP markers Xpsr129, Xpsr547, Xwmg380, Xabc461, Xwgs420, Xwmg2062, and Xpsr880. Molecular markers can also be used to transfer leaf rust resistance gene Lr10 present in chromosome 1A of the recurrent parent Pavon (3).

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. speltaoides 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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References and Notes


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Registration of 10 Wheat Germplasms Resistant to Septoria tritici Leaf Blotch

Ten spring wheat (Triticum aestivum L.) germplasms, CIMG90.248, CIMG90.250.1, CIMG90.250.2, CIMG90.358, CIMG 90.412, CIMG90.483, CIMG91.153, CIMG91.191, CIMG91.248, CIMG92.337, (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 Batan, 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 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 Mer82, Yao, Borl1ag M95, Opata M85, Kaur, 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 germplasm lines are F1 to F5, 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 (GS85), milk (GS71), dough (GS65) 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 (Pb0.05). In addition, we observed that these germplasms possessed resistance to leaf rust (caused by Puccinia graminis Pers./sp. tritici Eriks.) and stem rust (caused by Puccinia graminis Pers./sp. tritici Eriks. & E. Henn.). All germplasms