

Registration of Five Wheat Isogenic Lines for Leaf Rust and Stripe Rust Resistance Genes

We report here the release of four germplasm lines of hard red spring (HRS) wheat (*T. aestivum* L.) [Yecora Rojo *Yr36-Gpc-B1* (Reg. no. GP-793, PI 638740), Yecora Rojo *Lr47* (Reg. no. GP-791, PI 638738), Kern *Lr47* (Reg. no. GP-792, PI 638739), and Anza *Lr37/Yr17/Sr38* (Reg. no. GP-795, PI 638742)] and one durum wheat (*T. turgidum* L.) [UC1113 *Yr36-Gpc-B1* (Reg. no. GP-794, PI 638741)], isogenic for leaf rust (*Puccinia triticina* Eriks.) resistance gene *Lr47*, stripe rust (*P. striiformis* West. f. sp. *tritici*) resistance gene *Yr36*, and the *Lr37/Yr17/Sr38* leaf, stripe, and stem rust (*P. graminis* Pers.: Pers. f. sp. *tritici* Eriks. & E. Henn.) resistance gene complex. All genes were transferred by six backcrosses to their respective recurrent parents and molecular markers for each gene were used to select heterozygous plants for the targeted genes. After the sixth backcross plants were self-pollinated and homozygous BC₆F₂ plants were selected using markers. The isogenic lines are expected to be more than 99% identical to their recurrent parents.

Isogenic Lines for Stripe Rust Resistance Gene *Yr36* and Grain Protein Content Gene *Gpc-B1*

Chromosome 6B from *T. turgidum* ssp. *dicoccoides* (Körn.) Thell. accession 'FA15-3' from Israel (DIC hereafter) carries a gene that significantly increases grain protein content (Cantrell and Joppa, 1991). This gene was initially mapped as a quantitative trait locus within a 30-cM region of the short arm of chromosome 6BS using Recombinant Substitution Lines (RSLs) of the DIC 6B chromosome in the genetic background of Langdon (Joppa et al., 1997). The same DIC chromosome segment was found in the hexaploid wheat variety 'Glupro' ('Columbus'/*T. turgidum* var. *dicoccoides*/'Len') (Khan et al., 2000; Mesfin et al., 1999). The gene responsible for the differences in grain protein content was mapped as a single locus designated *Gpc-B1* proximal to the Nucleolar Organizer Region (Olmos et al., 2003; Distelfeld et al., 2004).

During field evaluations of the RSLs at University of California (UC) at Davis (Olmos et al., 2003), we observed that the lines with the DIC segment were more resistant to stripe rust than the lines with the Langdon segment. Two RSLs with the DIC 6BS region and two with the Langdon region were evaluated under controlled conditions at Washington State University. At the seedling stage, all lines were susceptible to the 15 different stripe rust races tested (including new races PST100 and PST101), but when the same lines were evaluated at the adult plant stage under a high-temperature cycle, the lines carrying the DIC segment showed significantly lower infection types (IT: 2.0 to 2.3) than the lines with the Langdon segment (IT: 7.0 to 7.3) with races PST100 and PST101. This high-temperature adult plant resistance gene was mapped as a single locus designated *Yr36* (McIntosh et al., 2005). *Yr36* was mapped on chromosome 6BS, 2 to 4 cM proximal to the *Gpc-B1* gene (Uauy et al., 2005).

Distal molecular markers *Xucw74* and proximal markers *Xucw77* or *Xbarc136* were used to introgress *Yr36* and *Gpc-B1* into the HRS common wheat variety 'Yecora Rojo' Cltr 17414 (Qualset et al., 1985) using Glupro as a donor parent; and into the durum breeding line UC1113 (UC Davis selection from CIMMYT cross CD52600 [KIFS/RSS/BD1419/3/MEXIS-CP/4/WAHAS/5/YAV79]) using Langdon RSL#65 as a donor parent. The BC₆F₃ seeds of the homozygous lines were deposited at the National Small Grains Collection (NSGC) as Yecora Rojo *Yr36-Gpc-B1* and UC1113 *Yr36-Gpc-B1*. These isogenic lines have been designated as the type germplasm

for the *Yr36* gene in *T. aestivum* and *T. turgidum* respectively (McIntosh et al., 2005).

The two pairs of isogenic lines were compared in field trials in Madera, CA, and Davis, CA, in 2004 under severe stripe rust infection pressure using a split plot design with five replications and large plots (1.2 by 4.0 m in Davis and 1.5 by 4.0 m in Madera). Lines with and without *Yr36-Gpc-B1* showed no significant differences in height and heading time for both the tetraploid and hexaploid pairs of isogenic lines.

The Yecora Rojo *Yr36-Gpc-B1* line showed a significant reduction in stripe rust infections (from 87 to 51% severity, Davis $P = 0.20$, Madera $P < 0.0009$), higher yields (average increase of 970 kg ha⁻¹, Davis $P = 0.05$, Madera $P = 0.02$), and an average increase of 850 g protein per 100 kg of grain relative to the isogenic line without the DIC 6BS chromosome segment (from 13.2 to 14.1% protein content, Davis $P = 0.03$, Madera $P = 0.0007$). Test weights of the lines with the *Yr36-Gpc-B1* genes (79.3 ± 0.5 kg hL⁻¹) and without these genes (78.8 ± 0.9 kg hL⁻¹) were not significantly different in this experiment.

The UC1113 *Yr36-Gpc-B1* line showed a significant reduction in stripe rust severity (from 36 to 2% severity, Davis $P = 0.03$, Madera $P = 0.006$), slightly higher yields (average increase of 242 kg ha⁻¹, although not significant in both locations), and an average increase of 1100 g of protein per 100 kg of grain relative to the isogenic line without the DIC 6BS chromosome segment (from 13.5 to 14.5% protein content, Davis $P = 0.006$, Madera $P < 0.0001$). Test weights of the lines with the *Yr36-Gpc-B1* genes (80.1 ± 0.5 kg hL⁻¹) and without these genes (81.0 ± 0.5 kg hL⁻¹) were not significantly different in this experiment.

Isogenic Lines for Leaf Rust Resistance Gene *Lr47*

The interstitial translocation line T7AS-7S#1-7AS-7AL carrying *Lr47* from *T. speltoides* (Tausch) Gren. was originally transferred to bread wheat by irradiating hybrid seed (CI15092/*T. speltoides*/'Fletcher'/3/5* 'Centurk') with fast neutrons (Wells et al., 1982). Interstitial segments of chromosome 7S#1 were transferred to chromosome 7A of hexaploid wheat using the *ph1b* mutation that promotes homeologous recombination (Lukaszewski 1995). The interstitial translocations were backcrossed three times into hard white spring variety 'Pavon 76' (PI 519847) and plants homozygous for the interstitial translocation were released as germplasm PI 603918 (Lukaszewski et al., 2000).

Resistance gene *Lr47* for leaf rust conferred resistance to the leaf rust races TBT, NBB, MBR, LCG, SDJ, MBG, NDB, MCG, and TDD (PRT codes, Long and Kolmer, 1989). The *T. speltoides* segment is located 2 to 10 cM from the centromere and is 20 to 30 cM long (Dubcovsky et al., 1998). This segment is generally transferred as a single linkage block. Here we report the transfer of the *Lr47-T. speltoides* segment from Pavon 76 into HRS varieties Yecora Rojo and 'Kern' (PI 612142) using molecular markers (Helguera et al., 2000).

The BC₆F₃ seeds of the homozygous lines were deposited at the National Small Grains Collection (NSGC) as Yecora Rojo *Lr47* and Kern *Lr47*. The two pairs of isogenic lines were compared in field trials at Kings, CA, in 2003 and Kings and UC Davis, CA, in 2004 using a split plot design with four replications [plot size (1.2 by 4.0 m in Davis and 1.5 by 4.0 m in Kings)]. Isogenic lines with and without the gene showed similar agronomic characteristics including height and heading time. Depending on the environment, some of the plants carrying the *Lr47* chromosome segment showed purple stems in some plants.

No significant differences in yield between isogenic lines with and without the *Lr47* gene were detected at Kings. How-

ever, at UC Davis under strong stripe rust infection pressure, the lines with the leaf rust resistance gene *Lr47* showed increased stripe rust infections (81 to 91% increase in severity for Yecora Rojo, and 58 to 75% increase in severity for Kern), which resulted in a significant decrease in yield (Yecora Rojo 12% decrease $P = 0.047$, Kern 21% decrease $P = 0.006$). These results suggest that the 7S chromosome segment carrying *Lr47* has replaced a gene located in chromosome 7A in Yecora Rojo and Kern that has a positive effect on resistance to the predominant stripe rust races in California (e.g., PST100, PST101). Therefore, the *T. speltoides* segment including *Lr47* would provide an advantage in areas under leaf rust infection but should be tested in other genetic background for its effect on stripe rust resistance.

No leaf rust was detected in the 2003 or 2004 field trials. However during the seed increases of these lines in 2002 at UC Davis we observed increased resistance to leaf rust in the Yecora Rojo *Lr47* line (no infection) compared to the adjacent recurrent parent Yecora Rojo (80% infection, susceptible reaction). The recurrent parent Kern was resistant to these leaf rust races.

The two isogenic lines carrying the *Lr47* gene showed a significantly higher ($P = 0.002$) grain protein content than the lines without the *T. speltoides* chromosome segment associated with the presence of the *Lr47* chromosome segment in the two locations tested in 2004 (average increase of 530 g of protein per 100 kg of grain).

Isogenic Lines for Genes *Lr37/Yr17/Sr38* from *T. ventricosum*

The *Yr17*, *Lr37*, and *Sr38* rust resistance genes, which confer resistance in wheat against stripe rust, leaf rust, and stem rust respectively, were initially introgressed in the winter bread wheat 'VPM1' from *T. ventricosum* (Tausch.) Cess., Pass. & Gib. (Maia, 1967) and are located in a 2NS/2AS translocation (Bariana and McIntosh, 1993). Rust races with virulence to *Yr17* and *Lr37* have been identified in some countries, but this gene cluster still provides resistance to a wide range of races and is useful in combination with other rust resistance genes.

Characterization of the 2NS/2AS translocation with molecular markers indicated that the 2NS translocation replaced approximately half of the short arm of chromosome 2A (distal 25–38 cM). A PCR assay (Helguera et al., 2003) was used to introgress the 2NS chromosome segment from HRW 'Madsen' into HRS 'Anza' C1tr15284 (Qualset et al., 1984). The BC₆F₄ seed of the Anza homozygous lines carrying the 2NS/2AS translocation was deposited at the National Small Grains Collection (NSGC) as Anza *Lr37/Yr17/Sr38*.

Isogenic lines were tested for leaf rust resistance at the Cereal Disease Laboratory (Helguera et al., 2003) and for stripe rust resistance in field trials at Davis (CA, 2004) and Kings (CA, 2004) using a split plot design with four replications (plot size 1.2 by 4.0 m at Davis and 1.5 by 4.0 m at Kings). The isogenic lines were morphologically similar and showed no significant differences in flowering time or height. The presence of the stripe rust resistance gene *Yr17* significantly reduced the severity of the stripe rust infection from 60% to almost no infection (Davis $P = 0.03$, Kings $P = 0.003$). The recurrent parent Anza has the slow rusting complex *Lr34/Yr18* (McIntosh et al., 1995) suggesting that the addition of *Yr17* increased the slow rusting resistance to stripe rust provided by *Yr18*. The improved resistance of the Anza *Lr37/Yr17/Sr38* line resulted in increased yields at both locations, but the differences were not significant (average increase 663 kg ha⁻¹, Davis $P = 0.07$, Kings $P = 0.17$). The

molecular and field data confirmed that the *Lr37/Yr17/Sr38* resistance gene complex was successfully transferred to Anza.

Small quantities of seed of these germplasm lines may be obtained from the corresponding author for 5 yr. Recipients of seed are asked to make appropriate recognition of the source of the germplasm if it is used in the development of a new cultivar, germplasm, parental line, or genetic stock.

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Acknowledgments

This project was supported by the National Research Initiative of the USDA Cooperative State Research, Education and Extension Service (CSREES), grant numbers 2005-00975 and IFAFS 2001-04462.

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doi:10.2135/cropsci2005.04-0048
Published in *Crop Sci.* 46:485–487 (2006).