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Kansas Rust-resistant Sweet Corn Populations A and B

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Common rust, caused by *Puccinia sorghi* Schw., can cause serious losses in sweet corn (*Zea mays* L.) production. Several of the *Rp* rust resistance genes commonly provide useful levels of resistance in the field (Groth et al., 1992). However, in recent years, common rust biotypes have been identified in North America that are virulent on lines carrying any single *Rp* gene (Hulbert et al., 1991). This indicates that the resistance conferred by any *Rp* gene would be unlikely to remain effective if deployed on a large scale.

Most of the common rust resistance genes that have been identified in maize have been mapped to a small area on the short arm of chromosome 10. This area includes a cluster of tightly linked resistance genes called the *rp1 complex*, and some others, such as *RpG*, that map one or more cM away from this complex. The tightly-linked arrangement of the genes in the *rp1* complex, coupled with a high frequency of mispairing (Sudupak et al., 1993) and recombination between the different genes, allows *Rp1* variants to be selected. These variants include *Rp1* genes with novel race specificities (Richter et al., 1995) and variants with combinations of existing *Rp1* genes. The latter class includes variants with two or more detectable *Rp1* genes tightly linked to each other in coupling (Hu and Hulbert, 1995). These 'compound' *Rp1* genes can be manipulated in breeding programs as though they are single genes.

Several of the compound genes that have been generated are highly resistant to all known common rust biotypes (Hu and Hulbert, 1995), but were constructed in dent corn backgrounds. Here we describe the transfer of two compound *Rp1* genes to sweet corn backgrounds to assist breeders' efforts in incorporating this potentially durable resistance into sweet corn varieties. These populations will allow the transfer of rust resistance into existing lines with a minimal number of backcrosses and may be suitable for the selection of parental lines for hybrid development.

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Origin and Description

Genes conditioning resistance. Two previously described (Hu and Hulbert, 1995) compound genes were used as sources of rust resistance. The *Rp1-DJ4* compound gene has *Rp1-J* and *Rp1-D* tightly linked together within 0.2 cM. The *Rp1-GFJ2* compound gene has the *Rp1-J*, *Rp1-F*, and *RpG* linked in coupling. *Rp1-F* and *Rp1-J* are within ≈0.2 cM while *RpG* maps ≈2.0 cM distally, toward the telomere of chromosome 10s. Both compound genes provide resistance to all North American rust biotypes in the Kansas State Univ. common rust collection (Hulbert et al., 1991), and are generally free of common rust in our crossing nursery at the Kansas State Univ. Rocky Ford Experimental Field, Manhattan, Kan. A Hawaiian biotype, collected in 1990, is virulent on lines carrying either *Rp1-J* and *Rp1-D*, and is virulent on lines carrying the *Rp1-DJ4* compound gene at the seedling stage. Greenhouse experiments have indicated, however, that the *Rp1-DJ4* compound gene provides partial resistance to this biotype and also to southern rust caused by *P. polysora* Underw. at the adult plant stage (Hu et al., 1997). This adult-plant resistance may be non–race-specific in nature. No common rust biotypes are available that are virulent on all components of the *Rp1-GFJ2* compound gene, so its potential for non–race-specific resistance to common rust has not been assessed.

Origin of the populations. Two sweet corn populations were made by crossing each of the two compound *Rp1* genes into a sweet corn (*su1*) background. Lines carrying each of the compound genes were crossed to the sweet corn hybrid variety 'Gold Cup' (Harris Moran, Pleasanton, Calif.), and rust-resistant plants were subsequently backcrossed to 'Gold Cup' three times (Fig. 1). Rust-resistant plants were selected in each generation by greenhouse inoculations of seedlings, as previously described by Hulbert et al. (1991). Four rust-resistant BC_3 plants for each of the two compound genes were selected and self-fertilized, and the progeny (BC_3S_1) were grown in a field nursery in Manhattan in 1995. Selections were made among these BC_3S_1 plants for early maturity (71 to 76 days to pollen shed), few (0 to 2) tillers, and intermediate ear height. Selection was also practiced for the absence, or low level of expression, of a chlorotic or necrotic-spotting phenotype which was present on the lower leaves of some individuals carrying the compound genes. Selected plants were self-pollinated, and BC_3S_2 lines were screened in a greenhouse in Manhattan for homozygosity of

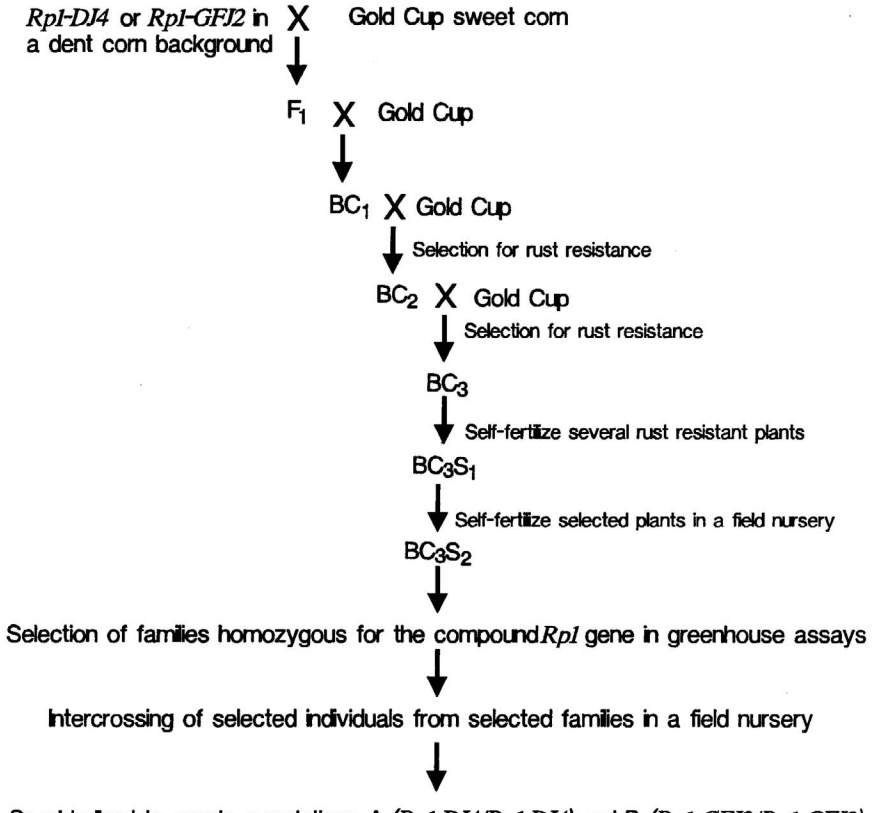

Fig. 1. Pedigrees of the rust-resistant sweet corn populations. The only difference in the pedigrees of the two populations is that a line carrying the *Rp1-DJ4* compound gene was used in the initial cross to generate population A, while a line carrying *Rp1-GFJ2* was used to generate population B.

the *Rp1* compound genes. Eight BC_3S_2 lines homozygous for the *Rp1-DJ4* compound gene were intercrossed in the field in 1996. Seed from these crosses was bulked to generate 'Population A'. Similarly, seven BC_3S_2 lines homozygous for the *Rp1-GFJ2* compound gene were intercrossed, and the seed bulked to generate 'Population B'.

Uses

Populations A and B can be used to transfer the compound genes into advanced breeding material with minimal numbers of undesirable dent corn genes. Following crosses to rust-susceptible material, the presence of the compound resistance genes may be detected with any known North American rust biotype, or can be assayed in the field in North America under natural inoculation conditions.

Availability

Small seed samples of populations A and B are available from S.H. Hulbert, Dept. of Plant Pathology, Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506-5502 (e-mail: shulbrt@plantpath.ksu.edu).

Literature Cited

Groth, J.V., J.K. Pataky, and G.R. Gingera. 1992. Virulence in eastern North American populations of *Puccinia sorghi* to *Rp* resistance genes in corn. Plant Dis. 76:1140–1144.

Hulbert, S.H., P.C. Lyons, and J.L. Bennetzen. 1991. Reactions of maize lines carrying *Rp* resistance genes to isolates of the common rust pathogen, *Puccinia sorghi*. Plant Dis. 75: 1130–1133.

Hu, G. and S.H. Hulbert. 1995. Construction of 'compound' rust resistance genes in maize. Euphytica 87:45–51.

Hu, G., C.A. Webb, and S.H. Hulbert. 1997. Adult-plant phenotype of the *Rp1-DJ* compound rust resistance gene in maize. Phytopathology 87:236–241

Richter, T.E., T.J. Pryor, J.L. Bennetzen, and S.H. Hulbert. 1995. New rust resistance specificities associated with recombination in the *Rp1* complex in maize. Genetics 141:373–381.

Sudupak, M.A., J.L. Bennetzen, and S.H. Hulbert. 1993. Unequal exchange and meiotic instability of *Rp1* region disease resistance genes. Genetics 133:119–125.