Rust-resistant sh2 Sweet Corn Populations

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The Rp1 area, on the short arm of maize (Zea mays L.) chromosome 10, carries most of the major genes that have been identified for resistance to common rust (Puccinia sorghi) Schwein. These include the rp1 complex, as well as Rp5 and RpG, which map 1-3 cM toward the telomere (Hulbert, 1997). The linkage among these genes enable the selection of recombinant individuals that carry Rp5 or RpG and an Rp1 gene by screening families consisting of a several hundred testcross progeny with the appropriate rust biotypes. Different genes, or alleles, within the rp1-complex can also be recombinated by screening larger populations. Once the appropriate alleles have been recombinated into coupling phase, they can be manipulated as single genes in breeding programs.

Some of the recombinant rp1 gene clusters, or “recombinant haplotypes,” that have been generated confer high levels of resistance to all known common rust biotypes (Hu and Hulbert, 1995). Some of the recombinant haplotypes appear to confer resistance that is broader than that expected from the component genes (Hu et al., 1997). The Rp1-D/J haplotype, which carries both Rp1-J and Rp1-D, confers partial resistance to a biotype that was virulent on both parental genes and also showed partial resistance to southern rust (P. polysora Underw.). The extent to which other recombinant haplotypes confer general rust resistance has not been investigated. General resistance is impossible to evaluate for recombinant haplotypes that confer race-specific resistance to all known common rust biotypes because of the combination of Rp genes that they carry.

To expedite the development of sweet corn cultivars with potentially durable resistance, we previously crossed two recombinant haplotypes into sh2 sweet corn backgrounds. Lines carrying each of the two compound genes were crossed with the sweet corn hybrid ‘Zenith’ (Harris Moran, Salinas, Calif.) and rust-resistant plants were subsequently backcrossed to ‘Zenith’ two times (Fig. 1). Rust-resistant plants were selected in each generation by greenhouse inoculations of seedlings (Hulbert et al., 1991). Rust-resistant BC3 plants were then crossed with the hybrid ‘Nordic’ (Illinois Foundation Seed, Inc. Champaign, Ill.). Plants carrying each of the recombinant haplotypes were then selected and sib-mated. Two families derived from sib-mating of each of the recombinant haplotypes were grown in a field nursery in Manhattan in 1997. Plants showing good vigor, intermediate ear height (0.3–1.0 m from soil), few tillers and early maturity (<62 d to pollen shed) were self-pollinated. We also selected for the absence of chlorotic and necrotic spotting, which is associated with both of the compound genes in some genetic backgrounds (unpublished). S1 families that were homozygous for each of

Rp1-GDJ or Rp1-FJC in

zeni corn background

F1 X ‘Zenith’ sweet corn

BC1 X ‘Zenith’

BC2 X ‘Nordic’

BC3 X Rust-resistant selected

BC3S1 Selected plants self-pollinated in field nursery

BC3S2 Families homozygous for the recombinant haplotype selected in greenhouse assays

Selected individuals from selected families intercrossed in field nursery

Seed bulked to create populations C (Rp1-GDJ/Rp1-GDJ) and D (Rp1-FJC/Rp1-FJC)

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ORIGIN OF THE POPULATIONS

Two sweet corn populations were made by crossing each of the two compound Rp1 genes into a sh2 sweet corn background. Lines carrying each of the two compound genes were crossed with the sweet corn hybrid ‘Zenith’ (Harris Moran, Salinas, Calif.) and rust-resistant plants were subsequently backcrossed to ‘Zenith’ two times (Fig. 1). Rust-resistant plants were selected in each generation by greenhouse inoculations of seedlings (Hulbert et al., 1991). Rust-resistant BC3 plants were then crossed with the hybrid ‘Nordic’ (Illinois Foundation Seed, Inc. Champaign, Ill.). Plants carrying each of the recombinant haplotypes were then selected and sib-mated. Two families derived from sib-mating of each of the recombinant haplotypes were grown in a field nursery in Manhattan in 1997. Plants showing good vigor, intermediate ear height (0.3–1.0 m from soil), few tillers and early maturity (<62 d to pollen shed) were self-pollinated. We also selected for the absence of chlorotic and necrotic spotting, which is associated with both of the compound genes in some genetic backgrounds (unpublished). S1 families that were homozygous for each of

Fig. 1. Development of the rust-resistant sweet corn populations. The only difference in the pedigrees of the two populations is that a line carrying the Rp1-GDJ compound gene was used in the initial cross to generate population C, while a line carrying Rp1-FJC was used to generate population D.
the compound genes were identified by rust inoculations. Twelve selected families, homozygous for $Rp$-$GDJ$, were grown in a field nursery in Manhattan in 1998. Selected individuals in each family were individually crossed with selected individuals in the other families. Over 100 individual crosses were bulked to make “population C.” Similarly, selected individuals from nine families homozygous for $Rp1$-$FJC$ were intercrossed and the resulting seed bulked to make “population D” (Fig. 1).

**Uses**

Populations C or D can be used to transfer the $Rp$-$GDJ$ or $Rp1$-$FJC$ recombinant haplotypes into rust-susceptible sweet corn lines with minimal undesirable dent corn traits. Following crosses with rust-susceptible genotypes, the presence of the recombinant haplotypes may be detected with any known rust biotype, or can be assayed in the field under natural inoculation conditions.

**Availability**

Seed samples of populations C and D are available from S.H. Hulbert, Dept. of Plant Pathology, Throckmorton Hall, Kansas State University, Manhattan, KS 66506-5502 (e-mail: shulbrt@plantpath.ksu.edu).

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