Analysis of Rust Resistance in the Dry Bean CNC

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Introduction

Compuesto Negro Chimaltenango (CNC) is part of the differential set of dry bean (*Phaseolus vulgaris*) genotypes used to detect races of *Uromyces appendiculatus*, the bean rust fungus. CNC is resistant to all races of *U. appendiuclatus* found in the northern Great Plains. Because of this, the resistance in CNC may be useful for breeding programs. However, little is known of the genetics of rust resistance in CNC.

The eventual objectives of this research are to understand the genetics of bean rust in CNC and to use the resistance for breeding purposes. Toward that goal we have used CNC as a parent to develop a dry bean population that segregates for rust resistance, determined reaction of progeny to different races of the fungus used to detect specific resistance genes, and developed AFLP markers linked to gene(s) of interest.

Methods and Materials

Population development. CNC was crossed to the rust-susceptible 'Othello'. An $F_{2:4}$ population of 100 recombinant inbred (RI) lines was developed in the greenhouse using the single seed descent method.

Disease evaluations. The 100 F_2 individuals used for population development were inoculated with races 49 and 73 of the bean rust fungus (Stavely 1983). F_3 families and select F_4 RI lines were inoculated with race 49. Disease reaction was evaluated 12 to 14 days post-inoculation as described (Stavely 1984).

AFLP markers. PstI/MseI markers were generated according to Vos et al. (1995). Bulked segregant analysis (Michelmore et al. (1991) was used to facilitate identification of markers linked to resistance. DNA from F_4 bean lines homozygous resistant and homozygous susceptible to race 49 were used to form the bulks.

Results and Discussion

Disease reactions. Othello pinto bean was susceptible and CNC was resistant to races 49 and 73 of the bean rust fungus. The 100 F_2 individuals analyzed from Othello/CNC segregated 3:1 (resistant:susceptible) to both races 49 and 73 (Table 1). All combinations of susceptibility and resistance to the two races were found in the F_2 population (Table 2). This suggests the segregation of at least two rust resistance genes in the population, one effective against race 49 and another against race 73. However, this conclusion is tentative. Disease reactions to race 73 have been determined only one time and only with the F_2 population. By comparison, F_3

families segregated 29:45:26 (homozygous resistant:heterozygous:homozygous susceptible) to race 49. This confirms the segregation of a single resistance gene effective against this race. (χ^2 = 1.18).

Table 1. Segregation ratios of 100 F_2 progeny to races 49 and 73. The expected ratio for a single dominant gene for resistance to each race was 75:25 (resistant:susceptible).

	Disease Reaction		
Race	Resistant	Susceptible	χ^2
49	74	26	0.053
73	76	24	0.053

Table 2. Reaction of parents and select F2 individuals to races 49 and 73.

	Disease Reaction[#]	
F_2 individual.	Race 49	Race 73
2	S	S
3	R	R
7	R	S
8	S	R
9	R	R
10	R	S
11	S	R
39	S	S

[#]S = susceptible, R = resistant

AFLP markers. Select lines were analyzed at the F_3 and F_4 generations to determine reaction to race 49. Homozygous susceptible and homozygous resistant lines were identified and DNA was isolated and pooled for bulked segregant analysis. Several polymorphic AFLP bands have been identified associated with resistance (data not shown).

Future work. The population is being advanced to the F_6 generation. Future plans include replicated testing of population against multiple races, confirming the segregation of two independent rust resistance loci in the population, identifying the loci in question, and mapping and tagging the loci with molecular markers.

References

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