

A TWO-GENE MODEL FOR POWDERY MILDEW RESISTANCE IN COMMON BEAN
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In 1993, while screening a common bean population for common bacterial blight resistance in the field in Mexico, an outbreak of powdery mildew (Erysiphe polygoni) occurred. An obvious variation in disease reaction among parental lines prompted an investigation of the reaction among segregating populations of F₂ plants and their parents. In studies by Dundas (1936, 1941), powdery mildew resistance seemed to be controlled by a single, dominant gene. Our objective was to determine if it was also a single, dominant gene that was responsible for resistance in our population.

MATERIALS AND METHODS

The crossing blocks that provided the progeny under evaluation involved ten parents: OAC Laser, OAC Gryphon, OAC Speedvale, and OAC 88-1 from Ontario; W-BB-11, W-BB-20-1, W-BB-52, and W-BB-II-56 from Puerto Rico; Jules from Nebraska; and XR-235-1-1 from Puerto Rico. The germplasm was selected for common bacterial blight resistance or adaptedness to Ontario growing conditions and nothing was known of their level of powdery mildew resistance. The parents were crossed in a conical mating design (Fouilloux and Bannerot, 1988). F₂ seeds, parents, and Peruano, a Mexican cultivar, were planted in the field at Huaquechula, Edo. de Puebla, Mexico. 22 seeds per entry were planted in a Type II modified augmented design (MAD) as described by Lin and Poushinsky (1985). Plants were evaluated for powdery mildew reaction on a scale of 0 (free from symptoms) to 4 (75-100% leaf infection).

RESULTS AND DISCUSSION

Although the powdery mildew infection was natural, analysis of the checks indicated no significant differences across the plot area and, therefore, the infection was assumed to be uniform and no adjustment of the data was made.

Although the crosses were originally designed to investigate common bacterial blight resistance, three biparental crosses happened to be between powdery mildew resistant and susceptible parents: W-BB-II-56 / XR-235-1-1 (susceptible / resistant), W-BB-11 / OAC Gryphon (susceptible / resistant), and OAC Gryphon / W-BB-II-56 (resistant / susceptible) (Table 1). By assuming scores of 0 and 1 to be resistant, and scores of 2, 3, and 4 to be susceptible, the F₂ progeny of W-BB-II-56 / XR-235-1-1 segregated into a 6:12 ratio of resistant:susceptible. The progeny of W-BB-11 / OAC Gryphon segregated into a 19:9 ratio, and progeny of OAC Gryphon / W-BB-II-56 segregated 4:14. The second ratio (19:9) is not significantly different from 3:1 ($p > .05$) suggesting that the resistance in OAC Gryphon is due to a single dominant gene. The ratios from the first and third crosses do, however, differ significantly from the hypothesised 3:1 ratio ($p < .05$).

Although the number of plants evaluated in the first and third crosses was low ($n=18$ in each), the population size was

sufficient to cast doubt on the adequacy of the hypothesis of a single dominant gene for resistance. The segregation ratios in crosses 1 and 3 are not significantly different from 1:3 resistant: susceptible.

We are proposing a two-gene model for this pathosystem. In this model, one resistance gene is dominant and the other is recessive, and both resistance genes must be present for resistance to be expressed. Under this model OAC Gryphon would have both the dominant and the recessive resistance genes (R1R1r2r2), W-BB-II-56 would be dominant at both loci (R1R1R2R2), and W-BB-11 would be recessive at both loci (r1r1r2r2). A cross between OAC Gryphon and W-BB-II-56 would segregate at the recessive resistance locus only, thus resulting in a ratio of 3:1 susceptible:resistant F2 progeny. A cross between OAC Gryphon and W-BB-11 would segregate at the dominant resistance locus only, resulting in 3:1 resistant: susceptible F2 progeny. This model would be confirmed if progeny from a cross between W-BB-II-56 and W-BB-11 were to segregate in a 13:3 ratio of susceptible to resistant plants.

Table 1. Disease rating and ratios of resistant to susceptible plants from crosses between susceptible and resistant parents (crosses 1 and 2) and resistant and susceptible parents (cross 3).

cross	disease rating					ratio+	X2++
	0	1	2	3	4		
W-BB-II-56 / XR-235-1-1	5	1	6	4	2	6:12	16.7*
W-BB-11 / OAC Gryphon	16	3	3	6	0	19:9	.76
OAC Gryphon / W-BB-II-56	1	3	2	4	8	4:14	26.7*

+ assumes ratings 0, 1 are resistant; 2, 3, 4 are susceptible.

++ X2 to test for resistant:susceptible ratio of 3:1.

* X2 values significant at 5% level.

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