

Inheritance of Anthracnose Resistance in the Common Bean Cultivar Widusa

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Genetic resistance is considered to be the most effective method of control of anthracnose caused by *Colletotrichum lindemuthianum* (Sacc. et Magn.) Scrib. in common bean (*Phaseolus vulgaris* L.). In a previous report, one symbol, *Co-I*⁵ was assigned to describe the gene that controls the resistance of the cultivar Widusa to race 7 of the pathogen. The inheritance of resistance in Widusa was confirmed to be monogenic by a single dominant gene (Alzate-Marin et al., 2002; Gonçalves-Vidigal et al., 2003), whereas Ferreira et al. (2003) affirmed that Widusa has two additional independent genes conferring resistance to race 38. In the present research we propose to confirm the inheritance in Widusa to races 7, 65, 73, and 453 through the evaluation of four F₂ populations and their respective families F_{2:3}, as well the allelism tests with previously characterized resistance genes.

Material and Methods

The common bean cultivar Widusa was crossed with Michigan Dark Red Kidney (MDRK), Cornell 49-242, TO, TU, BAT 93, and PI 207262. After this procedure the F₁, F₂, and F_{2:3} families were grown in the greenhouse and tested on their disease reaction to the races 7, 65, 73, and 453 of the fungal pathogen *C. lindemuthianum*. The fourteen-day-old seedlings of the plants were spray-inoculated with a spore suspension (1.2 x 10⁶ spores/ml) of each race.

Results and Discussion

The inheritance studies supported an expected 3R: 1S ratio presented in the four F₂ populations from the crosses Widusa x MDRK (p = 0.79), Widusa x BAT 93 (p = 1.0), Widusa x Cornell 49-242 (p = 0.95), and Widusa x TO (p = 0.51), when these populations were inoculated with races 7, 65, 73, and 453, respectively (Table 1). The results indicate that Widusa carries a single dominant gene that confers resistance to Middle American 65, 73, 453, and Andean race 7. The segregation 3R: 1S of the F₂ populations from the crosses Widusa x MDRK, Widusa x BAT 93, Widusa x Cornell 49-242 and Widusa x TO was confirmed by the analysis of the F_{2:3} families, which showed a good fit to a segregation ratio of 1:2:1. These results confirm that one dominant gene is responsible for the anthracnose resistance in Widusa to races 7, 65, 73 and 453.

Allelism tests in the cross (R x R), involving Widusa and Cornell 49-242, fitted a 15R:1S ratio in the F₂ population, when inoculated with race 7. The F₂ populations derived from the crosses Widusa x TO, Widusa x TU, and Widusa x BAT 93, were inoculated with races 7, and 73 to determine whether Widusa carries other resistant genes. The segregation ratio fitted was 15R: 1S and the p value varied from 0.53 to 0.92, indicating that each of the parents carries an independent dominant resistant gene. In the F₂ population derived from the cross Widusa and PI 207262, inoculated with race 65, the segregation fits a 15R:1S (269R:18S; p = 0.98) ratio, indicating the presence of two independent dominant genes, one of them is *Co-4*³ in PI 207262 (de Arruda et al., 2000), and the other *Co-I*⁵ gene in Widusa (Gonçalves-Vidigal, 2003). Otherwise, Alzate-Marin et al. 2003, reported that no segregation was observed in F₂ population from the cross Widusa x BAT 93 inoculated with race 65 (Bioagro). However, we observed that BAT 93 has a compatible reaction when inoculated with the race 65 collected in Parana State. The race 65 showed wide genetic variability, through the RAPD analysis of the isolates of this race, demonstrating an intra-race molecular variability (Gonçalves-Vidigal and Thomazella, unpublished data). This fact could be explained due to the origin of the race 65 and its different levels of virulence. After the inoculation with race 65, the F₂ population of the cross Widusa x PI 207262 segregated in ratio of 15R:1S, suggesting that PI 207262 possesses one dominant gene and Widusa another one. Since PI 207262 has previously shown to possess two dominant genes, thus the second gene in PI 207262 must have been defeated by race 65. Studies carried out by Ferreira et al. (2003) demonstrated results that do not agree

with the ones obtained by this experiment. The authors concluded that Widusa has two additional genes resistant to race 38. Besides that, they obtained in the F₂ population of the cross Widusa x A1183 (*Co-2*) a segregation ratio of 61R:3S with a p value = 0.71. In the meantime, if the observed data ratio had been considered to be 15R: 1S, it would have had a p value = 0.64. Furthermore, in the cross Widusa x TU, the authors considered an expected ratio of 61R:3S (p = 0.08), but if the data had been fitted a 15R:1S ratio, consequently the p value would have been 0.47. In addition, the segregation was fitted to a ratio 15R:1S in the F₂ population derived from the crosses Widusa x TO, and Widusa x SEL 1308 when inoculated with race 65 (Alzate-Marin et al. 2002).

In our experiment 200 individuals of the F₂ population derived from the cross Widusa x MDRK did not present segregation when inoculated with race 65. This result indicated that the dominant gene in Widusa is located at the same locus as the *Co-1* gene in MDRK. The inheritance studies supported an expected 3R:1S ratio observed in the four F₂ populations and confirmed by a ratio of 1:2:1 in their F_{2:3} families for resistance to races 7, 65, 73, and 453 of the *C. lindemuthianum*. In addition, allelism tests in F₂ populations derived from crosses Widusa and following cultivars: Cornell 49-242 (race 7); TO, TU, and BAT 93 (races 7 and 73), and PI 207262 (race 65), showed segregation ratio of 15R: 1S. This allelism test indicated that the single dominant resistance gene in Widusa is independent and located at a different locus from the *Co-2*, *Co-4*, *Co-5*, *Co-9*, and *Co-4³* genes. Since Widusa has a different resistance spectrum from all the other characterized *Co-1* alleles based on its position in the differential series, these data would indicate that it carries a new allele at this locus. The authors reaffirm that the anthracnose resistance allele in Widusa should be designated *Co-1⁵*.

Table 1. F₂ and F_{2:3} reactions and expected ratios of resistant (R) and susceptible (S) to *C. lindemuthianum* in cross R x S

Cross	Race	Phenotypic evaluation in the F ₂					Phenotypic evaluation in the F _{2:3}			
		Expected Ratio	R-	rr	χ^2	P value	RR	R-	rr	P value
Widusa x MDRK	7	3:1	164	57	0.074	0.79	23	43	24	0.90
Widusa x BAT 93	65	3:1	252	84	0.0	1.0	26	36	20	0.80
Widusa x Cornell 49-242	73	3:1	68	23	0.036	0.95	25	43	23	0.83
Widusa x TO	453	3:1	151	43	0.435	0.51	50	101	43	0.65

*R = Resistant; S = Susceptible; MDRK = Michigan Dark Red Kidney.

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