

CO-SEGREGATION OF RECOMBINANT INBRED LINES OF THE COMMON BEAN TO RACES 65 AND 73 OF *Colletotrichum lindemuthianum*

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is one of the most important legumes for direct human consumption (Lin et al. 2008). Anthracnose, caused by *Colletotrichum lindemuthianum* is the most widespread, recurrent and devastating disease of the common bean in Latin America and Africa (Pastor-Corrales and Tu 1989). The genetic mapping is carried out using segregating populations. Obtaining segregating populations for genetic mapping have been standard practice in the common bean research (Gepts et al. 1993; Blair et al. 2006). These populations have led to detailed studies and promising to greater efficiency in the genetic breeding of the crop worldwide, but have as limitation, the small size (Sanglard et al. 2013). Thus, the objective of this research was to phenotype the recombinant inbred lines (RIL's) population from AND 277 × Rudá cross with the 65 and 73 races of *Colletotrichum lindemuthianum*.

MATERIAL AND METHODS

This work was conducted at the Núcleo de Pesquisa Aplicada a Agricultura (Nupagri) of the Universidade Estadual de Maringá (UEM), Paraná state, Brazil. The genetic material consisted of 393 Recombinant Inbred Lines (RIL's), and two parent (AND 277 and Rudá). Seed samples of the RILs population were provided by Dr. Thiago Lívio Pessoa Oliveira de Souza of the CNPAF/Embrapa. These seeds were sown in plastic trays containing peat base substrates. In each tray were sown 10 RIL's to further inoculation with the races 65 and 73 of *C. lindemuthianum*, both obtained from the mycology collection of Nupagri. The inoculum preparation was performed according to the methodology proposed by Cárdenas et al. (1964). The counting of spores in each pathogen race was made with the aid of hemacytometer (Chamber of Neubauer- Preciss) and trinocular biological microscope, Motic® brand - mod BA210. After counting, the spore suspension was adjusted to a concentration of 1.2×10^6 spores mL⁻¹. The visual evaluation of symptoms in each plant was performed 7 to 10 days after inoculation. Severity scale proposed by Pastor-Corrales et al. (1995) was considered, with score ranging from 1 to 9. Plants with scores from 1 to 3 were considered resistant, whereas those having scores from 4 to 9 were considered susceptible.

RESULTS AND DISCUSSION

A total of 393 RIL's from cross Rudá × AND 277 were evaluated and it was observed a segregation of 202 resistant lines and 191 susceptible lines to race 65 ($\chi^2 = 0.307$; $p = 0.579$) and 203 resistant lines and 190 susceptible lines to the race 73 ($\chi^2 = 0.430$; $p = 0.512$), which set the monogenic ratio of 1:1. This results shows that the RIL's co-segregated for both inoculated races, indicating that a same gene confer resistance two races 65 and 73 of *C. lindemuthianum* (Table 1).

Table 1. Inheritance test in Recombinants Inbred Lines derived from the cross Rudá × AND 277 inoculated with races 65 and 73 of *C. lindemuthianum*

Races	Score		Observed ratio		Expected ratio		χ^2	<i>p</i> value
	AND 277	Rudá	R ^a	S ^b	R	S		
Race 65	1	5	202	191	1	1	0.307	0.579
Race 73	1	6	203	190	1	1	0.430	0.512

^a = Resistant; ^b = Susceptible

A segregation fitted a 1:1 (R:S) ratio in 393 RIL's population for races 65 and 73, indicating that there was no distortion of segregation (changing of genetic structure) for this character, which highlights the potential of these lines in genetic mapping. It was noted that the 393 RIL's showed similarity in the phenotypic behavior. Except one, all the lines resistant to the race 65 also were resistance to race 73, and susceptible lines to the race 65 were also susceptible to the race 73. This fact highlights the co-segregation of RIL's in relation to resistance to the both races (65 and 73). Genetic analysis revealed that the recombinant inbred lines co-segregated for 65 and 73 races of *Colletotrichum lindemuthianum*, showing that the *Co-1*⁴ gene present in AND 277 confers resistance to both races.

The reaction of RIL's to the races 65 and 73 of *Colletotrichum lindemuthianum* presented monogenic inheritance, being governed by a single gene. The recombinant inbred lines derived from the cross AND 277 × Rudá due to the large size, can be used in mapping genes that control quantitative and qualitative traits and molecular markers, hence they present the potential for the development of a consensus map to common bean.

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