

## EFFECTIVENESS OF RECURRENT SELECTION FOR ANTHRACNOSE RESISTANCE IN COMMON BEAN

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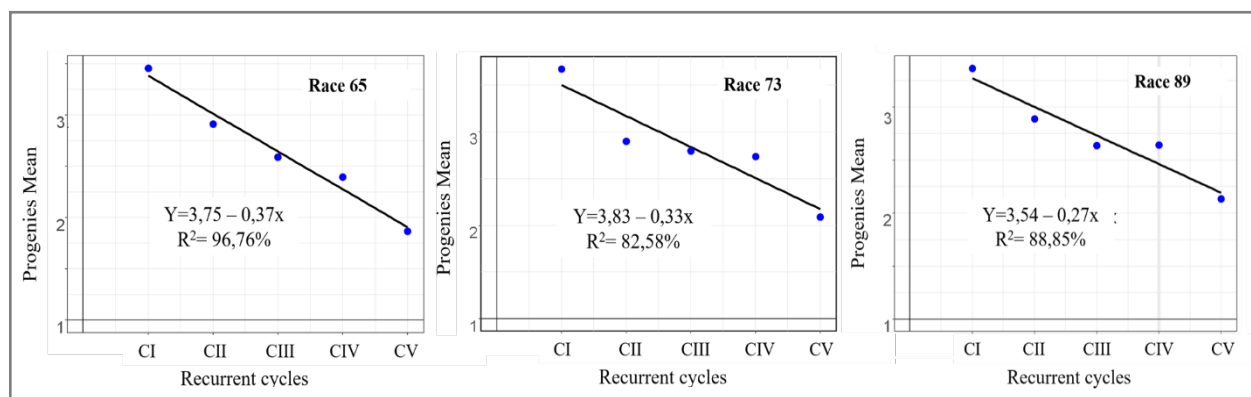
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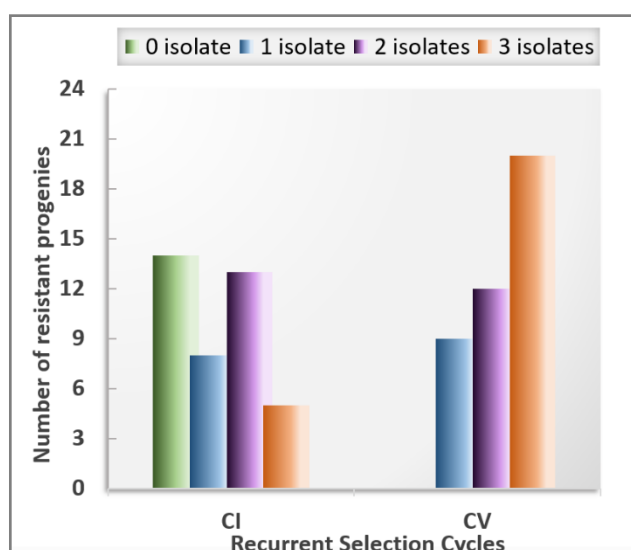
**INTRODUCTION:** *Colletotrichum lindemuthianum*, the causal agent of anthracnose in common bean, presents great evolutionary potential to overcome genetic resistance (Padder et al., 2017). Although a large number of genes have been identified in common bean conferring *C. lindemuthianum* race-specific-resistance (Meziadi et al., 2016), the development of varieties with durable resistance to anthracnose is still a challenge in breeding programs. Quantitative Resistance Loci (QRL) have also been reported (González et al., 2015), suggesting that resistance to anthracnose may involve more genetic complexity. Recurrent selection has been successfully used for accumulate favorable alleles of different traits in common bean, including resistance to diseases (Rezende et al., 2014; Leite et al., 2016). The objective of this study was to develop and evaluate the effectiveness of a recurrent selection program as an alternative to obtain common bean varieties resistant to different isolates of *C. lindemuthianum*.

**MATERIALS AND METHODS:** A mixture of 45 F<sub>2</sub> populations (S<sub>0</sub> population), derived from the diallel cross of ten common bean lines, with variability for the reaction to different isolates of *C. lindemuthianum*, was used to form the base population (Cycle 0). From Cycle 0, five cycles of evaluation, selection and recombination were carried out. In each cycle, S<sub>0</sub> plants were selected for resistance to races 65, 73 and 89 of *C. lindemuthianum*. About 40 S<sub>0:2</sub> progenies from each selective cycle were obtained. The progenies of the five cycles were evaluated for the reaction to isolates of races 65, 73 and 89 of *C. lindemuthianum* in a randomized complete blocks design with 3 replicates, being 9 seedlings per plot. Anthracnose severity was assessed according to the descriptive scale from 1 to 9 (Schoonhoven and Pastor-Corrales, 1987). The mean of anthracnose severity scores of the progenies of each cycle, for each isolate separately, were used to obtain the linear regression equations. The genetic progress (GP) for resistance to each isolate of *C. lindemuthianum* was estimated as follows:  $GP(\%) = \left( \frac{b_1}{\bar{X}_{CI}} \right) * 100$ , where  $b_1$  is the linear regression coefficient and  $\bar{X}_{CI}$  is the mean of anthracnose severity scores of S<sub>0:1</sub> progenies of Cycle I.

**RESULTS AND DISCUSSION:** The mean of anthracnose severity scores of the S<sub>0:2</sub> progenies decreased over the five recurrent selection cycles (Figure 1). Considering the S<sub>0:2</sub> progenies of the first cycle, the estimates of selection gain, per cycle, was 10.7%, 9.0% and 8.0% for the isolates of race 65, 73 and 89 of *C. lindemuthianum*, respectively. It was observed that there was a progressive increase in the number of resistant progenies to a greater number of isolates of *C. lindemuthianum* from the first to the last selective cycle. In the first cycle, 14 S<sub>0:2</sub> progenies were susceptible to the three isolates used. However, in the fifth cycle most of the progenies were resistant to these three isolates (Figure 2). Besides that, it is important to highlight that new sources of genetic resistance can be added in any cycle, so that the host can respond dynamically to the genetic variability of the pathogen. Therefore, the recurrent selection can be an effective breeding method to obtain common bean cultivars with broad spectrum of anthracnose resistance.



**Figure 1.** Linear regression for the mean of anthracnose severity scores of the S<sub>0:2</sub> progenies from selective cycles I to V of recurrent selection.



**Figure 2.** Frequency of progenies with favorable alleles (anthracnose severity scores 1.0 – 3.0) to none, one, two and three isolates of *C. lindemuthianum* in the first and fifth cycles of recurrent selection cycles aiming anthracnose resistance.

## ACKNOWLEDGEMENTS

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