GENERAL AND SPECIFIC COMBINING ABILITIES AS AN EFFICIENT APPROACH TO SELECT PARENTS AND SUPERIOR POPULATIONS FOR RESISTANCE TO WHITE MOLD IN COMMON BEAN

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INTRODUCTION

White mold (WM), caused by the soil borne fungus *Sclerotinia sclerotiorum* (Lib.) de Bary, is one of the most destructive diseases of common bean (*Phaseolus vulgaris* L.) in the world, mainly in the North and South American countries, including the United States, Canada, Argentina, and Brazil. This pathogen greatly undermines the seed yield and quality. In susceptible cultivars, WM can cause losses of 30 to 100%, especially in conducive weather of mean temperature around 10–25°C and high soil moisture, and in absence of disease management (Singh & Schwartz, 2010; Schwartz & Singh, 2013). The objective of this study was to select common bean parents and populations aiming to obtain elite lines resistant to WM by estimating general combining ability (GCA) and specific combining ability (SCA) for WM severity in three field nurseries carried out in Brazil.

MATERIAL AND METHODS

Partial diallel crosses were performed between parents from two groups: GI) three sources of partial resistance to WM identified abroad, and GII) nine Brazilian cultivars and elite lines. Twenty-seven populations were obtained and advanced in bulk up to F6 generation, when they were screened for WM severity in three field nurseries in Brazil (Oratórios-MG, Viçosa-MG, and Goianira-GO). The field nurseries were installed in a complete randomized block design. In Goianira, three replicates were used and each plot was two rows 2.0 m long, with 0.45 m between rows. In Oratórios, four replications were used and each plot was a single 3.0 m long row, with 0.50 m between rows. In Viçosa, five replications were used and each plot was a single 5.0 m long row, with 0.50 m between rows. BRS Requinte was used as a susceptible control and to fill the borders. The nurseries were sprinkler irrigated periodically. The WM severity was evaluated at the growth stage R8–R9, using a rating scale of 1 to 9 (1 = no disease symptoms and 9 = 80–100% diseased plants and/or 60–100% infected tissues) (Miklas et al., 2013). GCA and SCA estimates were obtained by the Griffing model IV, adapted by Geraldi & Miranda Filho (1988) for partial diallel. Statistics analyses were carried out using R software (R Care Team, 2013).

RESULTS AND DISCUSSION

Significant effects of populations (P) and of interaction between populations and environments (P × E) for WM severity were shown by the combined analysis of variance. The overall mean of WM severity in the combined analysis ranged from 2.83 to 5.03, in contrast with the mean severity of 7.21 presented by the susceptible control cultivar BRS Requinte. The results also showed the existence of variability for WM severity among parents from GII but not among the parents from GI, indicating that the selection should focus on cultivars and elite lines. In general, the GI parents contribute with favorable alleles for resistance to WM in the tested populations, but the genetic

effects depend of the environment. K-59, in Oratórios-MG and Viçosa-MG, and K-407, in Goianira-GO, contributed to increase the resistance to WM in the tested populations. Considering the GII parents, BRS Executivo and BRS Esplendor performed better across the three filed nurseries. The populations identified as most promising to be explored to obtain common bean lines resistant to WM were K-59/BRS Executivo, PI204717/BRS Campeiro, PI204717/Jalo Precoce, K-59/BRS Radiante and K-407/BRS Cometa, which presented significant and negative effects of the SCA. The results suggest that common bean breeding programs for WM resistance should use the strategy of selecting parents and populations resistant to WM based on estimates of GCA and SCA for WM severity in multi-field nurseries. Based on these evaluations, segregating populations that associate as many favorable alleles as possible to obtain resistant lines with broadly adaption to different environments may be achieved from crosses between selected parents.

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