RECURRENT SELECTION PROGRAM FOR TOLERANCE TO BEAN GOLDEN MOSAIC VIRUS IN BLACK COMMON BEAN

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Processes as parent selection, maintenance and exploitation of genetic variability, and conduction of the most promising segregating populations are basic steps for efficiency and success of all plant breeding program.Once new challenges are emerging worldwide on food production, the plant breeders, including those who work with autogamous plants, have considered the populational breeding and the breeding for quantitative traits as the main responsible for the yield increasing (Cargnin, 2007). Therefore, the recurrent selection could beconsidered as an important strategy to allow the stacking of favorable alleles associated to the target quantitative traits in each selection cycle, resulting in superior improved lines and populations. As a complementary tool to be used during the conduction of a recurrent selection program, the molecular markers can be extremely useful for parent selection to ensure the availability of initial genetic variability and monitor this variability over the program.

Bean golden mosaic virus (BGMV) is one of the heaviest constraints on bean production in Latin America, causing significant yield losses ranging from 40% to 100% (Morales *et al.*, 2004). In Brazil, it has been estimated that about 200,000 ha became inappropriate for common bean grow during the dry season due the severe incidence of BGMV. This virus is transmitted by the whitefly *Bemisia tabaci* (Gennadius) in a persistent and circulative manner. The disease is characterized by yellow-green mosaic of leaves, stunted growth and distorted pods, which may vary among genotypes. Control practices have focused primarily on controlling the vector by contact or systemic high-toxicity insecticides, with the concomitant problems of development of pesticide-resistant forms, low cost-benefit ratio and environmental concerns.

The main goal of this breeding program is to develop and conduct populations under recurrent selection design in order to obtain common bean black seeded lines tolerant to the BGMV. For this reason, it focuses on the development of base populations, performance testing of segregating progenies, and evaluation of the process efficiency by estimating the genetic progress over the selection cycles. SSR markers will also be used as background markers to assess and monitor the genetic variability over the program.

Based on previous studies on tolerance to BGMV developed by our research group, the following common bean lines were selected as parents for the composition of the original population (C0S0): Pinto 114, A 775, A 429, IAPAR 57, LM 21306-0, Ônix (LM 30630), Red Mexican 35, and Redlands Greenleaf C. Conical crosses were done using all these parents. Firstly, simple hybrids were obtained: Pinto 114 / Redlands Greenleaf C.; Ônix / LM 21306-0; IAPAR 57 / A 429; A 775 / Red Mexican 35. After that, the simple hybrids were crossed to develop double hybrids: (Pinto 114 / Redlands Greenleaf C.) // (A 775 / Red Mexican 35) and (IAPAR 57 / A 429) // (Ônix / LM 21306-0). The double hybrids were then crossed to obtain multiple hybrids from all eight parents. The F_1 generation formed by all multiple hybrids was conducted under shade house condition to obtain F_2 plants (the C_0S_0 generation), with selection

for black seeded plants. The base population (C_0S_0) composed by 4,910 plants was grown in the field and inoculated with BGMV seven days after germination, as described by Melo *et al.* (2005). Disease reaction was scored 50-60 days after inoculation, using the 1-9 degree scale proposed by Costa *et al.* (1990), where the degree 1 is equivalent to the absence of symptoms and 9 represents plants close to collapse or dead. Sixty-three $C_0S_{0:1}$ plants were initially selected as tolerant to the pathogen. Seeds from these plants were sown in the field using a plant-row design, and then inoculated with the virus. Fifty-five $C_0S_{0:2}$ progenies were selected as tolerant. Aiming to develop a new recombination cycle, these 55 tolerant genotypes were crossed following a circulant diallel design, resulting in the base population for the second cycle of selection (C_1S_0). This population was increased and, consequentially, the C_1S_1generation was obtained and inoculated with the pathogen under shade house condition, as described by Melo *et al.* (2005). Disease evaluation was done as previously described. The $C_1S_{1:2}$ progenies identified as most tolerant were selected to be sown and screened in the field. The top 20 $C_1S_{1:3}$ resulting progenies were selected and crossed to develop the third recombination cycle (C_2S_0), using a circulant diallel design. The C_2S_0 population was increased and about 15,000 C_2S_1 seeds were obtained and sown in the field. Out of them, 347 plants were selected based on their tolerance to BGMV. The resulting $C_2S_{1:2}$ progenies were also screened in the field and 201 $C_2S_{1:3}$ families were obtained and are being evaluated during the dry season of 2012 for reaction to BGMV and other diseases as well as for agronomic performance. The top 30 progenies will be selected and screened with a set of 40 SSR markers aiming to determine the allelic diversity present in these lines and identify the presence of genetic structuration in populations obtained by recurrent selection. In order to reduce the number of crosses and still keep the genetic variability, 10 $C_2S_{1:3}$ families tolerant to BGMV and most genetically divergent each other will be used for recombination and, consequently, begin a new cycle of recurrent selection (C_3S_0).

Aiming to estimate the recurrent selection efficiency per cycle, trials will be conducted to compare the mean performance of the best 30 families obtained from different selection cycles in relation to their parents. Despite of the transgenic solution already developed by Embrapa, this recurrent selection program aims also develop regularbreeding solutions for the genetic control of the BGMV to attend farmers that chose to grow conventional cultivars.

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