PARENTAL GENETIC REPRESENTATIVENESS IN BLACK SEEDED COMMON BEAN PROGENIES FROM THE EMBRAPA RECURRENT SELECTION PROGRAM FOR TOLERANCE TO BGMV

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Bean golden mosaic virus (BGMV) can seriously limit common bean (*Phaseolus vulgaris* L.) yield in some of the main production areas in Brazil. Unfortunately, up to now, no cultivars or elite lines have been developed with satisfactory levels of resistance or tolerance to the virus by conventional breeding methods. There is no consensus in regard to genetic control of the common bean reaction to BCMV, but there is evidence that it is a polygenic trait (Pessoni *et al.*, 1997). For this reason, the breeding program conducted by Embrapa is using recurrent selection (RS) as a strategy to develop carioca and black seeded elite lines tolerant to BGMV. Thus, the main goal of the present work was to identify progenies with greater parental genetic representativeness among the black seeded $C_2S_{1:4}$ progenies selected in this RS cycle as highest yielding and tolerant to the virus.

The initial population (C_0S_0) was formed from crosses among seven parents selected as tolerant to BGMV in field conditions ('Pinto 114', 'A775', 'A429', 'IAPAR 57', 'LM 21306-0', 'Ônix' and 'RGLC'). This population was advanced, evaluated and subjected to selection regarding to BGMV reaction throughout its generations. During the RS program for black seeded beans, 27 $C_2S_{1:4}$ progenies were developed and selected as the highest yielding and tolerant to the virus. These progenies would be recombined to form the base population in the next RS cycle (C_3). In the present work, these 27 progenies were then evaluated regarding to genetic representativeness of the seven parents. For this purpose, the presence of private alleles identified in the parents by microsatellite markers was used as criterion. The DNA extractions of the progenies and parents were carried out using samples composed of leaf tissue from 10 plants collected in bulk. Twelve fluorescent microsatellite markers were used. PCR reactions, electrophoresis and genotyping of the markers were done as described by Valdisser *et al.* (2013).

A total of 70 alleles were detected in the seven parents using the 12 microsatellite loci. Out of these 70 alleles, 34 were identified as private in at least one of the parents and thus used in the present work. Private alleles are useful in RS programs as they assist in estimating the real contribution of each parent in the genetic composition of the genotypes and progenies generated and selected for the subsequent steps of recombination (Brondani *et al.*, 2004). The parent that showed the greatest number of private alleles was 'RGLC' (10 alleles). In contrast, the parent 'LM21306-0' showed only two private alleles. However, 'LM21306-0' and 'A775' showed greater genetic representativeness in progeny formation, exhibiting at least one private allele in 21 and 25 progenies, respectively. Among the 27 $C_2S_{1:4}$ evaluated progenies, 10 were selected for the next recombination cycle (C_3) because they exhibited greater parental allele representativeness. This is a strategy aiming to maximize the genetic diversity of the base population in the next RS cycles and, thereby, also maximize the opportunity to get genetic gain for different traits during the future selection steps of the breeding program.

Table 1. Parental genetic representativeness in $C_2S_{1:4}$ black seeded progenies from the Embrapa recurrent selection program for tolerance to BGMV.

Progeny (Pro)	PA/Pro[a]	Parent (Par) - PA/Par[b]							GR (%)[c]
		Par1 - 5	Par2 - 5	Par3 - 5	Par4 - 3	Par5 - 2	Par6 - 4	Par7 - 10	
Pro1	3	1(33.3)	-	-	1(33.3)	1(33.3)	-		3/7 (42.9)
Pro2	8	2(25.0)	3(37.5)	2(25.0)	-	-	-	1(12.5)	4/7 (57.1)
Pro3	7	1(14.3)	3(42.8)	2(28.6)	-	-	-	1(14.3)	4/7 (57.1)
Pro4	8	3(37.5)	3(37.5)	-	1(12.5)	-	-	1(12.5)	4/7 (57.1)
Pro5	7	3(42.8)	2(28.6)	-	-	1(14.3)	-	1(14.3)	4/7 (57.1)
Pro6	6	3(50.1)	1(16.7)	-	-	1(16.7)	-	1(16.7)	4/7 (57.1)
Pro7	8	2(25.0)	3(37.5)	-	1(12.5)	1(12.5)	-	1(12.5)	5/7 (71.4)
Pro8	7	2(28.6)	3(42.8)	-	-	1(14.3)	-	1(14.3)	4/7 (57.1)
Pro9	6	2(33.3)	-	1(16.7)	2(33.3)	1(16.7)	-	-	4/7 (57.1)
Pro10	6	1(16.7)	1(16.7)	1(16.7)	1(16.7)	2(33.3)	-	-	5/7 (71.4)
Pro11	6	1(16.7)	2(33.3)	1(16.7)	1(16.7)	1(16.7)	-	-	5/7 (71.4)
Pro12	6	1(16.7)	2(33.3)	1(16.7)	1(16.7)	1(16.7)	-	-	5/7 (71.4)
Pro13	6	1(16.7)	1(16.7)	-	1(16.7)	1(16.7)	-	2(33.3)	5/7 (71.4)
Pro14	6	1(16.7)	1(16.7)	1(16.7)	1(16.7)	-	-	2(33.3)	5/7 (71.4)
Pro15	6	1(16.7)	2(33.3)	-	2(33.3)	1(16.7)	-	-	4/7 (57.1)
Pro16	4	-	1(25.0)	-	-	1(25.0)	-	2(50.0)	3/7(42.9)
Pro17	7	-	2(28.6)	-	2(28.6)	1(14.3)	-	2(28.6)	4/7 (57.1)
Pro18	4	-	2(50.0)	-	2(50.0)	-	-	-	2/7 (28.6)
Pro19	7	-	2(28.6)	-	2(28.6)	1(14.3)	-	2(28.6)	4/7 (57.1)
Pro20	5	-	2(40.0)	1(20.0)	1(20.0)	1(20.0)	-	-	4/7 (57.1)
Pro21	3	-	2(66.7)	-	1(33.3)	-	-	-	2/7 (28.6)
Pro22	5	1(20.0)	2(40.0)	-	1(20.0)	1(20.0)	-	-	4/7 (57.1)
Pro23	7	1(14.8)	2(28.6)	2(28.6)	1(14.3)	1(14.3)	-	-	5/7 (71.4)
Pro24	6	1(16.7)	2(33.3)	1(16.7)	1(16.7)	1(16.7)	-	-	5/7 (71.4)
Pro25	5	-	2(40.0)	2(40.0)	-	1(20.0)	-	-	3/7 (42.9)
Pro26	5	1(20.0)	2(40.0)	1(20.0)	-	1(20.0)	-	-	4/7 (57.1)
Pro27	3	-	2(66.7)	-	-	1(33.3)	-	-	2/7(28.6)

[a]PA/Pro: total number of private microsatellite alleles (PA) per $C_2S_{1:4}$ progeny (P).
[b]Parents: Par1-'Pinto114', Par2-'A775', Par3-'A429', Par4-'IAPAR57', Par5-'LM21306-0', Par6-'Onix' and Par7-'RGLC'; PA/Par: total number of private microsatellite alleles (PA) per parent (Par).
[c]GR: relative genetic representativeness of the seven parents in the $C_2S_{1:4}$ progenies.

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