PREDICTION OF GENETIC POTENTIAL OF COMMON BEAN SEGREGANT POPULATIONS FOR SLOW SEED-COAT DARKENING

Silva FC[1], Sousa LL[1], Melo PGS[1], Melo LC[2], Pereira HS[2]

[1]Universidade Federal de Goiás, [2]Embrapa Arroz e Feijão, GO- Brazil
eng.fernanda09@gmail.com

INTRODUCTION

In Brazil, Carioca common beans accounts for 70% of the consumer market (Pereira et al., 2017). For this type of grain, the darkening of the grains during storage has deserved attention because it is responsible for the low acceptance of the grains by the consumer. Some studies have demonstrated the possibility of selecting Carioca common bean with slow seed-coat darkening (Silva et al., 2008; Araújo et al., 2012). Thus, the objective of this study was to predict the genetic potential of common bean segregant populations for slow seed-coat darkening.

MATERIALS AND METHODS

Biparental crosses were carried out in a partial diallel scheme between 20 elite common bean lines with carioca seeds, divided into two groups: group I – two genotypes for slow seed-coat darkening (BRS Requinte and BRSMG Madrepérola); group II - ten genotypes for regular seed-coat darkening (BRS Estilo, Pérola, BRS Cometa, BRS Pontal, BRSMG Majestoso, IAC Alvorada, IPR Saracura, IPR Siriri, BRS Sublime and BRS Notável).

Populations and parents were evaluated in the $F_{3:4}$ generation, 2010/winter season, in Santo Antônio de Goiás, state of Goiás and in the $F_{4:5}$ generation, in the 2010/rainy season in Ponta Grossa, state of Paraná in an experimental randomized blocks design, with three replications, in which the plot was 7.2 m^2 .

> Seeds of 40 plants were collected individually in each replicate, totaling 120 plants per treatment. The seeds were stored for 155 days in room temperature and humidity. Seeds-coat darkening evaluation were carried out in each plant, which were ranked from 1 (very light colored grains) to 5 (very dark colored grains). Estimates of genetic and phenotypic parameters were obtained for each population in each environment, using the methodology of Melo et al. (1997). Data were submitted to analysis of variance and, later, the methodology of Jinks and Pooni (1976) was used for predicting the genetic potential of the populations. This methodology allows estimating the probability of extraction of lines that exceed a standard. In this case, the average of the population with the slow seed-coat darkening in each environment was used as a standard, subtracting 10%.

RESULTS AND DISCUSSION

Significant differences (p <0.01) were found between treatments in both generations, indicating the presence of genetic variability. The heritability estimates showed great variation, with values of high magnitude (0.00-0.95). The BRSMG Madrepérola populations presented consistent heritability values in both locations and generations (Table 1), demonstrating that genotype selection based on its respective phenotypes may be successful. The probabilities of populations exceeding the standard for the slow seed-coat darkening ranged in the $F_{3:4}$ generation from 0 to 37.1% and $F_{4:5}$ from 0 to 41.7%.

The highest probabilities for the achievement of promising lines were verified in the populations from the crossing with the cultivar BRSMG Madrepérola. High probability values

associated with high genetic variances and low means were found in populations 12, 13, 14, 18, 19 and 20. Based on these results, these populations present a possibility of success in the extraction of lines with slow seed-coat darkening.

Table 1. Means for seed-coat darkening, genetic variance (σ^2_G), heritability (h^2), Z value and P (Probability to obtain lines that exceed the best population by 10%), Santo Antônio de Goiás-GO and Ponta Grossa-PR in 2010/155 days storage.

Populations	$F_{3:4}$ Santo Antônio de Goiás					$F_{4:5}$ Ponta Grossa				
	Mean	σ^2_G	h^2	Z	P (%)	Mean	σ^2_G	h^2	Z	P (%)
1 (1 x 3)*	4.11	0.40	0.52	-1.72	4.27	4.82	0.00	0.00	-5.26	0.00
2 (1 x 4)	3.74	0.31	0.50	-1.46	7.21	4.67	0.26	0.63	-2.57	0.51
3 (1 x 5)	4.54	0.01	0.03	-2.92	0.18	4.37	0.33	0.71	-1.98	2.39
4 (1 x 6)	3.99	0.31	0.47	-1.71	4.27	4.46	0.35	0.72	-2.04	2.07
5 (1 x 7)	4.25	0.11	0.22	-2.36	0.91	4.85	0.02	0.09	-4.37	0.00
6 (1 x 8)	4.39	0.00	0.00	-3.26	0.06	4.73	0.05	0.24	-3.81	0.01
7 (1 x 9)	4.31	0.03	0.07	-2.65	0.40	4.77	0.09	0.36	-3.54	0.02
8 (1 x 10)	3.99	0.20	0.37	-1.89	2.94	3.77	0.01	0.04	-4.46	0.00
9 (1 x 11)	3.99	0.27	0.44	-1.77	3.84	4.27	0.30	0.75	-1.20	11.51
10 (1 x 12)	3.95	0.39	0.53	-1.58	5.71	3.83	0.28	0.69	-1.95	2.56
11 (2 x 3)	3.37	1.13	0.82	-0.66	25.46	3.62	1.11	0.92	-0.74	22.96
12 (2 x 4)	2.96	0.66	0.77	-0.42	33.72	3.46	1.10	0.92	-0.55	29.12
13 (2 x 5)	3.62	1.07	0.79	-0.87	19.22	3.35	1.68	0.95	-0.34	36.69
14 (2 x 6)	3.00	0.56	0.74	-0.49	31.21	3.62	0.85	0.92	-0.35	36.32
15 (2 x 7)	3.72	1.01	0.77	-0.97	16.60	3.46	1.41	0.94	-0.50	30.85
16 (2 x 8)	3.74	1.08	0.78	-0.96	16.85	3.35	1.32	0.93	-0.63	26.43
17 (2 x 9)	3.75	1.02	0.77	-0.99	16.11	3.62	1.37	0.93	-0.69	24.51
18 (2 x 10)	2.84	0.54	0.75	-0.33	37.07	3.77	0.71	0.90	-0.46	32.28
19 (2 x 11)	3.19	0.85	0.79	-0.59	27.76	3.85	1.04	0.93	-0.26	39.74
20 (2 x 12)	3.23	1.00	0.81	-0.58	28.10	3.42	1.07	0.94	-0.21	41.68

*Parents: 1- BRS Requinte; 2- BRSMG Madrepérola; 3- Pérola; 4- BRS Estilo; 5- BRS Cometa; 6- BRS Sublime; 7- BRS Notável; 8- BRS Pontal; 9- BRS Majestoso; 10- IAC Alvorada; 11-IPR Saracura;12- IPR Siriri.

REFERENCES
Araújo LCA et al. (2012). Ciênc agrotec, 36: 156-162.
Jinks JL and Pooni HS (1976). Heredity, 36:243-266.
Melo LC et al. (1997). Brazilian Journal of Genetics, 20: 283-292.
Pereira HS et al. (2017). Rev Ceres, 64: 159-166.
Silva GS et al. (2008). Crop Breed Appl Biotech, 8: 299-304.