

ARTICLE

Effect of environments on the estimated genetic potential of segregating common bean populations

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Received 29 June 2013

Accepted 06 September 2013

Abstract – *The objective of this study was to investigate the effect of environments on the estimated genetic potential of common bean populations for the traits hypocotyl diameter and grain yield. We evaluated 48 segregating bean populations in the growing seasons winter 2009 (F₂ and F₃ simultaneously) and drought 2010 (F₃ and F₄ generations simultaneously), and 16 controls. The genetic potential of the population was estimated using the methodology of Jinks and Pooni. The coincidence between the best and worst populations in the two growing seasons and different generations for the two characters was low, indicating that the environmental effect interferes with the selection of common bean populations when using the method of Jinks and Pooni. Thus, it is recommended that the genetic potential should be estimated based on the evaluation of a larger number of environments.*

Key words: *Phaseolus vulgaris, genetic and phenotypic parameters, plant architecture, grain yield selection.*

INTRODUCTION

In bean breeding programs, selection is mostly performed in segregating populations obtained through artificial hybridization followed by a few cycles of selfing. An important decision that defines the success of the selection is the choice of the populations with the greatest potential to produce superior lines. Prior knowledge about the potential of these populations can mean significant cost and time benefits, since breeders can focus on the most promising.

For the choice of a segregating population, aside from the mean, the variability is essential, since the genetic variability in the population may be low, since the genetic constitutions of the parents are similar for the target trait (Ramalho et al. 1993a). In some situations it is not possible to combine these two parameters (Santos et al. 2001).

One of the breeding procedures used to select segregating populations is that of Jinks and Pooni (1976). This method allows an estimated potential of a given population to generate lines superior to a certain standard reference, in the F_∞ generation. For this purpose, the mean and variance of the initial generations are estimated. Some studies have demonstrated the potential of this method to predict segregating common bean populations (Otubo et al. 1996, Abreu et al. 2002, Carneiro et al. 2002).

The selection of the most promising populations is based primarily on grain yield. However, other agronomic traits should be taken into consideration. In bean breeding, a decisive characteristic is the upright growth habit, which has been the focus of a number of studies (Cunha et al. 2005, Menezes Júnior et al. 2008, Rocha et al. 2012). An improved growth habit facilitates management practices and allows mechanical harvesting. However, the effect of environments, along with a visual assessment of plant architecture through scores assigned in the field, can hamper the choice of populations with more upright plants. Acquah et al. (1991) reported the efficacy of the hypocotyl diameter to determine the architecture of common bean plants. Thus, this trait is a promising indicator to identify more upright populations.

In general, the traits yield and plant growth of common bean are greatly influenced by environmental factors originating from, for example, the effect of years and yields (Ramalho et al. 1993b, Ramalho et al. 1998, Mendes et al. 2009). However, there is no information on the effect of environments in estimating the genetic potential of common bean populations by the methodology of Jinks and Pooni. For soybean, Triller and Toledo (1996) found that the interaction existing between genotype and environment affected the prediction process. These authors concluded

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that in the presence of interaction, the use of more than one reference cultivar and, particularly, data from two environments, increased the accuracy of grain yield estimates. Jinks and Pooni (1980) also emphasized the importance of obtaining variance estimates free of interaction effects, since the interaction with the environment resulted in misleading predictions for the trait flowering in tobacco.

The aim of this study was to verify the environment effect on the estimated genetic potential of common bean populations for hypocotyl diameter and grain yield by the method of Jinks and Pooni.

MATERIAL AND METHODS

The 48 segregating common bean populations derived from crosses of 14 parents in a partial diallel mating scheme in 2008, were divided in groups. Group 1 consisted of three common bean parents with black beans (BRS Valente, BRS Supremo and IPR Uirapuru), three with carioca grain (beige grains with light brown stripes) (BRS Horizonte, CNFC 9466 and A805) and two “mulatinho” (cream-colored grains) (A170 and A525). Group 2 consisted of six parents with carioca grain (BRSMG Majestoso, VC 6, BRSMG Madrepérola, L1, L2 and L3). The two groups differed in plant growth and type.

The 48 populations were evaluated in the F_2 and F_3 generations, along with the 14 parents and 2 commercial cultivars (Pérola and BRSMG Talismã), resulting in a total of 112 treatments in the winter season (sowing in the first half of August 2009). For the dry season (sowing in February 2010) a seed sample was taken from each treatment of the previous experiment. Thus, the populations evaluated in the dry season were in the F_3 and F_4 generations. The two experiments were conducted in an experimental field of the Federal University of Viçosa, in Coimbra/MG (lat 20° 45' S, long 42° 51' W, alt 690 m asl). Both experiments were arranged in a randomized block design with three replications, with plots of four 4-m rows, spaced 0.5 m apart, and 15 seeds per meter.

The populations and controls were evaluated for grain yield and hypocotyl diameter, measured in 20 randomly selected plants in the plots. Fertilization at planting consisted of 350 kg ha⁻¹ NPK fertilizer (8-28-16 of N, P₂O₅ and K₂O, respectively), and topdressing, 25 days after seedling emergence, of 30 kg ha⁻¹ N. All other cultural practices were applied according to the regional recommendations for the crop.

In the individual analyses of variance, all effects, except for error and block, were considered fixed. The genetic potential of the segregating populations of each generation and growing season was estimated by the methodology of

Jinks and Pooni (1976), which estimates the probability of a population to originate lines superior to a certain standard (PSS). This probability corresponds to the area to the right of a given value x on the abscissa of the normal distribution, calculated from the properties of a normal standard distribution, estimating variable Z by $Z = (x - m)/s$, where x = mean of the reference line (\bar{L}) which, for grain yield, was cultivar Pérola, plus 35%, and for hypocotyl diameter was the average of line A805, plus 10%; m = average of lines in the F_∞ generation which, in a model without dominance, correspond to the average of the generation under study (\bar{F}_m); s = phenotypic standard deviation among lines

$$(s = \sqrt{\hat{\sigma}_{F_L}^2}).$$

The genetic variance between lines ($\hat{\sigma}_{GL}^2$) is equivalent to twice the additive genetic variance ($\hat{\sigma}_a^2$) present in F_2 . For a model without dominance, the phenotypic variance in F_2 ($\hat{\sigma}_{F_2}^2$) contains $\hat{\sigma}_a^2 + \hat{\sigma}_E^2$. Thus, $\hat{\sigma}_a^2 = \hat{\sigma}_{F_2}^2 - \hat{\sigma}_E^2$. Since the environmental variance between lines is similar to the environmental variance of the F_2 generation, we have

$$s = \sqrt{\hat{\sigma}_{F_L}^2} = \sqrt{2\hat{\sigma}_a^2 + \hat{\sigma}_E^2} = \sqrt{2\hat{\sigma}_{F_2}^2 - \hat{\sigma}_E^2}. \text{ Therefore,}$$

$$\text{for a given population } i, Z_i = (\bar{L} - \bar{F}_{2i}) / \sqrt{(2\hat{\sigma}_{F_{2i}}^2 - \hat{\sigma}_{E_i}^2)}$$

. For populations evaluated in the F_3 generation, the phenotypic variance and estimate of variable Z_i were: $\hat{\sigma}_3^2 = 1.5$

$$\hat{\sigma}_A^2 + \hat{\sigma}_E^2 \text{ and } Z_i = (\bar{L} - \bar{F}_{3i}) / \sqrt{(1.332\hat{\sigma}_{F_{3i}}^2 - 0.332\hat{\sigma}_{E_i}^2)}.$$

For F_4 we used the following expressions:

$$\hat{\sigma}_{F_4}^2 = 1.75\hat{\sigma}_A^2 + \hat{\sigma}_E^2$$

$$\text{and } Z_i = (\bar{L} - \bar{F}_{4i}) / \sqrt{(1.143\hat{\sigma}_{F_{4i}}^2 - 0.143\hat{\sigma}_{E_i}^2)}.$$

The phenotypic variance for each population ($\hat{\sigma}_{F_i}^2$) was estimated in 20 plants per replication, sampled from the center rows, disregarding 0.5 m at either end. Subsequently, the average of these variances in the different replications was calculated. As an estimate of environmental variance of the populations the average of the environmental variances of each of the 16 controls was used. The environmental variance of each control corresponded to the phenotypic variance of these, estimated in the same way as for populations.

RESULTS AND DISCUSSION

In both growing seasons, significant differences ($P < 0.01$) were detected for the treatments and the partitioning in effects of populations (Pop.) and controls (Check), both for the hypocotyl diameter (HD) and for grain yield (YLD), indicating variability among genotypes (Table 1).

Table 1. Summary of individual analyses of variance for the traits hypocotyl diameter (HD) and grain yield (YLD) of common bean evaluated in the winter of 2009 (generations F₂ and F₃, simultaneously) and dry growing seasons of 2010 (generations F₃ and F₄, simultaneously)

Source of variation	df	Winter 2009		Dry 2010	
		Mean squares			
		HD	YLD	HD	YLD
Replications	2	0.0089	485150.82	0.00064	657386.61
Treatments	111	0.0056**	272967.17**	0.0068**	345733.15**
Populations	95	0.0035**	237045.28**	0.0046**	249662.05**
Generation F ₂ (F ₃) ¹	47	0.0026**	220253.73*	0.0041**	215994.00
Generation F ₃ (F ₄)	47	0.0043**	226681.08*	0.0053**	283622.02**
F ₂ vs F ₃ (F ₃ vs F ₄)	1	0.0036*	1513365.03**	0.00000056	235942.14
Controls	15	0.0174**	457164.42**	0.0207**	938225.53**
Pop. vs Check	1	0.0283**	922588.36*	0.0005	585101.15
Error	222	0.0009	149924.36	0.00095	154063.68
CV(%)		5.21	12.26	5.23	13.30
Means F ₂ (F ₃)		0.572	3252	0.588	2939
Means F ₃ (F ₄)		0.579	3107	0.588	2996
Population means		0.576	3180	0.588	2967
Control means		0.602	3030	0.592	2848

¹ Source of variation in parentheses refers to the experiment of the dry season of 2010; ** and * significant, at 1% and 5% probability, respectively, by the F test.

Significant population effects were also observed in the F₂, F₃ and F₄ generations, except for YLD in F₃, in the dry season. In the winter growing season, significant effects for the contrasts F₂ vs F₃ and Pop. vs Check indicated the presence of heterosis for the traits HD and YLD. However, in the dry season, the contrasts F₃ vs F₄ and Pop. vs. Check were not significant for either trait. These results suggest that the heterotic effects detected in F₂ are small. The predominance of dominance effects associated with grain yield in common bean was reported by Rodrigues et al. (1998) and Gonçalves-Vidigal et al. (2008). However, other studies reported predominantly additive effects for YLD (Santos et al. 1985, Kurek et al. 2001).

The probabilities that populations originate lines that are 10% superior to the reference line A805 (PSS), considering the hypocotyl diameter (Table 2) and 35% superior to cultivar Pérola for grain yield (Table 3), were inconsistent when compared in different generations and growing seasons, for most populations. The heritability estimates at the individual level for each population were generally low (Tables 2 and 3).

In the selection of the best 12 populations (25%), by the methodology of Jinks and Pooni (1976) based on the hypocotyl diameter or yield, it was observed that the number of coincident populations in all six possible contrasts, given by the combination of different growing seasons and/or by the generations, ranged from two to six (Figure 1). An analysis of the pairs of contrasts of these concordances showed less variation in HD than GY, indicating that the trait HD was less influenced by the environment.

When the 12 poorest populations were selected, the coincidence of the six prediction contrasts was also low (Figure 2). Thus, both in the selection of the best as in the elimination of the worst populations, the environmental effect on the prediction of the population potential by the methodology Jinks and Pooni (1976) was high. Triller and Toledo (1996) found that in soybean although the prediction by this method was not influenced by the heritability and complexity of the genetic control of the trait, the presence of genotype x environment interaction interfered with the prediction. These authors found that the use of two reference cultivars, and especially data from two environments, increased the accuracy of grain yield estimates.

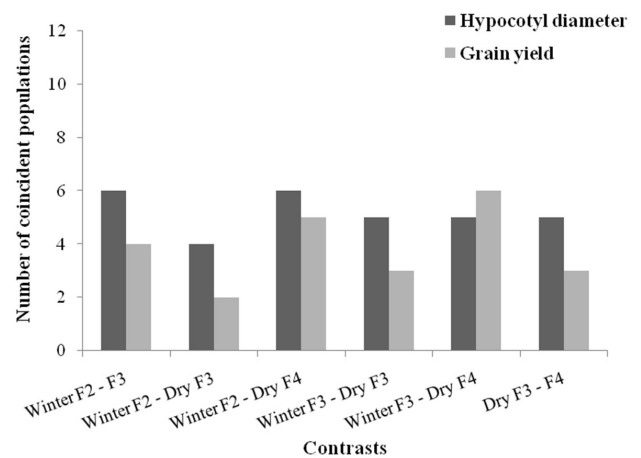


Figure 1. Number of coincident populations among the 12 best, considering the effects of seasons and generations, for the traits hypocotyl diameter and grain yield in the six possible contrasts.

Table 2. Probability of originating lines that are superior 10% (PSS, in %) to line A805, and heritability (h^2 , in %) of the hypocotyl diameter, of 48 common bean populations, evaluated in the winter 2009 (generations F_2 and F_3) and dry growing seasons of 2010 (generations F_3 and F_4)

Population	Winter 2009				Dry 2010			
	Generation F_2		Generation F_3		Generation F_3		Generation F_4	
	PSS	h^2	PSS	h^2	PSS	h^2	PSS	h^2
BRS Valente x VC6	7.93	13.25	0.94	0.00*	14.69	30.37	11.9	15.82
BRS Valente x BRS MG Majestoso	12.10	33.46	16.11	50.51	6.55	26.31	0.73	0.00
BRS Valente x BRS MG Madrepérola	5.16	21.74	1.16	7.51	4.09	0.00	9.01	37.09
BRS Valente x L1	1.13	0.00	7.64	7.41	12.1	31.77	11.12	16.88
BRS Valente x L2	0.23	0.00	0.89	0.00	0.19	0.00	0.80	0.00
BRS Valente x L3	0.38	0.00	13.79	28.10	11.31	25.44	5.16	0.00
BRS Supremo x VC6	8.69	13.24	5.82	0.00	10.75	0.00	2.07	0.00
BRS Supremo x BRS MG Majestoso	8.85	10.09	9.68	33.09	10.20	31.84	5.48	0.00
BRS Supremo x BRS MG Madrepérola	2.39	0.00	3.22	23.86	7.21	21.19	1.70	0.00
BRS Supremo x L1	6.81	0.00	6.94	0.00	3.36	0.00	9.01	0.00
BRS Supremo x L2	7.93	21.58	10.38	29.06	0.96	0.00	3.75	11.22
BRS Supremo x L3	1.32	0.00	16.85	37.60	14.46	43.66	5.37	0.00
IPR Uirapuru x VC6	17.36	21.96	13.14	8.68	14.69	0.00	6.30	0.00
IPR Uirapuru x BRS MG Majestoso	7.35	7.65	10.56	7.91	5.71	0.00	11.12	0.00
IPR Uirapuru x BRS MG Madrepérola	2.12	0.00	8.08	21.22	9.85	28.92	5.71	27.63
IPR Uirapuru x L1	9.85	8.58	5.94	0.00	16.11	0.00	15.15	19.87
IPR Uirapuru x L2	12.71	33.20	7.08	26.98	8.69	8.16	4.09	5.66
IPR Uirapuru x L3	5.59	0.00	11.90	42.31	14.46	6.25	23.58	29.27
BRS Horizonte x VC6	5.26	0.00	9.68	25.13	12.71	18.53	18.41	52.48
BRS Horizonte x BRS MG Majestoso	5.26	14.19	0.59	0.00	1.29	0.00	0.96	0.00
BRS Horizonte x BRS MG Madrepérola	5.37	11.36	0.26	0.00	5.05	23.74	8.69	45.19
BRS Horizonte x L1	0.78	0.00	10.56	31.32	14.46	24.84	0.57	0.00
BRS Horizonte x L2	0.02	0.00	0.12	0.00	7.08	42.92	2.68	10.81
BRS Horizonte x L3	10.03	22.38	0.55	0.00	11.90	23.75	13.14	29.86
CNFC 9466 x VC6	14.23	19.93	20.90	27.89	11.90	17.26	22.96	40.56
CNFC 9466 x BRS MG Majestoso	1.79	0.00	2.56	0.00	0.96	0.00	0.84	0.00
CNFC 9466 x BRS MG Madrepérola	1.58	0.00	2.62	16.15	0.39	0.00	3.36	7.79
CNFC 9466 x L1	9.85	25.55	16.60	41.63	12.51	36.44	14.01	21.53
CNFC 9466 x L2	10.75	45.15	17.62	43.84	2.68	7.14	4.95	9.31
CNFC 9466 x L3	0.01	0.00	15.15	28.06	9.01	18.92	4.27	11.32
A805 x VC6	8.38	0.00	14.01	22.62	24.51	45.94	7.64	0.00
A805 x BRS MG Majestoso	14.01	30.72	1.10	0.00	2.22	0.00	0.99	0.00
A805 x BRS MG Madrepérola	3.67	5.40	2.94	5.57	4.01	22.28	6.68	43.87
A805 x L1	6.55	18.94	7.64	23.09	23.27	33.57	6.30	7.52
A805 x L2	0.87	0.00	3.22	9.95	1.02	0.00	0.84	0.00
A805 x L3	14.69	34.24	6.94	12.26	15.62	28.75	7.35	0.00
A170 x VC6	2.33	0.00	0.87	0.00	15.15	17.74	17.62	18.68
A170 x BRS MG Majestoso	4.36	0.00	5.26	5.91	0.09	0.00	3.75	0.00
A170 x BRS MG Madrepérola	1.16	0.00	1.50	8.63	1.54	0.00	4.27	0.00
A170 x L1	2.56	0.00	16.35	32.52	3.67	0.00	8.23	0.00
A170 x L2	3.51	0.00	0.64	0.00	0.68	0.00	7.35	25.52
A170 x L3	0.00	0.00	2.81	0.00	10.75	9.39	22.36	37.48
A525 x VC6	23.89	28.21	14.01	0.00	31.92	47.60	44.04	37.04
A525 x BRS MG Majestoso	2.44	0.00	16.85	28.45	23.27	39.68	12.71	27.32
A525 x BRS MG Madrepérola	4.46	17.64	3.36	0.00	7.93	35.16	2.28	0.00
A525 x L1	16.11	21.23	19.49	18.90	12.51	14.40	15.15	41.00
A525 x L2	5.05	9.53	11.90	36.11	9.68	31.46	14.92	43.45
A525 x L3	9.34	12.06	31.92	42.57	20.90	38.40	44.04	54.65

*Heritability was considered zero, due to the negative or zero values estimated for genetic variance

Table 3. Probability of originating lines that are superior 35% (PSS, in %) to cultivar Pérola, and heritability (h^2 , in %) of the grain yield, of 48 common bean populations, evaluated in the winter 2009 (generations F_2 and F_3) and dry growing seasons of 2010 (generations F_3 and F_4)

Population	Winter 2009				Dry 2010			
	Generation F_2		Generation F_3		Generation F_3		Generation F_4	
	PSS	h^2	PSS	h^2	PSS	h^2	PSS	h^2
BRS Valente x VC6	44.83	39.29	21.18	0.00*	41.29	26.70	37.07	0.00
BRS Valente x BRS MG Majestoso	45.22	70.31	48.80	65.16	39.74	41.69	39.74	0.00
BRS Valente x BRS MG Madrepérola	45.22	18.50	37.07	51.27	41.29	48.50	46.02	47.75
BRS Valente x L1	43.64	9.52	32.27	18.58	40.52	36.13	35.94	0.00
BRS Valente x L2	42.47	0.00	35.94	33.48	31.21	0.00	42.07	0.00
BRS Valente x L3	39.36	0.00	45.62	30.24	39.36	44.71	40.52	13.70
BRS Supremo x VC6	46.02	0.19	29.80	13.52	30.50	0.00	28.77	0.00
BRS Supremo x BRS MG Majestoso	38.21	22.93	33.36	29.26	38.97	9.95	36.32	27.61
BRS Supremo x BRS MG Madrepérola	41.68	42.70	37.07	40.59	39.36	43.67	43.64	17.74
BRS Supremo x L1	41.68	21.01	41.29	0.00	38.97	0.00	45.62	36.48
BRS Supremo x L2	34.46	16.73	34.83	64.98	35.94	0.00	37.07	0.00
BRS Supremo x L3	35.20	0.00	43.25	49.61	40.13	58.08	43.64	4.43
IPR Uirapuru x VC6	39.36	33.75	33.36	0.00	40.13	13.18	48.40	0.00
IPR Uirapuru x BRS MG Majestoso	37.07	26.06	35.20	17.38	33.36	0.00	46.02	22.88
IPR Uirapuru x BRS MG Madrepérola	37.07	21.51	39.36	50.58	42.07	27.03	38.59	36.05
IPR Uirapuru x L1	40.13	26.05	29.80	24.41	46.41	0.00	41.29	37.70
IPR Uirapuru x L2	38.59	34.78	32.27	0.00	36.32	15.61	40.52	16.73
IPR Uirapuru x L3	40.90	0.00	38.59	20.84	30.85	0.00	44.43	32.96
BRS Horizonte x VC6	38.21	0.00	36.32	22.27	39.36	22.74	41.29	34.94
BRS Horizonte x BRS MG Majestoso	35.20	49.01	38.21	0.00	25.14	0.00	35.94	0.00
BRS Horizonte x BRS MG Madrepérola	39.36	41.24	37.07	27.57	43.64	21.98	34.46	26.86
BRS Horizonte x L1	38.21	0.00	32.27	51.43	42.47	35.57	44.83	2.53
BRS Horizonte x L2	23.58	0.00	16.85	0.00	44.83	59.96	34.83	1.14
BRS Horizonte x L3	40.52	37.19	28.77	0.00	44.43	40.31	34.09	27.04
CNFC 9466 x VC6	42.86	0.00	38.21	0.00	40.13	12.58	44.83	34.84
CNFC 9466 x BRS MG Majestoso	40.13	39.60	43.25	8.15	42.47	0.00	49.20	0.00
CNFC 9466 x BRS MG Madrepérola	48.4	36.35	46.81	36.41	41.29	0.00	40.52	0.00
CNFC 9466 x L1	36.32	20.36	38.97	41.30	38.21	28.64	45.62	35.52
CNFC 9466 x L2	47.61	44.93	43.25	50.32	43.25	29.78	47.61	0.00
CNFC 9466 x L3	41.29	0.00	39.36	9.05	40.13	5.54	34.09	17.20
A805 x VC6	14.46	0.00	30.85	0.00	33.72	17.25	28.43	12.12
A805 x BRS MG Majestoso	37.45	28.84	22.66	0.00	37.83	0.55	36.32	14.17
A805 x BRS MG Madrepérola	44.04	29.19	25.14	0.00	48.40	52.80	39.36	48.33
A805 x L1	22.36	0.00	33.00	16.98	42.47	35.02	37.45	0.00
A805 x L2	26.76	0.00	26.43	0.61	37.07	0.00	36.32	0.00
A805 x L3	17.36	0.00	26.76	0.00	34.46	28.70	41.29	12.46
A170 x VC6	14.46	0.00	18.94	0.00	32.64	2.99	43.64	28.28
A170 x BRS MG Majestoso	33.00	6.80	34.83	2.98	45.22	0.00	42.86	1.98
A170 x BRS MG Madrepérola	33.72	0.00	34.09	0.00	40.52	0.00	31.92	0.00
A170 x L1	26.76	0.00	31.92	9.06	39.74	0.00	32.27	0.00
A170 x L2	39.74	36.76	14.23	0.00	39.74	0.00	41.68	0.29
A170 x L3	32.27	0.00	31.21	0.00	41.68	22.48	41.68	11.28
A525 x VC6	15.15	0.00	18.94	0.00	22.36	0.00	18.14	11.24
A525 x BRS MG Majestoso	0.00	0.00	27.76	28.02	38.21	44.25	40.13	39.54
A525 x BRS MG Madrepérola	25.14	0.00	27.09	10.66	28.10	0.00	34.46	0.00
A525 x L1	36.69	40.04	21.18	0.00	28.77	0.00	35.94	30.25
A525 x L2	26.43	0.00	20.04	0.00	21.48	0.00	27.09	0.00
A525 x L3	14.01	0.00	39.36	30.80	28.43	22.94	33.72	41.16

*Heritability was considered zero, due to the negative or zero values estimated for genetic variance

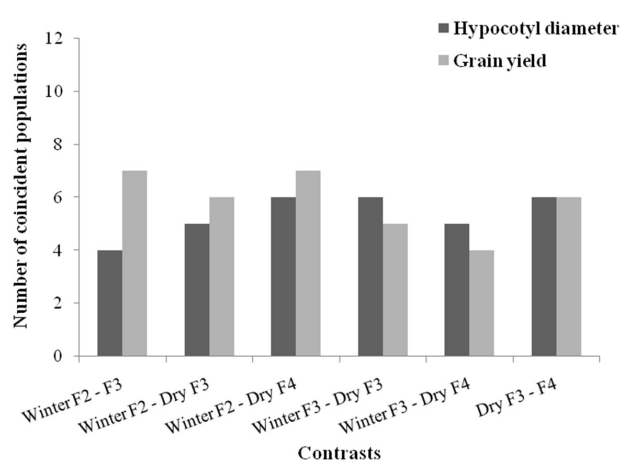


Figure 2. Number of coincident populations among the 12 poorest, considering the effects of seasons and generations, for the traits hypocotyl diameter and grain yield in the six possible contrasts.

The use of individual plants as the basic unit of assessment is another limitation in the methodology of Jinks and Pooni (1976), because the estimates of genetic variance within plants are usually associated with large errors (Vello and Vencovsky 1974). The estimates of genetic variance were negative for several populations, indicating that the estimated environmental variance, based on controls, may not represent the real variation of the populations evaluated in this study. In these cases, the heritability (h^2) for these populations was considered equal to zero (Tables 2 and 3). Importantly, for various populations, discrepant heritability estimates were obtained both between the two crops as within the same crop in different generations. An example of this situation was population BRS Valente x VC6, for both traits (Tables 2 and 3). Jinks and Pooni (1980), when assessing plant height and days to flowering in tobacco, stressed the importance of obtaining estimates of variances free of interaction effects, since the interaction with the environment for one of these traits led to deviations in predictions.

Because of the large number of values of zero heritability

Table 4. Classification of the six best and the six worst-performing common bean populations for hypocotyl diameter (HD) and grain yield (YLD) in the winter 2009 (F_2 and F_3) and dry growing seasons 2010 (generations F_3 and F_4)

Population	Classification (Six best - HD)				Sum of ranks
	WIN/F2	WIN/F3	DRY/F3	DRY/F4	
A525 x VC6	1	12	1	1	15
A525 x L3	13	1	5	2	21
CNFC 9466 x VC6	5	2	19	4	30
A525 x L1	3	3	16	9	31
CNFC 9466 x L1	12	7	15	11	45
A805 x VC6	16	11	2	21	50
Classification (Six worst - HD)					
BRS Horizonte x BRS MG Majestoso	25	45	41	43	154
CNFC 9466 x BRS MG Madrepérola	38	36	46	37	157
BRS Horizonte x L2	46	48	30	38	162
CNFC 9466 x BRS MG Majestoso	37	37	44	44	162
A805 x L2	42	33	42	45	162
BRS Valente x L2	45	42	47	46	180
Classification (Six best - YLD)					
CNFC 9466 x L2	2	6	7	3	18
CNFC 9466 x BRS MG Majestoso	17	5	9	1	32
BRS Valente x BRS MG Madrepérola	5	15	14	4	38
CNFC 9466 x BRS MG Madrepérola	1	2	15	23	41
BRS Valente x BRS MG Majestoso	4	1	22	25	52
CNFC 9466 x VC6	9	14	20	9	52
Classification (Six worst - YLD)					
A525 x L3	47	10	44	42	143
A525 x L1	29	43	43	36	151
A805 x VC6	45	32	37	46	160
A525 x BRS MG Madrepérola	40	37	45	39	161
A525 x L2	39	44	48	47	178
A525 x VC6	44	46	47	48	185

in this work, alternatives must be proposed for less biased variance estimates. An alternative would be to estimate the environmental variance of each segregating population from the mean coefficient of environmental variation of its two parents, as suggested by Melo et al. (1997). These authors stated that if the parents and their segregating populations are evaluated in different plots, the variances can have different environmental effects, resulting in low or overestimated genetic variances. A second possibility would be to calculate the environmental variance for each population based on the average environmental variance of its two parents, as done by Carneiro et al. (2002). A third interesting alternative would be the removal of outlier values from within the plots of controls, which are inbred lines, so the phenotypic variability contains only the environmental variance.

Based on the probabilities of obtaining lines superior to the standard cultivar (PSS), 48 populations of both generations of each growing season were classified to select the six populations with the best and eliminate the six with the worst performance (Table 4). This selection was based on the sum of ranks, being the best populations identified by the lowest sums and the worst by the highest values.

Lines A525 and VC6 stood out in the formation of the best populations for HD (Table 4). For GY, parent CNFC 9466 performed best, represented in four of the six populations classified as best. The population CNFC 9466 x VC6 proved most promising for both HD and YLD, with the advantage of having parents with carioca grain. It is interesting to note

that four of the six best populations for HD were also among the worst for GY, while two populations of the worst for HD were classified as promising for GY. This result shows that the elimination of the worst populations, mainly when based on YLD, leads to the elimination of promising populations for breeding of lines with upright growth. Consequently, a strategy that would tend to improve both growth habit and grain yield would be the establishment of a recurrent selection program with the six most promising populations for each of these traits.

CONCLUSIONS

By the method Jinks and Pooni, when based on the hypocotyl diameter as well as grain yield, the environmental effect interferes with the selection of common bean populations.

For greater reliability in selecting segregating common bean populations by the methodology of Jinks and Pooni, it is recommended to evaluate the populations in the greatest possible number of environments.

ACKNOWLEDGEMENTS

The authors are indebted to the Foundation for Research Support of the State of Minas Gerais (FAPEMIG) for financial support in the execution of the study, to the National Council for Scientific and Technological Development (CNPq) and the Coordination for improving Higher Education Personnel (CAPES) for scholarships.

Efeito de ambientes na predição do potencial genético de populações segregantes de feijão

Resumo – O objetivo deste trabalho foi verificar o efeito de ambientes na predição do potencial genético de populações de feijoeiro quanto ao diâmetro do hipocótilo e produtividade de grãos. Foram avaliadas 48 populações segregantes de feijão nas safras de inverno de 2009 (gerações F_2 e F_3 simultaneamente) e seca de 2010 (gerações F_3 e F_4 simultaneamente), além de 16 testemunhas. A predição do potencial genético das populações foi feita utilizando a metodologia de Jinks e Pooni. Verificou-se baixa coincidência entre as melhores e entre as piores populações nas duas safras e nas diferentes gerações para os dois caracteres, evidenciando que o efeito de ambientes interfere na escolha das populações de feijoeiro, quando se utiliza o método de Jinks e Pooni. Assim, é recomendável que a predição do potencial seja realizada com base nas informações de um maior número de ambientes.

Palavras-chave: *Phaseolus vulgaris*, parâmetros genéticos e fenotípicos, arquitetura de planta, produtividade de grãos, seleção.

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