



Selection of progenies of snap beans using mixed models (REML/BLUP)

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ABSTRACT. The purpose of this research was to select the development of superior genotypes of snap beans adapted to edaphoclimatic conditions of the North and Northwest of Rio de Janeiro State, Brazil, applying the mixed model methodology. The test was installed and carried out in the experimental area of the Instituto Federal Fluminense (IFF), located in the municipality of Bom Jesus do Itabapoana, Rio de Janeiro State, Brazil, using the modified SSD (Single Seed Descent) method. The experiment was of randomized block design with three replications. We evaluated weight of pod per plant and number of pod per plant in ten progenies from the snap bean breeding program of the Universidade Estadual do Norte Fluminense (UENF); individual plants were assessed in each plot and in each replication (block). All progenies had mean productivity superior to 1 kg of pod per plant and 144 pods per plant. The 7 and 2 progenies, which came from the crossings between (UENF 7-5-1) L6 × L20 (UENF 14-3-3) and (UENF 7-5-1) L6 × L13 (UENF 7-20-1), stood out from the others, as they led to a higher predicted additive gain for the two evaluated traits. We concluded that the selection for production of snap beans and grains applying BLUP enabled the prediction and achievement of significant genetic gains for breeding snap beans for subsequent generations

Key words: *Phaseolus vulgaris* L; Genetic breeding; Productivity

INTRODUCTION

Snap beans are characterized as being traditionally produced in small properties, either for own consumption or commercial purpose (Vieira et al., 2014). According to the Food and Agriculture Organization of the United Nations (FAO) (2014), world production is around 21 million tonnes, and China, Indonesia, and India are the largest producers. The South and Southeast Brazil produce around 75% of snap beans (Melo and Vilela, 2008). Rio de Janeiro State is one of the largest national markets of snap beans and is responsible for 21% of the total produced in the Southeast of the country. However, despite being valued, this culture presents low productivity in the North and Northwest of the state due to its lack of cultivars adapted to these regions (Vilela et al.; 2009; Francelino et al., 2011). It is possible to obtain superior and adapted genotypes by means of genetic breeding techniques. However, the development of researches on the snap bean culture is still scarce, especially with regard to the increase of traits related to the production and quality of pods, considering that there are few registered cultivars, when comparing to other registers (Brasil, 2017).

The REML/BLUP (Restricted Maximum Likelihood/ Best Linear Unbiased Prediction) method has proven to be efficient for data analysis, both balanced and unbalanced ones. In this methodology, the effects of treatments are considered as random effects, and the other main effects regarded as fixed effects (Resende, 2007b). Besides, this technique involves estimation of variance components and prediction of genetic values, simultaneously. Information about genetic progress is of fundamental importance, since it allows breeding programs to be evaluated regularly in order to evaluate their success. Moreover, it enables the study of new methodologies that will increase their efficiency and guide future researches. This way, the estimate of the genetic progress constitutes a relevant option used to evaluate breeding programs. As far as we know, the application of the REML/BLUP focusing on the assumption of the individual genotypic value has not been used in the process of selection of snap beans. However, this methodology was efficient in the study of adaptability and stability of common bean and cowpea (Carbonnel et al., 2007; Torres et al., 2015). Therefore, the aim of this work was to select snap bean progenies applying mixed models (REML/BLUP).

MATERIAL AND METHODS

The test was conducted in the experimental area of the Instituto Federal Fluminense, located in the municipality of Bom Jesus de Itabapoana, Northwest of Rio de Janeiro State (21°08, 41°40' W, 88 meters above sea level), Brazil. According to the Köppen-Geiger climate classification system (1928), its local climate is the Aw alternating hot and rainy season with dry season, annual temperature averaging between 22°C and 25°C, and annual average precipitation between 1200 mm and 1300 mm. To perform this research, we started characterizing and studying the genetic diversity of 25 accessions of the Germplasm Bank of the Universidade Estadual do Norte Fluminense, of indeterminate growth habit. Subsequently, crossings between the divergent accessions and desirable traits were executed, obtaining diallel hybrids. Lastly, generations were advanced to select the best genotypes to follow the breeding program (Table 1).

Table 1. Relation of the ten best F₃ progenies used for evaluation. Campos dos Goytacazes, RJ- 2016.

Progenies	Progenitors
G1	Feltrin × UENF 15-23-4
G2	UENF 7-5-1 × UENF 9-24-2
G3	Feltrin × UENF 14-3-3
G4	UENF 7-5-1 × UENF 14-3-3
G5	UENF 7-6-1 × UENF 15-23-4
G6	UENF 7-10-1 × UENF 7-20-1
G7	UENF 7-6-1 × UENF 14-3-3
G8	UENF 7-5-1 × UENF 7-20-1
G9	UENF 7-6-1 × UENF 7-12-1
G10	UENF 7-5-1 × UENF-1445

The F₃ population was conducted in a randomized block experimental design with three replications. The experimental plot was of ten plants in 1.0 m × 0.5 m spacing, which totaled 300 experimental units, and only the eight central plants of each line were evaluated. The sowing was performed with three seeds per pit. Ten days after sowing, the thinning was carried out, and one plant per pit was left; fifteen days after emerging, the plants were staked with bamboo and wire trellis. According to Filgueira (2013), the cultivation and phytosanitary treatments were performed as recommended for the culture. Data were collected from the physiological maturity of the culture, and the analyzed traits were the weight of pod per plant (PVP) – quantification of total weight in (kg) of pods of each plant obtained by means of a precision scale, and the number of pod per plant (NVP) – measured by the total count of pods in each plant after harvest. The individual statistic and genetic analyses were conducted based on the mixed model methodology for estimation of the variance components and of the genotypic parameters by means of the Restricted Maximum Likelihood (REML) and collection of the Best Linear Unbiased Prediction (BLUP) of the genotypic effects. Variables were analyzed according to the 61 models (Resende, 2016) with the following description:

$$Y = Xr + Za + Wp + Tb + \epsilon$$

in which *y* is the vector of data; *r* is the vector of the effect of populations and testimonies, considered as fixed effects; *a* is the vector of the individual additive genetic effects (assumed as random); *p* is the vector of plot effect (assumed as random); *b* is the vector of errors or residuals (random); and *X*, *Z*, *W*, *T* are incidence matrices for *r*, *a*, *p*, and *b*, respectively.

RESULTS AND DISCUSSION

Analyzing results in details, it can be seen that there was no difference in the coefficient of heritability for the two traits, which was considered of low magnitude; the coefficients of variation ($\sigma_g^2, \sigma_a^2, \sigma_{ep}^2, \sigma_{er}^2, e, \sigma_{fi}^2$) in the weight of pod per plant (PVP) character were lower than in the number of pod per plant (NVP) character (Table 2). This perception shows a possible difficulty when selecting this character, mainly in generations with a high percentage of heterozygotes, due to the low fixation of favorable alleles for the traits under study.

Table 2. Estimated genetic parameters for weight of pod per plant in kg/plant, and number of pod per plant, and the overall mean of the progenies.

Estimates	PVP	NVP
σ_g^2	0.028	382.404
σ_a^2	0.019	229.349
σ_{ep}^2	0.025	258.450
σ_{er}^2	0.135	1605.449
σ_{fi}^2	0.209	2475.653
h_a^2	0.092 ± 0.056	0.092 ± 0.056
c_{parc}^2	0.136	0.154
c_{proc}^2	0.123	0.104
$Cv_{gi} \%$	10.590	10.497
$Cv_e \%$	16.226	16.737
Overall Mean	1.313	144.266

Moreto (2008) states that genetic and phenotypic parameters are not easy to presume, since there are differences in the evaluation unit, experimental precision, number of plants, genotypic interaction \times environments, among other factors besides the genetic variation of populations that may interfere the estimates.

The heritability coefficient varies according to the various agronomic characters evaluated. For PVP and NVP traits, the individual heritability coefficient (h_a^2) presented low magnitude proving that only 9.2% of the existent variation are from genetic causes. The inherited value for the traits showed to be highly influenced by the expressive environmental variation, which hinders the success in the selection process.

As claimed by Borém (1997), characters that develop in a short period of time would be less subjected to the interaction with the environment. This way, they would express higher heritability value than the characters subjected to a higher period of development; and that can be seen in this study due to a constant formation and development of the snap beans and consequent impact on the heritability values for both traits under study.

The coefficients of determination of the plot effects (C_{parc}^2) and of determination of population effects (C_{porc}^2) which distinguish the experimental quality and measure the environmental variation between plots in blocks and populations, respectively, are also measured. The values of (C_{parc}^2) and (C_{porc}^2) were considered low for the two variables and indicated good experimental accuracy.

Besides, the estimates of the coefficient of experimental variation (CV_e) demonstrated considerably low values for both traits and validated good conditions and accuracy in the conduction of the experiment. The coefficient of individual additive genetic variation (CV_{gi} %) which quantifies the magnitude of the genetic variable available for the selection, presented 10.590 values for the PVP and 10.497 values for the NVP. It reveals that there may be higher emphasis of the genetic variation for the subsequent evaluations. Another important parameter as a selection strategy for breeding is the coefficient of relative variation (CV_r) or variation index (IV), which represents the ratio between the (CV_{gi}) and the (CV_e). According to Vencovsky (1987), when the index is close to or above 1, we can interpret that there are great conditions for selecting a specific trait.

Based on the coefficient of relative variable, the PVP and NVP traits can provide acceptable genetic gains, since the parameter magnitude for the traits were of 0.652 and of 0.627, respectively, considered moderate. Those values show a significant proportion of genetic variation with regard to the environmental influence and give condition to the selection process. With respect to classification, F_3 progenies, selected to obtain the weight of pod per plant, also ranked first for the number of pod per plant trait; it demonstrated a high level of interdependence between the evaluated characters (Figure 1). Therefore, G7 (UENF 7-5-1 \times UENF 9-24-2), G2 (UENF 7-5-1 \times UENF 7-20-1), G10 (UENF 7-6-1 \times UENF 15-23-4), and G6 (Feltrin \times UENF 14-3-3) genotypes were indicated as superior for the two evaluated traits, providing an increase in productivity. With the exception of G10, all of them were from crossings using at least one of the best testimonies (Feltrin and UENF 7-5-1).

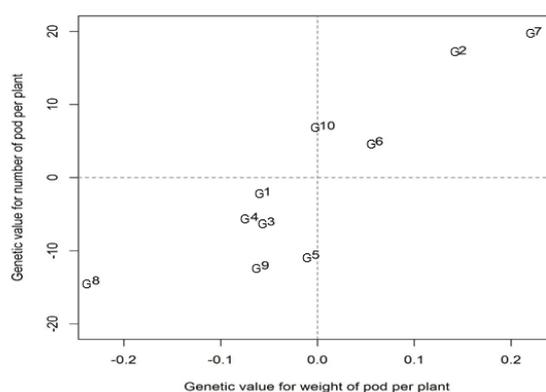


Figure 1. Prediction of genetic effects of bred population for weight of pod per plant (PVP) in kg/plant-1 and number of pod per plant (NVP) traits, in F_3 progenies of snap beans.

G2 and G7 progenies presented important values for number of pod per plant, which, when selecting, will be able to give mean predicted genetic gains of 16 pods per plant for the subsequent generation. In accordance with Chiorato et al. (2008), the effective selection of superior genotypes is associated with the components of the variance and with the components of the mean, and, to obtain significant genetic gains, the breeder genotypes of higher means and higher genetic variability should be selected. Thus, it is important to apply the rank and prediction of genetic values, based on criteria of high interest for the culture, emphasizing the increase of genetic gains by the selection of the best plants among the selected progenies. In the selection within progeny established by the BLUP methodology, it was possible to capture the total genotypic variation occurred between and within the progenies considering the best individuals of the best progenies (Tables 3 and 4). Four progenies and eight superior individuals of each of them were selected for the two traits applying a selection intensity of 10.6% in the original population, which totaled 32 plants to generate F₄ generation.

Table 3. Plants selected within the best F₃ progenies of snap beans for the weight of pod per plant (PVP) trait based on the predicted genetic value ($\mu+a$), genetic gain and new predicted mean.

Order	Rep	Progeny	Plant	$\mu+a$	Gain (kg)	New Mean
1	1	7	7	1.601	0.287	1.601
2	3	7	4	1.598	0.86	1.599
3	3	7	6	1.591	0.283	1.596
4	3	7	2	1.569	0.276	1.589
5	1	7	5	1.561	0.270	1.584
6	1	7	1	1.558	0.266	1.579
7	3	7	7	1.555	0.263	1.576
8	1	7	2	1.554	0.260	1.573
11	1	2	1	1.511	0.234	1.547
12	3	2	7	1.506	0.231	1.544
13	3	2	3	1.497	0.229	1.542
14	3	2	8	1.494	0.227	1.541
15	2	2	8	1.491	0.224	1.537
16	2	2	6	1.488	0.222	1.535
17	1	2	3	1.478	0.220	1.534
18	1	2	4	1.478	0.219	1.532
21	3	6	3	1.427	0.194	1.507
22	3	6	8	1.420	0.190	1.503
23	1	6	7	1.408	0.187	1.500
24	2	6	6	1.398	0.185	1.498
25	3	6	6	1.398	0.183	1.496
26	1	6	5	1.393	0.179	1.492
27	2	6	1	1.391	0.177	1.491
28	1	6	6	1.391	0.176	1.489
31	3	10	8	1.395	0.181	1.494
32	1	10	2	1.358	0.151	1.464
33	1	10	8	1.341	0.142	1.455
34	3	10	6	1.341	0.139	1.452
35	1	10	7	1.336	0.136	1.450
36	3	10	5	1.325	0.135	1.448

37	1	10	5	1.323	0.132	1.445
38	1	10	4	1.319	0.128	1.441

Table 4. Plants selected within the best F3 progenies of snap beans for the number of pod per plant (NVP) trait based on the predicted genetic value ($\mu+a$), genetic gain, and new predicted mean

Order	Rep	Progeny	Plant	$\mu+a$	Gain	New Mean
1	1	7	7	171.318	27.051	171.318
2	3	7	4	169.392	26.088	170.355
3	3	7	2	168.392	25.434	169.701
4	1	7	5	167.889	24.981	169.248
5	3	7	6	167.035	24.126	168.393
6	2	7	3	166.231	23.856	168.122
7	3	7	7	165.535	23.568	167.835
8	1	7	1	165.318	23.121	167.388
11	3	2	3	167.576	24.647	168.913
12	3	2	7	167.147	24.352	168.619
13	3	2	8	165.433	23.328	167.595
14	1	2	3	164.678	22.479	166.745
15	2	2	6	164.676	22.349	166.616
16	1	2	7	164.035	21.920	166.186
17	1	2	6	163.678	21.616	165.883
18	2	2	8	163.319	21.331	165.597
21	1	10	2	156.390	19.117	163.384
22	3	10	8	153.935	18.601	162.868
23	1	10	7	153.890	18.263	162.530
24	3	10	6	153.649	18.098	162.365
25	1	10	8	153.319	17.934	162.201
26	1	10	5	152.319	17.758	162.024
27	3	10	5	152.078	17.583	161.850
28	1	10	4	151.962	17.413	161.679
31	1	6	7	154.261	18.780	163.047
32	3	6	8	153.908	18.429	162.696
33	2	6	6	151.854	17.246	161.513
34	2	6	1	151.782	17.084	161.350
35	1	6	5	150.904	16.446	160.713
36	1	6	6	150.547	16.290	160.556
37	2	6	2	150.496	16.137	160.404
38	3	6	6	150.479	15.989	160.256

G7 progeny had the best productive performance for the weight of pod per plant (PVP) and number of pod per plant (NVP) traits, with mean predicted genetic value of 1.541 kg and 164.330 kg, respectively. The environmental variance had a high impact on the conduction of the experiment. As a result, low heritability values were obtained, which directly influenced in the genetic gain for both traits. The new selection of 32 plants (10.6% of selection intensity) based on the highest predicted genetic values, both for weight of pod per plant and number of pod per plant, will provide simultaneous predicted additive genetic gain of 15.765% for PVP and of 14.328% for NVP in relation to the mean of the original population (Table 5).

Table 5. Mean predicted genetic value ($\mu + a$) of the plants selected within the progenies for the weight of pod per plant (PVP) in kg/plant and number of pod per plant (NVP) traits.

Selected progenies	PVP	NVP
	$\mu + a$	$\mu + a$
G7 (UENF 7-5-1 \times UENF 14-3-3)	1.541	164.330
G2 (UENF 7-5-1 \times UENF 7-20-1)	1.502	163.022
G6 (UENF 7-6-1 \times UENF 14-3-3)	1.460	156.683
G10 (UENF 7-5-1 \times UENF-1445)	1.426	159.153
Overall Mean	1.313	144.266
Mean of the selected progenies	1.482	160.797
Mean of the selected plants	1.520	164.936
Predicted genetic gain	0.207	20.670
Predicted genetic gain (%)	15.765%	14.328%

CONCLUSION

The REML/BLUP methodology was efficient in the selection of progenies and superior individuals, and provided significant gains to the snap bean breeding. G7 and G2 progenies stood out from the others because of the high values obtained for weight of pod per plant and number of pod per plant. By means of the selection between and within the progenies for PVP and NVP, predicted additive gains of 15.765% and of 14.328% were respectively obtained.

CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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