

SOUSA, CMB; GRAVINA, GA; VIANA, AP; DAHER, RF; SOUZA, CLM. 2017. Selection of snap bean  $F_2$  progenies for production using the REML/BLUP methodology. *Horticultura Brasileira* 35: 033-040. DOI - <http://dx.doi.org/10.1590/S0102-053620170106>

## Selection of snap bean $F_2$ progenies for production using the REML/BLUP methodology

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### ABSTRACT

This study aimed to select snap bean  $F_2$  progenies for traits related to production of pods and grains using the REML/BLUP procedure. The experiment was carried out at the experimental area of Instituto Federal Fluminense, located in Bom Jesus do Itabapoana, Rio de Janeiro State, Brazil. The 55 genotypes were sown in lines, 42  $F_2$  progenies derived from diallelic crosses, and 13 parental genotypes used as controls. Each line consisted of 24 plants, without replications and at a spacing of 1.0x0.5 m. The plants were harvested and evaluated individually for production of green pods and grains per plant. The selection among and within progenies via BLUP using Selegen-REML/BLUP program was carried out. Based on the Restricted Maximum Likelihood (REML), we estimated genetic and residual coefficients of variation of 19.43% and 33.53%, respectively, for green pod production and grain production. We used 7.9% of selection intensity, totaling 100 plants selected based on individual genotypic value. The estimated accuracy for the selection of progeny was 0.5014 for pod production and 0.5130 for grain production, indicating difficulties in the selection of these traits due to the high environmental influence on the production traits. Nevertheless, the prediction of genetic values via BLUP, showed the progenies derived from crosses Feltrin x UENF 15-23-4, UENF 7-5-1 x UENF 9-24-2 and Feltrin x UENF 14-3-3 as the most promising progenies with gains of 65.66 g, 61.49 g and 57.63 g, respectively, for pod production and 52.45 g, 46.96 g and 49.29 g, respectively, for grain production. The predicted additive genetic gain with selection was of 36.05% for grain production and 33.5% for green pod production. We concluded that selection via BLUP for production of pods and grains enabled to predict and obtain significant genetic gains for genetic improvement of snap beans for the next generations.

**Keywords:** *Phaseolus vulgaris*, green pods, genetic gain.

### RESUMO

#### Seleção de progênies $F_2$ de feijão-vagem para produção via REML/BLUP

Este trabalho objetivou selecionar progênies  $F_2$  de feijão-vagem para caracteres relacionados à produção de vagens e grãos através do procedimento REML/BLUP. O experimento foi conduzido na área experimental do Instituto Federal Fluminense (IFF), localizado no município de Bom Jesus do Itabapoana-RJ. Foram semeadas linhas de 55 genótipos, entre eles, 42 progênies  $F_2$  oriundas de cruzamentos dialélicos, além dos 13 parentais, utilizados como testemunhas. Cada linha foi composta por 24 plantas, sem repetições e o espaçamento utilizado foi de 1,0x0,5 m. As plantas foram colhidas e avaliadas individualmente para as características produção de vagens verdes por planta e produção de grãos por planta. Foi realizada a seleção entre e dentro de progênies via BLUP utilizando-se o programa Selegen-REML/BLUP. Com base na Máxima Verossimilhança Restrita (REML), foi possível estimar os coeficientes de variação genético e residual de 19,43% e 33,53%, respectivamente para produção de vagens verdes por planta e produção de grãos por planta. Utilizou-se 7,9% de intensidade de seleção, totalizando 100 plantas selecionadas com base no valor genotípico individual. A acurácia estimada para a seleção de progênies foi de 0,5014 para a produção de vagens e 0,5130 para produção de grãos, indicando dificuldades na seleção dos caracteres devido à alta influência ambiental sobre as características de produção. Apesar disso, a predição dos valores genéticos estimados por meio do Melhor Preditor Linear Não-Viesado (BLUP), apontou os cruzamentos Feltrin x UENF 15-23-4, UENF 7-5-1 x UENF 9-24-2 e Feltrin x UENF 14-3-3 como as progênies mais promissoras, com ganhos de 65,66 g, 61,49 g e 57,63 g, respectivamente na produção de vagens verdes e 52,45 g, 46,96 g e 49,29 g, respectivamente na produção de grãos. O ganho genético aditivo predito com a seleção foi de 36,05% na produção de grãos, e 33,5% na produção de vagens verdes. Conclui-se que a seleção via BLUP para a produção de vagens e grãos possibilitou a predição e obtenção de ganhos genéticos significativos para o melhoramento do feijão-vagem nas próximas gerações.

**Palavras-chave:** *Phaseolus vulgaris*, vagens-verdes, ganho genético.

Received on August 21, 2015; accepted on May 11, 2016

Snap bean (*Phaseolus vulgaris*,  $2n=2x=22$ ), just like the common beans, is a predominantly autogamous, diploid species. It was domesticated

for over seven thousand years ago, in two centers of origin: Mesoamerican (Mexico and Central America) and Andean region (Vieira, 1999).

Snap bean is a very important vegetable worldwide. The pods are harvested when immature and they are consumed both *in natura* or

industrialized. In Brazil, this vegetable is traditionally produced by family farmers, who still use a small number of cultivars of indeterminate-growth-habit under protected cultivation (Peixoto *et al.*, 2002).

The crop has proven to be promising, among the vegetables which have been grown in Brazil, since it has reached the sixth position in production (CEASA, 2010); especially the Southeastern Region, producing about 37 thousand t/year and the state of Rio de Janeiro which is responsible for about 21% of this amount. Nevertheless, despite being very popular in the North and Northwest of the State, these regions still have low participation in this agricultural crop production due to the unfavorable weather conditions for cultivation (Vilela *et al.*, 2011).

UENF develops a snap-bean breeding program aiming to obtain promising cultivars for productivity of pods for the North and Northwest regions of the State. Silva (2013) characterized genetic diversity of 33 accessions from Active Germplasm Bank of snap bean of UENF using multivariate procedures based on 37 minimum morphological descriptors for snap bean. Then, diallelic crosses were carried out among 12 divergent accessions of the Bank, F<sub>1</sub> generation was evaluated together with parental genotypes based on Griffing's model 2 (1956). Thenceforth, the authors started this research aiming to select F<sub>2</sub> breeding lines with better pod yield under environmental conditions in the North region of the state of Rio de Janeiro, in order to ensure continuity of the breeding program.

Thus, the authors observed that the breeding programs of the species should be implemented to select and obtain genotypes more adapted with quality and production of superior pods in order to be recommended to the producers of these regions (Vilela *et al.*, 2011). The authors believe that superior genotypes should be selected based on, mainly, genetic components, contributing both as subsidy for planning efficient breeding strategies, as well as for identifying the nature of action of the genes involved in controlling the

traits to be improved. Another benefit of well estimated genetic components, according to Resende (2007b), is the possibility to predict the genotypic values of the selecting individuals, since the prediction procedure of genetic values depends on the identification of the genetic control of traits under selection, especially concerning individual heritability and repeatability parameters.

The authors consider the need of using specific methods when the aim is to estimate genetic parameters and to predict genetic values. According to Resende (2007b), the standard procedure recommended for quantitative and genetic analysis and for selection based on genotypic values is the REML/BLUP methodology. That means, the authors used the Restricted Maximum Likelihood Method (REML) to estimate the variance components and Best Linear Unbiased Prediction Method (BLUP) to predict genotypic values. The REML/BLUP methodology has been used as a tool associated with progeny selection in several crops like popcorn (Freitas *et al.*, 2013), coffee (Resende *et al.*, 2001; Pereira *et al.*, 2013), sugar cane (Resende & Barbosa, 2006), papaya (Oliveira *et al.*, 2012), common beans (Chiorato *et al.*, 2008) and others. In plant breeding, its use is relatively little, comparing to its use for animal breeding; the reason is because the experiments with plants are generally balanced (Resende, 2007b).

The aim of this work was to select snap bean F<sub>2</sub> progenies for production traits using REML/BLUP methodology.

## MATERIAL AND METHODS

The experiment was carried out in the experimental field of Instituto Federal Fluminense, located in the municipality of Bom Jesus de Itabapoana, Northwest of the state of Rio de Janeiro (21°08'S, 41°40'W, 88 m altitude). The local climate is Aw, according to Köppen classification, alternating hot and rainy season with dry season and average annual temperature ranging from 22 to 25°C and average annual rainfall from 1200 to 1300 mm.

The genetic material in this work consisted of F<sub>2</sub> population derived from a research carried out by Silva (2013), in which the author aimed to evaluate, through partial diallel 6 x 6, twelve snap bean genotypes (Table 1), chosen from 37 morphologic and agronomic traits, in accordance to the Form of Minimum Morphological Descriptors for Beans (Formulário de Descritores Morfológicos Mínimos de Feijão) (*Phaseolus vulgaris*), recommended by the National Service of Plant Varieties Protection [Serviço Nacional de Proteção de Cultivares (SNPC)], in order to select the best parents for generating productive populations and for the advancement of generations using SSD method (Single Seed Descent).

The authors evaluated 55 snap bean genotypes; 42 F<sub>2</sub> progenies were obtained from diallelic crosses and 13 parents used as control. Among the parents, three cultivars and 10 lines, from the Snap Bean Breeding Program of Universidade Estadual Norte Fluminense Darcy Ribeiro, were used.

The F<sub>2</sub> plants were arranged in the experimental field without the establishment of experimental plots, being 24 plants of each of F<sub>2</sub> progenies properly arranged and spaced with their parents. Each plant was arranged in spacing of 1.0x0.5 m.

Sowing was carried out at a depth of 2.5 cm, with two seeds per pit. During the experiment, cultural and phytosanitary practices were carried out according to the recommendations for the crop, according to Filgueira (2008), as well as sprinkler irrigation.

The progenies were evaluated in relation to pod and grain production traits, considering the weight of pods per plant (PVP), only the weight of green pods per plant, in grams, was considered (PGP). Analyses were carried out using the individual value of the plants of each progeny.

The authors used individual analyses referring to the values per plant for the two traits used for selection. The authors used the program SELEGEN – REML/BLUP (Restricted Maximum Likelihood – the Best Linear Unbiased Estimation) for estimation and prediction of genetic

**Table 1.** Genotypes used in crosses and main morphological characteristics. Campos dos Goytacazes, UENF, 2014.

Lines	Flowering	Genitor	Flower color	Mature pod color
L1- Progenitor 19 (UENF1445)	38 days	Male	White	Yellow
L2 – Feltrin	37 days	Female	White	Yellow
L3 - Top Seed Blue Line	40 days	Female	White	Yellow
L4 - UENF 7-3-1	37 days	Male	Pink	Purple
L6 - UENF 7-5-1	40 days	Female	Pink	Yellow
L7 - UENF 7-6-1	41 days	Female	White	Yellow
L10 - UENF 7-10-1	40 days	Female	Pink	Purple
L11 - UENF 7-12-1	40 days	Male	White	Purple
L12 - UENF 7-14-1	38 days	Female	Pink	Purple
L13 - UENF 7-20-1	40 days	Male	White	Yellow
L18 - UENF 9-24-2	39 days	Male	Purple	Yellow
L20 - UENF 14-3-3	35 days	Male	Purple	Purple

values. BLUP was the procedure adopted by the program for predicting the genetic values, using variance estimates obtained through REML method, presented by Resende (2007b). Variables were analyzed according to the following model (Resende, 2007b):

$$y = Xr + Za + e$$

Where **y**, **r**, **a**, and **e** are individual data vectors, repetition effects (fixed), individual additive genetic effects (random), respectively; **X** and **Z** are incidence matrices for repetition effects and for individual additive genetic

effects, respectively.

Random effects were assumed to be uncorrelated and to be normally distributed.

## RESULTS AND DISCUSSION

The traits grain production per plant (PGP) and pod production per plant (PVP) showed genetic variance of 465.69 and 792.08, respectively (Table 2). Estimate of genetic variance ( $s_g^2$ ) among the progenies, when presenting

positive values and different from zero, shows variability among progenies due to genotype and, consequently, the possibility of selecting superior breeding lines for each trait evaluated. Therefore, these values reflect considerable genetic variability or difference among genotypes to be used for selection, mainly for pod production, since this is the most economically relevant trait for the crop.

The authors highlight that the phenotypic variation should be composed, most part, of variations from genotype of the selection candidates, contributing to higher heritability of the selected character. From broad-sense heritability analysis ( $h_a^2$ ) for PGP and PVP traits, the authors observed values around 0.2632 for grain production and 0.2514 for pod production. These values show that 26.32% and 25.14% of the variation for traits PGP and PVP, respectively, are due to genetic causes. Heritability values for the traits showed to be seriously influenced by the high environmental variance obtained; this fact hinders the successful selection based on these traits. However, even being considered of low magnitude, these values are relevant in order to improve these traits, since they are polygenic traits, any gain for such traits should be considered.

Heritability values for PGP and PVP showed to be superior to the estimated by Coelho *et al.* (2002), which obtained

**Table 2.** Genetic parameters estimated for grain yield per plant (PGP) and pod production per plant (PVP) and the general mean of the progenies. Campos dos Goytacazes, UENF, 2014.

Estimates	PGP	PVP
$\sigma_g^2$	465.692198	792.08263
$\sigma_e^2$	1,303.4137	2,358.1849
$\sigma_f^2$	1,769.1059	3,150.2675
$h_a^2$	0,263236 ± 0,0408	0.251433 ± 0.0399
$h_{mp}^2$	0.26324	0.25143
$Ac_{prog}$	0.51307	0.50143
$CV_g$ (%)	20.4910	19.4345
$CV_e$ (%)	34.2811	33.5334
$CV_r$	0.5977	0.5795
Mean value	105.314	144.8142

$\sigma_g^2$  = genotypic variance;  $\sigma_e^2$  = environmental variance;  $\sigma_f^2$  = phenotypic variance;  $h_a^2$  = broad sense heritability;  $h_{mp}^2$  = heritability of progenies average;  $Ac_{prog}$  = progenies selection accuracy;  $CV_g$  (%) = genetic variation coefficient;  $CV_e$  (%) = environmental variation coefficient;  $CV_r$  = relative variation coefficient; ( $CV_r = CV_g / CV_e$ ).

**Table 3.** Prediction of genetic effects, predicted genetic gain and new mean of the improved population for the trait grain yield per plant in snap beans F<sub>2</sub> progeny evaluated at Bom Jesus do Itabapoana, Rio de Janeiro State, Brazil. Campos dos Goytacazes, UENF, 2015.

Sequence	Progenies	Genetic effect	Gain (g)	New mean (g)
1	14	52.455	52.455	157.769
2	12	46.135	49.295	154.609
3	24	42.295	46.962	152.276
4	26	38.811	44.924	150.238
5	27	30.112	41.961	147.275
6	16	24.372	39.030	144.344
7	25	21.716	36.557	141.871
8	19	19.017	34.364	139.678
9	21	16.900	32.424	137.738
10	36	16.044	30.786	136.100
11	18	14.158	29.274	134.588
12	15	13.151	27.930	133.244
13	32	13.109	26.790	132.104
14	22	12.266	25.753	131.067
15	13	11.585	24.808	130.122
16	31	11.465	23.974	129.288
17	34	8.693	23.075	128.389
18	41	6.827	22.173	127.487
19	30	5.786	21.310	126.624
20	23	5.044	20.497	125.811
21	20	4.327	19.727	125.041
22	33	3.376	18.984	124.298
23	11	3.301	18.302	123.616
24	3	2.685	17.651	122.965
25	28	2.093	17.029	122.343
26	6	1.808	16.443	121.757
27	9	1.464	15.889	121.203
28	51	0.801	15.350	120.664
29	35	0.260	14.830	120.144
30	17	-2.054	14.267	119.581
31	55	-2.252	13.734	119.048
32	47	-2.819	13.217	118.531
33	29	-3.845	12.700	118.014
34	39	-4.290	12.200	117.514
35	4	-5.435	11.696	117.010
36	2	-8.424	11.137	116.451
37	52	-10.978	10.539	115.853
38	8	-11.364	9.963	115.277
39	37	-11.848	9.404	114.718
40	53	-13.323	8.836	114.150
41	42	-15.571	8.240	113.554
42	38	-15.956	7.664	112.978
43	48	-17.412	7.081	112.395
44	43	-18.155	6.508	111.822
45	10	-18.267	5.957	111.271

broad-sense heritability values of 0.19 for grain production and 0.25 for pod production in the evaluation of F<sub>2</sub> common bean breeding lines from the cross Ouro 1919 x Milionário 1732 summer-autumn season. Evaluating production components in common bean genotypes, using REML/BLUP methodology, Chiorato *et al.* (2008) obtained heritability values for grain production superior to the ones obtained in this study, in which broad-sense heritability was estimated at 0.34, and heritability based on the line average estimated at 0.75. According to the authors, this fact allowed greater selective accuracy (0.87) due to the use of a greater number of replications in the experimental model and evaluation of fewer number of plants in a row.

Broad-sense heritability values can show great variation; factors like progenies of different origins and different levels of environmental influence on traits may be crucial in order to obtain better estimates for this parameter (Pereira *et al.*, 2013). Thus, the authors highlight that heritability is not an immutable trait, being not only a property of the characteristic, but also a property of population and environmental conditions in which the population was submitted (Cruz, 2005).

Heritability based on progeny average is determined considering the number of replications and plants evaluated per plot in the experiment (Chiorato *et al.*, 2008). In this work, heritability based on the progeny average for PGP and PVP maintained the same broad-sense heritability estimates. This fact occurred in order to estimate genetic parameters, the authors used only data at level of plants within progenies and consequently, without replications, being discarded the progeny averages.

Selective accuracy estimated for PGP showed an average of 0.513, whereas for PVP the average was 0.501; these values reflect difficulties for selecting based on these traits. According to Resende & Duarte (2007), selective accuracy can range from 0 to 1, classified very high ( $Ac_{prog} \geq 0.90$ ), high ( $0.70 \leq Ac_{prog} < 0.90$ ), moderate ( $0.50 \leq Ac_{prog} < 0.70$ ), and low ( $Ac_{prog} < 0.50$ ). The authors observed levels of accuracy for two traits within

**Table 3.** continuation

Sequence	Progenies	Genetic effect	Gain (g)	New mean (g)
46	5	-19.144	5.411	110.725
47	50	-19.447	4.882	110.196
48	44	-19.816	4.368	109.682
49	45	-21.327	3.843	109.157
50	1	-21.590	3.335	108.649
51	7	-26.521	2.749	108.063
52	46	-29.695	2.125	107.439
53	40	-30.223	1.515	106.829
54	49	-30.301	0.926	106.240
55	54	-49.998	0.000	105.314

**Table 4.** Prediction of genetic effects, predicted genetic gain and new mean of the improved population for the trait pods production per plant in snap beans F<sub>2</sub> progeny evaluated at Bom Jesus do Itabapoana, Rio de Janeiro State, Brazil. Campos dos Goytacazes, UENF, 2015.

Sequence	Progenies	Genetic effect	Gain (g)	New mean (g)
1	14	65.664	65.664	210.478
2	24	57.324	61.494	206.308
3	12	49.929	57.639	202.453
4	26	47.918	55.209	200.023
5	27	36.121	51.391	196.206
6	36	31.247	48.034	192.848
7	25	26.817	45.003	189.817
8	22	26.584	42.701	187.515
9	19	24.306	40.657	185.471
10	16	20.355	38.627	183.441
11	21	19.902	36.924	181.738
12	32	18.721	35.407	180.222
13	23	16.979	33.990	178.804
14	20	16.216	32.720	177.534
15	11	16.179	31.617	176.432
16	34	13.946	30.513	175.327
17	18	13.015	29.484	174.298
18	41	12.565	28.544	173.358
19	28	12.217	27.684	172.499
20	31	11.463	26.873	171.688
21	15	11.136	26.124	170.938
22	13	9.358	25.362	170.176
23	30	8.787	24.641	169.455
24	17	5.392	23.839	168.653
25	55	1.768	22.956	167.771
26	51	-1.169	22.028	166.843
27	47	-1.991	21.139	165.953
28	9	-2.472	20.296	165.110
29	3	-3.090	19.489	164.303
30	6	-4.042	18.705	163.519

the interval considered moderate. However, the authors verified the possibility to increase accuracy through experimental measures which search to minimize the environmental influence on genotypes and consequent increase in resulting heritability, keeping the size of the experiment.

Selective accuracy is associated to precision and represents correlation between the predicted genetic values and true genetic values of the candidate for selection. This reliability factor is a function of the coefficient of genotypic determination associated with the trait evaluated, which corresponds to the heritability coefficient, in a intrapopulation selection process (Resende & Duarte, 2007).

The traits PGP and PVP showed values close to CV<sub>g</sub> (%) (20.491 and 19.434, respectively), which indicate relative magnitude of changes of a character due to genetic action, being directly proporcional to genetic variance and allowing the breeder a better notion of genetic variability and, consequently, advances that can be obtained through the selection of a particular trait. These values for CV<sub>g</sub> show that the selection of better progenies will allow a significant increase of the population genetic value for the traits evaluated.

Another important parameter to define the best breeding strategy for each trait is the coefficient of relative variation (CV<sub>r</sub>) or variance index (I<sub>v</sub>), as this is the ratio between CV<sub>g</sub> and CV<sub>e</sub>. Therefore, this coefficient is not influenced by the average of the trait. According to Vencovsky (1987), when this ratio is close to or above 1, a favorable situation of selection for a particular trait is characterized. Based on this parameter, the traits PGP and PVP can provide acceptable genetic gains, since the magnitude of the CV<sub>r</sub> was 0.597 and 0.579, respectively. These values show a higher proportion of genetic variation in relation to the environmental influence, favoring selection process.

The authors highlight the importance of reporting the main advantages of using the mixed model methodology (REML/BLUP) in the simultaneous estimation of genetic parameters and

Table 4. continuation.

Sequence	Progenies	Genetic effect	Gain (g)	New mean (g)
31	39	-4.133	17.968	162.782
32	33	-4.153	17.277	162.091
33	35	-4.320	16.622	161.437
34	4	-5.090	15.984	160.798
35	53	-9.960	15.242	160.057
36	37	-11.611	14.497	159.311
37	42	-13.405	13.742	158.557
38	29	-13.476	13.026	157.840
39	38	-13.613	12.343	157.157
40	52	-14.387	11.675	156.489
41	2	-17.713	10.958	155.772
42	50	-19.391	10.236	155.050
43	8	-19.444	9.545	154.360
44	10	-19.592	8.883	153.697
45	44	-22.836	8.178	152.992
46	45	-24.170	7.475	152.289
47	48	-27.437	6.732	151.546
48	5	-29.526	5.977	150.791
49	43	-31.954	5.203	150.017
50	46	-32.846	4.442	149.256
51	40	-34.982	3.669	148.483
52	1	-37.030	2.886	147.700
53	7	-37.407	2.126	146.940
54	49	-43.186	1.287	146.101
55	54	-69.480	0.000	144.814

genotypic values prediction in a breeding program are presented by Resende *et al.* (2001): it can be applied to unbalanced data; (b) it does not require data obtained under strict experimental structures; (c) it allows simultaneous use of a great number of information from various experiments, generating more accurate estimates; (d) it corrects data for environmental effects and it predicts accurately and untainted genotypic values, maximizing genetic gain with selection. As a result, the authors can use the data sets that were taken, usually, in breeding programs, which had never been used in the estimation of genetic parameters, as a matter of appropriate methodology deficiency contemplating especially the unbalancing.

#### Selection among progeny

F<sub>2</sub> progenies obtained an average

value of 105.31 per plant for grain production and 144.81 for pod production per plant. Although these traits to selection of individual plants have been little used in previous studies on snap bean breeding program, these values are relatively low comparing to the ones obtained by Francelino *et al.* (2011), working with the parental lines present in this study under the same environmental conditions in Bom Jesus do Itabapoana. This indicates that direct interference of some environmental abnormalities on the experiment was noticed.

In a total of F<sub>2</sub> progenies (42 evaluated among 55 genotypes), 27 of these showed for their new averages, values superior than the best control for grain production in this study, the parental line UENF 7-5-1. The authors

highlight that this line has obtained satisfactory and constant productive performance considering the study carried out by Francelino *et al.* (2011), in which the same line was the most productive. These data reinforce not only the line potential but also contribute to indicate the possibility of selecting progenies with superior performance for this trait. Considering trait PVP, 24 F<sub>2</sub> progenies showed productive performance superior to the best control, which was the parental line UENF 7-10-1 for this trait. The high performance of this line for pod production compared to the other controls is also in accordance with the results obtained by Francelino *et al.* (2011). In this research, line UENF 7-10-1 showed to be the most productive for the trait under environmental conditions in the North region of Rio de Janeiro State.

The progenies 14, 12, 24, 26, 27, 16, 25, 19, 21 and 36 stood out among others (Table 3), since they showed greater genetic gains for PGP and will certainly contribute to further advances for the trait. From these progenies, the authors highlight that four of them are from line UENF 7-6-1 and three are from the just mentioned UENF 7-5-1. Ten progenies showing greater gains for PGP showed average genetic gain in the next generation of 40.876 g/plant; this value can vary according to the selection pressure to be exercised in the line selection.

Table 3 presents the top-ranked genotypes, which showed greater gains and higher new averages. The progeny 14, from the cross Feltrin x UENF 15-23-4, showed to be superior than the others, with a gain of 52.455 g/plant in relation to the population average if selected, thus providing a new average of 157.769 g/plant for PGP. Genotypes 46, 40, 49 and 54 obtained lower PGP in this study, with gains ranging from 2.215 to 0 g/plant. These genotypes, if selected, provided new population averages between 107.439 to 105.314 g/plant. Among them, the authors notice only one progeny, from the cross UENF 7-10-1 x UENF 14-3-3, and three parental lines used as controls, UENF 7-14-1, UENF 7-3-1 and UENF 15-23-4.

**Table 5.** Average predicted genetic value ( $\mu+g$ ) of the selected plants within progenies for the grain yield per plant (PGP) and pods production per plant (PVP) traits. Campos dos Goytacazes, UENF, 2015.

Selected progenies	PGP ( $\mu+g$ )	PVP ( $\mu+g$ )
(Feltrin) L2 x L31 (UENF 15-23-4)	167,510	221,600
(UENF 7-5-1) L6 x L18 (UENF 9-24-2)	155,861	213,435
(Feltrin) L2 x L20 (UENF 14-3-3)	158,371	203,469
(UENF 7-5-1) L6 x L20 (UENF 14-3-3)	153,044	204,071
(UENF 7-6-1) L7 x L31 (UENF 15-23-4)	141,843	188,907
(UENF 7-10-1) L10 x L13 (UENF 7-20-1)	126,117	182,827
(UENF 7-6-1) L7 x L20 (UENF 14-3-3)	135,269	182,207
(UENF 7-5-1) L6 x L13 (UENF 7-20-1)	125,435	182,953
(UENF 7-6-1) L7 x L11 (UENF 7-12-1)	130,122	176,489
(UENF 7-5-1) L6 x L1 (UENF-1445)	139,460	176,511
Mean of progenies	105,325	144,790
Mean of selected progenies	136,384	184,385
Mean of selected plants	143,303	193,247
Mean predicted genetic gain	37,978	48,457
Mean predicted genetic gain (%)	36,050	33,500
Mean of the witness UENF 1445	86,781	112,194
Mean of the witness Feltrin	83,543	120,141
Mean of the witness Top Seed Blue Line	102,434	142,780

Considering trait PVP (Table 4), the authors noticed a high degree of correspondence between progenies with the best performance for this trait and the best-ranked progenies for PGP, for the interdependence between both traits evaluated. Progenies 14, 24, 12, 26, 27, 36, 25, 22, 19 and 16 stood out for green pod production in this study; when selected, these progenies will provide predicted average genetic gain for the next generation population of 50.642 g/plant for this trait.

Once again, progeny 14, from the cross of the commercial variety Feltrin x UENF 15-23-4, stood out reaching the best productive performance for PVP and, consequently, the greatest predicted genetic gain of 65.664 g/plant, obtaining a new predicted average of 210.478 g/plant. Francelino *et al.* (2011) carried out selections among promising snap bean lines aiming to release improved material for producers from the North and Northwest regions of the State and showed line UENF 15-23-4 among the most productive lines both for grain production and green pod production in the region.

The lowest PVP were obtained by genotypes 1, 7, 49 and 54, showing predicted average gain of only 1.574 g/plant. Among these genotypes, two progenies and two parental lines are presented, UENF 7-3-1 and UENF 15-23-4. Although UENF 15-23-4 is one of the parents from which the line with the greatest PVP derived, the performance of the line itself was not satisfactory under the conditions of this study.

For an efficient selection of superior genotypes, Chiorato *et al.* (2008) state that this selection should be based both on variance components and on average components and for a considerable genetic gain, the genotypes with the highest averages and the greatest genetic variability should be selected. Based on criteria such as the greatest importance to good productive performance of green pods per plant, as well the greatest genetic variability for PVP, the authors concluded that the use of priority ranking and prediction of values for this trait becomes more feasible. This methodology aims to potentiate genetic gain by selecting the best plants within these selected progenies.

### Selection within progenies

Evaluating the traits in plants, the authors verified estimates for each plant or individual. Then, not only the selection among progenies was carried out but also the increase of gains in the population for the next generation, through the selection of ten best plants of each selected progeny, could be obtained.

Analysis of genetic parameters, showed in Table 2, allowed to verify that although in smaller proportions in relation to environmental variance, the authors noticed genetic variability in the population for both traits, with significant values which can be used through selection.

The selection of the most productive plant was carried out based on predicted genetic values of each individual. According to Resende (2007b), REML/BLUP methodology provides ordering potential genotypes for selection exploiting all the genotypic variation among and within progenies, considering each variable analyzed separately, though. Due to the different ordering of progenies by BLUP for selection among progenies for evaluated traits, the authors noticed that prioritizing the most relevant trait for the snap bean crop aiming subsequent selection within progenies (among progenies).

At this stage, 10 individuals of each progeny were selected, totalizing 100 plants in order to generate F<sub>3</sub> generation, allowing selection intensity about 7.9%.

The average of genotypic values of each progeny selected after selection of the best plants, general advances obtained through selection process carried out in this study, including genetic gains in relation to average of the original population from the selection among and within progenies and their performance in relation to the commercial controls are presented in Table 5.

Selecting plants with best productive performance for pods and grains, new predicted averages for progenies were obtained, especially for plants from the cross Feltrin x UENF 15-23-4, which obtained new averages ranking from 242.643 g to 219.729 g for PVP, production value above all commercial

controls used in the experiment.

Although the progenies were highly influenced by the environment, which resulted in low broad-sense heritability values estimated for the two traits, the selection of 100 plants (7.9% of selection intensity), considering the highest predicted genetic values, both for pod and seed production per plant, provided simultaneous predicted additive genetic gain of 36.05% for PGP and 33.5% for PVP in relation to the average of original population.

From this percentage, 29.48% of the gains for PGP resulted from selection among progenies and 6.57% due to individual selection within progenies. For PVP, selection among progenies provided 27.38% of gains and individual selection within progenies resulted in 6.12%, showing that most of variability present in population is among the different progenies evaluated.

Obtaining superior progenies and plants, from these crosses both for pod and grain production, was possible in low heritability conditions of traits, which makes REML/BLUP methodology an effective tool to obtain genetic gains in snap bean breeding program of UENF.

## ACKNOWLEDGEMENT

The authors thank to Instituto Federal Fluminense for the concession of the experimental area, to UENF for the research opportunity and to CAPES

for the Master scholarship granted to the first author.

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