

## Additive genetic prediction for F<sub>3</sub> families of common black beans (*Phaseolus vulgaris* L.) using linear mixed models

Ivan Ricardo Carvalho<sup>1</sup>, Vinícius Jardel Szarecki<sup>2</sup>, Luiz Leonardo Ferreira<sup>7</sup>, Gustavo Henrique Demari<sup>2</sup>, Maurício Horbach Barbosa<sup>2</sup>, Tiago Corazza da Rosa<sup>2</sup>, Francine Lautenchleger<sup>3</sup>, Jainara Fresinghelli Netto<sup>4</sup>, Daniel Boeno<sup>4</sup>, Suélen Matiasso Fachi<sup>4</sup>, Mayara Torres Mendonça<sup>4</sup>, Ricardo Boscaini<sup>4</sup>, Riteli Baptista Mambrin<sup>4</sup>, Darlene Sausen<sup>5</sup>, Velci Queiróz de Souza<sup>6</sup>

<sup>1</sup>Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Brazil

<sup>2</sup>Universidade Federal de Pelotas, Brazil

<sup>3</sup>Universidade Estadual do Centro-Oeste, Brazil

<sup>4</sup>Universidade Federal de Santa Maria, Brazil

<sup>5</sup>Universidade Federal do Rio Grande do Norte, Brazil

<sup>6</sup>Universidade Federal do Pampa, Brazil

<sup>7</sup>Centro Universitário de Mineiros, Brazil

\*Corresponding authors: carvalho.irc@gmail.com

### Abstract

The aim of study is to estimate the variance components and genetic parameters (REML), as well as to predict the genetic value (BLUP) of F<sub>3</sub> families of common black beans for the components of seed production. The experimental design was augmented blocks, where the 83 F<sub>3</sub> families were arranged only in each block, and the commercial controls were organized in three replicates. The additive genetic effects were determinant for plant height and first pod insertion height. The pronounced effects of the environment are expressed for the number of pods, seeds and seed mass per plant. Potentiality in the selection of higher F<sub>3</sub> families are revealed through the 2CBRS population for plant height and first pod insertion height, for the components of seed yield the selections should be directed to the populations 2CARS and 1FVRS. The number of seeds and seed mass per plant were potentiated in more than 28% of the selected F<sub>3</sub> families, and pronounceable genetic gains are obtained by the selection of families 66, 65 and 67. The inferences obtained in this study present theoretical and practical foundation, and can be applied in future studies of breeding and production of common black bean seeds.

**Keywords:** *Phaseolus vulgaris* L., breeding, production seeds, yield compounds.

**Abbreviations:** REML\_restricted maximum likelihood; BLUP\_Best linear unbiased prediction; PH\_plant height; FPI\_first pod insertion height; NPP\_number of pods per plant; NSP\_number of seeds per plant; SMP\_seed mass per plant.

### Introduction

The common bean (*Phaseolus vulgaris* L.) is one of the most important and constituent foods of the Brazilian diet, being an excellent source of protein and providing the body with energy, carbohydrates, vitamins, fibers, iron and zinc (Tavares et al., 2013; Schmutz, 2014). Among bean types, carioca is the most cultivated and consumed in the entire Brazilian territory and accounts for 60% of total bean consumption. The second most consumed type is black, being preferred mainly in the South Region and corresponds to 35% of the total bean consumed in Brazil (Silva et al, 2013; BorémandCarneiro, 2015). Brazil stands out as the world's largest producer and consumer of beans, producing in the 2016/2017 harvest a production of 3327 thousand tons and an average yield of 1076 kg ha<sup>-1</sup> of grains (IBGE, 2017). The state of Rio Grande do Sul, shows a production of 1038 thousand tons and average yield of 828 kg ha<sup>-1</sup> of grains (Conab, 2017). With the expansion of the agricultural

area cultivated with common bean, it is necessary the selection of superior genotypes in order to increase seed production. Higher genotypes are not easily identified, as there are several characters that demonstrate the quantitative inheritance, in this sense, genotypes can be controlled by a large number of genes, have low heritability and great effect of the environment on the phenotype (RamalhøAraujo, 2011; Szarecki et al., 2017).

The early selection of families with higher potential consists of a crucial step, since it maximizes the use of human and financial resources in a breeding program (Abreu et al., 2002; Rocha et al., 2013). At the time of progeny evaluation, the genetic effects of different generations, populations and families are often confounded (Resende et al., 2015). Thus, the application of methodologies based on mixed linear models, proposed by Henderson (1975), is indicated as an excellent procedure in the genetic evaluation, since it allows

to include all the sources of variation, estimates of the accurate genotypic values free of any effects of the environment (Paternelli; Resende, 2015). Through the REML / BLUP procedure, there can be obtained estimates of variance components extracted by the restricted maximum likelihood (REML), as well as the prediction of genetic values through the best linear unbiased prediction (BLUP). Studies using mixed models applied in different segregating generations of common black bean are scarce, so this work aimed to estimate the variance components and genetic parameters (REML), as well as to predict the genetic value (BLUP) of  $F_3$  families of common black beans for the components of seed production.

## Results and discussion

### *Variance components and genetic parameters*

The Deviance analysis (LRT) revealed significance at 5% of probability by the chi-square test ( $X^2$ ) for the characters plant height (PH), first pod insertion height (FPI), number of pods per plant (NPP), number of seeds per plant (NSP) and seed mass per plant (SMP). This allowed verifying the reliability of the REML / BLUP estimates and predictions obtained in this study with populations and segregating families of common black bean (Table 2).

The estimation of the variance components made it possible to stratify the phenotypic expression of the characters of interest and to identify the genetic, additive, genealogical contributions from the  $F_2$  population, as well as those resulting from the effects of segregating  $F_3$  families. The phenotypic manifestation of plant height (PH) was determined by 18.1% due to the additive genetic effects, where the source population was responsible for 10.9% and the selected  $F_3$  family represented 8.1% of effects on the magnitude of the character. In this context, it is clear that the identification of superior genotypes for plant height should be proceeded from segregating  $F_3$  generation, since in previous generations there is high expression of non-additive effects. For the first pod insertion height (FPI) it was possible to verify that the additive genetic effects determine the phenotype by 18.1%, and the genetic contribution of the  $F_3$  generation was 4.2% higher than the effect attributed to the  $F_2$  generation for the measured phenotype. Similar genetic trends were expressed for the number of pods per plant (NPP) and seed mass per plant (SMP), where the additive genetic effects influenced the phenotype by 0.4%. These low magnitudes can be attributed to the genetic nature of these traits, since they are controlled by the expression of many genes and the growing environment has proniable effects on the phenotype. The  $F_3$  generation influenced the phenotype more than the  $F_2$  generation, because the families analyzed were based on the selection of the best individuals contained in each population of origin; therefore, the results obtained follow the expected genetic and phenotypic trend. The number of seeds per plant (NSP) shows that the phenotype was determined by 3.5% of additive genetic effects, but the selection of the best  $F_2$  population resulted in 30.2% of effects in the magnitude of this character, being these effects 14.0% higher than those from the segregating families. Narrow sense heritability ( $h^2a$ ) revealed higher magnitudes through plant height (PH) and first pod insertion height (FPI), which were

of low heritability but were pronibly controlled by genetic additive effects. On the other hand, the number of pods per plant (NPP), number of seeds per plant (NSP) and seed mass per plant (SMP) were affected by more than 97% of effects resulting from the growing environment. For the measured characters, we observed that the plant height (PH) and first pod insertion height (FPI) have greater genetic variability in this situation. But for the ratio between the genetic variations and the residual effects (CVg / CVe) we observed that possible selections were through the characters that reflect the stature of common black bean plants. This can be understood through the possibility of proceeding with positive selection of superior genotypes for these attributes of agronomic interest.

### *Best linear unbiased prediction (BLUP) applied in the selection of segregating $F_2$ populations*

Regarding the ranking of the  $F_2$  segregating populations, we selected the populations that presented potential to obtain progenies higher than the characters of agronomic interest for plant height (PH) (Table 3), where 12 populations such as 2CBRS, 2CARS, 1FVRS, 1PJRS, 5SRRS, 2FVRS, 2PJRS, 6SRRS, 3PMRS, 2PMRS, 1CARS and 1CARS showed genetic gain to the character. For these conditions, genetic gains greater than 10.41% can be obtained with the population 2CBRS where their selection can increase the plant in 5.57cm and reveal progenies of 33.79 cm on average. The first pod insertion height (FPI) showed genetic gains in 11 segregating populations such as 2CBRS, 6SRRS, 5SRRS, 2PMRS, 1PJRS, 3PJRS, 2PJRS, 3PMRS, 3BGRS, 1BGRS and 3FVRS. Higher increase of this character can be obtained by the selection of the 2CBRS population, as it results in a genetic gain of 10.53% representing 1.85 cm of FPI, in this way, in the next generation the progenies evidenced on average 16.57 cm. The number of pods per plant (NPP) was genetically increased by selection of the populations 1FVRS, 2CARS, 1CARS, 2CBRS, 1PJRS, 3PMRS, 1CBRS, 4SRRS, 1PMRS, 2RSRRS, 2FVRS and 4BGRS. However, to increase on three pods on average, progenies should be selected in the 1FVRS population with genetic gains of 10.55%. For the number of seeds per plant (NSP), genetic gains were obtained by selecting the populations 1FVRS, 2CARS, 1CARS, 2CBRS, 2PMRS, 1PJRS, 2RSRRS, 1PMRS, 3CBRS, 4SRRS and 5RSR. However, it is possible to obtain transgressive families through the specific selection of the 1FVRS and 2CARS population that result in a genetic increase of more than 10.5%, representing a phenotype with more than 38 seeds per plant. Seed mass per plant (SMP) revealed that 12 populations 2CARS, 1FVRS, 1CARS, 2CBRS, 4SRRS, 1PJRS, 3PMRS, 3PJRS, 2BGRS, 3FVRS, 1PMRS and 3CBRS genetically increase the trait. The selection aimed at enhancing this character can be carried out through the populations 2CARS and 1FVRS, being possible to obtain genetic gains higher than 10.3% and increase in more than 1.7 grams of seeds per plant.

### *Best linear unbiased prediction (BLUP) applied in the selection of segregating $F_3$ families*

In relation to the selection carried out in the  $F_3$  segregating families, we observed that positive genetic gains at plant

**Table 1.** Genealogy organization of the F<sub>2</sub> segregant populations and the F<sub>3</sub> segregating families derived from the common black bean.

F <sub>2</sub> Population	Origin	Abbreviation	F <sub>3</sub> Families
1	Campos Borges - RS	1CBRS	1 to 5
2	Campos Borges - RS	2CBRS	6 to 9
3	Campos Borges - RS	3CBRS	10 to 11
4	Palmeira das Missões - RS	1PMRS	12 to 13
5	Palmeira das Missões - RS	2PMRS	14
6	Palmeira das Missões - RS	3PMRS	15 to 19
7	Palmeira das Missões - RS	4PMRS	20 to 24
8	Palmeira das Missões - RS	5PMRS	25
9	Santa Rosa - RS	1SRRS	26
10	Santa Rosa - RS	2SRRS	27
11	Santa Rosa - RS	3SRRS	.
12	Santa Rosa - RS	4SRRS	28
13	Santa Rosa - RS	5SRRS	29 to 38
14	Santa Rosa - RS	6SRRS	39 to 43
15	Pejuçara - RS	1PJRS	44 to 48
16	Pejuçara - RS	2PJRS	49 to 52
17	Pejuçara - RS	3PJRS	53 to 54
18	Pejuçara - RS	4PJRS	55
19	Braga - RS	1BGRS	56
20	Braga - RS	2BGRS	57
21	Braga - RS	3BGRS	58 to 64
22	Braga - RS	4BGRS	65
23	Cruz Alta - RS	1CARS	66
24	Cruz Alta - RS	2CARS	67 to 68
25	Cruz Alta - RS	3CARS	69 to 72
26	Fortaleza dos Valos - RS	1FVRS	73 to 74
27	Fortaleza dos Valos - RS	2FVRS	75 to 77
28	Fortaleza dos Valos - RS	3FVRS	78 to 81
29	Fortaleza dos Valos - RS	4FVRS	82 to 83

**Table 2.** Estimation of variance components and genetic parameters (REML) for plant height (PH), first pod insertion height (FPI), number of pods per plant (NPP), number of seeds per plant (NSP), seed mass per plant (SMP) referring to the F<sub>3</sub> segregating generation of common black bean.

Variance components and Genetic parameters	Characters				
	PH	FPI	NPP	NSP	SMP
$\sigma^2a$	21.68	5.29	0.07	11.07	0.04
$\sigma^2EF$	13.01	2.54	2.59	50.86	1.27
$\sigma^2EPop$	9.73	1.33	1.86	58.53	0.80
$\sigma^2E$	75.25	19.25	12.24	193.88	7.71
$\sigma^2F$	119.67	28.41	16.77	314.34	9.82
$\hat{h}^2a$	0.18	0.19	0.00	0.03	0.00
$C^2F$	0.11	0.09	0.15	0.16	0.13
$C^2POP$	0.08	0.05	0.11	0.19	0.08
$Cvg(\%)$	16.50	15.64	4.58	16.04	5.01
$Cve(\%)$	18.77	17.18	37.39	45.64	42.50
Overall mean	28.22	14.71	6.00	20.74	3.95

<sup>1</sup> $\sigma^2a$ : additive genetic variance,  $\sigma^2EF$ : variance between F<sub>3</sub> families,  $\sigma^2EPop$ : variance between F<sub>2</sub> populations,  $\sigma^2E$ : residual variance,  $\sigma^2F$ : phenotypic variance,  $\hat{h}^2a$ : narrow sense heritability,  $C^2F$ : determination coefficient of the F<sub>3</sub> family effects,  $C^2POP$ : determination coefficient of F<sub>2</sub> populations,  $Cvg(\%)$ : coefficient of genetic variation,  $Cve(\%)$ : coefficient of residual variation and *Overall mean*: overall mean of the experiment.

**Table 3.** Predictions for the best linear unbiased prediction (BLUP) referring to plant height (PH), first pod insertion height (FPI), number of pods per plant (NPP), number of seeds per plant (NSP), seed mass per plant (SMP) for 29 segregating populations of common black bean.

PH			FPI		SMP		NSP		NPP	
R*	P	G	P	G	P	G	P	G	P	G
1	2CBRS	10.41	2CBRS	10.53	2CARS	10.76	1FVRS	11.93	1FVRS	10.55
2	2CARS	8.18	6SRRS	9.34	1FVRS	10.34	2CARS	10.63	2CARS	8.89
3	1FVRS	7.10	5SRRS	8.47	1CARS	8.96	1CARS	9.53	1CARS	7.42
4	1PJRS	6.51	2PMRS	7.43	2CBRS	7.34	2CBRS	7.87	2CBRS	6.48
5	5SRRS	6.06	1PJRS	6.68	4SRRS	6.30	2PMRS	6.78	1PJRS	5.67
6	2FVRS	5.74	3PJRS	6.07	1PJRS	5.56	1PJRS	5.94	3PMRS	5.07
7	2PJRS	5.44	2PJRS	5.49	3PMRS	5.02	2SRRS	5.27	1CBRS	4.58
8	6SRRS	5.21	3PMRS	4.95	3PJRS	4.61	1PMRS	4.66	4SRRS	4.15
9	3PMRS	4.87	3BGRS	4.48	2BGRS	4.25	3CBRS	4.16	1PMRS	3.80
10	2PMRS	4.53	1BGRS	4.08	3FVRS	3.89	4SRRS	3.75	2SRRS	3.48
11	1CARS	4.21	3FVRS	3.75	1PMRS	3.60	5SRRS	3.41	2FVRS	3.21
12	1PMRS	3.89	2CARS	3.41	3CBRS	3.30	5PMRS	3.12	4BGRS	2.96
13	1BGRS	3.53	1FVRS	3.12	4BGRS	3.02	3PMRS	2.85	3CBRS	2.74
14	1CBRS	3.21	4BGRS	2.86	2FVRS	2.78	2BGRS	2.62	3PJRS	2.53
15	5PMRS	2.91	3CBRS	2.63	1CBRS	2.55	3PJRS	2.40	3FVRS	2.34
16	4SRRS	2.64	4PJRS	2.41	5SRRS	2.35	3FVRS	2.19	5SRRS	2.16
17	2SRRS	2.39	2BGRS	2.18	4PJRS	2.17	3SRRS	2.01	3SRRS	1.98
18	3FVRS	2.15	5PMRS	1.97	2SRRS	2.00	1CBRS	1.83	2BGRS	1.82
19	1SRRS	1.92	4PMRS	1.77	3SRRS	1.84	6SRRS	1.64	5PMRS	1.65
20	2BGRS	1.72	2FVRS	1.59	5PMRS	1.69	2FVRS	1.46	4FVRS	1.49
21	3CBRS	1.52	1CARS	1.42	3BGRS	1.53	4FVRS	1.30	4PMRS	1.34
22	4BGRS	1.35	3CARS	1.25	4FVRS	1.38	1SRRS	1.13	2PMRS	1.18
23	3PJRS	1.18	4SRRS	1.09	6SRRS	1.21	4BGRS	0.97	3BGRS	1.01
24	3SRRS	1.02	3SRRS	0.92	2PMRS	1.05	3BGRS	0.81	1SRRS	0.83
25	4PMRS	0.86	1CBRS	0.76	3CARS	0.89	4PJRS	0.66	6SRRS	0.67
26	3BGRS	0.67	1SRRS	0.61	1BGRS	0.73	1BGRS	0.51	4PJRS	0.48
27	4FVRS	0.48	1PMRS	0.46	1SRRS	0.54	4PMRS	0.38	1BGRS	0.23
28	4PJRS	0.30	2SRRS	0.25	4PMRS	0.32	3CARS	0.19	3CARS	0.00
29	3SRRS	0.00	4FVRS	0.00	2PJRS	0	2PJRS	0.00	2PJRS	0.00

\* R: ranking; P: F<sub>2</sub> segregating population; G: predicted genetic gain.

**Table 4.** Predictions for the best linear unbiased prediction (BLUP) for plant height (PH) estimated for 83 F<sub>3</sub> segregating families of common black bean.

PH (cm)											
R	F	G	R	F	G	R	F	G	R	F	G
1	32	3.92	22	41	1.65	43	24	1.04	64	25	0.49
2	33	3.49	23	17	1.62	44	28	1.01	65	63	0.46
3	74	3.30	24	59	1.58	45	79	0.99	66	54	0.44
4	5	3.07	25	40	1.55	46	1	0.96	67	58	0.41
5	48	2.92	26	31	1.52	47	16	0.94	68	61	0.39
6	7	2.77	27	80	1.49	48	27	0.91	69	62	0.36
7	75	2.65	28	2	1.46	49	8	0.88	70	82	0.33
8	66	2.56	29	35	1.42	50	47	0.86	71	22	0.31
9	46	2.44	30	34	1.39	51	3	0.83	72	72	0.28
10	44	2.33	31	43	1.36	52	55	0.80	73	83	0.25
11	67	2.25	32	38	1.33	53	36	0.78	74	69	0.23
12	13	2.17	33	81	1.29	54	64	0.75	75	78	0.20
13	42	2.10	34	65	1.26	55	76	0.72	76	56	0.17
14	73	2.03	35	4	1.24	56	19	0.70	77	20	0.14
15	53	1.97	36	18	1.21	57	50	0.67	78	21	0.12
16	60	1.92	37	30	1.18	58	49	0.65	79	26	0.09
17	52	1.87	38	12	1.16	59	77	0.62	80	68	0.06
18	15	1.82	39	29	1.13	60	23	0.60	81	70	0.04
19	6	1.77	40	37	1.11	61	51	0.57	82	71	0.01
20	9	1.73	41	39	1.08	62	10	0.55	83	57	0.00
21	45	1.69	42	14	1.06	63	11	0.52			

\* R: ranking; F: F<sub>3</sub> segregating family; G: predicted genetic gain.**Table 5.** Predictions for the best linear unbiased prediction (BLUP) referring to the first pod insertion height (FPI) estimated for 83 F<sub>3</sub> segregating families of common black bean.

FPI (cm)											
R*	F	G	R	F	G	R	F	G	R	F	G
1	33	4.12	22	51	1.58	43	37	1.00	64	82	0.54
2	32	3.80	23	6	1.54	44	14	0.98	65	63	0.52
3	5	3.42	24	44	1.50	45	3	0.96	66	71	0.50
4	59	3.13	25	74	1.47	46	35	0.94	67	67	0.48
5	40	2.92	26	80	1.44	47	61	0.91	68	54	0.45
6	42	2.72	27	66	1.40	48	24	0.89	69	11	0.43
7	41	2.57	28	49	1.37	49	55	0.87	70	22	0.41
8	60	2.44	29	45	1.35	50	81	0.85	71	64	0.39
9	39	2.33	30	9	1.32	51	17	0.83	72	25	0.37
10	46	2.23	31	16	1.30	52	56	0.80	73	27	0.34
11	12	2.15	32	47	1.27	53	70	0.78	74	62	0.32
12	31	2.08	33	38	1.24	54	73	0.76	75	8	0.29
13	29	2.02	34	34	1.22	55	28	0.74	76	78	0.27
14	13	1.96	35	58	1.19	56	65	0.72	77	76	0.25
15	52	1.90	36	69	1.17	57	1	0.70	78	36	0.22
16	30	1.85	37	79	1.14	58	72	0.68	79	10	0.20
17	50	1.80	38	18	1.12	59	57	0.65	80	20	0.17
18	7	1.75	39	75	1.09	60	77	0.63	81	21	0.14
19	15	1.70	40	4	1.07	61	2	0.61	82	26	0.12
20	48	1.66	41	19	1.05	62	23	0.59	83	83	0.08
21	53	1.62	42	43	1.02	63	68	0.57			

\* R: ranking; F: F<sub>3</sub> segregating family; G: predicted genetic gain.

**Table 6.** Predictions for the best linear unbiased prediction (BLUP) referring to the numbers of pods per plant (NPP) estimated for 83 F<sub>3</sub> segregating families of common black bean.

NPP (units)											
R*	F	G	R	F	G	R	F	G	R	F	G
1	73	6.08	22	25	1.63	43	26	0.77	64	24	0.21
2	66	5.76	23	8	1.57	44	30	0.74	65	61	0.19
3	67	5.59	24	64	1.51	45	21	0.71	66	57	0.16
4	65	4.96	25	75	1.45	46	19	0.68	67	58	0.14
5	45	4.28	26	76	1.40	47	18	0.65	68	43	0.11
6	5	3.83	27	6	1.35	48	20	0.62	69	38	0.09
7	48	3.50	28	7	1.30	49	23	0.60	70	40	0.06
8	46	3.24	29	53	1.26	50	22	0.57	71	42	0.03
9	44	3.03	30	80	1.21	51	81	0.54	72	39	0.01
10	47	2.87	31	36	1.17	52	17	0.52	73	41	0.00
11	4	2.69	32	77	1.13	53	82	0.49	74	54	0.00
12	14	2.53	33	52	1.09	54	83	0.46	75	55	0.00
13	2	2.40	34	33	1.05	55	13	0.44	76	72	0.00
14	3	2.29	35	37	1.02	56	15	0.41	77	71	0.00
15	1	2.18	36	79	0.98	57	12	0.39	78	69	0.00
16	28	2.09	37	34	0.95	58	16	0.37	79	68	0.00
17	27	2.00	38	78	0.92	59	63	0.34	80	70	0.00
18	9	1.92	39	32	0.88	60	60	0.31	81	50	0.00
19	10	1.84	40	35	0.86	61	59	0.29	82	49	0.00
20	11	1.76	41	29	0.83	62	62	0.26	83	51	0.00
21	74	1.69	42	31	0.80	63	56	0.24			

\* R: ranking; F: F<sub>3</sub> segregating family; G: predicted genetic gain.

**Table 7.** Predictions for the best linear unbiased prediction (BLUP) referring to the numbers of seeds per plant (NSP) estimated for 83 F<sub>3</sub> segregating families of common black bean.

NSP (units)											
R*	F	G	R	F	G	R	F	G	R	F	G
1	73	6.40	22	34	1.64	43	22	0.67	64	59	0.12
2	66	6.26	23	13	1.57	44	18	0.63	65	62	0.09
3	67	5.88	24	74	1.51	45	31	0.60	66	17	0.06
4	65	5.63	25	80	1.45	46	79	0.57	67	64	0.03
5	14	4.84	26	12	1.39	47	52	0.54	68	61	0.01
6	5	4.30	27	24	1.34	48	78	0.52	69	54	0.00
7	48	3.87	28	10	1.28	49	2	0.49	70	57	0.00
8	45	3.53	29	77	1.23	50	43	0.46	71	56	0.00
9	46	3.24	30	7	1.18	51	1	0.44	72	15	0.00
10	6	3.01	31	53	1.14	52	38	0.41	73	55	0.00
11	9	2.82	32	4	1.09	53	39	0.39	74	58	0.00
12	33	2.65	33	23	1.04	54	60	0.36	75	16	0.00
13	36	2.51	34	29	1.00	55	30	0.34	76	72	0.00
14	44	2.38	35	19	0.96	56	26	0.32	77	71	0.00
15	47	2.26	36	21	0.92	57	41	0.29	78	68	0.00
16	37	2.15	37	81	0.88	58	75	0.27	79	70	0.00
17	25	2.05	38	8	0.84	59	82	0.24	80	69	0.00
18	32	1.96	39	20	0.81	60	42	0.22	81	50	0.00
19	11	1.87	40	3	0.77	61	76	0.19	82	49	0.00
20	27	1.78	41	35	0.73	62	63	0.17	83	51	0.00
21	28	1.71	42	40	0.70	63	83	0.14			

\* R: ranking; F: F<sub>3</sub> segregating family; G: predicted genetic gain.

**Table 8.** Predictions for the best linear unbiased prediction (BLUP) referring to the seed mass per plant (SMP) estimated for 83 F<sub>3</sub> segregating families of common black bean.

SMP (grams)											
R	F	G	R	F	G	R	F	G	R	F	G
1	66	6.16	22	10	1.64	43	25	0.71	64	40	0.18
2	67	6.11	23	6	1.58	44	30	0.69	65	42	0.15
3	73	5.92	24	8	1.52	45	19	0.65	66	41	0.13
4	65	5.34	25	7	1.46	46	23	0.63	67	43	0.11
5	5	4.54	26	74	1.40	47	21	0.60	68	12	0.08
6	28	4.00	27	33	1.34	48	26	0.57	69	13	0.06
7	27	3.59	28	4	1.29	49	20	0.54	70	71	0.04
8	45	3.28	29	64	1.23	50	60	0.52	71	72	0.01
9	48	3.04	30	36	1.19	51	22	0.49	72	68	0.00
10	44	2.84	31	32	1.14	52	63	0.47	73	69	0.00
11	47	2.67	32	34	1.09	53	57	0.44	74	70	0.00
12	53	2.53	33	76	1.05	54	59	0.41	75	55	0.00
13	46	2.41	34	75	1.01	55	56	0.39	76	24	0.00
14	14	2.31	35	1	0.97	56	81	0.37	77	18	0.00
15	52	2.21	36	3	0.94	57	62	0.34	78	17	0.00
16	9	2.10	37	37	0.90	58	58	0.32	79	16	0.00
17	77	2.01	38	2	0.87	59	61	0.30	80	15	0.00
18	80	1.92	39	54	0.84	60	82	0.27	81	50	0.00
19	11	1.84	40	35	0.81	61	83	0.25	82	49	0.00
20	78	1.77	41	29	0.78	62	38	0.23	83	51	0.00
21	79	1.70	42	31	0.75	63	39	0.20			

\* R: ranking; F: F<sub>3</sub> segregating family; G: predicted genetic gain.

height (PH) can be obtained in 53% of the evaluated progenies, these results in a genetic gain of at least 3.43 cm and plants with 31.66 cm in average. However, in order to enhance the character, it is possible to specifically target the selection (Table 4) for families 32 and 33 from the 6SRRS population, 74 from the 1FVRS population and 5 from the 1CBRS population. With the selection of these families, genetic gains greater than 3% can be obtained, this will reflect in increments greater than 10 cm and plants with more than 38.5 cm in height. One of the greatest difficulties of bean sowing in large areas is the availability of genotypes adapted to the mechanized harvest, being necessary to select erect type genotypes and appropriate first pod insertion to minimize crop losses (Silva et al., 2009; Silva and Wander, 2015). For the first pod insertion height (FPI) it was found (Table 5) that 50.6% of the F<sub>3</sub> families evaluated revealed genetic gains for this character, where a general selection can increase by at least 1.36 cm and obtain plants of 16.07 cm of FPI. Superior genetic gains can be obtained by selecting the families 33 and 32 from the 5SRRS population, with the family 5 extracted from the 1CBRS population and the 59 family selected in the 3BGRS population. The selection targeting for these families results in the genetic increase of at least 3.1% that influences a phenotype 4.3 cm higher and the progenies with 19 cm of first pod insertion height. The number of pods per plant (NPP) revealed that 33.7% of F<sub>3</sub> families allowed genetic gains of at least 1.3% to the character through selection (Table 6). In this context, it is possible to genetically potentiate the magnitude of pods per plant by 4.2 to 6.0% by selecting families 73, 66, 67, 67 and 45 from the 1FVRS, 1CARS, 2CARS and 4BGRS populations, respectively. By using this strategy, it will be possible to increase 2 to 3 pods per plant and indirectly to increase the seed yield of the future genotype. The number of seeds per plant (NSP) follows a similar tendency (Table 7) to the number of pods per plant (NPP), and it is possible to identify positive genetic gains through 30.1% of F<sub>3</sub> families evaluated, and a minimum increment of 4.3 seeds per plant and progenies of 25.15 seeds. However, it is possible to potentiate the phenotypic expression of this character by selecting the families 73, 66, 67 and 65 that genetically increase in 16.95 the number of seeds per plant, as well as, reveal plants with more than 37 seeds. The seed mass per plant (SMP) revealed that 28.9% of the progenies presented genetic gains to the character, this indicates the possibility of having superior genotypes and that can be selected for higher seed yield (Table 8). In this context, a minimum increase of 0.44 grams of seeds per plant can be obtained by means of the predicted genetic gain of 1.52. However, the targeting of the selections may improve the character with genetic gains higher than 3.5% obtained by the selection of the families 66, 67, 73, 65, 5, 28 and 27 from the populations 1CARS, 2CARS, 1FVRS, 4BGRS, 1CBRS, 4SRRS and 2RSRRS, respectively. This would provide an increase of 1.05 to 1.8 grams of seeds per plant, indicating a valid indication of the high genetic potential of these genotypes to obtain high yields of common black bean seeds.

## Materials and methods

### Location and experimental design

This experiment was carried out in the agricultural crop of 2017 in the municipality of Tenente Portela - RS, in the state

of Rio Grande do Sul, Brazil. At the coordinates, latitude 27°22 '16"S and longitude 53°45 '30"W, with an altitude of 420 meters. Soil is classified as a Ferric Red Latosol (Streck, 2008), and the climate is characterized by Köppen as subtropical humid Cfa. The experimental design used was of augmented blocks, where the 83 F<sub>3</sub> families were arranged only in each block, and the commercial controls were organized in three replicates. The families come from populations collected in the cities of Campos Borges - RS, Palmeira das Missões - RS, Santa Rosa - RS, Pejuçara - RS, Braga - RS, Cruz Alta - RS and Fortaleza dos Valos - RS (Table 1). The experimental units consisted of two lines with two meters in length, spaced by 0.5 meters. For sowing, 12 seeds per linear meter were used in the population density of 24 plants per m<sup>2</sup>. For base fertilization, 250 kg ha<sup>-1</sup> of N, P<sub>2</sub>O<sub>5</sub>, K<sub>2</sub>O (10-20-20) were used. For top dressing 50 kg ha<sup>-1</sup> of nitrogen in the form of urea (46% of N) was applied at the phenological stage V<sub>4</sub>. Crop management, weed control and insect pest control were performed according to the crop needs.

### Traits measured

The agronomic characters were evaluated in ten plants per experimental unit, these being: *Plant height (PH)*: measured through the distance between the soil surface to the stem end, results in centimeters (cm). *First pod insertion height (FPI)*: obtained by the distance at the ground level until the insertion of the first pod, results in centimeters (cm). *Number of pods per plant (NPP)*: measured by counting the total number of pods per plant, results in units. *Numbers of seeds per plant (NSP)*: obtained after the pod track, where the total number of seeds produced per plant was measured, results in units. *Seed mass per plant (SMP)*: the cleaned seeds were submitted to measurement of the mass in precision scale, results in grams.

### Statistical analysis

The data obtained were submitted to the assumptions diagnosis of the statistical model (Ramalho et al., 2000). Subsequently, based on the phenotypic information, the variance components and genetic parameters were estimated (Resende, 2016). The mixed linear model  $y = Xr + Za + Wp + Ts + e$  was used; where  $y$  is the data vector;  $r$ : is the vector of the repetition effects assumed as fixed and summed to the general mean;  $a$ : are the individual additive genetic effects assumed to be random;  $p$ : are the parcel effects assumed to be random;  $s$ : are population effects (random); and  $e$ : are random residual effects. The capital letters  $X$ ,  $Z$ ,  $W$  and  $T$  represent the incidence matrices for the effects  $r$ ,  $a$ ,  $p$  and  $s$ , respectively.

### Conclusion

The additive genetic effects were determinant for plant height and first pod insertion height. The pronounced effects of the environment are expressed for the number of pods, seeds and seed mass per plant. Potentiality in the selection of higher F<sub>3</sub> families are revealed through the 2CBRS population for plant height and first pod insertion height, for the components of seed yield the selections should be directed to the populations 2CARS and 1FVRS.



The number of seeds and seed mass per plant were potentiated in more than 28% of the selected F<sub>3</sub> families, and pronounceable genetic gains are obtained by the selection of families 66, 65 and 67. The inferences obtained in this study present theoretical and practical foundation, and can be applied in future studies of breeding and production of common black bean seeds.

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