

Combining ability in snap bean lines in Brazil

A.B.S. Gomes¹, T.R.A. Oliveira¹, G.A. Gravina¹, D.P. Cruz¹,
C.Q.S.S. Sant'Anna¹, R.F. Daher¹, L.C. Araújo², K.C. Araújo²,
G.H.F. Oliveira³, R.S. Rocha¹ and I.M. Pereira¹

¹ Universidade Estadual do Norte Fluminense "Darcy Ribeiro",
Campos dos Goytacazes, RJ, Brasil

² Instituto Federal Fluminense, Bom Jesus de Itabapoana, RJ, Brasil

³ Universidade Federal de Sergipe, Nossa Senhora da Glória, SE, Brasil

Corresponding author: T.R.A. Oliveira

E-mail: tamara_rebecca@hotmail.com

Genet. Mol. Res. 18 (2): gmr18214

Received November 14, 2018

Accepted April 08, 2019

Published May 13, 2019

DOI <http://dx.doi.org/10.4238/gmr18214>

ABSTRACT. The search for genetic material of snap beans with desirable yield traits is of utmost importance for yield increase in Brazil. We evaluated 12 snap bean genotypes by diallel crosses that presented characteristics of interest, so as to select the best genitors to generate productive populations in the snap bean breeding program of the Universidade Estadual do Norte Fluminense in Rio de Janeiro state, Brazil. Diallel crosses were performed applying Method 2 of Griffing. The F₁ generation, composed of 36 hybrid combinations, was evaluated in a greenhouse, in a completely randomized design with two replicates. The traits evaluated were: pod weight, length, width and thickness, number of seeds and seed weight. There were significant differences among genotypes for most variables, indicating genetic variability between snap bean lines. The following genitor genotypes proved to be the most suitable when the trait to be improved was yield: Top Seed Blue Line, UENF 1445, UENF 7-20-1, and UENF 7-10-1. The hybrids with higher values of combining ability estimates are indicated to generate promising segregating populations. Thus L3 (Top Seed Blue Line) × L18 (UENF 9-24-2), and L12 (UENF 7-14-1) × L1 (UENF 1445) hybrid combinations showed the best estimates of specific combining ability for the traits under evaluation, suggesting a high probability of obtaining superior

genotypes. The efficiency of selection for these traits is based on additive genic action and demonstrates progress in the of snap bean breeding program.

Key words: *Phaseolus vulgaris*; Genetic breeding; General and specific combining ability; Gene action

INTRODUCTION

Snap bean product can improve social conditions by reducing the level of unemployment in rural areas and generating opportunities for diversification for small producers. This is a widely consumed and commercialized crop in Brazil, with production distributed among the Northeast, Midwest, Southeast and South regions (Melo and Vilela, 2007). Rio de Janeiro state, considered one of the largest Brazilian centers of production and marketing of this vegetable, has been very promising in snap bean production, being responsible for 21% of the total produced in the southeast region (IBGE, 2006).

The cultivation of snap beans in Rio de Janeiro is a traditional activity and, given its relevance for the agriculture of the state, the search for genetic materials with desirable traits for yield is of great interest. However, this state still exhibits a productivity considered low because it does not have a cultivar with high productivity for this region.

In this way the search for genetic materials with characteristics desirable to the production is of high importance. High yields can be obtained from the use of more enhanced cultivation techniques or from using genetically superior cultivars, which are considered to be the most promising.

The hybridization stage among contrasting genitors that display traits of interest is the first stage of a breeding program. Among all the analyses, diallels are allow estimating the best hybrid combinations, enabling to advance generations applying the selected genotypes, as they present favorable alleles for the traits of interest (Engelsing et al., 2011; Carvalho et al., 2016).

In genetic breeding programs, the identification of snap bean lines with a high potential for pod and grain yield should be prioritized, and then line selection be made based fiber content (Londero et al., 2006). Moreover, breeding programs must satisfy the consumer market, focusing on the nutritional quality of the crops.

Consequently, this research was conducted to select snap bean genotypes that present promising agronomic traits.

MATERIAL AND METHODS

Genetic Material and Conduction of the Experiment

At first, diallel crosses among 12 snap bean genotypes were conducted, three commercial varieties and nine lines from the snap bean breeding program of the Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Rio de Janeiro State, Brazil. The genotypes used as genitors were selected regarding the traits of interest, evaluated from 37 morphological and agronomic traits, in accordance with the Minimum Morphological Descriptor List for Bean (*Phaseolus vulgaris*) (Formulário de Descritores

Morfológicos Mínimos de Feijão), recommended by the National Service for Cultivar Protection (Serviço Nacional de Proteção de Cultivares – SNPC) (Table 1).

Table 1. Lines used as genitors and respective morphological markers applied.

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

The F₁ generation and the genitors were evaluated, in 2013, at a greenhouse in the Research Support Unit (Unidade de Apoio à Pesquisa - UAP) of the Universidade Estadual do Norte Fluminense, in a completely randomized design with two replicates, resulting in 48 treatments, being 12 genitor genotypes and 36 hybrid combinations. Plants were sown by hand in 5 L pots with three seeds per pot. Thinning was carried out 10 days after sowing, leaving one plant per pot, and the tutoring was made using pieces of flat zinc wire and string. Irrigation was manually done, and phytosanitary treatments were performed following the recommendations of Filgueira (2013).

Traits Evaluated

The evaluated traits comprised the crop cycle of snap bean, estimated by the number of days from the date of planting to the date of flowering, when at least 50% of the plants had open flowers; flower color, evaluated during flowering; pod color, analyzed during physiological maturation; pod weight (PW), total weight in grams (g) of dry pods/plant in precision scale; seed weight per plant (SWPP), weighing of seeds/plant, after pod threshing, in a calibrated precision scale; pod length (PL), measurement in centimeters (cm) of dry pods with a ruler; pod width (PWID), measurement in millimeters (mm) at the central position of dry pods, with a digital pachymeter; pod thickness (PT), measurement in millimeters (mm) of dry pod with a digital pachymeter; and number of seeds per plant (GNPP), count of seeds per plant.

Statistical Analyses

The analyses of variance of all the agronomic traits were individually conducted for each trait regarding the effect of treatments as fixed. The statistical model used for the analysis of combining ability, derived from the mean of replicates, followed the model indicated by Geraldi and Miranda Filho (1988) adapted from the method 2 and model I of

Griffing (1956), in which the genitors are included in the analysis, and the experimental material is considered a fixed set of lines, according to the following model:

$$Y_{ij} = \mu + 1/2(d_1 + d_2) + g_i + g_j + s_{ij} + \varepsilon_{ij} \quad (\text{Eq. 1})$$

in which Y_{ij} = cross mean involving the i -th genitor of group I and the j -th genitor of group II; μ = overall mean of the diallel; d_1, d_2 = contrasts comprising means of groups I and II and the overall mean; g_i = effect of the general combining ability of the i -th genitor of group I; g_j = effect of the general combining ability of the j -th genitor of group II; s_{ij} = effect of the specific combining ability; ε_{ijk} = average experimental error. The analyses were conducted using the Genes software (Cruz, 2013).

RESULTS AND DISCUSSIONS

The analysis of variance proved significant differences for the variables, other than seed weight and number of seeds (Table 2). Thus, the selected lines revealed that it is possible to succeed in the breeding program, given that genetic gains, in terms of hybrid crosses, depend on the existing variability (Krause et al., 2012; Machado, 2014). The PL values determined are similar to the means of estimates for coefficients of variation described in other experiments with snap bean crop (Silva et al., 2004).

Table 2. Analysis of variance for pod weight (PW), grain weight (GWPP), grain number (GNPP), pod length (PL), pod width (PWID), pod thickness (PT) analyzed in 12 genotypes of snap bean.

Sources of variation	DF	Mean Squares					
		PW	GWPP	GNPP	PL	PWID	PT
Treatment	47	316.35*	141.64	541.40	8.20**	6.01**	0.84*
Residue	48	178.24	117.57	423.95	0.94	0.75	0.46
Phenotype		158.17	70.82	270.70	4.10	3.00	0.42
Genotype		69.05	12.03	58.72	3.63	2.62	0.19
Environment		89.12	58.78	211.97	0.47	0.37	0.23
Heridabilitv		43.65	16.99	21.69	88.52	87.36	44.86
V.C.		28.80	35.16	33.50	6.62	8.15	8.86

* and ** significant effects at 5% and at 1% by the F Test, respectively.

Pod weight, seed weight, and number of seeds displayed high values for phenotype and environment, and medium to low heritability. These results are explained because the traits are of quantitative nature, strongly influenced by the environment (Carvalho et al., 2016). Concerning pod length, pod width, and pod thickness traits, which are not much influenced by the environment, low environmental values and high heritability are noticed.

The application of the original means in the grouping by the mean test makes it easier the verification of the best genitors before the diallel analysis (Table 3). The existing genetic variability among the genitors is relevant to selecting the promising genotypes aiming at exploring the heterosis (Baldissera et al., 2012).

Among the 12 genitor genotypes, line 7 (UENF 7-6-1) showed to be superior to the other ones concerning pod weight (PW), seed weight (SWPP), number of seeds (NSPP), and pod length (PL). For the PW trait, five groups were set. Some crosses also had high pod

weight, in which the main genitors were L3 (Top Seed Blue Line), L10 (UENF 7-10-1), and L12 (UENF 7-14-1).

Table 3. Mean values of pod weight in grams (PW), grain weight in grams (GWPP), grain number (GNPP), pod length in cm (PL), pod width in cm (PWID), pod thickness in cm (PT) of 12 genitors and 36 hybrids from the partial diallel. Campos dos Goytacazes, RJ, Brazil, 2013.

Treatment	PW	GWPP	GNPP	PL	PWID	PT
L1	39.80 b-e	23.51 b-d	45 c-d	17.52 a-b	11.20 d-l	8.12 a-g
L2	48.73 b-e	35.94 a-d	75 a-d	12.45 i-n	7.87 p-q	9.14 a-b
L3	35.70 b-e	24.23 b-d	50 b-d	10.60 n	7.75 p-q	9.32 a
L4	44.53 b-e	23.19 b-d	45 c-d	13.66 e-l	9.86 i-p	6.84 f-g
L6	62.59 b-c	37.88 a-c	55 b-d	15.28 b-f	12.43 b-f	7.64 b-g
L7	92.62 a	55.38 a	110 a	18.87 a	14.92 a	7.74 a-g
L10	49.89 b-e	32.84 a-d	60 a-d	19.42 a	10.55 f-o	8.88 a-c
L11	44.74 b-e	30.72 a-d	65 a-d	17.52 a-b	12.14 b-h	8.34 a-f
L12	35.06 b-e	22.01 b-d	43 c-d	14.55 c-i	12.32 b-g	7.49 b-g
L13	60.71 b-c	34.52 a-d	70 a-d	18.80 a	11.57 b-i	8.48 a-f
L18	36.94 b-e	21.36 c-d	48 c-d	14.64 c-i	13.41 a-c	7.01 e-g
L20	44.50 b-e	28.95 a-d	60 a-d	12.53 h-n	11.92 b-i	7.09 e-g
L2 × L1	33.92 c-e	24.29 b-d	50 b-d	14.83 c-i	10.13 h-o	6.90 f-g
L2 × L4	26.07 d-e	19.29 c-d	40 c-d	11.58 l-n	7.83 p-q	7.74 a-g
L2 × L11	44.54 bcde	29.85 abcd	60 abcd	14.90 c-h	9.25 k-q	7.34 c-g
L2 × L13	57.06 b-d	41.05 a-c	85 a-c	15.10 c-g	9.99 i-o	7.25 c-g
L2 × L18	41.06 b-e	29.54 a-d	50 b-d	11.25 m-n	9.19 l-q	6.84 f-g
L2 × L20	41.88 b-e	23.39 b-d	48 c-d	13.22 f-m	8.60 o-q	7.17 d-g
L3 × L1	55.51 b-d	30.44 a-d	65 a-d	13.80 d-l	11.06 d-l	7.79 a-g
L3 × L4	53.92 b-d	41.54 a-c	80 a-c	11.82 k-n	7.18 q	8.05 a-g
L3 × L11	38.87 b-e	28.16 b-d	60 a-d	16.13 b-d	8.67 n-q	7.34 c-g
L3 × L13	61.97 b-c	42.46 a-c	85 a-c	14.05 c-k	10.76 e-n	8.83 a-d
L3 × L18	67.45 a-b	48.54 a-b	100 a-b	12.23 j-n	11.58 b-i	7.89 a-g
L3 × L20	43.29 b-e	22.58 b-d	50 b-d	14.09 c-k	10.20 g-o	8.12 a-g
L6 × L1	52.34 b-d	38.96 a-c	80 a-c	14.93 c-g	10.87 e-m	7.82 a-g
L6 × L4	50.11 b-e	32.23 a-d	65 a-d	13.72 e-l	12.70 b-e	8.64 a-e
L6 × L11	51.56 b-d	36.27 a-d	75 a-d	15.86 b-e	12.36 b-f	7.04 e-g
L6 × L13	52.92 b-d	39.75 a-c	80 a-c	13.91 d-l	9.64 j-p	7.51 b-g
L6 × L18	17.73 e	11.07 d	25 d	14.09 c-k	13.52 a-b	8.63 a-e
L6 × L20	37.67 b-e	34.14 a-d	70 a-d	15.71 b-e	11.88 b-i	7.64 b-g
L7 × L1	44.35 b-e	31.44 a-d	60 a-d	15.04 c-g	10.56 f-o	7.69 a-g
L7 × L4	35.12 b-e	31.47 a-d	65 a-d	13.08 f-m	13.51 a-b	8.41 a-f
L7 × L11	34.88 b-e	23.11 b-d	50 b-d	15.15 c-g	12.14 b-h	6.65 g
L7 × L13	43.07 b-e	26.58 b-d	55 b-d	14.93 c-g	10.45 f-o	7.25 c-g
L7 × L18	35.16 b-e	18.88 c-d	40 c-d	13.22 f-m	13.14 a-d	7.86 a-g
L7 × L20	35.57 b-e	24.66 b-d	50 b-d	15.04 c-g	11.36 c-k	8.26 a-g
L10 × L1	54.59 b-d	29.08 a-d	55 b-d	15.43 b-f	10.85 e-m	7.45 c-g
L10 × L4	54.76 b-d	35.75 a-d	60 a-d	16.12 b-d	8.67 n-q	7.41 c-g
L10 × L11	39.25 b-e	33.03 a-d	65 a-d	16.35 b-c	11.17 d-l	7.55 b-g
L10 × L13	39.76 b-e	24.40 b-d	50 b-d	19.57 a	9.39 k-p	8.25 a-g
L10 × L18	55.89 b-d	38.71 abc	80 a-c	14.15 c-k	12.40 b-f	7.77 a-g
L10 × L20	44.26 b-e	31.25 a-d	60 a-d	14.82 c-i	11.03 d-l	7.68 a-g
L12 × L1	56.24 b-d	43.10 a-c	85 a-c	14.72 c-i	8.86 m-q	7.23 c-g
L12 × L4	34.34 c-e	26.18 b-d	55 b-d	12.06 k-n	9.21 l-q	6.90 f-g
L12 × L11	50.96 b-d	39.96 a-d	70 a-d	15.26 b-f	9.46 i-p	7.21 c-g
L12 × L13	26.90 d-e	19.25 c-d	40 c-d	13.84 d-l	10.19 g-o	6.61 g
L12 × L18	53.74 b-d	33.42 a-d	65 a-d	14.63 c-i	9.11 l-q	7.47 b-g
L12 × L20	61.95 b-c	28.80 a-d	52 b-d	12.85 e-n	10.14 h-o	7.55 b-g

Means with different letters in the same column differ at 5% by the Duncan Test

Considering the SWPP trait, the genitor genotypes that demonstrated the best hybrids were L3 (Top Seed Blue Line) and L6 (UENF 7-5-1). The other variables formed 4, 15, 17, and 7 groups for NSPP, PL, PWID, and PT variables, respectively. These results confirm the findings of Oliveira et al. (2018), besides proving the existing variability among the lines under study, ensuring success in the crosses.

The effects of genotypes of group I, when applied as female genitors, were significant for all variables; however, for group II, when used as male genitors, the

significance was only for PL, PWID, and PT (Table 4). That points to the occurrence of variability in the expression of those traits, validating the possibility of selection gain.

Table 4. Analysis of variance for pod weight (PW), grain weight (GWPP), grain number (GNPP), pod length (PL), pod width (PWID), and pod thickness (PT) analyzed in diallel crosses in 12 genitors of snap beans. Campos dos Goytacazes, RJ, Brazil, 2013.

Sources of variation	FD	Mean Squares					
		PW	GWPP	GNPP	PL	PWID	PT
Treatment	47	316.35*	141.64	541.40	8.20**	6.01**	0.84*
Genitors	11	523.67*	185.97	706.43	16.90**	8.73**	1.41**
Group I	5	921.44*	285.41*	1192.08*	24.17**	15.87**	1.38*
Group II	5	135.67	53.11	242.08	12.60**	2.72**	1.10*
Group I×II	1	474.81	353.12	600.00	2.04	3.02*	3.10**
Genitor×Cross.	1	350.19	0.05	34.72	22.31**	13.15**	2.94**
Cross	35	250.23	131.75	504.00	5.06**	4.95**	0.60
GCA G-I	5	372.69	138.72	628.88	10.81*	16.21**	1.44*
GCA G-II	5	81.67	44.15	204.72	12.95**	3.83	0.69
SCA I×II	25	259.45	147.87	538.88	2.34**	2.93**	0.42
Residue	48	178.24	117.57	423.95	0.94	0.75	0.46

* and ** indicate significant effects at 5% and at 1% of probability by the F Test, respectively.

The diallel cross method proposed by Griffing (1956) is founded on the concepts of general and specific combining ability defined by Sprague and Tatum (1942). They described general combining ability (GCA) as the average behavior of a line in hybrid combinations, and specific ability (SCA) as the behavior that leads specific hybrid combinations to be superior or inferior regarding the average line implied in the process.

The estimate effects of the general combining ability were expressive for LP, PWID, and PT variables. These results prove the presence of, at least, one genitor that has a superior average performance in hybrid combinations (Oliveira et al., 2016). Moreover, the significance shows a strong influence of the additive effects on the control of these traits, along with the possibility of achieving promising lines (Arunga et al., 2010). Likewise, the estimate effects of specific combining ability were also significant for the same traits, suggesting that there is also an influence of the dominance effects on the expression of those traits and complementarity among the genitors (Cruz et al., 2012; Oliveira et al., 2016).

It is worth mentioning that works approaching diallel analysis in snap beans are unusual, having, among those few studies, divergence regarding results achieved. Rodrigues et al. (1998), when analyzing the genic effects in diallel, showed that the dominance effects were predominant for plant height. In turn, when Leal et al. (1979) applied the potential of the partial diallel in the snap bean to evaluate the genic effects on the yield trait, they inferred that the additivity and the epistasis were predominant.

In breeding programs, selections are made in advanced segregating generations to obtain greater genetic progress, considering the occurrence, in these generations, of several pure lines in the population with additive effects of the genes. In the opinion of Cruz et al., (2012), this is why the GCA is of greater relevance to the breeders, given that it depends on the additive variance.

By the estimates of the GCA effects on the PW, SWPP, and NSPP traits, it can be confirmed that the L1 Progenitor 19 (UENF 1445) and L3 (Top Seed Blue Line) genitors showed high and positive estimates, which suggests a possible contribution to the increase

of these traits (Table 5). Similar results for pod weight and number of seeds per plants were found by Rainey and Griffiths (2005) and Francelino et al. (2011).

Table 5. Values of the general combining ability (gi) of six traits in 12 snap bean genitors for pod weight (PW), grain weight (GWPP), grain number (GNPP), pod length (PL), pod width (PWID), and pod thickness (PT).

Genitors	PW	GWPP	GNPP	PL	PWID	PT
L1	4.25	2.06	4.02	0.41	-0.08	-0.12
L2	-4.48	-2.92	-6.38	-0.89	-1.30	-0.39
L3	8.26	4.79	11.52	-0.68	-0.56	0.39
L4	-2.85	0.25	-0.97	-1.31	-0.62	0.25
L6	-1.52	1.24	4.02	0.32	1.35	0.27
L7	-7.21	-4.79	-8.47	0.03	1.38	0.08
L10	2.84	1.21	-0.13	1.70	0.11	0.07
L11	-1.89	0.40	1.52	1.23	0.03	-0.41
L12	2.11	0.46	-0.55	-0.48	-0.97	-0.44
L13	1.70	1.42	4.02	0.85	-0.40	0.01
L18	-0.06	-0.79	-1.80	-1.11	1.01	0.13
L20	-1.13	-3.35	-6.80	-0.08	0.06	0.13

With regard to PL, the L10 (UENF 7-10-1) and L11 (UENF 7-12-1) genitors were the ones that presented positive values for GCA, which allows their indication in crosses to promote gains for that trait. For PWID, a higher contribution of the L7 (UENF 7-6-1) and L18 (UENF 9-24-2) genitors was seen; and the best genitors for PT, according to the GCA, were the L3 (Top Seed Blue Line) and L4 (UENF 7-3-1).

The L1 and L3 genitors were the ones proving the best GCA, being always among the best for PW, SWPP, and NSPP, with high and positive values. These results show higher potential to enhance those traits, suggesting their use on the crosses in breeding programs of snap bean. Nevertheless, the hybrid from the cross between L1 \times L3 did not present good performance, confirming Cruz and Vencovsky (1989), when they compared some methods of diallel analysis, revealing that not always two genitors of high general ability originate the best hybrid of the diallel when they are crossed.

The highest SCA effect for PW was in the L3 (Top Seed Blue Line) \times L18 (UENF 9-24-2), L3 (Top Seed Blue Line) \times L13 (UENF 7-20-1), and L6 (UENF 7-5-1) \times L1 (UENF 1445) hybrids, proving that the use of their genitors in the breeding program should lead to superior lines and possible promising cultivars. The L3 (Top Seed Blue Line) \times L13 (UENF 7-20-1) cross tends to be more promising than the L3 (Top Seed Blue Line) \times L18 (UENF 9-24-2) cross because the L13 (UENF 7-20-1) genitor has better agronomic and quality traits over the L18 (UENF 9-24-2).

The hybrids of L2 (Feltrin) \times L11 (UENF 7-12-1) and L2 (Feltrin) \times L13 (UENF 7-20-1) were the only ones with positive SCA for all traits. Nevertheless, as stated by CRUZ et al. (2004), the significance of the SCA is not enough to recommend these crosses; there should be, at least, one of the genitors with high GCA. Thus, as none of these genitors showed a high estimate of GCA, these crosses should be carefully considered.

The SCA estimates for SWPP evidence that the hybrids of higher and more positive values were L3 (Top Seed Blue Line) \times L18 (UENF 9-24-2) and L12 (UENF 7-14-1) \times L1 (UENF 1445). For NSPP, the L3 (Top Seed Blue Line) \times L18 (UENF 9-24-2), L2 (Feltrin) \times L13 (UENF 7-20-1), and L12 (UENF 7-14-1) \times L1 (UENF 1445) crosses provided higher values (Table 6).

Table 6. Estimate of the effects of the specific combining ability for pod weight (PW), grain weight (GWPP), grain number (GNPP), pod length (PL), pod width (PWID), and pod thickness (PT) from a diallel cross involving 12 genitors of snap bean and their 36 hybrids.

Genitors	PW	GWPP	GNPP	PL	PWID	PT
L2 × L1	-11.08	-5.67	-9.44	0.93	1.05	-0.18
L2 × L4	-11.83	-8.86	-14.44	-0.59	-0.71	0.27
L2 × L11	5.68	1.54	3.05	0.18	0.05	0.55
L2 × L13	14.59	11.72	25.55	0.75	1.23	0.02
L2 × L18	0.37	2.43	-3.61	-1.11	-0.99	-0.50
L2 × L20	2.26	-1.16	-1.11	-0.17	-0.62	-0.16
L3 × L1	-2.24	-7.24	-12.36	-0.30	1.23	-0.08
L3 × L4	3.26	5.66	7.63	-0.55	-2.10	-0.21
L3 × L11	-12.73	-7.86	-14.86	1.20	-1.27	-0.24
L3 × L13	6.76	5.41	7.63	-0.49	1.25	0.81
L3 × L18	14.01	13.71	28.47	-0.34	0.65	-0.25
L3 × L20	-9.07	-9.68	-16.52	0.48	0.23	-0.01
L6 × L1	4.36	4.82	10.13	-0.19	-0.87	0.06
L6 × L4	9.24	-0.09	0.13	0.32	1.49	0.50
L6 × L11	9.73	3.79	7.63	-0.07	0.50	-0.42
L6 × L13	7.49	6.25	10.13	-1.65	-1.78	-0.38
L6 × L18	-25.92	-20.20	-0.39	0.49	0.67	0.60
L6 × L20	-4.91	5.42	10.97	1.09	-0.01	-0.37
L7 × L1	2.07	3.35	2.63	0.21	-1.21	0.12
L7 × L4	-0.05	5.18	12.63	-0.01	2.27	0.46
L7 × L11	-1.24	-3.32	-4.86	-0.49	0.24	-0.62
L7 × L13	3.33	-0.86	-2.36	-0.33	-1.00	-0.44
L7 × L18	-2.79	-6.34	-11.52	-0.07	0.26	0.03
L7 × L20	-1.31	1.99	3.47	0.71	-0.55	0.43
L10 × L1	2.25	-5.01	-10.69	-1.05	0.34	-0.11
L10 × L4	9.53	3.45	-0.69	1.35	-1.29	-0.53
L10 × L11	-6.93	0.58	1.80	-0.95	0.54	0.28
L10 × L13	-10.03	-9.06	-15.69	2.63	-0.78	0.55
L10 × L18	7.87	7.47	20.13	-0.81	0.80	-0.05
L10 × L20	-2.68	2.56	5.13	-1.16	0.38	-0.13
L12 × L1	4.63	9.73	19.72	0.40	-0.55	0.18
L12 × L4	-10.16	-5.35	-5.27	-0.52	0.33	-0.51
L12 × L11	5.50	5.26	7.22	0.13	-0.07	0.46
L12 × L13	-22.15	-13.46	-25.27	-0.90	1.10	-0.56
L12 × L18	6.45	2.93	5.55	1.84	-1.39	0.17
L12 × L20	15.73	0.86	-1.94	-0.95	0.58	0.25

The L10 (UENF 7-10-1) × L13 (UENF 7-20-1), L10 (UENF 7-10-1) × L4 (UENF 7-3-1), and L3 (Top Seed Blue Line) × L11 (UENF 14-3-3) crosses are suitable to generate promising segregating populations for the PL trait, once they are composed of, at least, one genitor genotype with a positive and significant GCA value. For the PWID trait, the L7 (UENF 7-6-1) × L4 (UENF 7-3-1) and L10 (UENF 7-10-1) × L18 (UENF 9-24-2) crosses displayed the best estimates for the SCA.

The L3 (Top Seed Blue Line) × L13 (UENF 7-20-1) and L6 (UENF 7-5-1) × L4 (UENF 7-3-1) crosses were the hybrids with the best positive and significant SCA values for the PT trait, thus the most indicated to be used in crosses to increment this trait in the population. It is verified that the crosses L3 (Top Seed Blue Line) × L18 (UENF 9-24-2) and L12 (UENF 7-14-1) × L1 (UENF 1445) almost always provided the best SCA estimates for the traits under evaluation, showing a high probability to obtain superior genotypes, using them in the artificial crosses.

ACKNOWLEDGMENTS

This study was financed in party by the Coordenação de Aperfeiçoamento de Pessoas de Nível Superior – Brasil (CAPES) – Finance Code 001. In addition we thank FAPERJ and CNPq for scholarships granted.

REFERENCES

- Arunga EE, Rheenen HAV and Owuoche (2010). Diallel analysis of snap beans (*Phaseolus vulgaris* L.) varieties for important traits. *Afr. J. Agric. Res.* 5: 1951-1957.
- Baldissera JNC, Bertoldo JG, Valentini G, Coan MMD, et al. (2012). Uso do melhor preditor linear não-viesado (BLUP) na predição de híbridos em feijão. *Biosci. J.* 28: 395-403.
- Carvalho ADF, Silva GO and Pereira RB (2016). Capacidade de combinação de genitores de cenoura para caracteres de rendimento de raízes e tolerância à queima-das-folhas. *Ceres.* 63: 183-190. <http://dx.doi.org/10.1590/0034-737X201663020009>.
- Carvalho M, Castro I, Matos M, Lino-Neto T, et al. (2016). Caracterização agromorfológica de acessos de feijão frade (*Vigna unguiculata*): bases para o melhoramento. *Rev. Ciênc. Agrár.* 39: 506-517. <http://dx.doi.org/doi.org/10.19084/RCA16091>.
- Cruz CD (2013). GENES: software para análise de dados em estatística experimental e em genética quantitativa. *Acta Sci. Agron.* 35: 271-276. <http://dx.doi.org/10.4025/actasciagron.v35i3.21251>.
- Cruz CD and Vencovsky R (1989). Comparação de alguns métodos de análise dialélica. *Rev. Bras. Genet.* 12: 425-438.
- Cruz CD, Regazzi AJ and Carneiro PCS (2012). Modelos Biométricos Aplicados ao Melhoramento Genético. Editora UFV, Viçosa, 514p.
- Engelsing MJ, Simon Rozzetto D, Coimbra JLM, Zanin CG, et al. (2011). Capacidade de combinação em milho para resistência a *Cercospora zea-maydis*. *Rev. Ciênc. Agron.* 42: 232-241. <http://dx.doi.org/10.1590/S1806-66902011000100029>.
- FAO. Food and Agriculture Organization. Faostat (2014). Available in: < http://www.fao.org/index_en.htm.
- Filgueira FAR (2013). Novo manual de Olericultura: agrotecnologia moderna na produção e comercialização de hortaliças. Editora UFV, Viçosa, 421p.
- Francelino FMA, Gravina GA, Manhães CMC, Cardoso PMR, et al. (2011). Avaliação de linhagens de feijão-de-vagem para as regiões Norte e Noroeste Fluminense. *Rev. Ciênc. Agron.* 42: 554-562.
- Geraldi IO and Miranda Filho JB (1988). Adapted models for the analysis of combining ability of varieties in partial diallel crosses. *Rev. Bras. Genét.* 11: 419-430.
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* 9: 463-493.
- IBGE - Instituto Brasileiro de Geografia e Estatística (2006). Sistema IBGE de Recuperação automática. Available in: < <http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=19&i=P&c=818>>.
- Krause W, Rodrigues R and Leal NR (2012). Capacidade combinatória para características agrônômicas em feijão-de-vagem. *Rev. Ciênc. Agron.* 43: 522-531. <http://dx.doi.org/10.1590/S1806-66902012000300015>
- Leal NR, Hamad I and Bliss F (1979). Combining ability estimates for snap bean traits using early and advanced generations. *Hort. Sci.* 14: 405-405.
- Londero PMG, Ribeiro ND, Cargnelutti Filho A, Rodrigues JÁ, et al. (2006). Herdabilidade dos teores de fibra alimentar e rendimento de grãos em populações de feijoeiro. *Pesq. Agrop. Bras.* 41: 51-58.
- Melo PCT and Vilela NJ (2007). Importância da cadeia produtiva brasileira de hortaliças. Available at: http://www.abhorticultura.com.br/downloads/cadeia_produtiva.pdf.
- Machado A (2014). Construção histórica do melhoramento genético de plantas: do convencional ao participativo. *Rev. Bras. Agroecol.* 9: 35-50.
- Oliveira GHF, Buzinaro R, Revolti LTM, Giorgenon CHB, et al. (2016) An accurate prediction of maize crosses using diallel analysis and best linear unbiased predictor (BLUP). *Chil. J. Agric. Res.* 76: 294- 299. <http://dx.doi.org/10.4067/S0718-58392016000300005>
- Oliveira TRA, Gravina GS, Oliveira GHF, Araújo LC, et al. (2018) Multivariate analysis used as a tool to select snap bean (*Phaseolus vulgaris* L.) genotypes. *Aust. J. Crop Sci.* 12: 67-73. <http://dx.doi: 10.21475/ajcs.18.12.01.pne661>.
- Rainey KM and Griffiths PD (2005). Diallel analysis of yield components of snap beans exposed to two temperature stress environments. *Euphytica.* 142: 43-53. <https://doi.org/10.1007/s10681-005-0480-3>
- Rodrigues R, Leal NR and Pereira MG (1998). Análise dialélica de seis características agrônômicas em *Phaseolus vulgaris* L. *Bragantia.* 57: 241-250. <http://dx.doi.org/10.1590/S0006-87051998000200005>.
- Silva MP, Amaral Júnior AT, Rodrigues R, Daher RF, et al. (2004). Análise dialélica da capacidade combinatória em feijão de vagem. *Hort. Bras.* 22: 77-280.
- Sprague GF and Tatum LA (1942). General vs. specific combining ability in single crosses of corn. *J. Amer. Soc. Agron.* 34: 923-932. <http://dx.doi: 10.2134 /agronj1942.00021962003400100008x>