

*Full Length Research Paper*

## Combining ability for morphoagronomic traits in common bean and snap bean

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The present study aimed to estimate the combining ability for agronomic traits of interest in genotypes of *Phaseolus vulgaris* by means of the Griffing diallel. To this end, six parents were crossed in a complete diallel scheme without reciprocals, namely, two common bean genotypes (PI207262 and BAC 6) and four accessions of snap-bean (UENF 1482, 1486 UENF, UENF 1487, UENF 1579). Twelve morphoagronomic traits of interest for the culture of the snap bean were evaluated. There were significant differences for all morphoagronomic traits evaluated, except for the fiber content in the pod. Concerning the source of variation general and specific combining ability (GCA and SCA, respectively), there was a significant effect for most traits studied, except for the dry mass of the aerial part and diameter of the pod, which were not significant for SCA. Based on the data obtained, the cross between the parents of common bean PI207262 and BAC 6 and the parents of snap bean UENF 1487 and UENF 1486 is recommended, so as to obtain superior genotypes in advanced generations. Due to the occurrence of effects of both GCA and SCA in the control of morphoagronomic traits in the population assessed, the use of methods of conducting segregating populations focused on parental control is recommended, such as the Pedigree method.

**Key words:** *Phaseolus vulgaris* L., yield components, general combining ability, specific combining ability.

### INTRODUCTION

Snap bean (*Phaseolus vulgaris* L.) is one of the most consumed vegetables in the world (Blair et al., 2010). World production is approximately nine million tons (FAO, 2010), but in Brazil, it is difficult to measure the dimension and importance of this market due to the lack of reliable statistical data. The main difference between snap bean and common bean is in the pods, which have juicy mesocarp and low fiber content. They are used for feeding when the seed is at the immature stage, after cooking or industrial processing (Singh, 2001). In Brazil, snap bean is mainly cultivated by small producers, who use a small number of cultivars of narrow genetic base and limited technological resources and inputs, resulting

in low productivity and increased susceptibility of culture to pathogens (Peixoto et al., 2002; Vilela et al., 2009; Barbé et al., 2010). The identification and introgression of genes from other gene backgrounds in *P. vulgaris* are necessary to broaden the genetic basis of snap beans. Common bean is a primary source for this increased variability, due to the constant breeding process of this culture for improving yield and resistance to diseases (De Ron et al., 2004).

Aimed to achieve superior and divergent genotypes, the diallel analysis provides the identification of the best crosses for the recombination of genes of interest, the estimation of the genetic effects resulting from different crosses, and the understanding of the mechanism of inheritance of different characters, which allows the selection of the most efficient method for conducting the segregating population (Kurek et al., 2001; Cruz et al., 2004). Among the known methods of diallel analysis, the

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**Table 1.** Morphoagronomic traits of six parents of *Phaseolus vulgaris* L. used in the diallel crosses.

Genotypes	Flower color	Pods color	Seeds color	Cross section of the pod	Pods type	Days to flowering
<b>Common bean</b>						
PI 207262	White	Green	Beige	Flat	Manteiga	41
BAC-6	White	Green	Beige	Flat	Manteiga	44
<b>Snap bean</b>						
UENF 1482	Purple	Yellow	Black	Flat	Manteiga	54
UENF 1579	Purple	Green	White	Elliptical	Macarrão	50
UENF 1487	White	Green	White	Flat	Macarrão	49
UENF 1486	White	Green	White	Flat	Manteiga	45

one proposed by Griffing (1956) is based on the estimation of the effects of general combining ability (GCA) of a group of parents and specific combining ability (SCA) of their respective hybrid combinations. According to Sprague and Tatum (1942), GCA is the result of the average behavior of lineages when crossed with each other, and the SCA represents the behavior of two individuals in a number of hybrid combinations.

This study aimed to evaluate the combining ability of genotypes of *P. vulgaris* (snap bean and common bean) for 12 morphoagronomic traits, identify superior hybrid combinations to advance generations, and make inferences about the modes of gene action involved in the expression of the characters under study.

## MATERIALS AND METHODS

Based on a previous work that evaluated bean-pod genotypes of determinate habit from the vegetable germplasm collection of the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) (Teixeira et al., 2004), four accessions of snap bean of determinate habit were selected: UENF 1482, UENF 1486, UENF 1487 and UENF 1579, which were added to two common bean genotypes, BAC 6 and PI 207262 (Table 1). These six genotypes were used as parents in a complete diallel without reciprocals, resulting in the achievement of 15 F<sub>1</sub> hybrids. The crosses occurred between July and October 2008 and February and May 2009. To this end, plantings of seven pots were carried out weekly for five weeks. When the parents started to flower, daily crosses were carried out among them through the technique of opening and emasculation of flower buds, using smears. The crosses occurred at times of mild weather to favor their fixation, precisely between 6 and 10 am, and 3:30 and 5:45 pm. At harvest, pods from cross were harvested separately, identified according to the cross that originated them and shelled, and their seeds were set aside for further stages.

The diallel evaluation occurred in a greenhouse located in the Research Support Unit of the Center for Agricultural Science and Technology of the UENF, between May and September 2009. The experiment was arranged in a randomized block experimental design with three replications and six pots for each genotype per experimental plot. The six parents and their 15 hybrids were sown in 5-liter pots, with a substrate composed of 50% soil, 30% cattle manure and 20% sand, with the application of 3 g of NPK mineral fertilizer at a ratio of 4-14-8 per pot. The pots were randomly arranged in six rows per block, with 126 pots in each block, totaling 378 pots. Later, top dressing with 1 g of ammonium sulfate per pot

was carried out at the beginning of pod formation. Four seeds were sown in each pot, with thinning of two plants per pot after seedling emergence. The confirmation of the crosses was given by the dominance of the purple color in the flowers observed in F<sub>1</sub> hybrids. In the case of crosses between parents of the same color of flower, *inter simple sequence repeat* markers (ISSR) were used and the confirmation of the crosses was performed by the identification of bands belonging to the male parent in the hybrids obtained from these crosses.

The following morphoagronomic characteristics were evaluated: plant height (PH), in meters; dry mass of the aerial part (DMAP), in grams; length of pod (LP), in mm; pod diameter (PD), in mm; height of the insertion of the first pod (HIFP), in meters; total number of pods (TNP), number of pods per plant (NPP); total number of grains (TNG); number of grains per plant (NGP); total weight of grains (TWg); fiber content in the pod (FP), obtained according to Frank et al. (1961); and harvest index (HI).

The statistical analysis was performed by the Method 2 of the diallel analysis proposed by Griffing (1956), based on the average of the replications, including the parents and F<sub>1</sub>s, using the Model B, which considers the effect of genotypes as fixed. This model is represented by:

$$Y_{ij} = m + g_i + g_j + s_{ij} + \bar{\epsilon}_{ij},$$

Where  $Y_{ij}$  = is the average value of the hybrid combination ( $i \neq j$ ) or of the parent ( $i = j$ );  $m$  = overall mean of all treatments;  $g_i$  = refers to the effect of the general combining ability of the parent  $i$ ;  $g_j$  = refers to the effect of the general combining ability of the parent  $j$ ;  $s_{ij}$  = refers to the effect of the specific combining ability for the crosses between parents  $i$  and  $j$ ; and  $\bar{\epsilon}_{ij}$  = refers to the average experimental error.

The estimators of the general and specific combining abilities were obtained through the Least Squares Method and the normal equations  $X'Y = X'X \hat{\beta}$ , derived from the linear model  $Y = X\beta + E$ , in which  $E \sim \text{NID}(\varphi, I\sigma_q^2)$  (Cruz et al., 2004). All the analyses were achieved by using the GENES software system (Cruz, 2006).

## RESULTS AND DISCUSSION

There was a significant genotype effect for all morphoagronomic traits evaluated, excepting FB (Table 2). Although this result is different from the expected, it is

**Table 2.** Estimate of the mean squares of *Phaseolus vulgaris* L. (parents and F<sub>1s</sub>) of the general and specific combining abilities (GCA and SCA) and residue, and quadratic component of the CGC ( $\Phi^2_g$ ) and CEC ( $\Phi^2_g$ ) for 12 agronomic traits assessed in a complete diallel scheme without reciprocals.

Sources of variation	DF	Mean Squares <sup>1/</sup>											
		PH	DMAP	LP	PD	HIFP	TNP	NPP	TNG	NGP	TWG	FB	HI
Repetitions	2	0.04	42.20	544.18	13.88	0.0018	711.87	20.31	4120.02	114.43	1018.01	0.018	22.07
Genotypes	20	0.43**	14.92*	1803.20**	5.84**	0.0026**	1377.51**	37.46**	59952.06**	1665.32**	5850.92**	0.0261 <sup>ns</sup>	181.93**
GCA	5	1.03**	35.78**	6594.09**	14.71**	0.0029**	2193.53**	56.90**	141907.98**	3941.43**	10816.95**	0.0189 <sup>ns</sup>	398.28**
SCA	15	0.22**	7.96 <sup>ns</sup>	206.19*	2.88 <sup>ns</sup>	0.0023**	1105.56*	31.02*	32634.18**	906.55**	4195.51**	0.0282 <sup>ns</sup>	109.81**
Error	40	0.09	7.91	95.13	2.14	0.0008	433.08	12.00	6550.66	181.95	787.09	0.0408	18.80
<b>Quadratic components</b>													
$\Phi^2_g$		0.043	1.1615	270.7898	0.5236	0.0001	73.3518	1.8710	5639.8882	156.6448	417.9108	-	15.8120
$\Phi^2_g$		0.0455	0.0197	37.0193	0.2471	0.0005	224.1596	6.3409	8694.5083	241.5322	1136.1379	-	30.3369
$\Phi^2_g / \Phi^2_g$		0.94	58.96	7.31	2.12	0.20	0.33	0.29	0.65	0.65	0.37	-	0.52
Mean		1.12	21.53	143.58	7.63	0.24	106.38	Ntr	407.27	67.88	148.95	0.78	52.31
CV <sup>2/</sup>		26.66	13.06	6.79	19.17	11.33	19.56	19.52	19.87	19.87	18.83	25.81	8.29

<sup>1/</sup>PH: Plant height, DMAP: dry mass of the aerial part, LP: length of pod, PD: pod diameter, HIFP: height of the insertion of the first pod, TNP: total number of pods, NPP: number of pods per plant, TNG: total number of grains, NGP: number of grains per plant, TWG: total weight of grains, FP: fiber content in the pod and HI: harvest index; <sup>2/</sup>CV = coefficient of variation. <sup>ns</sup> = Not significant at the 0.05 level; \*\* = significant at the 0.01 level; and \* = significant at the 0.05 level.

known that while snap bean breeding is focused on production and quality of pods (Soutiriou and Mavrana, 2008), common bean breeding is targeted at grain yield and quality. Thus, crosses between snap bean genotypes and common bean genotypes may lead to changes in traits of agronomic interest. The values of variation coefficient for the characters under evaluation ranged from 6.79 to 26.66%, indicating acceptable levels of environmental variation (Table 2). Unfolding the sum of the genotypes squares in addition to the general (GCA) and specific combining ability (SCA) revealed that all of the traits were significant by the F test, except for the traits DMAP and PD, which were not significant for SCA, and FB, which was not significant for GCA

or SCA (Table 2). The estimates of quadratic components demonstrated that the traits DMAP, LP and PD expressed superiority of additive genetic effects in relation to the non-additive, indicating the possibility of satisfactory gains with selection for these traits in segregating generations. The opposite was observed for PH, HIFP, TNP, NPP, TNG, NGP and TWG, that is, non-additive effects were prevalent, suggesting that gains or losses for these characteristics demand the implementation of more complex breeding strategies to allow segregating populations to achieve recombinant lines (Table 2).

However, Cruz et al. (2004) and Pereira et al. (2007) point out that the pre-selection of parents,

such as that carried out for this experiment, can reduce the differential for additive effects, thus increasing the importance of non-additive effects. Through the evaluation of three genotypes of snap bean and two of common bean as parents of a complete diallel without reciprocals, Rodrigues et al. (1999) observed the predominance of additive effects for NPP, NGP, LP and FB, and non-additive effects for PH. However, Gonçalves-Vidigal et al. (2008) evaluated six common bean parents and verified the prevalence of non-additive effects for PH, NPP and NGP. The selection of parents for the formation of segregating populations is crucial for successful breeding programs. Combining ability, with the presence of complementary genes, is also

**Table 3.** Estimates of the effects of general combining ability and standard deviations (SD) for 12 morphoagronomic traits evaluated in six parents of *Phaseolus vulgaris* L. in a complete diallel scheme without reciprocals.

Genitors	Evaluated Traits <sup>1/</sup>											
	PH	DMAP	LP	PD	HIFP	TNP	NPP	TNG	NGP	TWG	FB	HI
PI 207263	0.2913	0.3763	-27.9125	-0.6250	-0.0125	15.2470	2.5287	125.9679	20.9937	20.8371	0.0521	3.6350
BAC 6	0.2363	-0.3275	-11.4025	-0.7863	0.0125	2.5833	0.4175	56.0941	9.3475	32.3083	-0.0104	6.1000
UENF 1482	-0.0963	0.2313	3.9775	-0.2238	0.0000	4.4983	0.1787	-21.2820	-3.5475	-16.3429	-0.0267	-4.6913
UENF 1579	-0.1038	2.0338	7.1600	0.6088	0.0138	-7.5804	-1.2775	-29.0195	-4.83375	-6.3792	0.0096	-2.8513
UENF 1487	-0.1825	-1.5688	13.5538	1.2575	-0.0100	-3.4129	0.0550	-48.9358	-8.15625	-16.7842	-0.0142	-1.0188
UENF 1486	-0.1450	-0.7450	14.6238	-0.2313	-0.0038	-11.3354	-1.9025	-82.8245	-13.8037	-13.6392	-0.0104	-1.1738
SD(g <sub>j</sub> -g <sub>j</sub> )	0.0859	0.8117	2.8157	0.0423	0.0079	6.0075	1.0000	23.3642	3.8939	8.0989	0.0583	1.2516

<sup>1/</sup>PH: Plant height, DMAP: dry mass of the aerial part, LP: length of pod, PD: pod diameter, HIFP: height of the insertion of the first pod, TNP: total number of pods, NPP: number of pods per plant, TNG: total number of grains, NGP: number of grains per plant, TWG: total weight of grains, FP: fiber content in the pod and HI: harvest index.

fundamental for success. According to Sprague and Tatum (1942), a low GCA value indicates that the average of hybrids in which the lineage *i* participates does not differ from the general average of the diallel. On the other hand, high values, either positive or negative, reveal that the lineage *i* is much better or worse than the other lineages included in the diallel, compared to the average of their hybrids. According to the GCA estimate, the parent UENF 1579 achieved the highest value for DMAP and a negative value for PH. A plant with high mass of the aerial part, short stature and thicker stem is an extremely advantageous ideotype in *P. vulgaris* L., since it prevents plants from bending and gives them a more upright position (Moreira et al., 2009; Trindade et al., 2010). For the characters LP and PD, related to the quality of pods, the parents UENF 1486, UENF 1487, UENF 1579 and UENF 1482 expressed high and positive values of GCA for LP, while for PD, the parents PI 207262, BAC 6, UENF 1482 and UENF 1486 presented negative values. This is consistent with the desires of the Brazilian market, which requires long and thin pods. For TNP, NPP, TNG, NGP,

TWG and HI, components of productivity in *P. vulgaris* L., the parents PI 207262 and BAC 6, both genotypes of common bean, expressed the highest values of GCA, strengthening their ability to produce pods and grains.

The estimates of the SCA effects reveal the prevalence of negative dominance effects for almost all the characters evaluated in the six parents used (Table 4). These values are estimates of the genetic divergence among the genotypes present in the experiment, and are relevant for autogamous plants, mainly when the values  $\hat{\sigma}_{ii}$  and  $\hat{\sigma}_{ij}$  are consistent with the estimates of GCA for signal and magnitude, indicating that the gains observed in  $F_1$  can be capitalized with the advancement of generations (Mavrona et al., 2001; Silva et al., 2004). Considering the characters TNP, NPP, TNG, NGP, TWG and HI, related to the production of pods and grains, the positive estimates of  $\hat{\sigma}_{ii}$  in BAC 6 (Table 4) stood out, agreeing with the GCA estimates, in signal, for these characters (Table 3). For the traits LP, PD and FB, related to the quality of pods, it is worth mentioning that with the

exception of the parent UENF 1579, all parents expressed positive values for LP, and the negative values observed for PD and FB for most parents, mainly for the negative values and of great magnitude of the parents (Trindade et al., 2010).

The selection of the best crosses among the hybrids obtained should focus on parents with high estimates of  $\hat{\sigma}_{ij}$ , aiming to capitalize the gains per selection in advanced generations. Seeking crosses presenting high GCA estimates and signals that agree with that desired for breeding, the parents UENF 1487 and UENF 1486 have higher and positive values of  $\hat{\sigma}_{ij}$  for LP and negative values for PD and FB. Thus, the cross between these two parents can result in lineages with high-quality pods in advanced generations. Regarding the characters TNP, NPP, TNG, NGP, TWG and FB, related to the production of beans and grains, higher values of  $\hat{\sigma}_{ij}$  occurred for all these traits in the crosses among UENF 1579, UENF 1487 and UENF 1579 and UENF 1486 for TNP, NPP, TNG, NGP and TWG (Table 4). On the other hand, the parent PI 207262

**Table 4.** Estimates of the effects of specific combining ability ( $\hat{S}_{ii}$  and  $\hat{S}_{ij}$ ) and standard deviations (SD) for 12 morphoagronomic traits evaluated in six parents of *Phaseolus vulgaris* L. in a complete diallel scheme, without reciprocals.

Hybrids <sup>2/</sup>	Evaluated Traits <sup>1/</sup>											
	PH	DMAP	LP	PD	HIFP	TNP	NPP	TNG	NGP	TWG	FB	HI
P <sub>1</sub> × P <sub>1</sub>	-0.1996	-1.6439	7.9793	-0.6943	-0.0179	-7.5475	-1.2446	-65.2110	-10.8675	-34.5989	-0.0375	-3.8171
P <sub>1</sub> × P <sub>2</sub>	-0.2646	-0.2701	-2.1907	-0.5631	-0.0029	-11.5437	-1.9133	7.3326	1.2188	-25.3301	-0.0150	-4.4221
P <sub>1</sub> × P <sub>3</sub>	0.1879	1.7711	-2.8907	-0.4356	0.0096	11.87125	2.5453	4.3689	0.7237	40.2111	0.0613	6.1491
P <sub>1</sub> × P <sub>4</sub>	0.0754	1.1986	0.1068	-1.1081	0.0458	4.6200	0.7816	92.4464	15.4100	-6.4027	-0.0250	-3.0309
P <sub>1</sub> × P <sub>5</sub>	0.2841	0.1811	-4.2570	2.4132	-0.0004	9.1125	0.8892	-83.6373	-13.9375	35.9723	-0.0212	5.7266
P <sub>1</sub> × P <sub>6</sub>	0.1167	0.4073	-6.7270	1.0819	-0.0167	1.0350	0.1867	109.9114	18.3200	24.7474	0.0750	3.2116
P <sub>2</sub> × P <sub>2</sub>	-0.3296	-2.4564	1.6193	-0.0218	-0.0279	11.1200	1.8679	19.2064	3.2050	-51.7014	-0.0825	-5.3771
P <sub>2</sub> × P <sub>3</sub>	0.1629	0.9048	7.0993	-0.3843	0.0446	-29.4650	-4.3433	-51.4174	-8.5700	47.9699	0.0038	7.4641
P <sub>2</sub> × P <sub>4</sub>	0.3804	1.0524	-7.7932	0.4232	0.0409	12.6137	2.1128	100.3202	16.7163	32.5361	0.0175	3.5842
P <sub>2</sub> × P <sub>5</sub>	0.3191	1.5949	-0.8269	0.8444	-0.0154	19.1162	2.5604	34.5664	5.7587	27.9611	0.0313	2.5716
P <sub>2</sub> × P <sub>6</sub>	0.0616	1.6311	0.4731	-0.2768	-0.0117	-12.9612	-2.1521	-129.214	-21.5337	20.2661	0.1275	1.5566
P <sub>3</sub> × P <sub>3</sub>	-0.1946	-1.1439	2.4193	-0.2068	-0.0229	-21.3800	-4.6646	-121.711	-20.2850	-63.2089	-0.0300	-13.294
P <sub>3</sub> × P <sub>4</sub>	-0.0471	0.6236	2.6968	0.5307	0.0134	4.6987	1.3516	-46.9735	-7.8287	28.8573	0.1437	6.3254
P <sub>3</sub> × P <sub>5</sub>	-0.1384	-0.5739	9.4031	0.5519	-0.0129	24.5312	4.0191	159.6127	26.6037	-17.2177	0.0475	-1.0071
P <sub>3</sub> × P <sub>6</sub>	0.2241	-0.4376	-21.1469	0.1507	-0.0092	31.1237	5.7567	177.8314	29.6413	26.5974	-0.1962	7.6579
P <sub>4</sub> × P <sub>4</sub>	-0.3296	-2.7989	-2.9457	-0.1918	-0.0504	7.9900	-3.3021	-84.9061	-14.1525	-30.8264	-0.0125	-2.8346
P <sub>4</sub> × P <sub>5</sub>	-0.1108	2.4536	6.1406	-0.0606	-0.0067	7.9900	0.7054	82.7801	13.8000	13.4386	-0.0687	0.0529
P <sub>4</sub> × P <sub>6</sub>	0.3616	0.2698	4.7406	0.5982	0.0071	9.8625	1.6529	-58.7611	-9.7925	-6.7764	-0.0425	-1.2621
P <sub>5</sub> × P <sub>5</sub>	-0.1221	-1.4339	-5.0232	-1.5593	0.0071	-23.5575	-2.6371	-64.4035	-10.7375	-22.1064	-0.075	-2.6896
P <sub>5</sub> × P <sub>6</sub>	-0.1096	-0.7877	-0.4132	-0.6306	0.0208	-13.6350	-2.8996	-64.5148	-10.7500	-15.9414	0.1613	-1.9646
P <sub>6</sub> × P <sub>6</sub>	-0.3271	-0.5414	11.5368	-0.4618	0.0046	-7.7125	-1.2721	-17.6260	-2.9425	-24.4464	-0.0625	-4.5996
SD ( $\hat{S}_{ii}$ - $\hat{S}_{ij}$ )	0.1719	1.6234	5.6313	0.8451	0.0158	10.6501	2.0001	46.7285	7.7878	16.1977	0.1166	2.5031

<sup>1/</sup>PH: Plant height, DMAP: dry mass of the aerial part, LP: length of pod, PD: pod diameter, HIFP: height of the insertion of the first pod, TNP: total number of pods, NPP: number of pods per plant, TNG: total number of grains, NGP: number of grains per plant, TWG: total weight of grains, FP: fiber content in the pod and HI: harvest index; and <sup>2/</sup>P<sub>1</sub>: PI 207263, P<sub>2</sub>: BAC 6, P<sub>3</sub>: UENF 1482, P<sub>4</sub>: UENF 1579, P<sub>5</sub>: UENF 1487, and P<sub>6</sub>: UENF 1486.

expressed positive and high values of GCA and  $\hat{S}_{ij}$  in the cross between this parent and the accessions UENF 1579 and UENF 1487 for all yield components assessed (Tables 3 and 4), indicating that PI 207262 gathers genes related to the production of pods and grains that are transmitted to the genotypes from these crosses.

From the values of GCA and SCA ( $\hat{S}_{ii}$  and  $\hat{S}_{ij}$ ) obtained, it was concluded that the parents PI207262 and BAC 6 have genes that favor the production of pods and grains, while the parents UENF 1487 and UENF 1486 expressed values favorable to the quality of pods. Therefore, strains derived from crosses between UENF 1487 and

UENF 1486 are recommended to be used with the common bean genotypes evaluated.

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