

## Genetic parameters of grain production and its components in common bean (*Phaseolus vulgaris* L.) under drought stress

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### Abstract

Appropriate methods in breeding programs can reduce time and costs. Additionally, selection strategies related to production traits are favourable due to their high detection efficiency and low cost. This research aimed to evaluate the genetic parameters of grain production and its primary components in F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations derived from crosses between the common bean cultivar IPR-Uirapuru, which is highly tolerant to drought stress, and the line LP 97-28, which has a low tolerance to drought stress, under conditions of water deficit during the year 2011. The plants were subjected to water stress during three different developmental stages: vegetative growth (V<sub>3</sub> stage), flowering (R<sub>6</sub> stage) and pod-filling (R<sub>8</sub> stage). The drought intervals lasted four days, and the plants were subsequently irrigated for 20 days. At physiological maturity (R<sub>9</sub>), the plants were harvested individually, and the following characteristics were evaluated: grain production (GP), the average weight of 100 seeds (W100s), the number of pods per plant (NPP) and the number of seeds per pod (NSP). From the phenotypic data, genetic analyses were performed to estimate the means and variances for each of the generations. Estimates of genetic variance components enabled the calculation of heritability estimates in a broad and narrow sense. The results show that additive genetic effects were involved in the majority of the total genetic variances, indicating a significant contribution for all traits evaluated. The values for heritability in a broad ( $H^2$ ) and narrow ( $h^2$ ) sense were high, indicating reliability in the transmission of traits to offspring. Thus, the additive effects played a greater role in the total genetic variance in relation to the genetic control of drought tolerance, and satisfactory genetic gains were made with the selection of tolerant individuals in early generations. Selection contributed to gains of 2.93 for grain production, 3.29 for the average weight of 100 seeds, 2.37 for the number of pods per plant and 0.73 for the number of seeds per pod. After selection in the F<sub>2</sub> generation, the predicted genetic gains in these same traits for the F<sub>3</sub> population were 9.79, 24.58, 9.39 and 5.34, respectively.

**Keywords:** Backcross, drought tolerance, heritability, *Phaseolus vulgaris* L., variances.

**Abbreviations:** BC\_backcross, GP\_grain production, W100s\_average weight of 100 seeds, NPP\_number of pods per plant, NSP\_number of seeds per pod,  $\sigma^2$ \_phenotypic variance,  $\sigma_e^2$ \_environment variance,  $\sigma_g^2$ \_genotypic variance,  $\sigma_a^2$ \_additive variance,  $\sigma_d^2$ \_dominance variance,  $H^2$ \_%broad sense heritability,  $h^2$ \_%narrow sense heritability, *add*\_average degree of dominance, *mng*\_minimum number of genes, *DS*\_differential of selection, *GS*\_gain by selection, and *PGG*\_predicted gain genetic.

### Introduction

The common bean crop is an important economic option for producers with access to advanced technology in their area and for the model of family farming (Broughton et al., 2003) because it is a low-cost source of protein and carbohydrates (Abdellatif et al., 2012) and has high levels of minerals, mainly iron and zinc (Carvalho et al., 2012). Drought is common in many areas with agricultural potential, especially tropical regions, and causes an increase in temperature and a decrease in relative humidity (Muñoz-Perea et al., 2006). Drought stress in crops can be provoked by irregular rainfall (Asfaw et al., 2012a; Blair et al., 2012) and inadequate irrigation for crops such as the common bean (Antonino et al., 2000; Fereres and Soriano, 2007). When exposed to drought stress during the reproductive stage, *Phaseolus vulgaris* experiences significant losses in grain production (Ramirez-Vallejo and Kelly, 1998) because fewer pods are produced (Muñoz-Perea et al., 2007) as a result of water deficiency and the ensuing abortion of reproductive organs

(Lizana et al., 2006). Cultivation of the common bean requires basic and applied research on the impacts caused by water deficit due to the frequency and severity of production losses linked to this abiotic stress (Beebe et al., 2013) and the high economic and nutritional importance for producers and consumers of the grain in countries such as Brazil (Londero et al., 2008). Appropriate methods in selective breeding programs can reduce time and costs by determining plants that can be discarded (Clarke et al., 1992). Therefore, selection strategies related to production traits such as grain production, the average weight of 100 seeds, the number of pods per plant and the number of seeds per pod is favourable due to their high detection efficiency and low cost (Subbarao et al., 1995). Therefore, this study aimed to estimate genetic parameters for grain production and its primary components in F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations derived from crosses of the common bean cultivar IPR-Uirapuru, which is highly

tolerant to drought, and the line LP 97-28, which has a low tolerance to drought, under water deficit conditions.

## Results

### Production components

The grain production (GP) results reveal that the evaluated plants had values between 0.01 and 9.78 g. The low and high means for all populations were 2.30 and 6.86 g, respectively (Table 1). The  $F_2$  generation showed the best performance. The low and high values for variance were obtained in the parental  $P_1$  (1.51) and  $F_2$  (8.88) generations, respectively. In relation to the average weight of 100 seeds (W100s), the values ranged between 12.56 and 29.64 g. In addition, the low and high means were 18.49 and 21.83 g, with the greatest means observed in the  $F_1$  and  $P_2$  populations (Table 1). The greatest variance of 11.12 was obtained in the  $F_2$  generation. For the number of pods per plant (NPP), the plants studied had values between 1 and 19, and the lowest and highest means were 2.70 and 7.02, respectively (Table 1). The best result was found in the  $F_2$  generation, while the lowest value was observed in the  $BC_1$  generation. The highest variance of 8.08 was observed in the  $F_2$  generation (Table 1). For the number of seeds per pod (NSP), the plants collected in this study had values between 1.0 and 6.8. The low and high means were 4.17 and 4.64 in populations  $P_1$  and  $BC_2$ , respectively (Table 1). Additionally, the best result was found in generation  $BC_2$ . The low and high variances were 0.38 and 1.54 (Table 1) and were obtained in the  $P_2$  and  $F_2$  generations, respectively.

### Genetic control

The values of the phenotypic ( $\sigma_p^2$ ), environmental ( $\sigma_e^2$ ), genotypic ( $\sigma_g^2$ ), additive ( $\sigma_a^2$ ) and dominance variances ( $\sigma_d^2$ ) for grain production were 8.88, 2.97, 5.91, 5.75 and 0.16, respectively (Table 2). The genotypic variance corresponded to 66.6% of the phenotypic variance (total), and the additive variance accounted for 97.3% of the genetic variance.

The phenotypic, environmental, genotypic, additive and dominance variances for the W100s were 11.12, 2.55, 8.57, 7.66 and 0.91, respectively (Table 2). For this characteristic, the genotypic variance accounted for 77.1% of the total variance, while the additive variance corresponded to 89.4% of the existing genetic variance. The phenotypic, environmental, genotypic, additive and dominance variances for the NPP were 8.08, 2.33, 5.75, 4.73 and 1.02, respectively (Table 2). The phenotypic variance accounted for 71.2% of the genetic variance. Additionally, the additive variance corresponded to 82.3% of the genotypic variance. For the NSP, the phenotypic, environmental, genotypic, additive and dominance variances were 1.54, 0.56, 0.98, 0.76 and 0.22, respectively (Table 2). The genotypic variance represented 63.7% of the phenotypic variance in this characteristic. The additive and dominance variances contributed to 77.6 and 22.4% of the genotypic variance, respectively. The estimates of broad sense heritability ( $H^2$  %) ranged between 63.6 and 77.0% (Table 2), and the high and low values were found in the W100s and NSP characteristics, respectively. The estimates of narrow sense heritability ( $h^2$  %) oscillated between 49.2 and 68.9% (Table 2), and the high and low values also corresponded to the W100s and NSP characteristics. The average degree of dominance ( $add$ ) values were 0.22, 0.48, 0.65 and 0.76 for the GP, W100s, NPP and NSP characteristics, respectively (Table 2). The

minimum number of genes ( $mng$ ) that controlled the GP, W100s, NPP and NSP characteristics were 4.7, 4.4, 8.6 and 5.5, respectively (Table 2).

### Differential of selection, gain by selection and predicted genetic gain

The characteristics of grain production, average weight of 100 seeds, number of pods per plant and number of seeds per pod had differential of selection (DS) values ranging from 1.49 to 4.85 (Table 3). The high and low values were obtained for the W100s and the NSP, respectively. In relation to gain by selection (GS), the GP, W100s, NPP and NSP characteristics had values of 2.93, 3.29, 2.37 and 0.73, respectively (Table 3). When expressed as a percentage (% GS), the grain production trait had the highest value for gain by selection at 42.7%. The lowest value was found for the average weight of 100 seeds. The predicted genetic gain (PGG) values were 9.79, 24.58, 9.39 and 5.34 for the GP, W100s, NPP and NSP characteristics, respectively (Table 3).

### Correlations between characteristics

Correlation coefficients indicated that all characteristics were directly proportional (Table 4), except between the NSP and NPP, which were inversely proportional. Additionally, the results show a high correlation (0.96) between the NPP and GP. Moderate associations were found between the GP and W100s and the W100s and NSP within six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) derived from crosses between LP 97-28 and IPR-Uirapuru.

## Discussion

The estimated means of the segregating generations and the genetic variance ( $\sigma^2$ ) composed of high additive genetic variance indicated the presence of transgressive individuals. These findings enabled the selection of promising genotypes for drought tolerances higher than those of IPR-Uirapuru and LP 97-28, the parent lines in this study. In terms of the estimated variances in the study populations, the best performances were observed for the segregating generations ( $F_2$ ,  $BC_1$  and  $BC_2$ ), which demonstrated higher values for all traits compared to the parent ( $P_1$  and  $P_2$ ) and  $F_1$  generations (Table 1). These results can be attributed to the large segregation of genes and, consequently, the higher amplitude in the distribution of the drought stress tolerance values, indicating genetic variation for the evaluated traits (Gravina et al., 2004). Similar results to those found in this study in terms of the GP of the  $F_2$  generation were reported by Szilagy (2003) for experiments with the common bean grown under adequate conditions (irrigation) and drought stress. This author studied production components in six populations derived from crosses between F332 and Ardeleana. Genotypes that are tolerant to drought stress often do not exhibit high levels of production because productive cultivars have no tolerance genes and are thus sensitive to drought. This characteristic works as a limiting factor during the selection of cultivars for use in production systems (Santos and Carlesso, 1998). The results of present study corroborate this information; the grain production obtained in line LP 97-28 was higher than that observed in cultivar IPR-Uirapuru, which has a tolerance to water deficits. For W100s, the genotypic variance observed in the  $F_2$  population was high, suggesting a high rate of transmission of this characteristic to generations from crosses between LP 97-28

**Table 1.** Number of evaluated plants (n), means (m) and variances ( $\sigma^2$ ) from grain production (GP), average weight of 100 seeds (W100s), number of pod per plant (NPP) and number of seeds per plant (NSP) obtained in six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>), derived of cross between LP 97-28 × IPR-Uirapuru, Maringá-PR, Brazil, 2011.

LP 97-28 × IPR-Uirapuru	GP (g)			W100s (g)		NPP		NSP	
	n	m	$\sigma^2$	m	$\sigma^2$	m	$\sigma^2$	m	$\sigma^2$
LP 97-28 (P <sub>1</sub> )	16	4.60	1.51	18.49	1.19	5.69	1.29	4.17	0.68
IPR-Uirapuru (P <sub>2</sub> )	18	4.48	1.89	21.83	1.37	4.39	2.13	4.60	0.38
F <sub>1</sub>	7	4.19	4.25	21.83	3.81	4.43	2.95	4.29	0.59
F <sub>2</sub>	166	6.86	8.88	21.29	11.12	7.02	8.08	4.61	1.54
BC <sub>1</sub>	10	2.30	4.92	19.29	6.44	2.70	5.34	4.54	1.43
BC <sub>2</sub>	39	3.31	7.07	20.52	8.13	3.44	6.09	4.64	0.88

**Table 2.** Estimates of phenotypic variance ( $\sigma_p^2$ ), environmental variance ( $\sigma_e^2$ ), genotypic variance ( $\sigma_g^2$ ), additive variance ( $\sigma_a^2$ ), dominance variance ( $\sigma_d^2$ ), broad sense heritability ( $H^2_{\%}$ ), narrow sense heritability ( $h^2_{\%}$ ), average degree of dominance (*add*) and minimum number of genes (*mng*) related to grain production (GP), average weight of 100 seeds (W100s), number of pod per plant (NPP) and number of seeds per plant (NSP) obtained in six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>), derived of cross between LP 97-28 × IPR-Uirapuru, Maringá-PR, Brazil, 2011.

LP 97-28 × IPR-Uirapuru	GP	W100s	NPP	NSP
Phenotypic variance ( $\sigma_p^2$ )	8.88	11.12	8.08	1.54
Environmental variance ( $\sigma_e^2$ )	2.97	2.55	2.33	0.56
Genotypic variance ( $\sigma_g^2$ )	5.91	8.57	5.75	0.98
Additive variance ( $\sigma_a^2$ )	5.75	7.66	4.73	0.76
Dominance variance ( $\sigma_d^2$ )	0.16	0.91	1.02	0.22
Broad sense heritability ( $H^2_{\%}$ )	66.4	77.0	71.1	63.6
Narrow sense heritability ( $h^2_{\%}$ )	64.7	68.9	58.5	49.2
Average degree of dominance ( <i>add</i> )	0.22	0.48	0.65	0.76
Minimum number of genes ( <i>mng</i> )	4.7	4.4	8.6	5.5

and IPR-Uirapuru (Table 1). A study conducted with Preto Carioca and Jalo, which are Brazilian cultivars of *P. vulgaris*, demonstrated high variability in terms of size and grain weight (Ribeiro et al., 2000). Additionally, Lima et al. (2005) reported that larger seeds positively influenced growth and production as well as the total dry matter and average weight of 100 seeds in common bean plants. In relation to the NPP, the highest value was found in the F<sub>2</sub> population (Table 1), revealing the presence of a transgressive segregant because the F<sub>2</sub> value was greater than those observed in LP-97-28 and IPR-Uirapuru, the parental lines. A reduction in the number of pods per plant is a common response in plants exposed to drought stress (Leport et al., 1999) due to the accumulation of organic solutes such as amino acids in the leaves. In the common bean, this effect is caused by the plant's attempt to adjust the osmotic pressure (Sassi et al., 2010) and results in reduced flowering and pod formation. Similar behaviour related to a decrease in the number of pods per plant was observed by Leport et al. (1998) in experiments with six legume species under the influence of drought. Rezene et al. (2013) tested 49 common bean genotypes under water deficit and field conditions and produced higher results than those observed in the present study. The average values of the NSP in the study populations showed low variations (4.17 and 4.64) and smaller variances (Table 1) compared to the values of the other characteristics. Similar NSP results were reported by Guimarães et al. (2011) in experiments with 49 common bean genotypes under drought stress conditions, which were simulated by applying half of the recommended water depth to the crop. Higher variances for GP, W100s, NPP and NSP were observed in the F<sub>2</sub> generation, revealing greater plant heterogeneity and suggesting great variability within this population. Genetic variability is extensively explored in breeding programs; it serves as the basis for selection and provides opportunities to establish a desired characteristic (Franco et al., 2001). Smaller variances were obtained in the parents, confirming homozygosity in these populations due to the line and cultivar. The GP, W100s, NPP and NSP results indicate that through selection, the F<sub>2</sub> generation contained plants that were tolerant to drought stress and had high grain production. This generation performed better than crosses between LP 97-28 and IPR-Uirapuru. The environmental variances for GP, W100s, NPP and NSP contributed from 22.9 to 36.6% of the total variances (phenotypic). These values were relatively low given that the study evaluated production characteristics and incorporated significant environmental influences. The smaller influence of the environment demonstrates the adequate execution of this experiment because this study was conducted in a greenhouse environment with uniform edaphoclimatic and drought stress conditions. Melo et al. (2006) evaluated the GP of 36 populations of common bean and found similar results for the contribution of environmental variance. Asfaw et al. (2012a) analysed quantitative trait loci (QTL) in common bean plants exposed to drought under field conditions and found a higher contribution of environmental variance (59%) to GP compared to the variance obtained in this research. The results indicate high contributions of additive variances in relation to genotypic variance and intense additive allelic interactions on all the evaluated traits. The existence of high additive variance suggests the identification of superior genotypes (Cruz et al., 2012). Typically, breeding methods that take advantage of high additive variance to obtain genetic gains are more important for the improvement of autogamous species, such as *Phaseolus vulgaris* (Gravina et al., 2004). Roberts et al. (1998) observed a high contribution

of additive variance for the NPP and NSP in crosses of *P. vulgaris*. According to this research, the use of additive variance is recommended as an indicator when studying GP, W100s, NPP and NSP in the cross (LP 97-28 × IPR-Uirapuru) because it accounts for a significant portion of genotypic variance. The results related to broad and narrow sense heritabilities described in this study are high because studies involving populations are normally conducted under field conditions and high levels of environmental interference reduce genetic variances and produce lower heritabilities. The broad sense heritability is responsible for providing the proportion of genetic variance present in the phenotypic or total variance. Consequently, higher heritability coefficients may be caused by greater additive genetic variance, lower environmental variance or minor interactions between genotype and environment (Acquaah, 2007). Additionally, similar results for broad and narrow sense heritabilities indicate that the dominance effect is null. However, if the broad sense heritability is higher than the narrow sense heritability, the dominance effect is present (Abney et al., 2001). Nunes et al. (1999), working with common bean genotypes, reported lower broad sense heritability for the GP characteristic (35%) compared to the present study (Table 2). In relation to broad sense heritability, Coelho et al. (2002) reported lower values (0-34%) for the GPROD, W100s, NPP and NSP characteristics in experiments on the production and primary components in *P. vulgaris*. Zacharisen et al. (1999) studied yield components in common bean plants and reported higher values of narrow sense heritability for GP, W100s and NSP and lower values for NPP compared to the values found in the present study (Table 2). Szilagy (2003) evaluated the influence of drought under field conditions in populations of *P. vulgaris* and obtained lower results for GP, W100s, NPP and NSP. The average degree of dominance values varied from 0.22 to 0.76 (Table 2), revealing that the intra-allelic interactions were of partial dominance. The average degree of dominance expresses the relationship between the genotypic value of the heterozygote and the homozygote, with possible interactions characterised by absence of dominance, partial dominance, complete dominance and overdominance (Cross et al., 2012). The results for the minimum number of genes indicate that at least five genes control the GP and W100s characteristics and six and nine genes control the NSP and NPP, respectively. This estimate is useful for revealing the nature of polygenic traits (Rocha et al., 2009). However, the small numbers of genes found in the characteristics were associated with the interference of the statistical model, disproving any possible link between the loci. Lopes et al. (2003) found five genes that determined seed size. Blair et al. (2012) used molecular techniques to detect quantitative trait loci (QTL) linked to water deficit tolerance in the common bean and described 49 loci, 27 which were related to the W100s and 10 of which were related to GP. The gain by selection and predicted genetic gain were high in the F<sub>2</sub> generation, indicating that the choice of parents LP 97-28 (low tolerance) and IPR-Uirapuru (high tolerant) was adequate. Vale et al. (2012) demonstrated that the cultivar IPR-Uirapuru behaved satisfactorily when subjected to stress drought and was considered similar to cultivar Pérola because it showed the best performance for drought tolerance. Knowledge of the gain by selection and the consequent predicted genetic gain is essential to determine appropriate selection criteria, including those related to grain production components in the common bean plant (Acquaah, 2007).

**Table 3.** Mean initial in F<sub>2</sub> generation (Mi), mean of selected plants in F<sub>2</sub> generation (Ms), differential of selection (DS), gain by selection (GS), gain by selection expressed in percentage [(GS (%))], and predicted gain genetic (PGG) related to grain production (GP), average weight of 100 seeds (W100s), number of pod per plant (NPP) and number of seeds per plant (NSP) obtained in six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>), derived of cross between LP 97-28 × IPR-Uirapuru, Maringá-PR, Brazil, 2011.

Characteristic	Genetic component					
	Mi	Ms	DS	GS	GS (%)	PGG
GP	6.86	11.45	4.59	2.93	42.7	9.79
W100s	21.29	26.14	4.85	3.29	15.5	24.58
NPP	7.02	11.12	4.10	2.37	33.8	9.39
NSP	4.61	6.10	1.49	0.73	15.9	5.34

**Table 4.** Coefficients of phenotypic correlation between grain production (GP), average weight of 100 seeds (W100s), number of pod per plant (NPP) and number of seeds per plant (NSP) obtained in six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>), derived of cross between LP 97-28 × IPR-Uirapuru, Maringá-PR, Brazil, 2011.

Characteristic	GP	W100s	NPP	NSP
GP	-	0.36	0.96**	0.01
W100s		-	0.13	0.41
NPP			-	-0.20
NSP				-

Asterisks (\*\*) indicate significance to 0.01 of probability by the t test.

The differential of selection connected to GP described in this research (Table 3) was higher than that described by Londero et al. (2006). Gonçalves-Vidigal et al. (2008), working with *P. vulgaris*, found lower results for the differential of selection related to the W100s. Takeda et al. (1991) showed a lower gain by selection (5.6%) for GP compared to the results in Table 3. Ramirez-Vallejo and Kelly (1998) reported that gain by selection caused changes in GP, NPP and NSP of 17, 7 and 11.0%, respectively, which were lower than the values observed in the present study (Table 3). For the gain by selection of the W100s, NPP and NSP characteristics, the results in the present study are higher (Table 3) than those reported by Gonçalves-Vidigal et al. (2008), who described changes of 5.7, 10.9 and 4.7% in the W100s, NSP and NPP, respectively. In relation to the predicted genetic gain (Table 3), the results in this study are lower compared to those of Abreu et al. (2002), who estimated the GP in common bean crosses. The predicted genetic gain values reported by Londero et al. (2006) were similar to the values found in this study. Molina et al. (2001) studied lines and cultivars of *P. vulgaris* under drought stress and found positive correlations between GP and NPP, GP and W100s and W100s and NPP, with coefficients of 0.64, 0.83 and 0.38, respectively. These authors also reported a negative correlation between NPP and NSP. Guimarães et al. (2011) evaluated drought tolerance in common bean genotypes and describe a positive correlation between NPP and GP, as reported in the present study (Table 4). In another study with the common bean, Gonçalves-Vidigal et al. (2008) reported positive correlations between NSP and W100s. Balcha (2010) also found an inverse association between NSP and NPP in experiments on the genetic variation of 26 genotypes of the common bean.

## Materials and methods

### Experiment localization and climatic conditions

The experiment was implemented and executed during the year 2011 in a greenhouse of the Núcleo de Pesquisa Aplicada a Agricultura (Nupagri), of the Universidade Estadual de Maringá (UEM), Maringá, Paraná, Brazil (23°26'S and 51°53'W). During the experimental period, the minimum, mean and maximum temperatures were 17, 22 and 29, respectively, while the average value to air relative humidity was 63%, with temperature and air relative

humidity measured air with thermohygrometer installed into greenhouse (Minipa, model 241).

### Obtaining of segregation populations

The seeds from cultivar IPR-Uirapuru and line LP 97-28 were obtained in Instituto Agronômico do Paraná (Iapar). The segregating generations F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> derived from artificial crosses between IPR-Uirapuru and LP 97-28, in order to perform this research connected with genetic control aiming tolerance to water deficit and high production (Acquaah, 2007). The controlled hybridizations were carried out in a greenhouse located in Iapar, being used the technique of emasculation of flowers, and following the procedures described by Ramalho et al. (1993).

### Experimental design

The experiment was composed of six populations, with two parents P<sub>1</sub> and P<sub>2</sub>, and F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations derived from the cross between LP 97-28 (low tolerance to drought) × IPR-Uirapuru (high tolerant to drought). The experiment consisted of 16 plants for line LP 97-28, 18 plants for cultivar IPR-Uirapuru, and 7, 166, 10 and 39 plants in F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations, respectively. The plant numbers in each population are adequate to evaluate these crosses (Cruz et al., 2012). The experimental design was completely randomized. In this study, each plant within respective generation was considered as one repetition, and experimental unit was represented by one plant per pot.

### Experiment implementation, plant conduction and fertilization

After hybridizations, the hybrid seeds were multiplied to obtain the F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations. In each pot was placed only one seed. In this study were used containers with capacity of 3 L containing holes in bottom, aiming to drain excess water. The substrate was composed of a mixture of susbtrato Plantmax<sup>®</sup> and sand in the ratio 2:1 (v/v). Fertilization was performed according to exigencies of common bean crop and previous substrate analyze, with the fertilization applied at regular intervals of 15 days until the R<sub>8</sub> stage.

### **Irrigation and water deficit application**

All plants were irrigated time per day for 15 minutes at 11:00 and 15:00 h. The irrigation within the greenhouse was performed by a microsprinkler system, with a flow rate of 10 L h<sup>-1</sup>. The three cycles of moderate stress was induced by irrigation suspension for four days (Santos et al., 2009b) at 20, 40 and 60 days after seedling emergence, whose periods coincided with the phenological stages V<sub>3</sub>, R<sub>6</sub> and R<sub>8</sub>, respectively. In common bean crop these periods described are related to vegetative, flowering and pod filling, respectively (Fernández et al., 1985).

### **Evaluated characteristics**

The characteristics measured were grain production (GP), determined by the total weight of seeds in each generation and dividing by the number of plants to each generation, standardized to 13% of moisture, being expressed in grams.plant<sup>-1</sup>. The average weight of 100 seeds (W100s) was obtained by weighing of 100 seeds collected to random in each generation, which was expressed in grams. The number of pods per plant (NPP) was represented by the ratio between the total number of pods and the total number of plants in each generation, expressed in numbers, and the number of seeds per pod (NSP), described by the ratio between the total number of seeds and the total number of pods in each generation, expressed in numbers.

### **Components of the variances**

Estimates of phenotypic, genotypic, additive, dominance and environmental variances were obtained from data of P<sub>1</sub> and P<sub>2</sub> parents, as well as F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations, with the environmental variance being calculated in population with better performance, in agreement with formulas described by Cruz et al. (2012). The genetic-statistic analyzes were performed using software GENES (Cruz, 2006).

$$\begin{aligned}\sigma_p^2 &= \sigma^2_{(population\ in\ each\ population)} \\ \sigma_g^2 &= [\sigma_p^2(P_1) + 2\sigma_p^2(F_1) + \sigma_p^2(P_2)] / 4 \\ \sigma_g^2 &= \sigma_p^2 - \sigma_e^2 \\ \sigma_a^2 &= 2\sigma_p^2(F_2) - [\sigma_p^2(BC_1) + \sigma_p^2(BC_2)] \\ \sigma_d^2 &= \sigma_g^2 - \sigma_a^2\end{aligned}$$

Where,  $\sigma_p^2$  = phenotypic variance,  $\sigma_e^2$  = environmental variance,  $\sigma_p^2(P_1)$  = phenotypic variance in P<sub>1</sub>,  $\sigma_p^2(F_1)$  = phenotypic variance in F<sub>1</sub>,  $\sigma_p^2(P_2)$  = phenotypic variance in P<sub>2</sub>,  $\sigma_g^2$  = genotypic variance,  $\sigma_a^2$  = additive variance,  $\sigma_p^2(F_2)$  = phenotypic variance in F<sub>2</sub>,  $\sigma_p^2(BC_1)$  = phenotypic variance in BC<sub>1</sub>,  $\sigma_p^2(BC_2)$  = phenotypic variance in BC<sub>2</sub>, and  $\sigma_d^2$  = dominance variance.

### **Heritability and average degree of dominance**

The broad sense heritability, narrow sense heritability and average degree of dominance were calculated for the crossing between parents (LP 97-28 x IPR-Uirapuru). These estimates were based on variances obtained from the parents and investigated generations (Mather and Jinks, 1984), being performed with the software GENES (Cruz, 2006).

$$\begin{aligned}H^2\% &= (\sigma_g^2 / \sigma_p^2) \times 100 \\ h^2\% &= (\sigma_a^2 / \sigma_p^2) \times 100 \\ add &= \sqrt{(2\sigma_d^2 / \sigma_a^2)}\end{aligned}$$

Where,  $H^2\%$  = broad sense heritability,  $h^2\%$  = narrow sense heritability, *add* = average degree of dominance,  $\sigma_g^2\%$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance,  $\sigma_a^2$  = additive variance, and  $\sigma_d^2$  = dominance variance.

### **Minimum number of genes**

To estimate the minimum number of genes that control each characteristic was used the equation described by Burton (1951), in which it utilizes the amplitude between parents and genotypic variance. This model is indicated to evaluate these crosses (Cruz et al., 2012), but despises any possible connection between loci.

$$mng = [R^2 (1 + 0,5 add^2 / 2)] / 8\sigma_g^2$$

Where, *mng* = minimum number of genes, R = total amplitude in evaluated population, *add* = average degree of dominance, and  $\sigma_g^2$  = genotypic variance.

### **Differential of selection, gain by selection and predicted gain genetic**

The differential of selection is represented by the difference between the mean of plants selected under the selection intensity of 20% and population mean (Frey and Horner, 1955), being selected the plants within population with better performance. The gain by selection was calculated using the narrow sense heritability, being estimated according to the methodology described by St Martin and Futi (2000). For the predicted gain genetic was calculated by sum of the population mean and gain by selection, using the formula reported by Cruz et al. (2012).

$$\begin{aligned}DS &= Ms - Mi \\ GS &= DS \times h^2 \\ GS(\%) &= (GS / Mi) / 100 \\ PPG &= Mi + GS\end{aligned}$$

Where, DS = differential of selection, Ms = mean of selected plants within population, Mi = mean initial within population, GS = gain by selection,  $h^2$  = narrow sense heritability, GS (%) = gain by selection expressed in percentage and PPG = predicted gain genetic.

### **Relationship between characteristics**

The relationships were estimated using the Pearson correlation coefficients between traits, and it were calculated using the mean values of the parents and generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) derived from the cross LP 97-28 x IPR-Uirapuru, being determined to association between two characteristics.

### **Conclusion**

The genetic control of grain production aimed at increasing tolerance to water deficit was heavily influenced by additive effects in populations derived from crosses between line LP 97-28 and cultivar IPR-Uirapuru of the common bean plant. The heritability in a broad and narrow sense observed in this study can be considered high for all evaluated traits. Additionally, the gain by selection obtained for grain production was also high at 42.7%. This result demonstrates the potential of segregating individuals with superior characteristics for drought stress tolerance.

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