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Research Article Estimates of Genetic Parameters and Efficiency in Selection for Branching Capacity in Soybean Genotypes

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Abstract

In soybean breeding programs, research which seek to increase the efficiency of selection of soybean lines more productive have proved promising. The objective of this research was to estimate the efficiency of selection of genotypes with greater branching capacity and more productive, as well as to estimate genetic parameters for these traits. To estimate the expected gain from selection, 11 progenies in F3 generation were used, conducted in a randomized block design with six replications. The progenies had their gains estimates which were compared with the real gain obtained on F4 generation, which were conducted on experimental field in a randomized block design, with three replications. It was concluded that there are genetic variability for the productivity among evaluated progenies and also to issuing capability of lateral branches in soybean, however, the selection seeking to intensify or reduce this characteristic does not imply achievement of production gains.

Key words: Glycine max, breeding, lateral branches, phenotypic correlation, gain selection, variation index

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

The soybean (*Glycine max* (L.) Merrill) has been great importance in the economic and food sectors, especially in the leading countries in production and exports, as the United States, Brazil and Argentina (SEAB., 2014). Large portion of increased production and the competitiveness of Brazilian soybean are associated with accomplishment of scientific research in order to obtain cultivars with high productivity and wide adaptation (Costa *et al.*, 2004).

There are essentially two basic strategies for the development of new soybean; average of seed mass is responsible for significantly reducing in the number of seeds per pod and number of pods per plant, because the lower the number of pods per plant, the greater the availability of photoassimilates produced by plant for seed filling. Thus, the selection based upon these components may prejudice gains in productivity.

The second strategy for development of more productive plants looking improved total biomass production, as the vegetative part and reproductive without altering the association between them, consequently resulting in modification of plant architecture.

Whereas, the mathematical model that explains the grain production of soybean is given by:

$Y = NP \times NSP \times ASW$

where, Y is the seed yield per plant, NP is the number of pods per plant, NSP is the number of seeds per pod and ASW is the average seed weight, yield increases may be obtained with raise in the number of pods per plant and also in number of nodes. The increase of this last characteristic may be obtained by selecting plants with higher capacity of lateral branches emission. Thus, the search for genotypes with high capacity of branching can result in more productive varieties.

Vernetti (1983) reported that the genetic capacity of soybean production can be expressed by certain morphological traits of the plant, including the number of branches, number of pods per branch and number of seeds per branch.

Evidence of genetic variability in soybean capacity for branching was found in studies by Nelson (1996), Basavaraja (2002) and Bangar *et al.* (2003). Despite the explicit importance of the issue capacity of lateral branches in soybean, the works available on literature are scarce and inconsistent as the genetic parameters of the characteristic and how much their selection efficiency in seek for more productive genotypes. The estimation of genetic parameters such as heritability, correlation coefficients and genotypic, phenotypic and environmental variances, allows the breeder information about the nature of genes involved in the control of interest traits and defines the best strategy to be adopted in the improvement of a given population (Santos *et al.*, 1995).

Therefore, the objectives of this study were to estimate genetic parameters for the branch capacity in soybean and to estimate the efficiency of genotype selection with this characteristic, seeking for much more productive materials.

MATERIALS AND METHODS

The study was divided into two stages. At first, an experiment was conducted under greenhouse conditions at the Plant Science Department of the Federal University of Viçosa (UFV), Minas Gerais, Brazil. Eleven F3 progenies were used from the soybean breeding program of UFV.

The experimental design was a randomized block with six replications. Each experimental unit was consisted in a pot with two plants, evaluated individually.

Of this set, were selected 10 and 50% of genotypes with greater branching capacity and the same percentage of genotypes with lower capacity to emit lateral branches.

In the second stage, to estimate the selection efficiency of trait in study, all genotypes were advanced to F4 generation under field conditions. The experiment was conducted in the experimental field of Federal University of Viçosa. The experimental design was randomized block with three replications. Each experimental plot consisted of a line with 1.5 m long containing three plants spaced 0.50 m, adopting as useful part, the central plant. The lines were spaced 0.70 m in order to maximize the capacity of lateral branches emission by the plants. Previously the sowing, the seeds were treated with fungicide carbendazin at a rate of 60 mL 100 kg⁻¹ of seeds and then inoculated with *Bradyrhizobium japonicum*. The control of pests and diseases was conducted in accordance with the recommendations for soybean (Sediyama *et al.*, 2015).

Initially, it was preceded the analysis of variance of the first experiment, to identify the existence of genetic variability between progenies based on the following characters: Number of Branches (NB), productivity (PROD), Number of Pods per plant (NP), Number of Seeds per Pod (NSP), 100-Seed Weight (100 SW), Length of Branches (LB) and Number of Nodes of the Branches (NNB).

From the values of mean square obtained from the analysis of variance, were estimated to genotypic variance average $(\hat{\sigma}_g^2)$, environmental variance average $(\hat{\sigma}_e^2)$, phenotypic variance average $(\hat{\sigma}_f^2)$, genetic variation

coefficient (CV_g (%)), variation index (I_v) and average heritability (h^2) by the following equations:

Genotypic variance average:

$$\hat{\sigma}_g^2{=}\frac{MSG{\text -}MSR}{r}$$

Where:

MSG = Mean square of the genotype MSR = Mean square of residue r = Number of repetitions

Environmental variance average:

$$\hat{\sigma}_e^2 = \frac{MSE}{r}$$

Average phenotypic variance:

$$\hat{\sigma}_{f}^{2} = \frac{MSG}{r}$$

Genetic coefficient of variation:

$$CV_{g}(\%) = \frac{(100 \times \sqrt{\hat{\sigma}_{g}^{2}})}{m}$$

Where:

m = Medium

Index of variation:

$$I_V \!=\! \sqrt{\frac{\hat{\sigma}_g^2}{\hat{\sigma}_e^2}}$$

Average heritability:

$$h^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_f^2}$$

On F3 generation were estimated the phenotypic correlations between the basic yield components: (number of pods per plant (NP), Number of Seeds per pod (NSP) and 100-Seed Weight (100 SW)) and characteristics related to

branching capacity of soybean plant (Number of Branches (NB), Number of Nodes of Branches (NNB) and Length of Branches (LB)).

In the selection of the best genotypes and estimates of genetic progress, it was used as a criterion for selection, the indirect selection. In this case, the gain estimated by indirect selection of the j character, by selecting in the character i is given by:

$$GS_{j(i)} = DS_{j(i)}h_j^2$$

where, $DS_{j(i)}$ is the indirect selection differential obtained depending on the average of the character those individuals whose superiority was evidenced in another character on the which is practiced direct selection.

The estimate of the gain realized on the j character, by selecting in the character i is obtained by:

$$GSr_{j(i)} = (XS_{j(i)F4} - XO_{jF3})$$

where, $XS_{j(i)F4}$ is the average of F4 progenies selected on F3 for the character j, with selection in i and XO_{jF3} is the original average for the j character on generation F3.

Gain prediction efficiency was checked by their agreement in magnitude and direction with the gain realized.

In addition of the estimates of genotypic, phenotypic and environmental variance was also estimated the genetic variation coefficient, variation index and the heritability in the broad sense.

Statistical analyzes were performed using the Genes Program: Computer Application in genetics and statistics (Cruz, 2013).

RESULTS AND DISCUSSION

The results of the variance analysis presented in Table 1 showed a significant difference (p<0.01) for all characteristics studied. These results represents that there are variability among the evaluated progenies and as well the possibility of using these in obtaining superior genotypes for the traits studied.

The coefficient of variation values found for the number of branches, number of nodes per branch, number of pods, number of seeds per pod and productivity (Table 1) were apparently high. However, were acceptable values as they are less than found by Okonkwo and Idahosa (2013). Thus, the experimental accuracy can be considered high. Estimates of genetic parameters obtained are given in the Table 2. The greatest genetic variation were observed for number of pods, weight of hundred seeds, productivity and number of branches, indicating that this population there are favorable conditions for selection and breeding of these characters. The greater the genetic variation, the greater the possibilities of genetic gains with the selection. This fact also shows the existence of genetic variability for issuing capacity of lateral branches in soybean, legitimizing the work of Nelson (1996), Basavaraja (2002), Bangar *et al.* (2003) and Sirohi *et al.* (2007).

The coefficient of genetic variation, besides allowing inferences about the genetic variability presents in different genotypes, environments and characters also helps in the selection of superior genotypes. In this study, these values ranged from 9.69% (NSP) to 34.41% (NB and LB) showed in Table 2 in agreement with related by Agrawal *et al.* (2000), Malik *et al.* (2011) and Chandel *et al.* (2013).

The estimates values for the heritability of all characters were considered high. High heritability had been previously reported for these traits (Aditya *et al.*, 2011; Chandel *et al.*, 2013; Okonkwo and Idahosa, 2013). According to Oliveira *et al.* (2015), high heritability estimates suggest the possibility of selecting superior genotypes safely. Therefore, it

Table 1: Summary of the variance analysis of the characters

Variables	Sources of variation					
	Genotypes	Residues	Mean	CV (%)		
NB	13.11**	1.57	4.03	31.08		
PROD	42.73**	6.25	17.92	13.96		
NP	753.84**	35.79	43.40	13.79		
NSP	0.28**	0.02	2.16	5.98		
100 SW	101.20**	4.57	20.19	10.60		
LB	603.72**	52.36	24.25	29.84		
NNB	4.52**	0.60	4.04	19.26		

**Significant at 1% probability by F test, NB: Number of branches per plant, PROD: Productivity, NP: Number of pods, NSP: Number of seeds per pod, 100 SW: 100-seed weight, LB: Length of branches, NNB: Number of nodes of the branches, on 11 progenies of soybean in generation F3 (Crop season, 2013/14), CV: Coefficient of variation can be expected gains from the selection of more branched and productive genotypes. The variation index (I_v) proposed by Vencovsky (1987) gives the proportion of genetic variance in relation to the residual error and there is not, therefore, influence the population average. The variation index were higher than a unit for NB, NP, NSP, 100 SW, LR and NNB, which according to Silva *et al.* (2009), confer the possibility of successfully selecting for the traits under study.

Faced with the possibility of success in the selection of genotypes with greater number of branches, it has been estimated the influence of that selection in the main soybean yield components in two instances with different selection intensities.

It is important to note that all estimates of selection are overrated, as were calculated considering the heritability in the broad sense. As a result they were segregating genotypes in generation F3, it was not possible to estimate separately the genotypic variance additive component. However, this fact was not interfering on the results, since all methods used are subject to this same problem. Similar fact described by Costa *et al.* (2004), in his study comparing different selection criteria in segregating populations.

As shown in the Table 3, the selection of plants with greater ability to branch results in loss of less than 1% in productivity of grain in the two situations of selection pressure. From the selection of plants more branched, noted increase in the number of pods, however, there was reduction in the number of seeds per pod and 100-seed weight (Table 3). This balance in the modification of yield components gains explains the absence of influence of the selection of soybean plants more branched in the increments in weight of the seeds.

With 10% of selection pressure, screening plants less branched promoted almost 17% reduction in grain production. This reduction was attributed to the reduction in the average number pods per plant, which, according to

Table 2: Estimation of variance components and genetic parameters of the character

Genetic parameters	NB	PROD	NP	NSP	100 SW	LB	NNB
$(\hat{\sigma}_g^2)$	1.9236	6.0793	119.6757	0.0436	16.1035	1.9236	0.6528
$(\hat{\sigma}_e^2)$	1.5688	6.2545	35.7904	0.0166	4.5746	1.5688	0.6039
$(\hat{\sigma}_{f}^{2})$	0.5465	5.4772	22.8636	0.0013	2.8325	5.7067	0.2973
Cvg (%)	34.4100	13.7600	25.2100	9.6900	19.8800	34.4100	20.0200
l _v	1.1100	0.9900	1.8300	1.6200	1.8800	1.1100	1.0400
h² (%)	88.0300	85.3600	95.2500	94.0400	95.4800	88.0300	86.6400

 $\hat{\sigma}_{g}^{2}$: Genotypic variance average, $\hat{\sigma}_{e}^{2}$: Environmental variance average, $\hat{\sigma}_{f}^{2}$: Phenotypic variance average, CVg: Genetic variation coefficient, I,: Index of variation, h²: Average heritability, NB: Number of branches per plant, PROD: Productivity, NP: Number of pods per plant, NSP: Number of seeds per pod, 100 SW: 100-seed weight, LB: Length of branches, NNB: Number of nodes of the branches, of 11 progenies of soybean on generation F3 (Crop season, 2013/14)

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Parameters	PROD	NP	NSP	100 SW
X _o	17.92	43.40	2.16	20.19
h²	0.85	0.95	0.94	0.67
Selection pressure 10%				
Xs [_]	14.39	24.57	2.29	21.30
Xs ⁺	17.79	55.86	1.95	16.36
Gse ⁻ (%)	-16.80	-41.34	5.56	3.67
Gse+ (%)	-0.61	27.35	-9.26	-12.63
Selection pressure 50%				
Xs [_]	17.97	36.41	2.25	23.08
Xs ⁺	17.86	50.37	2.05	17.29
GSe ⁻ (%)	0.22	-15.37	3.70	9.56
Gse+ (%)	-0.28	15.30	-4.63	-9.56

X_o: Original population average, Xs: Population average with less ability of branching, Xs⁺: Population average with greater ability of branching, h²: Heritability of character, GSe⁻:Gain selection expected for populations with less ability of branching, GSe⁺: Gain selection expected for populations with greater ability of branching, PROD: Productivity, NP: Number of pods per plant, NSP: Number of seeds per pod, 100 SW: 100-seed weight evaluated in 11 progenies of soybean in F3 generation, in experiment on greenhouse, with selection pressure of 10 and 50% (Crop season, 2013/14)

Table 4: Phenotypic correlation coefficients between the characters

Parameters	PROD	NB	NSP	100 SW
NB	0.0272	0.8757**	-0.6197*	-0.9267**
LB	0.1362	0.9038**	-0.6003*	-0.8975**
NNB	0.3736	0.9208**	-0.3851	-0.9095**

****Significant at 5 and 1% levels, respectively, NB: Number of branches, LB: Length of branches, NNB: Number of nodes of the branches, PROD: Productivity, NP: Number of pods per plant, NSP: Number of seeds per pod, 100 SW: 100-seed weight

Table 5: Real gain for characters

Parameters	PROD	NP	NSP	100 SW
X _o	17.92	43.40	2.16	20.19
Selection pressure 10%				
Xs ⁻	14.86	49.76	2.15	21.43
Хs ⁺	17.94	89.15	1.94	9.36
GSr [_]	-17.08	14.65	-0.46	6.14
GSr ⁺	0.11	105.41	-10.19	-53.64
Selection pressure 50%				
Xs [_]	16.17	57.38	2.11	14.92
Xs ⁺	17.24	77.47	2.01	12.95
GSr [_] (%)	-9.77	32.21	-2.31	-26.10
Gsr+ (%)	-3.79	78.50	-6.94	-35.86

X_o: Original population average, Xs⁻: Population average with less ability of branching, Xs⁺: Population average with greater ability of branching, Gse⁻: Gain selection realized for populations with greater ability of branching, PROD: Productivity, NP: Number of pods, NSP: Number of seeds per pod, 100 SW: 100-seed weight in experiment conducted on field evaluated in F4 generation of soybean genotypes, with selection pressure of 10 and 50%. (Crop season, 2014/15)

Nogueira *et al.* (2012), this is the component of greatest weight in the composition of soybean productivity. The reduction in the number of pods in turn, may be as a result of the reduction in the number of total nodes of the plant due to the reduction in the number of branches. Still under 10% pressure in selection, also occurred an increment in the number of seeds per pod and mass of seeds, however, insufficient to compensate for the magnitude of the loss in number of pods and provide gains in production (Table 3).

By correlation analysis (Table 4), it is observed that in addition to the number of branches, the selection based on the length of the branches and on the number of nodes of the branches would imply no gains in grain production. Interrelationships presented in the Table 4 corroborate with the real gain obtained in the second experiment (Table 5). This phenomenon occurs due to the additional demand of photo assimilates diverted to the issuance and growth of these vegetative parts, that otherwise could be used in the production and development of reproductive structures.

In possession of predicted values (Table 3) and obtained experimentally (Table 5), it is possible to verify that there was agreement between the expected and the obtained experimentally by selecting soybean plants more branched, both with selection pressure of 10 or 50%. However, the same was not observed when selected plants less branched, demonstrating that the efficiency gains through prediction of indirect selection is variable depending on the characteristic used in the selection, the trait that is sought gains and selection pressure.

This fact occurs due to the environmental conditions of the crop season of prediction, which does not always coincide with those of the crop season, which the selected material was conducted in the field.

CONCLUSION

There is genetic variability for productivity between progenies evaluated. There is genetic variability for issuance of lateral branches in soybean plants. The selection seeking to intensify or reduce the ability of issuing side branches, from generation F3-F4, does not imply achievement of production gains.

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