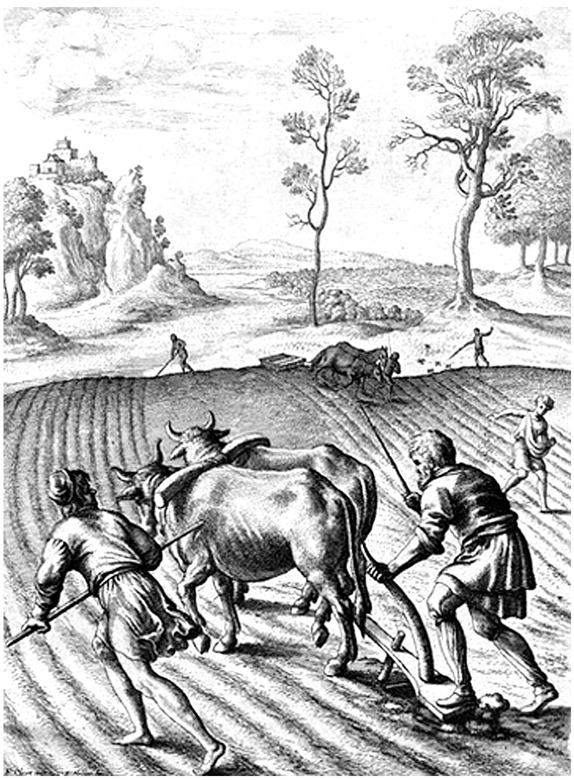
ISSN : 1812-5379 (Print)
ISSN : 1812-5417 (Online)
http://ansijournals.com/ja

JOURNAL OF AGRONOMY



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Journal of Agronomy 13 (3): 117-121, 2014
ISSN 1812-5379 / DOI: 10.3923/ja.2014.117.121

Correlations and Genetic Parameters Between Morphological Descriptors in Soybean

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Abstract: Determining the genetic variability and correlations between traits of interest for selection in a population is one of the stages in a breeding program. The objectives of this study was to evaluate the potential for genetic improvement of a population composed of twelve commercial soybean genotypes, were estimated genetic and phenotypic descriptors and correlations between morphological traits of the population. The experimental design was used in randomized block design with four replications. The descriptors measured were plant height and first pod insertion, number of pods and ramifications, mass of hundred grains and yield grains. The yield grains presented more genotypic coefficient of variation, ratio b and herdability. This descriptor obtained phenotypic correlations significant positive ($p<0.01$), with number of pods, ramifications and mass hundred grains, indicating that the selection of plants with larger number of ramifications entailed, therefore, more productive genotypes. The genotype correlations had the same sign and in most cases superior to their corresponding phenotypic correlations values, indicating that the phenotypic expression is decreased compared to environmental influences. Environmental correlations between descriptors with differences in magnitude and sign, in relation to the respective genotype correlations, revealed that the environment favored one character over another and that the genetic and environmental causes of variation have different physiological mechanisms, defaulting the indirect selection.

Key words: Cultivars, *Glycine max* L., plant

INTRODUCTION

The soybean (*Glycine max* (L.) Merrill) is currently subject of intense research activity directed to getting information that enables productivity increases, since this culture assumes great socioeconomic value by the importance of their products, especially bran, vegetable oil and its derivatives (Motta *et al*., 2000).

Brazil is the second largest world soybean producer reaching in the 2012/2013 crop a production of 81 million tons of grain. The expansion of cultivated area and the genetic breeding are among the major factors that have provided an increase in productivity of soybean, which in the current crop has obtained an average yield of 2,933.0 kg ha^{-1} (Conab, 2013).

Almeida *et al.* (2010) argue that knowledge of the association between characters is of great importance in the genetic breeding of any kind, particularly when the low heritability or measurement problems cause difficulties in selecting. In these cases, the indirect selection can be recommended using another character that has high heritability and easy evaluation, long as it is highly correlated with that one character difficult to direct selection.

According to Correa *et al.* (2003) the best selection strategies for obtaining superior genotypes are defined by estimates of genetic parameters such as variances, heritability, genotypic coefficient of determination, coefficient of genetic variation and coefficient b (CVg/CVe) of a population that it is intended explore for genetic improvement.

When the variability is explored through the selection of certain character, simultaneously other characters may be changed due to genetic correlation between characters (Santos and Vencovsky, 1986). Falconer (1987), distinguishes two causes of correlation between two variables: The genetic, resulting from genetic linkage (temporary cause) or pleiotropism (main cause)

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and environmental causes. This latter becomes cause correlation when two characters are influenced by the same differences in environmental conditions. The association between two characters directly observed is the phenotypic correlation (Falconer, 1987; Carvalho *et al*., 2004; Goldenberg, 1968).

In research of soybean genetic breeding the studies about genotypic, phenotypic and environmental correlations have involved morphological descriptors such as plant height, insertion height pods, number of pods, number of branches, mass of 100 grains and yield grain (Almeida *et al*., 2010; Lopes *et al*., 2002; Peluzio *et al*., 1998, 2005; Oliveira *et al*., 2000; Taware *et al*., 1997; Churata and Ayala-Osuna, 1996; Lemos *et al*., 1992; Moro *et al*., 1992; Sakiyama, 1989; Miranda, 1998).

In this context, the objective of this study was to estimate the phenotypic, genotypic and environment correlations among agronomic descriptors of soybean.

MATERIALS AND METHODS

Experimental site: The experiment was installed in the experimental area of the State University of Mato Grosso do Sul-Unit University Aquidauana (UEMS/UUA), located in the Brazilian Savanna (or Cerrado), located in the municipality of Aquidauana, comprising the following coordinates 20°27'S and 55°40'W with an average elevation of 170 m (Schiavo *et al*., 2010).

The soil was classified as Ultisol sandy loam texture (Embrapa, 2006), with the following layer 0-0.20 m: pH (H_2O) = 6.2; Al exchangeable ($cmol_c\ dm^{-3}$) = 0.0; Ca+Mg ($cmol_c\ dm^{-3}$) = 4.31; P ($mg\ dm^{-3}$) = 41.3; K ($cmol_c\ dm^{-3}$) = 0.2; Organic matter ($g\ dm^{-3}$) = 19.7; V (%) = 45.0; m (%) = 0.0; Sum of bases ($cmol_c\ dm^{-3}$) = 2.3; Cation Exchange Capacity (or CEC) ($cmol_c\ dm^{-3}$) = 5.1. The climate of the region, according to the classification described by Köppen-Geiger is Aw (Savanna Tropical) with cumulative rainfall during the experiment 450 mm and maximum and minimum temperatures of 91.4 and 66.2°F, respectively.

Experimental design: Twelve commercial soybean genotypes were grown (P98Y70, CD238, CD241, BRS255, VMAX, NK7059, Magna, BRS245, Potência, SYN3358, MSOY7909 e SYN5909) in randomized block design with four replications. The *Brachiaria decubens* was grown as previous and preceding sowing soybean plant was dried out with the active ingredient glyphosate, in the dose 1 kg ha^{-1}. The soybean seeding was performed manually in on 2011-12, under 0.45 m row spacing with 16 seeds per meter, with the fertilizer of corresponte 400 kg ha^{-1} de fertilizante 4-20-20.

The seeds were treated with fungicide (Thiram 480 TS® in dose of 300 mL 100 kg^{-1}) and insecticide (Imidacloprid 350 SC® in dose of 150 mL 100 kg^{-1} seeds) and preceding sowing were inoculated with *Bradyrhizobium japonicum* in dose of 240 g 100 kg^{-1}.

Analysis of descriptors: At 80 Days After Emergence (DAE) were measured Plant Height (PH) and first pod insertion (PIH), by means of ten plants per plot. At complete maturity (115 DAE), the Number of Pods (NP) and Number of Ramifications (NR) were analyzed by means of ten plants per plot, while the yield (YG) and Mass of Hundred Grains (MHG) were evaluated in the two central rows soybean, being corrected for moisture 13%.

Data analysis: In the analysis of results was used the analysis of variance, adopting the following statistical model (Cruz *et al*., 2004):

$$Yij = \mu+gi+bj+eij$$

Where:

Yij = Characteristic value of the i-ésimo genotype on the j-ésimo block
μ = Overall average of test
gi = Effect of i-ésimo genotype (i = 1,2,. .., g)
bj = Effect of j-ésimo block (j = 1,2. .., r); e
ϵij = Random error associated with the genotype i and block j ϵij~ NID (0, s 2)

Genetic parameters and their estimators were analyzed for each characteristic using the following expressions (Cruz *et al*., 2004):

- Genotypic variance:

$$S^2g = \frac{QM_g - QM_r}{k}$$

- Environmental variance:

$$S^2e = \frac{QM_r}{k}$$

- Genotypic coefficient of variation:

$$CVg = \left(\frac{\sqrt{S^2g}}{m}\right)\times 100$$

- Experimental coefficient of variation:

$$CVe = \left(\frac{\sqrt{QM_e}}{m}\right) \times 100$$

- $$b = \frac{CVg}{CVe}$$

- Herdability:

$$h^2 = \frac{S^2g}{S^2f}$$

In the estimates of the correlations were employed in the mentioned expressions by Ramalho *et al.* (2000):

- Phenotypic correlation:

$$r_{F(xy)} = \frac{COV_{F(xy)}}{\sqrt{(S^2_{Fx}) \times (S^2_{Fy})}}$$

- Genotypic correlation:

$$r_{G(xy)} = \frac{COV_{G(xy)}}{\sqrt{(S^2_{Gx}) \times (S^2_{Gy})}}$$

- Environmental correlation:

$$r_{E(xy)} = \frac{COV_{E(xy)}}{\sqrt{(S^2_{Ex}) \times (S^2_{Ey})}}$$

Where:
r_{xy} = Correlation between characters X and Y
COV_{xy} = Covariance between characters X and Y
S^2_x and S^2_y = Variance of characters X e Y, respectively

The estimates of variance and parameters components genetic and phenotypic and were obtained using the computer application GENES (Cruz, 2006).

RESULTS AND DISCUSSION

Table 1 presented the summary of estimates of genetic parameters. The experimental coefficient of variation (CVe) ranged from 5.0 (NR) and 14.1 (YG), which according to Lucio *et al.* (1999), classified high experimental precision. Moreover, it is below the maximum acceptable estimate of CVe to productivity of soybeans, which is 16.0% (Carvalho *et al.*, 2003).

Table 1: Genetic parameter estimates for six morphological descriptors evaluated in twelve soybean genotypes

Description	PH[1] (m)	PIH (m)	NP	NR	MHG (g)	YG (kg ha^{-1})
Minimum	34.3	7.1	32.9	3.0	15.5	663.0
Maximum	92.6	16.1	125.3	11.4	29.1	3,213.3
CVg (%)[2]	19.1	14.5	28.9	37.3	16.7	39.0
CVe (%)	10.3	13.4	14.0	5.0	8.9	14.1
b	1.9	0.9	2.1	7.4	1.9	2.8
S^2g	121.1	1.7	734.5	7.7	13.0	550,882.2
S^2e	35.4	1.9	171.1	0.1	3.6	72,186.7
h^2	93.2	78.0	94.5	99.6	93.5	96.83

[1]PH: Plant height, PIH: Pod insertion height, NP: Number of pod, MHG: Mass of hundred grains, YG: Yield grains, [2]CVg: Genotypic coefficient of variation, Cve: Experimental coefficient of variation, b: Relation between Cvg and Cve, S^2g: Genotypic variance, S^2g: Environmental variance and h^2: Herdability

The genotypic coefficient of variation (CVg) ranged from 14.5 (PIH) and 39.0 (YG), among the morphological descriptors, the YG is showing greater variability, being highly promising for performing the selection (Table 1). Considering that the existence of genetic variability in a population is crucial factor to any breeding program (Ramalho *et al.*, 2000), the germplasm under study proves the principle, promissory for works sorting or hybridization with potential for development of new cultivars.

The ratio b was below 1.0 only PIH (Table 1), indicating favorable situations to selection for all other descriptors according to the interpretation of this value according to Vencovsky (1978).

Following this trend, were found values above 93.0% for herdability (h^2), with the exception of PIH (78.0%) (Table 1) being that values higher than those observed by Mauro *et al.* (1995) and Santos *et al.* (1995) in soybean.

According to Polizel (2004), the maximum and minimum herdability for YG is 58.0 and 3.0%, respectively, with the majority between 33.0 and 58.0%. This can be attributed to the purely quantitative behavior of this character, due to the large number of genes that control, allowing greater environmental influence and concomitantly, a decrease of the relationship between S^2g and S^2e. However, the data obtained for this descriptor corroborate the results of Rossmann (2001), that noted the estimation of h^2 moderate to high in a soybean population evaluated in four years.

Estimates of high h^2 are associated with greater genetic variability, higher selective accuracy (Filho *et al.*, 2009) and greater chance of success in the selection of soybean lines with higher grain yield.

Significants phenotypic correlations (r_F) ($p<0.01$) (Table 2), were identified between the descriptors ND×PIH, NR×NP×NP MHG, MHG×NR, being the values obtained of superior magnitude to those observed by

Table 2: Estimates of phenotypic, genotypic and environmental correlations between six morphological descriptors evaluated in twelve soybean genotypes

Descriptors	PH[1] (m)	PIH (m)	NP	NR	MHG (g)	YG (kg ha^{-1})
PH (m)						
r_F	---	-0.0053	0.0517	0.0144	-0.1442	0.0564
r_G	---	-0.0099	0.0210	0.0107	-0.1519	0.0644
r_E	---	0.0256	0.5224	0.2287	-0.0377	-0.1030
PIH (m)						
r_F		---	-0.8044*	-0.5051	-0.5428	-0.5720
r_G		---	-0.8924	-0.5560	-0.6217	-0.6572
r_E		---	-0.3463	-0.4783	-0.0990	-0.0095
NP						
r_F			---	0.8899*	0.8602*	0.8352*
r_G			---	0.9129	0.9067	0.8720
r_E			---	0.2864	0.1348	0.0252
NR						
r_F				---	0.8772*	0.8498*
r_G				---	0.9082	0.8666
r_E				---	0.0721	-0.0818
MHG (g)						
r_F					---	0.8899*
r_G					---	0.9056
r_E					---	0.6259
YG (kg ha^{-1})						
r_F						---
r_G						---
r_E						---

[1]PH: Plant height, PIH: Pod insertion height, NP: Number of pod, NR: Number of ramifications, MHG: Mass of hundred grains, YG: Yield grains, *Significant at 1% probability by t-test

Peluzio *et al.* (1998, 2005). The YG descriptor obtained r_F significant positive ($p<0.01$) with NP, NR and MHG, indicating that the selection of plants with larger number of ramifications entailed, therefore, more productive genotypes.

Positive correlations indicate the occurrence of pleiotropism or gene ligation imbalance between pairs of characters and promote the simultaneous selection of two or more characters, whith the selection in only one of these (Falconer, 1987; Goldenberg, 1968; Johnson *et al.*, 1955). Moreover, the selection of a character can cause an undesirable selection of another.

The genotype correlations (r_G) had the same sign (Table 2) and in most cases superior to their corresponding r_F values, indicating that the phenotypic expression is decreased compared to environmental influences. These results corroborate those obtained by Almeida *et al.* (2010), Lopes *et al.* (2002), Peluzio *et al.* (1998, 2005), Oliveira *et al.* (2000), Taware *et al.* (1997), Churata and Ayala-Osuna (1996), Lemos *et al.* (1992), Moro *et al.* (1992), Sakiyama (1989) and Miranda (1998). Thus, r_F may be useful in the absence of estimates of r_G.

Environmental correlations (r_E) between descriptors with differences in magnitude and sign, in relation to the respective r_G, revealed that the environment favored one character over another and that the genetic and environmental causes of variation have different physiological mechanisms (Table 2), defaulting the indirect selection. Among these are cited PIH×PH and YG×PIH, agreement with the results obtained by Almeida *et al.* (2010).

The results section should provide details of all of the experiments that are required to support the conclusions of the study. There is no specific word limit for this section. The section may be divided into subsections, each with a concise subheading. Large datasets, including raw data, should be submitted as supporting information files, these are published online alongside the accepted article.

CONCLUSION

The population presented genetic variability and potential for genetic improvement and gain of the yield grain can be obtained mainly through selection based on descriptor number of ramification.

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