Multivariate exploratory approach and influence of six agronomic traits on soybean genotypes selection

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ABSTRACT: A comprehensive analysis for selection of superior genotypes can be useful and necessary. The aim of this study was to select soybean genotypes with superior agronomic traits through the use of multivariate exploratory analysis and to identify those traits that are most influent over grain productivity and selection. We evaluated 29 soybean genotypes in a randomized block design with three replications. Agronomic traits analyzed were: plant height at flowering (PHF), plant height at maturity (PHM), height at insertion of the first pod (HIP), grain productivity (GP), number of nodes (NN) and number of pods (NP). Data were submitted to principal component analysis. Two eigenvalues explained 68.17% of the variance contained in the original information, generating two components with relevant amount of information. These were characterized by the traits PHF, PHM, HIP, NP and GP which allowed to discriminate and select 6 genotypes with good agronomic traits with emphasis on grain productivity. Direct (positive) relationships were observed between GP and the traits PHF, PHM, HIP and NP, as these were observed to influence the distribution of genotypes with greater GP in the two-dimensional plane. The traits that were more related and favorably influencing GP of selected genotypes were plant height at maturity and number of pods.

Keywords: *Glycine max*, principal components, genetic improvement, trait selection, grain productivity.

Abordagem exploratória multivariada e influência de seis caracteres agronômicos na seleção de genótipos de soja

RESUMO: Uma análise mais abrangente para seleção de genótipos superiores pode ser útil e necessária. O objetivo do presente estudo foi selecionar genótipos de soja com caracteres agronômicos superiores por meio de análise exploratória multivariada, e identificar aqueles caracteres que mais influenciam na produtividade de grãos e na seleção. Para tanto, foram avaliados 29 genótipos de soja, conduzidos no delineamento de blocos ao acaso, com três repetições. Os caracteres agronômicos avaliados foram: altura da planta no florescimento (APF) e na maturidade (APM), altura de inserção da primeira vagem (AIV), produtividade de grãos (PG), número de nós (NN) e número de vagens (NV). Os dados foram submetidos à análise de componentes principais. Na análise de componentes principais dois autovalores explicaram 68,17% da variância contida nas informações originais, gerando dois componentes com quantidades de informações relevantes, sendo caracterizados pelos caracteres APF, APM, AIV, NV e PG que permitiram discriminar e selecionar 6 genótipos com bons atributos agronômicos com ênfase em produtividade de grãos. Relações diretas (positivas) foram observadas entre PG com os caracteres APF, APM, AIV e NV, pois estes tiveram influência na distribuição dos genótipos com PG superior no plano bidimensional. Os caracteres que mais relacionaram e influenciaram favoravelmente a PG dos genótipos selecionados foram altura da planta na maturidade e número de vagens.

Palavras-chave: *Glycine max*, componentes principais, melhoramento genético, seleção para caracteres, produtividade de grãos.

1. INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of the most important crops worldwide, with significant impact on the economy of various countries. In Brazil, soybean is one of the largest generators of foreign exchange, in addition to ensuring generation of employment and income. The demand for soybeans has been strong and growing, because this product

is used as an ingredient of many food and industrial products. Thus, the development of new cultivars with good performance of agronomic traits, specifically for the various growing regions, is of fundamental importance (HAMAWAKI et al., 2010; PRIOLLI et al., 2004). The identification of superior genotypes based on only one character often leads to the failure of new cultivars. It is, therefore, important to identify the components that are more influential on obtention of productive genotypes (BERTINI et al., 2010; SILVA et al., 2015).

The complexity of the most agronomically important traits requires the accurate and efficient selection of productive genotypes. This is importante particularly because, usually, these characters present a certain degree of association (genetic correlations), so that the direct selection of an isolated character may cause a disadvantage on other trait that is economically important (AKRAM et al., 2011; LEITE et al., 2015; NOGUEIRA et al., 2012; RODRIGUES et al., 2013).

A more comprehensive analysis for selection of the best genotypes may be useful and necessary. In this sense, multivariate analyses are a manner to run and provide in a single analysis results what would require several univariate analysis (HAIR et al., 2009). Multivariate exploratory analysis is often associated with the objective of reducing the original space to a minimum necessary size in order to obtain the description of relevant information contained in the original observations (BARBOSA et al., 2013; VALLADARES et al., 2008) . Several multivariate methods can be applied to selection of superior genotypes, allowing also to observe the influence of agronomic traits in the selection of genotypes and the relationships between them. We emphasize the use of principal component analysis can be used in experimental data based on the average of genotypes for each trait, as used by Dallastra et al. (2014); Viana et al. (2013); Pitta et al. (2010).

Principal component analysis reduces the space of agronomic traits of studied genotypes, creating orthogonal axes that are linear combinations of the original variables, which are called principal components. The power of each trait is measured in its respective component, transforming the original structure into a new smaller structure (FERRAUDO, 2014).

Multivariate analysis can be used in the selection of superior genotypes for agronomic traits, as they are useful to unify the information of the total set of traits, allowing more rigorous selection and obtaining specific genotypes for the traits of interest. In this context, it may be possible to obtain desirable genetic gain, depending on the variability between genotypes and the differential selection after the selection cycle through principal components. Given the lack of studies with the use of multivariate exploratory techniques as alternatives for selection of superior genotypes, new studies using selection strategies such as these are important. Therefore, the aim of the present study was to select soybean genotypes with good performance of agronomic traits through the use of multivariate exploratory analysis and identify the more influente traits over grain productivity and over the selection process.

2. MATERIALS AND METHODS

2.1. Experiment onset

The experiment was started in 2011/12 and run from December 2011 to April 2012 in the Sabiá farm (08º36'25"S, 44º38'49" W and 569 meters a.s.l.) located in the Serra das Laranjeira, in the municipality of Currais, PI. Currais is a municipality inserted in the Cerrado of the south of Piauí. The soil is dystrophic Yellow Latosol cultivated with soybeans in previous crops, containing 201 g kg^{-1} of clay, 729 g kg^{-1} of sand and 70 g kg^{-1} of Silt. The climate is Aw according to Köppen-Geiger Climate Classification and has two well defined seasons, the dry season from May to September and the rainy season from October to April (ANDRADE et al. 2014). The accumulated rainfall during the experiment was 1,180 mm measured by a pluviometer installed in the experimental area.

The experimental design consisted in a randomized block with 29 soybean genotypes (G1, G2, G3, ..., G29) with three replications. Each plot consisted of four rows, 0.45 m apart from each other and with 5.0 m in length, using 10 plants per linear meter. The usable area was represented by the two central rows of each plot, excluding 0.50 m from each end as borders.

As basis fertilizer, 420 kg ha^{-1} fertilizer were used in the formulation 02-24-12. Seed treatment was performed with thiamethoxan (200 mL/100 kg of seed) and fludioxonil + metalaxyl-M (100 ml/100kg seed) and subsequently inoculated with strains of *Bradyrhizobium japonicum* in the dosage of 150 g of the inoculant per 100 kg of seeds. Fifteen days after plant emergence, 120 kg ha^{-1} of potassium chloride were applied in coverage. During the crop cycle, control of weeds, pests and diseases were carried out by incidence, with products recommended for the culture.

2.2. Evaluation of agronomic traits

Genotypes were assessed as they reached the phenological stages of soybean ideal for assessment (FEHR; CAVINESS, 1977). We evaluated the following agronomic traits: plant height at flowering (PHF) - height from the plant lap up to the apex of the main stem (cm) when approximately 50% of the plants in the plot usable area were at the stage R1; plant height at maturity (PHM) - height measured from the plant lap up to the apex of the main stem (cm) when plants were at the stage R8; height at insertion of the first pod (HIP) - height measured from the plant lap up to the insertion of the first pod on the main stem (cm) when they were at the stage R8; number of nodes per plant (NN) - obtained by counting the number of nodes of plants; number of pods per plant (NP) - obtained by counting the total number of pods of plants, and grain productivity (GP) - obtained by weighing the grains produced by plants of the plot usable area, adjusted to 13% moisture, converted into kg ha^{-1}. Based on the assessment of the number of days to maturity of soybean, which is approximately 120 days, the cycle of all strains was evaluated.

2.3. Statistical analysis

Because of the interdependency and interrelationship of agronomic traits, principal component analysis was performed. For this analysis, data from all agronomic traits were standardized, resulting in a mean equal to zero and variance equal to unit, according to recommendation (FERRAUDO, 2014). All statistical analyses were performed using Statistica v.10 (STATSOFT, 2004).

For the principal component analysis, eigenvalues above one (1.0) were considered because they generate components with significant amount of information of the original variables (SILVA; LIMA, 2012).

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For selection of genotypes using principal component analysis, scales in the axes of the graphs were predetermined through elipse in order to obtain a better discrimination of genotypes based on the projection of vectors of agronomic traits. The range of the ellipse highlighted in red on the X axis and Y axis comprises values from 2 to -2 and this is in line with Dallastra et al. (2014).

Genotypes in the center of the graph, within the ellipse, were not significant. Genotypes located outside the highlighted range are specific and differ significantly from the others, precisely because they have highly specific traits (DALLASTRA et al., 2014; VIANNA et al., 2013). After selection of genotypes through principal component analysis, the differential selection was estimated using the Eq. 1 for all evaluated traits based on the difference between the mean of the selected genotypes and the overall mean of all genotypes, according to Nascimento et al. (2014).

$$DS = MSG - MG_0 \qquad (1)$$

where:

DS - differential of selection;
MSG - average of selected genotypes;
MG_0 - overall mean of genotypes.

3. RESULTS AND DISCUSSION

The principal component analysis (PCA) of soybean genotypes showed two eigenvalues above one, generating two primary components with relevant amount of information. The eigenvalue of the first principal component (PC1) was 2.53, which is a significant value when considering that the sum of all eigenvalues was 6. The proportion of the variance retained by CP1 was 42.29% of the original variance. The main variables that explained that retention of variance were plant height at flowering (PHF), plant height at maturity (PHM), height at insertion of the first pod (HIP) and grain productivity (GP), with factor loadings (correlations) above 0.5 (Table 1). Only correlations above 0.5 were considered important

Table 1. Correlations between agronomic traits and the principal components (PC1 and PC2) of soybean genotypes.
Tabela 1. Correlações entre os caracteres agronômicos e os componentes principais (CP1 e CP2) dos genótipos de soja.

Traits	PC1	PC2
PHF	0.758	-0.371
PHM	0.861	-0.003
HIP	0.848	-0.157
GP	0.560	0.729
NN	0.415	-0.259
NP	0.130	0.890

PHF = plant height at flowering (cm); PHM = plant height at maturity (cm); HIP = height at insertion of the first pod (cm); GP = grain productivity in kg ha⁻¹; NN = number of nodes; NP = number of pods per plant.

(FERRAUDO, 2014). Traits with values of correlation with the principal components above such value are the ones that haveh discriminatory power over the respective components. For the second principal component (PC2) the eigenvalue was 1.55, which corresponds to 25.88% of the original remaining variance, and the traits number of pods (NP) and grain productivity (GP) showed discriminatory power over the PC2, with factor loadings (correlations) of 0.729 and 0.890 respectively.

For each main componente, equal signs mean that the traits are positively correlated and opposite signs mean that the traits are negatively correlated (Hair et al., 2009).

In Figure 1, the two-dimensional plane composed by PC1 (42.29%) and PC2 (25.88%) retained 68.17% of the total original variance and was characterized by the traits PHF, PHM, HIP, NP and GP. This allowed the discrimination and selection of soybean genotypes G11, G12, G14, G22, G25 and G29 with superiority for grain productivity. For the genotypes G11, G12 and G25, grain productivity was influenced by traits related to plant height (APF, APM and AIV) but also by the component of number of pods per plant. The grain productivity for the G22 was mainly influenced by the traits related to plant height (PHF, PHM and HIP). In the case of genotypes G14 and G29, these were influenced almost exclusively by the character number of pods per plant. Among the agronomic traits under study, only the NN had low influence on selected genotypes. Specific
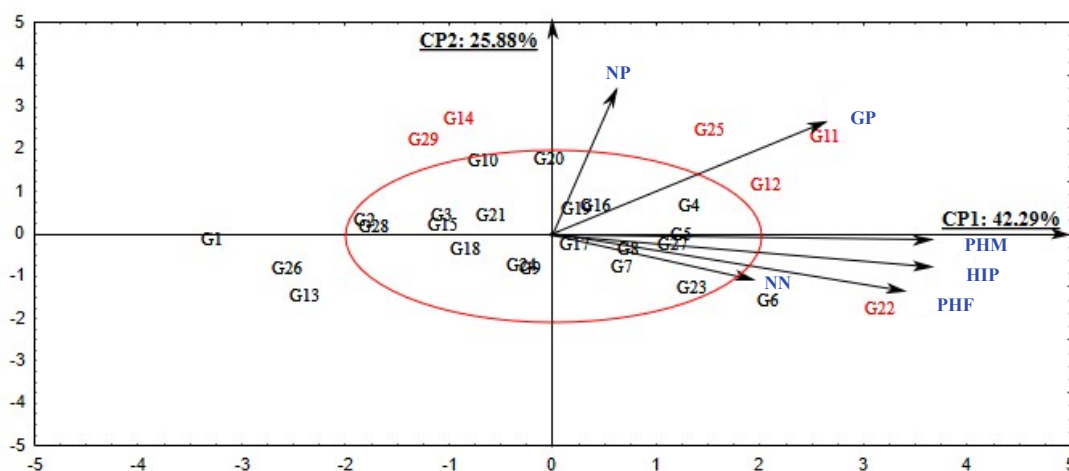

Figure 1. Biplot graph with dispersion of 29 soybean genotypes according to the principal components: PC1 x PC2 and projection of vectors of traits: plant height at flowering (PHF) in cm, plant height at maturity (PHM) in cm, height at insertion of the first pod (HIP) in cm, grain productivity (GP) in kg h⁻¹, number of nodes (NN) and number of pods (NP).
Figura 1. Gráfico biplot com dispersão dos 29 genótipos de soja em função dos componentes principais: CP1 x CP2 e projeção dos vetores dos caracteres: Altura da planta no florescimento (APF) em cm, altura da planta na maturidade (APM) em cm, altura de inserção da primeira vagem (AIV) em cm, produtividade de grãos (PG) em kg h-1, número de nós (NN) e número de vagens (NV).

genotypes for these traits were located at the ends, outside the range highlighted in red (Figure 1).

The center of the range representes one confidence interval of 95%, meaning that the genotypes centered on the graph plane have mean values for each character, without significant differences. It is possible to check the dispersions of vectors of agronomic traits and, consequently, the relations between them. Direct (positive) relationships were observed between GP and PHF, PHM, HIP and NP. In this context, the traits PHF, PHM, HIP and NP were important in the principal component analysis, as they allowed to discriminate genotypes with higher grain productivity, with strong direct influence on this trait. The trait number of pods showed high positive correlation with grain productivity, both positioned in the same quadrante what means that the higher the value of this trait, the higher the value of grain productivity of genotypes. This result is in line with Dallastra et. (2014); Viana et al. (2013); Silva et al. (2015).

Depending on the number of genotypes to be studied, it is up to the breeder to define what will be the appropriate rigor for selection in the analysis and hence on the number of genotypes to be selected for traits of interest. The principal component analysis helped in the selection of superior genotypes, with superiority for grain productivity, coupled with great contribution of the PHF, PHM, HIP and NP. Leite et al. (2015) observed positive and significant phenotypic and genotypic correlations at 1% probability for plant height at maturity with plant height at flowering, height at insertion of the first pod, number of nodes and grain productivity, and stated that the selection of taller plants at maturity would have great influence on grain prductivity. Alcântara Neto et al. (2011) found positive indirect effect of plant height at maturity over grain productivity via number of pods. Number of pods was a favorable character for indirect selection of soy grain productivity. In the studies of Akram et al. (2011) and Nogueira et al. (2012), the character that most influenced grain productivity was number of pods. This trait had the highest value for favorable direct effect, with great contribution to grain productivity. In the present study the characters that were more related and directly influenced in favorable way the most productive genotypes were plant height at maturity and number of pods.

Table 2 shows the means for agronomical traits of discriminated and selected genotypes according to the principal component analysis, considering the favorable selection for traits desirable in soybean that showed discriminatory power in the principal components (PC1 and PC2). The agronomic traits plant height at flowering, at maturity and the height of the first pod must have desirable values in the selected productive genotypes. Sediyama et al. (2009) recommend values height at flowering and at maturity of 55.0 cm and 80.0 cm, respectively, that satisfactory for crops. Almeida et al. (2011); Carvalho et al. (2010) point out that the selection of plants with height at maturity above 80 cm and height of insertion of the first pod below 10 cm may cause losses in mechanical harvesting. For the trait insertion of the first pod, satisfactory height is around 15.0 cm, although most modern harvesters can make good harvest with plants showing first pods at 10.0 cm (ROCHA et al., 2012).

All genotypes selected through principal components showed mean value higher than the overall mean for productivity. The

Table 2. Mean values for agronomic traits of soybean genotypes discriminated and selected through principal component analysis.
Tabela 2. Valores médios para os caracteres agronômicos dos genótipos de soja discriminados e selecionados pela análise de componentes principais.

Genotypes	PHF	PHM	HIP	GP	NN	NV
G11	54.40	58.00	12.80	4.447.22	12.17	105.00
G12	50.00	57.40	13.80	2.727.78	13.67	109.20
G14	36.00	55.80	9.20	2.905.56	12.00	110.00
G22	53.27	73.53	14.80	2.054.63	13.39	46.13
G25	46.87	61.40	11.80	3.279.63	12.50	120.00
G29	39.20	51.90	7.90	2.329.17	13.00	115.00
MSG	46.62	59.67	11.72	2.957.33	12.79	100.89
MG$_0$	45.95	53.66	11.02	1.964.94	12.64	81.98
DS	0.68	6.01	0.70	992.39	0.14	18.91

DS = differential of selection; MSG = Average of selected genotypes; MG$_0$ = overall average of genotypes; PHF = plant height at flowering (cm); PHM = plant height at maturity (cm); HIP = height at insertion of the first pod (cm); GP = grain productivity (PG) in kg ha^{-1}; NN = number of nodes; NP = number of pods per plant.

genotype G11 had higher mean grain productivity than the overall mean of selected genotypes. The genotypes selected through principal components in the outer region of the ellipse compared to the overall mean observed are characterized as specific for the agronomical traits that defined them.

The differential selection between genotypes selected through principal components and the overall mean showed higher amplitudes for the traits grain productivity, number of pods and plant height at maturity. According Borém & Miranda (2009), in breeding pratice, the differential parameter for selection can be used to get an indication of the genetic gain obtained with the selection for the evaluated traits. In this study, the characters plant height at maturity and number of pods favorably influenced grain productivity of selected genotypes, confirming the relationship verified in the principal component analysis.

The most productive selected genotypes had higher dispersion of the traits and, consequently, greater genetic variability and may be used for formation of segregating populations. This aims to obtain promising genotypes, with the following agronomic characteristics: greater plant height at maturity and higher values for the production component (number of pods), which may result in more productive genotypes.

The principal components multivariate exploratory technique allowed the exploration of information on the group of genotypes, analyzing simultaneously all agronomic traits, and allowing the breeder to identify the most important results. Therefore, this is an approach that can be further explored in genotype selection studies. The combination of the linear relationship between the traits and the distribution of genotypes according to the projection of the vectors of the traits in the same analysis can be considered comprehensive and thorough analysis. Dallastra et al. (2014), in a study on the selection of soybean genotypes carriers of the RR gene, and Pitta et al. (2010), in a study on the selection of genotypes of groundnut resistant to *Anticarsia gemmatalis,* noted that principal componente analysis was efficient in the process of selection, leading to genetic gains for agronomic traits of interest, which is an advantageous and appropriate situation to identify superior genotypes.

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4. CONCLUSIONS

Multivariate exploratory approach by principal components allowed the discrimination and assisted in the selection of six soybean genotypes with good agronomic traits, with emphasis on grain productivity.

The selected genotypes as well as grain productivity were discriminated by plant height at flowering and at maturity, height at the first pod and number of pods, which had the strongest influence on the distribution of genotypes in the two-dimensional plane.

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