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RESEARCH ARTICLE

PATH ANALYSIS AND DISSIMILARITY IN SOYBEAN WITH INDETERMINATE HABIT

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ABSTRACT

The relationships between characteres are established through correlation coeficientes of path analysis, wich provides understanding of cause and effect directs and indirects on the main variable. Itaimed to determine the direct and indirect phenotypic effects of the agronomically important characters related to grain yield of soybean with indeterminate growth habit and genetic dissimilarity between genotypes. The experiment was conducted at the Federal University of Santa Maria, at Frederico Westphalen – RS *Campus*, in 2013/2014 crop. The experimental design was randomized block with ten genotypes of soybean (FPS Paranapanema RR, BMX Classe RR, FPS Solimões RR, BMX Potência RR, BMX Força RR, BMX Energia RR, BMX Turbo RR, FPS Iguaçu RR, BMX Tornado RR, BMX Alvo RR), organized in three repetitions. It was evaluated yield components. The data were subjected to analysis of phenotypic path analysis, and the significant variables were subject to genetic dissimilarity analysis the method of Mahalanobis, through the UPGMA clustering method, and relative contribution of morphological characters in dissimilarity for method of Singh. The path analysis reveals for the characters thousand grain weight and length of branches direct effects with correlation coefficient of magnitude higher to grain yield, reveals through the length of internode significant indirect effects. The method of Singh reveals that the characters number of branches and nodes in the branches largest contribution to distinguish between genotypes. The Mahalanobis distance reveals formation of three groups.

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INTRODUCTION

The soybean (*Glycine max* L.) characterized as legume belonging to the Fabaceae family, is coming from to Asian continent. In the 70 was implemented in Brazil and currently is the main cultivated commodity. This oilseed has a high nutricional value and yield, it can be used as green manure, forage, silage, hay (SEDIYAMA, 2009). Accordint to the National Food Suply Company (2014) the soybean crop in 2013/2014 shows increases of 8,7% in acreage and grain yield around 2,860.00 pounds per hectare. The yield potential of soybeans is determinate through of contribution of several agronomic traits, such as number of plants per unit area, legumes per plant, seed per legume, grain weight, branches per plant, reproductive nodes and length of branches (THOMAS & COSTA, 2010). Thus, it becomes necessary to know the relationship between these characters, setting their contribution to grain yield. The relationships between characters are established through the correlation coefficients of path analysis (WRIGHT, 1921), which provides understanding of cause and effect, directly and indirectly on the main variable. According Ramalho *et al.* (2012), the correlation coefficients allow to identify the changes of a particular character over another. The definition of the inter-relationships between these characters may contribute to genetic improvement through indirect selection of characters less complex heritage, promoting gains in yield potential of soybeans. The classification of soybean genotypes as the genetic relatedness and distance may be measured through genetic divergence based on the phenotype of the individual, and can quantify the similarity and dissimilarity between genotypes, the distinction between groups and how these groups can be contrasted in their characteristic. The distinction of the groups may contribute to the choice of parents and increase genetic variability in segregating population (CRUZ *et al.*, 2004). Thus, the present study aimed to determine the direct and indirect phenotypic

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effects of the agronomically important characters related to grain yield of soybean with indeterminate growth habit and genetic dissimilarity between genotypes.

MATERIALS AND METHODS

The experiment was conducted in the 2013/2014 crop at the Federal University of Santa Maria of FredericoWestphalen *Campus*, the Plant Breeding Laboratory and Manufacturing Plant, located in the coordinates 27º39'S, 53º42'O, with an altitude of 490 meters. According to Mota (1953) the climate is characterized as humid subtropical CFA, the soil is classified as Typicalalumino Ferric. The experimental design was randomized blocks, ten soybean cultivars with indeterminate growth habit, arranged in three repetitions. The genotypes used were FPS Paranapanema RR, BMX Classe RR, FPS Solimões RR, BMX Potência RR, BMX Força RR, BMX Energia RR, BMX Turbo RR, FPS Iguaçu RR, BMX Tornado RR, BMX Alvo RR. The experimental units were consisted of four rows of three feet long, spaced 0.45 meters, with a population density of 300,000.00 plants ha^{-1}. The culture was implanted under direct seeding system, using base fertilization with 200 kg ha^{-1}NPK of formulation 5-20-20. The control of insect pests and diseases was done preventively. The evaluations were conducted in the central rows of each experimental unit, despising the first meter from each end in order to reduce the effects of border. Ten plants were randomly collected for measurement of agronomic interest characters, compounding the average of each variable in the experimental unit. The characters evaluated were:

- Insertion of the first legume (IFL): measure of the stem of each plant to the insertion of the first legume, in centimeters.
- Plant height (PH): measure from the stem of each plant to the apex of the plant.
- Number of legumes in main stem (NLMS): total of viable legumes in main stem.
- Number of legumes in braches (NLB): total of viable legumes in branches.
- Number of legumes per plant (NLP): total of legumes of main stem and branches.
- Number of reproductive nodes in main stem (NRNS): count of nodes that issued viable legumes in main stem.
- Number of reproductive nodes in branches (NRNB): count of nodes that issued viable legumes in branches.
- Number of branches (NB): total of branches per plant.
- Branch lenght (BL): measure between the insertion of branch to apex, considered those with more than tem centimeters.
- Number of legumes per node in main stem (NLNS): ratio between of the total legumes in main stem and the number of reproductive nodes.
- Number of legumes per node in branches (NLNB): ratio between of the total legumes in branches and the number of reproductive nodes.
- Internode length (IL): ratio between the number of nodes in main stem and branches length, in centimeters.
- Thousand grain weight (TGW); measure through of sampling of eight subsamples of 100 seeds per experimental unit, after proceeded to the average of the character, in grams.
- Grain yield (YIELD): measure through of the total mass of grains on experimental unit, with hinder correction of humidity for 13%, set the grain mass by the number of plants per experiment unit, getting the grain yield per plant correct, after set for the employed population of plants, in kg ha^{-1}.

The data were subjected to analysis of variance to 5% level of probability. Afterwards, it was preceded to the phenotypic path analysis between agronomic characters. The variables that showed significant results were analyzed for genetic dissimilarity by Mahalanobis, through the clustering method "Unweighted Pair Group Method with Arithmetic Mean" (UPGMA), and the relative contribution of morphological dissimilarity in the method of Singh (1981). For path analysis, the estimates of direct and indirect effects, were performed considering the statistical model: $y = p_1x_1 + p_2x_2 +...+ p_nx_n+ p_eu$, where y = dependent variable grain yield; $x_1, x_2,....,x_n$: explanatory variables; $p_{a,}$ $p_2,...p_n$: path coefficients. The estimates of path coefficient are based in equations system X´Xβ = X´Y (Li, 1975), being:

$$X'Y= \begin{matrix} r_{1y} \\ r_{2y} \\ \vdots \\ r_{ny} \end{matrix} \quad , X'Y= \begin{matrix} 1 & r_{12} & \cdots & r_{1n} \\ r_{12} & 1 & \cdots & r_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ r_{1n} & r_{2n} & \cdots & 1 \end{matrix} \quad e\ \beta= \begin{matrix} p_1 \\ p_2 \\ \vdots \\ p_n \end{matrix}$$

Thus, performing the decomposition of the correlation between the dependent and the independent variables, was obtained (CRUZ *et al*., 2004):

$$\begin{matrix} r_{1y} = p_1+p_2r_{12} + \dots + p_nr_{1n} \\ r_{2y} = p_1r_{12}+ p_2+ \dots+ p_nr_{2n} \\ \dots \qquad \dots \qquad \dots \end{matrix}$$

$$r_{ny}= p_1r_{1n}+ \underset{n}{p_{n2}}+ \dots + p_n$$

$$r_{iy}= p_i+ \underset{j\neq i}{} \quad p_j\ r_{ij}$$

Where:r_{iy}: correlation between the main variable selecting the investigator (y) and the ith explanatory variable; p_i: measure the direct of variable i on the main variable; p_ir_{ij}: measure of indirect effect of variable i, via variable j, on the main variable. As Cruz *et al*. (2004), when the exclusion of the variables is not desired by the researcher adopts is similar to ridge regression analysis procedures.This methodology in the presence of multicollinearity, the least squares estimator obtained X'Y can be linked to very high variance.This adverse effect can slightly modify the system of normal equations with the introduction of the constant K on the diagonal of the matrix X'X. Thus, the path coefficients are obtained: (X´X + Kl) = X´Y;

$$\sigma= \begin{matrix} p_1^* \\ p_2^* \\ \dots \\ p_n^* \end{matrix}$$

With the inclusion of the constant K the decomposition of the correlation between the explanatory variables and the basic variable is given by:

$$\begin{matrix} r_{1y} = (1+K)p_1^*+p_2^*r_{12} + \dots + p_n^*r_{1n} \\ r_{2y}= p_1^*r_{12} +(1+K)p_2^*+ \dots + p_n^*r_{2n} \end{matrix}$$

... ...

$$r_{ny} = p^*_1 r_{1n} + p^*_2 r_{n2} + \dots + (1+K)\ p^*_n$$

Thus, it hasbeen:

$$r_{iy} = \ 1+K\ p^*_{1i} + \overset{n}{\underset{j\neq i}{}}\ p^*_j\ r_{ij}$$

For the K value are considered values from 0 to 1, where Cruz *et al*. (2004) point out that between the values, you should opt for the lower value of the constant, for which the majority of the path coefficients, related to the various characters, are stabilized. The determination of pathdiagramsgivenby:

$$R^2 = p_1 r_{1y} + \ p_2 r_{2y} + \dots + p_n r_{ny}$$

The net effect is estimated by:

$$\rho_{\varepsilon =}\ \overline{1\text{- }R^2}$$

Performing the analysis we used the statistical software Genes (CRUZ, 2013).

RESULTS AND DISCUSSION

The grain yield is characterized as a quantitative character controlled by the joint action of several genes, theses contribute in small proportions to phenotype performance, but directly dependent on the environment (Allard, 1971). Thus, the soybean breeding for superior genotypes should be grounded knowledge of the characters and the interconnections of these characters. These relationships show direct and indirect effects of characters to grain yield (Coimbra *et al*., 1999). The multicollinearity can express high coefficients, resulting in values without regard to the biological phenomenon under study (Coimbra *et al*., 2005). In this case, it performs the elimination of variables and applies the methodology proposed by Carvalho (1995) Least squares or ridge pathanalysis. In evaluating multicollinearity of the phenotypic correlation matrix, it’s observed severe effects of multicollinearity through the characters: number of nodes on the main stem, number of nodes on branches, number of legumes per node on the main stem and number of legumes per node in the branching. As well, the characters were removed from the analysis purpose of circumventing the effects of multicollinearity. Performed the inclusion of the character number of legumes per node on the main stem. The genotypes of soybean with indeterminate growth habit show grain yield, direct influences of characters thousand grain mass, length of branches, number of legumes on the main stem, plant height and internode length (Table 1). Studies conducted by Nogueira *et al*. (2012), show to grain yield coefficients of moderate to high correlation to the direct effects through the characters number of pods per plant, weight of hundred grains and grain number per legume.According Kurek *et al*. (2001), in bean direct contributions to grain yield are revealed through the number of legumes per plant and grain yield. The insertion of the first pod influences mechanized harvesting process where smaller magnitudes of this character allow more losses in the harvest (Braz *et al*., 2010). The direct effects are observed coefficients of low and negative correlation (Table 1), revealing that genotypes with lower height of the first legume insertion tend to increase the grain yield through the number of reproductive nodes on the main stem or branches. The indirect effects, it observe positive anddowncorrelation coefficients to the character plant height, low and negative via number of legumes on the main stem and internode length. Therefore, an increase in height of the first legume insertion allows the genotype increase his stature, but does not influence on effect on yield. Almeida *et al*. (2010), reveals positive effects of the height of the first legume insertion and grain yield. The Pearson correlation shows intermediateand negative coefficients (r = -0.30). The plant height shows the direct effects, positive and low coefficient of correlation to the main variable. Low and positive indirect effect is evidenced by the internode length (Table 1). Therefore, the increase in height of the soybean causes to elongation of the main stem and distance between reproductive nodes. Low and negative indirect effects are observed through the height of the first legume insertion.Studies of Coimbra *et al*. (2004), show no relationship between plant height with the thousand grain weight and grain yield. According to Souza *et al*. (2013), smaller in stature soybeans result in increased number of grains per legume, grains per plant and grain yield, been contributing to crop yield potential. The total Pearson correlation (r = 0.219) shows low and positive, confirming the relationship between the explanatory variables and the main parameter. The number of legumes per plant reveals major contribution to productive potential of soybeans with high fluctuations as cultivation environment, with speeches by abiotic factors, availability of water and photoperiod (Lima *et al*., 2009). To the direct effects observe low and positive correlation coefficients to grain yield (Table 1.). Indirectly there is positive and low coefficient of correlation across the length of the branches, in this way, the number of legumes on the main stem plus the length of the branches, enables the increase of total legumes per plant. Low and negative coefficients are revealed indirectly through the internode length and thousand grain weight of soybeans.

The grain yield can be explained through increase in main stem legumes, reducing the distance between nodes and increased reproductive branches. Proven results for studies of AlcantaraNeto *et al*. (2011), show a high contribution of the number of legumes per plant with grain yield. The total Pearson correlation showed a low positive correlation (r= 0.139) between the number of legumes per plant and grain yield.Therefore, soybean genotypes with indeterminate habit advocate the formation of smaller magnitude in branches, on the other hand contributes to the increase of total legumes per plant. The Pearson correlation is evident in low magnitude and negative (r = -0.221) between the number of legumes on the branches and the main character. The number of branches per plant reveals the direct effects of low and negative correlation coefficient for grain yield (Table 1). Indirectly observed were low and positive coefficients through the characters plant height and length of the branches, and low and negative via insertion of the first legume and thousand grain weight.Thus, the indeterminate soybeans, recommends higher plants with less number of branches but on the other hand reduce the weight of grain. According Barbosa *et al*. (2014), soybean reveals ability to modify itself in relation to environmental conditions, nutrient management and planting date, mostly by changing the magnitude of the of characters number of reproductive nodes on the main stem and branches per plant.The Pearson correlation is evident in intermediate and positive (r = 0.359), demonstrates the relationship between the magnitude and branches of the productive potential of soybeans.

Table 1. Estimate of the phenotipic direct and indirect effects of eight characters on the grain yield, coming to ten soybean genotypes with indeterminated growth habit. FredericoWestphalen, RS, 2014

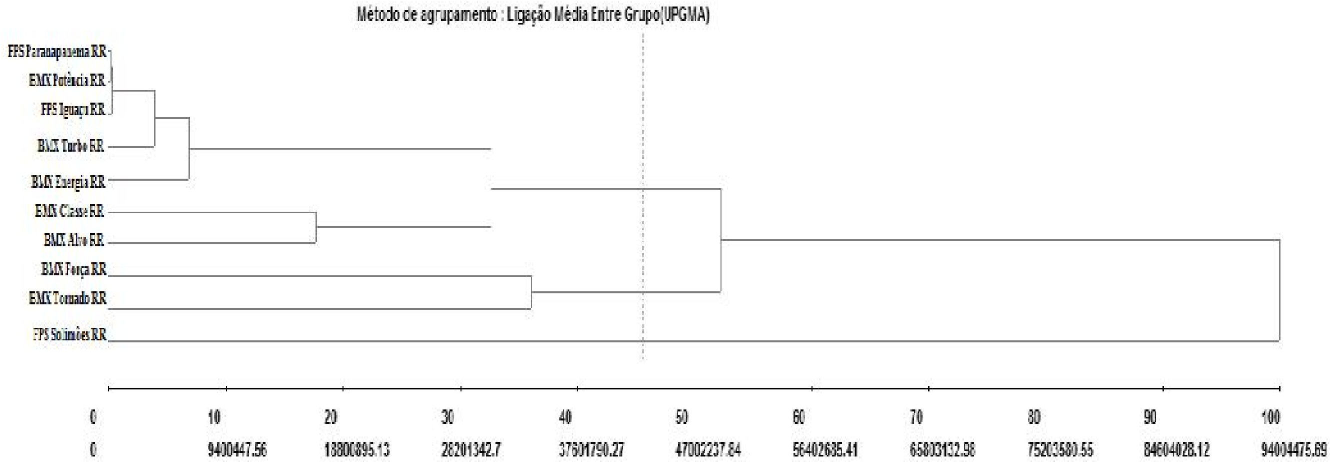
Effects	Explanatory variable							
	IFL	PH	NLMS	NLB	NB	BL	LINT	TGW
Direct via YIELD	-0.232	0.237	0.286	-0.074	-0.124	0.595	0.217	0.624
Indirect via IFL	-	-0.191	0.083	-0.066	-0.154	0.035	-0.127	0.023
Indirect via PH	0.196	-	-0.073	0.056	0.121	0.035	0.162	0.031
Indirect via NLMS	-0.103	-0.088	-	-0.070	-0.098	0.119	-0.176	-0.165
Indirect via NLB	-0.021	-0.017	0.018	-	-0.066	-0.040	0.023	0.024
Indirect via NB	-0.082	-0.063	0.042	-0.111	-	-0.039	0.004	0.041
Indirect via BL	-0.090	0.088	0.247	0.324	0.186	-	-0.270	-0.248
Indirect via LINT	-0.118	0.148	-0.134	-0.067	-0.007	-0.098	-	0.145
Indirect via TGW	-0.063	0.082	-0.366	-0.207	-0.205	-0.260	0.417	-
Total (r)	-0.300	0.219	0.139	-0.221	-0.359	0.405	0.272	0.539
Determination coefficient								0.859
K value used in the analyse								9.831
Residual effect of variable								0.376
Determining variable								2.998

YIELD = grain yield; IFL= insertion of first legume, PH = plant height, NLMS= number of legumes in main stem; NLB=number of legumes in branches; NB=number of branches; BL=branches lenght; LINT= internode lenght; TGW= thousand grain weight.
Source: data from the search.

Table 2. Relative contribution of characters for divergence – Singh (1981) in tem genotypes of soybean. Frederico Westphalen, RS, 2014

Variables	Vale (%)
Insertion of the first legume	9.06
Plan the height	0.18
Number of legumes in main stem	0.11
Number of legumes in branches	1.71
Number of nodes in main stem	0.68
Number of nodes in branches	11.66
Number of branches	12.30
Branches length	0.11
Number of legumes per node in main stem	0.51
Number of legumes per node in branches	57.50
Branches length	1.73
Number of legumes per plant	0.59
Thousand grain weight	0.02
Grain yield	3.81

Source: data from the search.



Source: data from the search.

Figure 1. Dendrogram with ten soybean genotypes of indeterminate growth habit through the clustering method of average linkage between groups (UPGMA). Genotypes: FPS Paranapanema RR, BMX Classe RR, FPS Solimões RR, BMX Potência RR, BMX Força RR, BMX Energia RR, BMX Turbo RR, FPS Iguaçu RR, BMX Tornado RR, BMX Alvo RR. FredericoWestphalen, RS, 2014

The length of the branches reveals the direct effects of intermediate low and positive correlation coefficients for grain yield (Table 1). The indirect effects can be observed coefficients of low and positive correlation via the main number of vegetables, and low and negative stem through the thousand grain weight. The Pearson correlation demonstrates correlation (r = 0.405) positiveandintermediate. The internode length reveals direct effects with low and positive correlation coefficients to grain yield (Table 1). Indirectly can be observed intermediate to low coefficients, but both positives thought of thousand grain weight and plant height. Low and negative indirect effects are observed by inserting the first legume, number of legumes and length in the main stem of the branches. Study of Souza *et al.* (2013), show correlation coefficients of high magnitude and positive through the character number of legumes, grains per plant and thousand grain weight, in relation to grain yield of soybean. The Pearson correlation proves to be low and positive (r = 0.272), explaining the relationship between internode length and the main character. The thousand grain weight presents itself as one of the most important characters to the productive potential of soybeans. Thus, if the direct effects observed, intermediate and positives coefficients to the main variable (Table 1.).Studies reveal that the dimensions and the weight of the grains influence to grain yield (Coimbra *et al*., 1999). The indirect effects observed were low and positive coefficients via internode length, low and negative through the number of legumes in the main branches and length of stem. Thus, heavier grains can be obtained by genotypes with reduced magnitude of vegetables and branches per plant. With this, the formation of structures less expensive energy, can contribute to better partitioning of assimilates between grains, favoring an increase in the size and for the weight of these grains, thus contributing to soybean yield.Study by Souza *et al.* (2014), point out the potential of soybean is due to leaf expansion, solar radiation interception, assimilation, conversion efficiency and entrainment of assimilates to reproductive structures. The Pearson correlation is revealed (r = 0.539) intermediate and positive towards thousand grain weight and grain yield. Phenotypic estimates of cause and effect in path analysis, are reliable due to the high value obtained in the coefficient of determination (0.859) and low residual effects (0.376). This way, highlights the importance of identifying the direct and indirect effects between the explanatory character and the main parameter in soybean with indeterminate growth habit. The method of Singh aims to determine the relative contribution of agronomic characters that influence the differentiation of genotypes (Table 2.). Thus, it is noteworthy that the dissimilarity of 10 soybean genotypes is grounded in characters, number of legumes per node in branches with 57.50% contribution, followed by number of branches with 12.30% and number of nodes per branch 11.66%.However, studiesby Almeida *et al.* (2011), show that the variable hundred grain weight reveals 26.56% of contribution to the genetic similarity between the soybean genotypes.

The characters, plant height, number of legumes on the main stem, number of nodes on the main stem, branch length, number of legumes per node on the main stem, number of legumes per plant and thousand grain weight, contributing to lower magnitudes 1.00% for the discrimination of genotypes.In studies performed by Adams *et al.* (2011), show lower contribution of the character number of legumes per plant for genetic dissimilarity. Cluster analysis aims at forming groups of contrasting genotypes for their characteristics. Thus, the genetic dissimilarity is estimated based on the Mahalanobis distance (Figure 1) which allows differentiating the genotypes into three groups. The group I is characterized as the largest group, consisting of six genotypes, such as, FPS Paranapanema RR, BMX Potência RR, FPS Iguaçu RR, BMX Turbo RR, BMX Energia RR , BMX Classe RR. The group II is formed by three genotypes: BMX Alvo RR, BMX Tornado RR e BMX Força RR. The group III is formed by only one genotype: FPS Solimões RR, this being the farthest in relation the other genotypes studied.

According to Bueno (2006), knowledge of dissimilarity between genotypes may contribute to the choice of the parents who will compose a block of crosses in a breeding program, which is extremely important to success of the activity for allowing the targeting of combinations between parents, where the hybridization between more dissimilar parents may result in increasing the variability in the segregating population.

Conclusion

The path analysis reveals the characters thousand grain weight and length of the branches direct effects with correlation coefficient of higher magnitude to grain yield. Significant indirect effects are revealed through the length of the internode. The method of Singh reveals that the characters number of branches and nodes in the branches largest contribution to distinguish between genotypes. The Mahalanobis distance reveals formation of three groups, where genotypes belonging to grups I and II are more distant, and may increase genetic variability in the formation of a crossing block.

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