COMMUNICATIONS IN PLANT SCIENCES

Path analysis and traits correlation in soybean

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This work aimed to study agronomic traits of soybean genotypes by path analysis and correlation estimates. We have used a randomized complete block design to assess 35 soybean genotypes with three replications, which 31 lines were from the breeding program of the Federal University of Uberlândia, Brazil, plus four commercial cultivars. We have assessed features number of days to the blooming, plant height at blooming, number of days to maturity, plant height at maturity, first pod height, number of nodes on the main stem at maturity, number of pods with one, two and three seeds per plant, total number of pods per plant, number of seeds per pod and grain yield. The features plant height at maturity and number of nodes at maturity have presented significant correlations phenotypic and genotypic positive. 100-seed weight was positively correlated with grain yield shown high direct phenotypic and genotypic effects being, therefore, useful for indirect selection aiming the grain yield increase.

Highlighted Conclusion
The approaches correlation and path analysis of agronomic traits of major importance in soybean lines are efficient in assessing interconnections between yield and other agronomic traits in soybean. The features plant height at maturity and number of nodes are positively correlated. 100-seed weight is positively correlated to grain yield, and correlations between the number of days to the blooming and average weight of 100 seeds are negative.

Correlation coefficients are dimensionless and might fluctuate, positively or negatively, over a range from -1 to 1 (Cruz et al. 2012); it is a intensity measure of linear association between two variables. Correlation coefficients might be phenotypic, genotypic and environmental; its main function is to evaluate the relation between the traits. Phenotypic correlation is estimated by phenotypic measures which are made up by genetic and environmental causes. Therefore, genotypic correlation is the genetic portion of the phenotypic correlation used in breeding programs; because only genes can be inherited by the offspring (Ferreira et al. 2003).

Knowledge of characteristics correlated to grain yield allows the breeder to use additional information in order to either, rule out or precisely promote genotypes of interest (Pandini et al. 2002). Rodrigues et al. (2010) claim that simple correlation coefficients do not represent the relationship of cause and effect between characteristics. It is because the high correlation between two characters can be misleading due the indirect effect promoted by other features (Dewey and Lu 1959). Therefore, Wright (1921) developed a method in order to better understand the causes of associations between characters originated from the analysis of correlations, which is called path analysis. This method allows unfolding the correlations into direct and indirect effects of variables in just on a base variable (Wright 1921).

According to Cruz et al. (2012), path analysis is set up as a standardized regression coefficient, being an analytical expansion of multiple regression. The success of such procedure lies upon the correct formulation of the cause and effect relationship between variables (Gondim et al. 2008). In addition, the unfolding of correlations depends on the set of the studied characters, which are established by the breeder's knowledge, its importance and its possible interrelations, which are demonstrated in the track diagrams (Cruz et al. 2012).

The main objective of this study was studying the correlation and path analysis of agronomic traits in soybean lines, which were originated from the breeding program of the Federal University of Uberlandia.

MATERIAL AND METHODS

The experiment was carried out during the 2011/12 season. Treatments were made up by 35 soybean genotypes. That included 31 lines from the Improvement Program of the Federal University of Uberlandia plus four cultivars recommended to the region. Cultivars UFOS 7910, BRSGO7560, UFUS Xavante, M-Soy 8866, were used as witnesses.

Randomized complete block design with three replications was used. Due the reduced number of seeds available for every line, each experimental was made up by soybean plants disposed in rows of 5 m length. Spacing between rows was 0.5 m. Only data from central 4 m of each row was used to evaluations, disregarding 0.5 m at the row ends. Remaining a study area that was equals to 2 m^2 in each plot.

Agronomic traits of major importance was used in order assess correlations between yield and other agronomic traits in soybean. Data were obtained through measuring of phenological stages of development of the culture, recommended by Fehr and Caviness (1977). Agronomic traits evaluated were: number of days to the blooming (NDF), plant height at blooming (APF), number of days to maturity (NDM), plant height at maturity (APM), first pod height (AIV), number of nodes on the main stem at maturity (NNM), number of pods with one grain (NV1), number of pods with two grains (NV2), number of pods with three grains (NV3), total number of pods per plant (NVT), average 100-seed weight (PMG), number of grains per pod (NGV) and grain productivity (PROD).

Phenotypic and genotypic correlations were estimated by using equations:

a) Phenotypic correlation:

$$rf = \frac{PMGxy}{\sqrt{QMGx\ QMGy}}$$

where:

PMGxy: average product between the genotypes of the characters X and Y; QMGx: mean square between genotypes of the X character; QMGy: mean square between genotypes of the Y character;

b) Genotypic Correlation:

$$r_g = \frac{PMG_{xy} - PMR_{xy})/r}{\sqrt{\widehat{\emptyset}_{g(X)}\widehat{\emptyset}_{g(Y)}}} = \frac{\widehat{\emptyset}_{g(xy)}}{\sqrt{\widehat{\emptyset}_{g(X)}\widehat{\emptyset}_{g(Y)}}}$$

$$\widehat{\emptyset}_{g(X)} = \frac{QMG_X - QMR_X}{r}$$

$$\widehat{\emptyset}_{g(Y)} = \frac{QMG_X - QMR_X}{r}$$

where: $\widehat{\emptyset}_{g(XY)}$: genotypic covariance estimator; $\widehat{\emptyset}_{g(X)}$ and $\widehat{\emptyset}_{g(Y)}$: estimators of the squared components associated to genetic variability of the X and Y characters, respectively.

Significant phenotypic correlations were observed by T test with n-2 degrees of freedom, where n is the number of genotypes. Significance of genotypic correlation was assessed by bootstrap with 5,000 simulations.

Explanation of the soybeans production was given by the multiplicative mathematical model: Grain production (PROD) = number of pods per plant (NVT) x number of seeds per pod (NGV) x average weight of a grain (PMG). As requirement for using dynamic path analysis is an additive model, logarithm was taken in order to reach this purpose (Santos et al. 1995).

Diagnosis of multicollinearity was carrying out to twelve characters. Multicollinearity of X'X matrix was established according to criteria suggested by Montgomery and Peck (1981), wherein the values of the determinant and the number of condition (NC) were given by the ratio between the largest and smallest matrix eigenvalue. Elements of the eigenvectors associated to eigenvalues were analyzed in order to identify the characters which contributed to the emergence of multicollinearity, according Belsley et al. (1980). Variables that contribute to multicollinearity from moderate to severe levels were eliminated from the path analysis, as recommended by Bizeti (2004).

Analyses were performed using the GENES software (Cruz 2006).

RESULTS AND DISCUSSION

Table 1 shows the outcomes of genotype determination coefficient (H2) outcomes. It was found H2 ranged from 44.42 to 95.04% for the total number of pods and seed number per pod, respectively. High values of H2 coefficient indicates that the nature of the variability observed is made up mainly by genetic causes (Cruz et al. 2012, Ramalho et al. 2012). Similar results were found by Yokomizo & Vello (2000), Lopes et al. (2002) and Silveira et al. (2006), who studied some of these soybean characteristics.

Table 1. Genotypic determination coefficient for agronomic traits of soybean genotypes evaluated in 35 genotypes, 2011/12 season, Uberlândia, MG, Brazil.

Characteristic	(H^2)
Number of days to the blooming (NDF)	82.15
Plant height at the blooming (APF)	66.89
Number of days to maturity (NDM)	91.64
Plant height at maturity (APM)	86.30
Height of the first pod (AIV)	81.71
Number of nodes on the main stem at maturity (NNM)	81.32
Number of pods with one grain (NV1)	74.60
Number of pods with two grains (NV2)	74.65
Number of pods with two grains per plant (NV3)	84.50
Number of pods per plant (NTV)	44.42
100-seed weight (PMG)	77.37
Number of grain per pod (NGV)	95.04
Grain yield (PROD)	72.95

Table 2 shows the phenotypic and genotypic correlations outcomes. In order to perform the interpretation of correlations three aspects must be taken into account: magnitude, direction and significance (Cruz et al. 2012). Positive correlation coefficients indicate that the studied variable tends to increase along with the correlated variable, whereas negative correlation coefficients indicate the opposite effect, meaning a variable tends to increase while the other variable decreases.

According to Lopes et al. (2002), although there are estimates for the levels of significance of the statistical correlations, there is a tendency among plant breeders to interpret just the sign, that might be positive or negative, and the magnitude of those values. Therefore, the criteria used in the valuation take into account estimates above

-0.5 and below 0.5. For this reason, in the interpretation of the results concerning the correlations found this study, we adopted the criteria suggested by Lopes et al. (2002) and Cruz et al. (2012).

Table 2. Phenotypic (rf) and genotypic (rg) correlations of nine agronomic characters in 35 soybean genotypes, 2011/12 season, Uberlândia, MG, Brazil.

Characteristic		APF	NDM	APM	AIV	NNM	NV3	NVT	NGV	PMG	PROD
NDF	rf	0,13^{ns}	0,33^{ns}	0,12^{ns}	0,41*	0,34*	0,08^{ns}	0,31^{ns}	-0,09^{ns}	-0,48**	-0,35*
	rg	0,30^{ns}	0,35^{+}	0,17^{ns}	0,50^{++}	0,47^{+}	0,12^{ns}	0,55^{+}	-0,09^{ns}	-0,56^{++}	-0,42^{+}
APF	rf		0,10^{ns}	0,41*	0,40*	0,13^{ns}	0,05^{ns}	0,23^{ns}	-0,08^{ns}	0,25^{ns}	0,2^{ns}
	rg		-0.10^{ns}	0,44^{+}	0,48^{+}	0,09^{ns}	0,02^{ns}	0,25^{ns}	-0,09^{ns}	0,31^{ns}	0,28^{ns}
NDM	rf			0,09^{ns}	0,41*	0,34*	-0,05^{ns}	-0,07^{ns}	0,05^{ns}	-0,16^{ns}	-0,55**
	rg			0,13^{ns}	0,49^{++}	0,41^{+}	-0,04^{ns}	-0,09^{ns}	0,06^{ns}	-0,20^{ns}	-0,68^{++}
APM	rf				0,44**	0,68**	-0,28^{ns}	-0,16^{ns}	-0,2^{ns}	0,20^{ns}	0,07^{ns}
	rg				0,48^{++}	0,74^{++}	-0,38^{+}	-0,34^{ns}	-0,24^{ns}	0,19^{ns}	0,07^{ns}
AIV	rf					0,38*	0,18^{ns}	0,09^{ns}	0,14^{ns}	0,02^{ns}	-0,21^{ns}
	rg					0,42^{+}	0,19^{ns}	0,14^{ns}	0,15^{ns}	0,04^{ns}	-0,20^{ns}
NNM	rf						-0,07^{ns}	0,05^{ns}	-0,08^{ns}	0,16^{ns}	-0,07^{ns}
	rg						-0,17^{ns}	-0,12^{ns}	-0,12^{ns}	0,16^{ns}	-0,12^{ns}
NV3	rf							0,29^{ns}	0,82**	0,16^{ns}	0,34*
	rg							0,14^{ns}	0,87^{++}	0,19^{ns}	0,37^{ns}
NVT	rf								-0,28^{ns}	-0,01^{ns}	0,30^{ns}
	rg								-0,36^{ns}	-0,05^{ns}	0,31^{ns}
NGV	rf									0,17ns	0,12^{ns}
	rg									0,19ns	0,14^{ns}
PMG	rf										0,67*
	rg										0,70^{++}

**, *: Significance level 1% and 5%, respectively. ++, +: Significance level 1% and 5%, respectively, by the bootstrap method with 5000 simulations.. NDF and NDM: number of days to the blomming and to maturity, respectively; APF and APM: plant height at blooming and at maturity, respectively; NNM: number of nodes on the main stem at maturity; AIV: first pod height; PROD: grain yield; NVT: total number of pods per plant; PMG: average 100-seed weight; NV3: number of pods with three grains; NGV: number of grains per pod.

Table 2 shows that highest significant estimates of phenotypic and genotypic correlations were found to plant height at maturity and number of nodes at maturity, average 100-seed weight and grain yield, number of days to maturity and grain yield, number of days to the blooming and average weight of hundred grains, number of days to the blooming and height of the first pod, number of days to the blooming and total number pods per plant, number of days to the blooming and grain yield, number of pods with three grains and grain yield.

Pods with three grains and the number of seeds per pod presented significant positive correlation and high magnitude, showing that the evaluated lines exhibit large numbers of pods with three grains, reflecting the competitiveness of the lines studied against the current elite cultivars.

Results of phenotypic and genotypic correlations between plant height at maturity and number of nodes at maturity were significant and positive, showing high magnitude that corroborate results found by Bizeti et al. (2004) and Nogueira et al. (2012).

Correlations between number of days to the blooming and 100-seed weight were significant and negative. Bizeti et al. (2004) and Nogueira et al. (2012) also found such results when they evaluated correlations between soy characters in two sowing dates.

Estimates of correlation between number of days to the blooming and height of the first pod, and number of days to the blooming and total number of pods, were significant and positive. Nogueira et al. (2012) and Pelúzio et al. (2005) found similar outcomes in sowing carried out in December and in evaluations of those characteristics in nine cultivars sown in 2000/01 in Gurupi-TO, respectively. Nogueira et al. (2012) found no significant correlations between the number of days to the blooming and the total number of pods in the sowing of February. However, the study of correlation evaluations between characters in twelve soybean genotypes planted during the off-season in Tocantins 2007 (Almeida et al. 2010) found differs results from the current study. Thus, it is noted that the correlation between those characters might vary as a function of the genotypes and environments evaluated.

Phenotypic and genotypic correlations between grain yield and number of days to blooming and maturity were significant and negative (Table 2). These results differ from those found by Nogueira et al. (2012), who observed positive and significant correlations studding 90 soybean genotypes grown in two sowing dates. As well as the results found in the current work differ from those results found in the study made by Carvalho et al. (2002), who evaluated correlations between agronomic traits of soybean lines from different crossings in three sowing times in two seasons.

On the other hand, similar results were found by Salimi and Moradi (2012), who studied correlations between soy characters in normal conditions of humidity and water stress conditions. These authors observed significant and positive correlations between the number of days to maturity and grain yield under normal humidity conditions; however, under water stress conditions they found statistically significant and negative correlations. By observing the meteorological data that was collected during the experiment it was found that in the growing season precipitation occurred around 500 mm. According to Embrapa (2011) in order complete its cycle soybean crop requires between 500 and 800 mm of water; depending on climate. Arshad et al. (2006) as well as Machikowa and Laosuwan (2011) also found negative correlations between days to maturity and grain yield under normal growing conditions.

In the current study, assessment of correlations between 100-seed weight and grain yield it was statistically significant and positive estimates (Table 2). This result implies that productivity is positively affected by the average weight of the seeds, but it is also opposite to the results found by other authors (Carvalho et al. 2002, Nogueira et al. 2012). Those authors also point out that soy often promotes compensation in grain size as a function to the number of pods. Thus, it can be explain the lack of correlation between total number of pods and seed yield.

The simultaneous inclusion of number of pods with one and two grains, number of grains per pod and number and days to the blooming in the analyses generate multicolinearity in the matrix of phenotypic and/or genotypic correlations. Therefore, based on the criteria suggested by Bizeti (2004) it was excluded from the path analysis.

Table 3 shows the path analysis outcomes was resulting by unfolding the phenotypic and genotypic correlations. Phenotypic correlation coefficients and genotypic obtained for path analysis were 0.8 and 1.0, respectively. It implies that most of the variation of the basic variable, that is grain yield, was explained by characters included in the path diagram. Correlation analysis suggested that the characters such as number of pods with three grains and the average 100-seed weight are useful for indirect selection aiming grain yield. By observing the path analysis results shown in Table 3, it was noted that the number of pods with three grains offer a low direct effect on the phenotypic grain yield.

Moreover, it was detected high magnitude of phenotypic and genotypic direct effects of the average 100-seed weight character over the grain yield; this indicates that there is potential for indirect selection by the average grain weight, since this character has a high coefficient of genotypic determination (above 70%). These results corroborate those outcomes reported by El-Badawy and Mehasen (2012), who evaluated the correlation between agronomic traits belonging to five soybean genotypes, sown in three planting densities in two years of cultivation.
Results found to the other direct and indirect effects, whether phenotypic and genotypic were irrelevant and therefore rejected, as it showed low magnitudes and values below the residual effects.

CONCLUSION

Most of variability observed to the total number of pods and seed number per pod is due to genetic causes.
Correlations between features plant height at maturity and number of nodes at maturity are positive.
Correlations between number of days to the blooming and 100-seed weight are negative.
Character 100-seed weight is positively correlated to grain yield therefore, useful for indirect selection aiming grain yield increase.

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Table 3. Estimation of direct effects, indirect phenotypic (E.F) and genotypic (E.G.) of characters APF, NDM, APM, AIV, NNM, NV3, PMG and NTV regarding grain yield in 35 soybean genotypes in Uberlândia, MG, Brazil.

Effects Description	Primary Component		Effects Description	Primary Component	
	Yielding			Yielding	
	E.F	E.G		E.F	E.G
Direct effect of APF	0,0608	-0,4947	Direct effect of NNM	-0,1567	-0,9652
Indirect effect via NDM	-0,0332	-0,0047	Indirect effect via APF	0,0078	-0,0442
Indirect effect via APM	0,1370	0,7555	Indirect effect via NDM	-0,1172	-0,0135
Indirect effect via AIV	-0,1087	-0,2940	Indirect effect via APM	0,2279	1,2598
Indirect effect via NNM	-0,0201	-0,0863	Indirect effect via AIV	-0,1053	-0,2529
Indirect effect via NV3	0,0362	0,0966	Indirect effect via NV3	-0,0086	-0,0768
Indirect effect via PMG	0,1219	0,1353	Indirect effect via PMG	0,0666	0,0580
Indirect effect via NTV	0,0618	0,1776	Indirect effect via NTV	0,0111	-0,0873
Total	0,2558	0,2853	Total	-0,0744	-0,1222
Direct effect of NDM	-0,3434	-0,0325	Direct effect of NV3	0,2761	0,7384
Indirect effect via APF	0,0059	-0,0710	Indirect effect via APF	0,0080	-0,0648
Indirect effect via APM	0,0300	0,2294	Indirect effect via NDM	-0,0124	-0,0017
Indirect effect via AIV	-0,1133	-0,2949	Indirect effect via APM	-0,0844	-0,5498
Indirect effect via NNM	-0,0535	-0,4003	Indirect effect via AIV	-0,0498	-0,1181
Indirect effect via NV3	0,0099	0,0396	Indirect effect via NNM	0,0048	0,1004
Indirect effect via PMG	-0,0609	-0,0689	Indirect effect via PMG	0,1551	0,1670
Indirect effect via NTV	-0,0225	-0,0785	Indirect effect via NTV	0,0766	0,1386
Total	-0,5477	-0,6769	Total	0,3741	0,4097
Direct effect of APM	0,3353	1,6969	Direct effect of PMG	0,4902	0,4530
Indirect effect via APF	0,0249	-0,2203	Indirect effect via APF	0,0151	-0,1478
Indirect effect via NDM	-0,0308	-0,0044	Indirect effect via NDM	0,0427	0,0049
Indirect effect via AIV	-0,1223	-0,2890	Indirect effect via APM	0,0528	0,2396
Indirect effect via NNM	-0,1065	-0,7166	Indirect effect via AIV	-0,0128	-0,0378
Indirect effect via NV3	-0,0695	-0,2392	Indirect effect via NNM	-0,0213	-0,1235
Indirect effect via PMG	0,0772	0,0639	Indirect effect via NV3	0,0874	0,2721
Indirect effect via NTV	-0,0348	-0,2164	Indirect effect via NTV	0,0052	0,0206
Total	0,0734	0,0750	Total	0,6593	0,6814
Direct effect of AIV	-0,2776	-0,6066	Direct effect of NVT	0,2530	0,7432
Indirect effect via APF	0,0238	-0,2398	Indirect effect via APF	0,0149	-0,1182
Indirect effect via NDM	-0,1401	-0,0158	Indirect effect via NDM	0,0306	0,0034
Indirect effect via APM	0,1477	0,8086	Indirect effect via APM	-0,0461	-0,4941
Indirect effect via NNM	-0,0595	-0,4024	Indirect effect via AIV	-0,0240	-0,0669
Indirect effect via NV3	0,0496	0,1437	Indirect effect via NNM	-0,0069	0,1134
Indirect effect via PMG	0,0226	0,0282	Indirect effect via NV3	0,0836	0,1377
Indirect effect via NTV	0,0219	0,0820	Indirect effect via PMG	0,0100	0,0125
Total	-0,2115	-0,2021	Total	0,3151	0,3311
Residual effect				0,4417	0,0000
R^2				0,8049	1,1059

R^2: coefficient of determination; APF: plant height at the blooming; NDM: number of days to maturity; APM: plant height at maturity; AIV: First pod height; NNM: number of nodes on the main stem at maturity; NV3: number of pods with three grains; PMG: average weight of hundred seeds; NVG: number of grains per pod.

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