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Genetic parameters, correlations and path analysis in cowpea genotypes for yield and agronomic traits grown in *Cerrado*/Amazon Rainforest ecotone

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Abstract: The development of superior genotypes is the main objective of all plant breeding programs. To determine the genetic variability, heritability and correlations, 20 cowpea genotypes were grown in a randomized block design with four replications in *Cerrado*/Amazon Rainforest ecotone region. The data recorded were plant height, pod length, pod mass, pod grain mass, grain index, pod grain number and yield. Analysis of variance revealed significant differences between genotypes for all traits studied. The genotypic determination coefficient was high for all traits evaluated. Similarly, the accuracy parameter presented high estimates (>0.90). The magnitudes of the genotypic correlation coefficients were higher than the environmental and phenotypic correlations for most correlations, showing a greater influence of the genetic factor than the environmental factors. The direct and indirect effects provided greater reliability in the cause and effect interpretations between the studied traits, indicating that yield can be explained through the effects of the analyzed traits. The traits pod mass (0.9628) and pod grain mass (0.7835) showed the greatest favorable direct effect, showing a strong association between the analyzed characters and can be used in direct or indirect selection for yield in cowpea.

1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the oldest crops known to man and, because its moderate drought resistance, grows mainly in tropical climate areas (Egbadzor *et al.*, 2014). Recent studies suggest it originated from Central Africa over 4,000 years ago (Ogunkanmi *et al.*, 2014). According to Rocha *et al.* (2009), cowpea is a valuable legume, predominantly cultivated in Brazil, Africa and the United States. In the Brazilian North and Northeast regions, it is one of the main population's diet components, especially in rural areas (Santos *et al.*, 2014).

This crop still has low yields, despite the fact that its high adaptive potential to the conditions of tropical climate environments is verified

(Leite *et al.*, 2009). Teixeira *et al*. (2010) point out as causes the management techniques adopted and, mainly, the inefficiency of the technologies used and the use of traditional cultivars without breeding for yield. In Brazil there are cultivars with good commercial acceptance, but breeding programs aimed at evaluation and recommendation in specific environments are concentrated only in large producing centers (Oliveira *et al*., 2002; Barili *et al*., 2015).

One of the cowpea breeding programs basic goals is to obtain more productive genotypes. The availability of variance components estimates and genetic parameters such as coefficient of genetic variation, heritability and correlation coefficients for yield and their components are essential for the plant breeding programs development. These genetic parameters are characteristic of each population and may change in consequence of selection, changes in management, methods and estimation models, among other causes.

However, an important aspect about yield is that it is characterized as a complex variable, i.e., resulting from the expression and different components association (Santos *et al*., 2018). Correlation quantifies the association between any two variables. However, it does not allow inferences about cause and effect (Furtado *et al.*, 2002). The path analysis, proposed by Wright (1921), allows to partition the correlation coefficient into direct and indirect effects (path coefficient). For Cruz *et al.* (2014), this analysis can be defined as a standardized regression coefficient, being an expansion of the multiple regression analysis when complex interrelationships are involved.

In this sense, knowing the association between these traits allows the breeder to explore the possibility of indirect selection in cases of traits with complex inheritance and low heritability, such as yield. Correlation coefficient estimates make it possible to evaluate the magnitude and direction of the relationship between two traits and, consequently, the possibility of obtaining gains for one of them using indirect selection for the other trait. In some cases, indirect selection based on correlated response may be more effective and faster than direct selection of the desired trait (Cruz *et al*., 2014).

Thus, this research was conducted with the objective of estimating the genetic parameters for the yield and its components in 20 cowpea genotypes population cultivated in the Cerrado/Amazon Rainforest ecotone region in Brazil. As well as, investigate the associations between traits to direct selection strategies in breeding programs with this crop. Study results may assist in strategies for breeding and manipulation of traits by cowpea breeders in Brazil or other similar environments.

2. Materials and Methods

The experiment was carried out in Imperatriz city, Maranhão State, Brazil, in the experimental field of the *Centro de Difusão Tecnológica* (CDT) on premises of *Empresa Brasileira de Infraestrutura Aeroportuária* (INFRAERO) of geographic coordinates Latitude South 5°31’32’’ and Longitude West 47°26’35’’, and altitude of 123.30 meters. According to the Köppen climate classification, the region’s climate is Aw, tropical savanna, with tropical wet and dry climate (Peel *et al*., 2007).

The survey of climate monitoring data for the region over the past 20 years was carried out. Data on annual total precipitation, maximum, minimum and average annual temperatures were collected. The data were obtained from an automatic climate monitoring station made available in the governmental meteorological database *Banco de Dados Meteorológicos para Ensino e Pesquisa* (BDMEP) administered by the Brazilian meteorology institute *Instituto Nacional de Meteorologia* (INMET). The time series graphs were produced using the ggplot2 package in the R software.

The treatments consisted in twenty erect habit cowpea genotypes from the Active Germplasm Bank (AGB) from the *Empresa Brasileira de Pesquisa Agropecuária* (EMBRAPA Meio Norte) cowpea genetic breeding program, located in Teresina, Brazil, 15 lines and 5 cultivars, respectively: LF-3; LF-21; LF-30; LF-48; LF-49; LF-62; LF-104; LF-143; LF-144; LF-148; LF-153; LF-154; LF-155; LF-159; LF-168; BRS-Guariba; BRS-Tumucumaque; BRS-Nova Era; BRS-Itaim; and BRS-Cauamé.

The soil physical and chemical characteristics were determined before the experiment beginning, from the superficial soil samples collected at random points in the experimental field up to 0.20 m depth. Soil texture was analyzed by the modified soil sedimentation Bouyoucos method after addition of a dispersing agent. Potential acidity was estimated from SMP pH after pH determination in calcium chloride 0,01 mol L^{-1} (Shoemaker *et al.*, 1961). Soil macronutrients and micronutrients analysis was performed to develop fertilizer recommendations.

The experimental design was a randomized complete block with 20 treatments and four replications.

The experimental plot consisted of two lines of 4.0 m and spacing of 0.50 m between lines and 0.20 m between plants, constituting a total experimental area of 220.00 m². Soil tillage was carried out in a conventional manner with one plow and two harrows. The digging and sowing operations were manual. From the chemical soil analysis, was performed the fertilization according to the requirements of the crop (Table 1). Irrigation was carried out by means of a sprinkler system sized to the crop and the region requirements, applying a daily water of 3.8 mm h^{-1}.

Invasive plants were controlled by hand weeding, performed weekly. Phytosanitary treatments were carried out through regular monitoring of pests and diseases, using the commercial insecticide Conect® when necessary. The harvest was performed when the pods of the plot were dry, totaling two harvests. The drying of the pods was completed in a forced air circulation oven, where the pods remained for two days at a temperature of 38°C.

In the useful area of each plot were recorded the following data: plant height (PH): average height in cm randomly measured in five plants of the plot; pod length (PL): average length in cm of five randomly harvested pods in the plot useful area; pod mass (PM): in grams, considering the five previously harvested pods; pod grain mass (PGM): in grams, considering the grains of the five pods submitted to the aforementioned evaluations; grain index (GI): refers to the dry grain mass in the dried pods. It is obtained by the expression:

$$GI = PGM/PM \text{ X } 100$$

seeds per pod (SPP): performed by counting the seeds in the five pods harvested for the previous samples; and yield: estimate considering the yield in all the useful plot area (m^2), extrapolating the value obtained for kg ha^{-1} correcting the value for grain mass to 13% moisture.

The collected data were initially submitted to the Shapiro-Wilk test to verify the data set normality and the Bartlett test to verify if the error has homogeneity of variance (homoscedasticity), not presenting the need for data transformation. Subsequently, one-way analysis of variance was performed to test the variability between genotypes, adopting the statistical model described in the equation below:

$$Y_{ij} = \mu + G_i + B_j + \mathcal{E}_{ij}$$

where:
Y_{ij} = observed trait value of the i-th genotype in the j-th block;
μ = general experimental mean;
G_i = effect of the i-th genotype considered fixed;
B_j = effect of the j-th block considered random;
$\mathcal{E}_{ij}$ = random error associated to the i genotype and j block observations.

To understand the genotypic variability between the different traits measured, the components of phenotypic variance and genetic parameters were also estimated using the expressions suggested by Cruz *et al*. (2014):

a) Phenotypic variance: $\sigma^2_P = MS_g/b$
b) Environmental variance: $\sigma^2_E = MS_E/b$
c) Genotypic variance: $\sigma^2_G = (MS_g - MS_E)/b$
d) Genotypic determination coefficient: R^2 $(\sigma^2_G/\sigma^2_P) \times 100$
e) Intraclass correlation coefficient:
$ICC = \sigma^2_G/(MS_E+\sigma^2_G) \times 100$
f) Phenotypic coefficient of variation (%):

$$PVC = \frac{\sqrt{\sigma^2_P}}{\bar{x}} \times 100$$

g) Genotypic coefficient of variation (%):

$$GCV = \frac{\sqrt{\sigma^2_G}}{\bar{x}} \times 100$$

h) Environmental coefficient of variation (%):

$$ECV = \frac{\sqrt{MS_E}}{\bar{x}} \times 100$$

i) b quotient: $\frac{GCV}{ECV}$ ratio = $\sqrt{\frac{\sigma^2_G}{MS_E}}$

where: MS_g is the mean square of genotypes; MS_E is the mean square of error; b = number of blocks (replications) and $\bar{x}$ is the is the average of each trait.

j) Accuracy: $\hat{r} = (1 - 1/F)^{0.5}$
where Snedecor's F is the value of the variance ratio

Table 1 - Soil chemical characterization used in the field experiment

pH ($CaCl_2$)	OM (g Kg^{-1})	P (mg dm^{-3})	K (cmol dm^{-3})	Ca (cmol dm^{-3})	Mg (cmol dm^{-3})	Al (cmol dm^{-3})	H+Al (cmol dm^{-3})	SB (cmol dm^{-3})	CEC (cmol dm^{-3})	V (%)
4.8	18.4	13.5	0.26	1.66	0.69	0.00	1.70	2.61	4.31	60.5

OM= organic matter; P= phosphorus; K= potassium; Ca= calcium; Mg= magnesium; Al= Aluminium; H+Al= potential acidity; SB= sum of bases; CEC= Cation exchange capacity; V= base saturation.

for treatment effects (genotypes) associated with analysis of variance (ANOVA).

In the estimates of the correlations were used the expressions cited by Falconer (1987) and Ramalho *et al.* (1993):

a) Phenotypic correlation: $\Upsilon_{P(XY)} = \dfrac{COV_{P(XY)}}{\sqrt{\sigma^2{}_{PX} . \sigma^2{}_{PY}}}$

b) Genotypic correlation: $\Upsilon_{G(XY)} = \dfrac{COV_{G(XY)}}{\sqrt{\sigma^2{}_{GX} . \sigma^2{}_{GY}}}$

c) Environmental correlation: $\Upsilon_{E(XY)} = \dfrac{COV_{E(XY)}}{\sqrt{\sigma^2{}_{EX} . \sigma^2{}_{EY}}}$

where: Υ_{XY} is the correlation between the characters X and Y; COV_{XY} is the covariance between the characters X and Y; and, and $\sigma^2{}_Y$ ad $\sigma^2{}_X$ are the variances of the characters X e Y, respectively.

The unfolded of these correlations into direct and indirect effects of the six agronomic traits on yield was performed using the path analysis described by Cruz *et al*. (2014). The level of the multicollinearity of the *X'X* singular matrix was established by the product of the respective diagonal element of *X'X* by the component of the residual variance according to the methodology proposed by Montgomery *et al*. (2012). After verifying the multicollinearity of the phenotypic correlation matrix, this was implanted in direct and indirect effects, considering the following equation:

$Y = p_1X_1 + p_2X_2 + ... + p_nX_n + p_\varepsilon u$

where Y is the main dependent variable yield. X_1, X_2......, Xn are the independent variables. p_1, p_2, .. p_n are the path coefficients. The coefficient of determination was calculated by the expression

$R^2 = p^2{}_{1y} + p^2{}_{2y} + ... 2p_{2y}.p_{2n\Upsilon 2n}$

The estimates of the components of the phenotypic variance, genetic parameters, correlations between traits and path analysis were obtained using the computational application GENES (Cruz, 2013).

3. Results and Discussion

Timeless climate data and information

Over the past 20 years, the average annual air temperature has varied between 27.37 and 28.84°C (Fig. 1). The highest annual temperature observed was 35.22, in 2015. On the other hand, the lower annual temperature observed was 20.78°C, in 2018. The deviations observed for the maximum, minimum and average annual temperatures were ±0.57°C, ±0.70°C and ±0.41°C, respectively. Total annual precipitation ranged from 1961.30 mm in 2016, to 498.50 mm in 2000 (Fig. 1). Because this great difference between the results collected for total annual precipitation, there was a large deviation for this parameter, value equal to ±0358.38. The average of annual total precipitation over the last 20 years was 1395.85 mm.

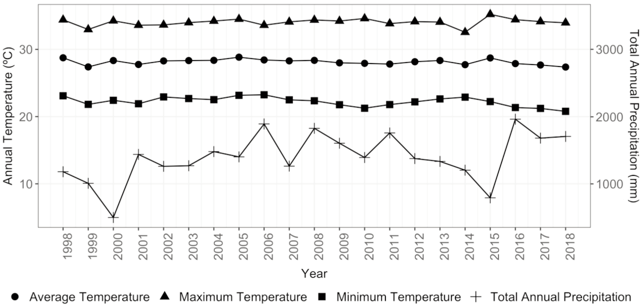

Fig. 1 - Annual maximum temperature, annual minimum temperature, average annual temperature and total annual precipitation of the last twenty years (1998-2018) in a region characterized by the Cerrado/Amazon Rainforest ecotone (INMET, 2019).

Estimates of genetic parameters

The analysis of variance showed a significant effect (p<0.01) between the genotypes according to the F test for all evaluated characteristics (Table 2), showing genetic variability presence in the population. Considering the existence of genetic variability in a population is a determining factor for any breeding program (Ramalho *et al*., 2012), at first, the germplasm under study is promising for selection or hybridization work with potential for new cultivars development. Similarly, Araméndiz-Tatis *et al*. (2018) also detected significant differences for the same traits evaluated in an assay where they estimated the genetic parameters of traits associated with yield in 42 white seed cowpea genotypes.

The relative standard deviation (RSD), which is used to estimate the experiments precision, presented values considered low for the traits PH, PL, PM, MGV and GI, which indicates excellent experimental precision. While for the characteristics SPP and Yield presented RSD equal to 12.24% and 21.86%, therefore, they are considered regular values, indicating good experimental precision (Cruz *et al*., 2014; Ferreira, 2018) (Table 2). Similar results for the same

Table 2 - Analysis of variance summary for the traits plant height (PH), pod length (PL), pod mass (PM), pod grain mass (PGM), grain index (GI), seeds per pod (SPP) and Yield in 20 cowpea genotypes evaluated in Cerrado/Amazon Rainforest ecotone region, Brazil, 2019

Variation source	DF	PH (cm)	PL (cm)	PM (g)	PGM (g)	GI (%)	SPP	Yield (Kg ha-1)
		Mean square						
Blocks	3	46.46	1.61	5.54	5.05	112.71	75.61	120831.01
Genotypes	19	319.08 **	4.28 **	34.85 **	13.43 **	112.71 **	238.99 **	136000.33 **
Error	57	6.46	0.70	0.99	0.55	16.19	21.72	20004.46
Mean	-	65.36	20.22	18.57	14.40	78.12	75.74	647.03
RSD (%)	-	3.89	4.14	5.35	5.17	5.15	6.15	21.86
I.V. (%)	-	1.95	2.07	2.68	2.59	2.58	3.08	10.93

DF= degrees of freedom; (**) significant at 1% probability of error by the F test; RSD= relative standard deviation; VI= variation index.

traits were obtained by Carvalho *et al.* (2012) and Correa *et al*. (2015).

The variation index (VI), another parameter related to the experimental precision, proposed by Gomes (1991), which is more adequate than the RSD, as it also considers the number of repetitions used in the experiment, besides the residual variation, presented low values for all traits, except for productivity that presented value of IV considered of medium magnitude.

The success of the selection depends on the existence and magnitude of the observed genetic variability for yield and its components in the material under breeding (Adewale *et al.*, 2010; Raturi *et al.*, 2015; Shereen and El-Nahrawy, 2018). Table 3 shows there was low phenotypic variation (s) for the traits PL, PM, PGM, while for PH, GI and SPP a certain phenotypic variation was observed. For yield, there is a high phenotypic variation (s).

The values estimated for genotypic variance (s) ranged from 0.89 for pod length (PL) to 78.15 for plant height (PH) (Table 3). Analyzing the genotypic variance (s) in relation to the phenotypic variance (s), it was observed there was a major contribution of genotypic variance (s) to the present phenotypic variability. These results were confirmed by the estimates of the genotypic determination coefficient (R^2) (Table 3).

Table 3 - Estimates of genetic parameters for traits plant height (PH), pod length (PL), pod mass (PM), pod grain mass (PGM), grain index (GI), seeds per pod (SPP) and Yield in 20 cowpea genotypes evaluated in Cerrado/Amazon Rainforest ecotone region, Brazil, 2019

Genetic parameters	Traits						
	PH (cm)	PL (cm)	PM (g)	PGM (g)	GI (%)	SPP	Yield (Kg ha^{-1})
σ^2_F	79.77	1.07	8.71	3.36	28.18	59.75	34000.08
σ^2_E	1.61	0.17	0.71	0.14	4.05	5.43	5001.11
σ^2_G	78.15	0.89	8.46	3.22	24.13	54.32	28998.96
R^2 (%)	97.98	83.15	97.17	95.87	85.64	90.91	85.29
ICC (%)	92.37	56.15	89.55	85.30	59.85	71.44	59.18
PCV (%)	13.66	5.12	15.89	12.73	6.80	10.21	28.50
GCV (%)	13.52	4.68	16.67	12.46	6.29	9.73	26.32
ECV (%)	3.89	4.14	5.35	5.17	5.15	6.15	21.86
b = GCV/ECV	3.48	1.13	2.93	2.41	1.22	1.58	1.20
$\hat{r}$	0.99	0.91	0.99	0.98	0.93	0.95	0.92
Mean	65.36	20.22	18.57	14.40	78.12	75.74	647.03

σ^2_F = phenotypic variance; σ^2_E = environmental variance; σ^2_G = genotypic variance; R^2= genotypic determination coefficient; ICC= intra class correlation coefficient; PCV= phenotypic coefficient of variation; GCV= genotypic coefficient of variation; ECV= environmental coefficient of variation; *b* quocient = GCV/ECV ratio; $\hat{r}$ = accuracy.

Cruz *et al*. (2014) mention that when the adopted statistical model considers genotypes as a fixed effect, as in the present study, heritability becomes the genotypic determination coefficient. The values of the genotypic determination coefficient (R^2) ranged from 83.15% for PL to 97.9% for PH. All evaluated traits presented high (R^2) estimates (>75%). This parameter provides indications of the expected performance of a given population for traits selection, which allows us to infer that the population in study is promising for the trait selection under study.

However, it is noteworthy that for complex inheritance characteristics such as yield, which are the expression result of many alleles and they are greatly influenced by the environmental conditions to which population undergoes, the high values of R^2 may be overestimated by genotype x environment interaction, since the present study was conducted in only one year and in a single environment.

Torres *et al.* (2015), in a study to determine the number of measurements required, evaluated 40 genotypes of prostrate and semi-prostrate cowpea types in the state of Mato Grosso do Sul, in ten assays, the R^2 ranged from 51.50% to 92.64%. While Shimelis and Shiringani (2010), in a study to determine the variance components and heritability in ten cowpea lines, obtained the genotypic determination coefficient of 55.00% for yield, lower than the value found in the present work.

Given the high value of R^2, it can be inferred that it is caused by the inherent genetic variability of the tested genotypes, because each of them contributes a distinct genetic identity (Teixeira *et al*., 2007). Fehr (1987) mentions that higher genotypic determination coefficients may be associated with lower environment variation and lower genotype-environment interaction. And according to Gomes (2009), there is low to medium accuracy in environmental control, since the relative standard deviations (RSD) were below 21% for all characters.

The intraclass correlation coefficient (ICC), which corresponds to the repeatability coefficient, indicates an estimate of the total measurement variability fraction owing to variations between individuals. The ICC ranged from 56.15% to 92.37% for pod length and plant height, respectively (Table 3). When characteristics have a lower intraclass correlation coefficient require a greater number of measurements (replications) to predict the real value of a given trait and vice versa. Therefore, it can be inferred for the superior genotypes selection, the number of measurements in the present study is satisfactory.

The coefficients of variation provide information about the variation nature and magnitude. They clarify if the variations are owing to genetic or environmental causes. Typically, the GCV values are bigger than ECV. If the differences between GCV and ECV are excessive, so the environmental effects will be more noticeable on the trait. Thus, in the observed results, the relative proportion (%) of the deviations from the mean because of genetic effects (GCV) were higher when compared to the environmental ones (ECV), for all traits (Table 3).

The genotypic coefficient of variation (GCV) ranged from 4.68% for pod length and from 26,32 to 26.32% for yield (Table 3). The highest estimates (GCV) were recorded for pod grain mass (12.46%), plant height (13.52%), pod mass (16.67%) and yield (26.32%), indicating that these traits offer greater selection perspectives to obtain genotypes much more aligned to the proposed, as they are erect habit and determined growth genotypes.

These results are consistent with those found by Lopes *et al.* (2017) for yield and pod mass; Regis *et al*. (2014) for pod grain mass and grain index, and Bhagasara *et al.* (2017) for yield in this species. The characteristics plant height, pod length and seeds per pod showed lower GCV and, therefore, present greater difficulties in the selection process and expected genetic advance. Fact in agreement with Correa *et al*. (2015) and Silva and Neves (2011). However, Gerrano *et al.* (2015), found higher GCV values for plant height (67.41%), pod length (19.97%) and seeds per pod (24.82%).

The *b* quotient is an auxiliary tool for the breeder. According to the interpretation of Cruz *et al.* (2014) for this parameter, when the value is greater than or equal to 1.00, it indicates that there is genetic variability within the population in study, which can therefore, be explored, and in the case, the trait is favorable to selection. The quotient b ranged from 1.13 for PL to 3.48 for PH (Table 3). Thus, it can concluded that the *b* quotient values found for all evaluated characteristics are favorable to selection in order to obtain more productive genotypes.

Genotype evaluation assays should be approached from a genetic and statistical point of view, not just from a statistical perspective. In the context of genotypic evaluation, accuracy is the most important statistical parameter. It has the property of informing about the correct ordering of genotypes for selection purposes and also about the effectiveness of inference about the genotypic value of each genotype (Resende, 2002).

Accuracy depends not only on the residual variation magnitude and the number of replication, but also on the proportion between the genetic and residual variations associated with the trait under evaluation. Accuracy refers to the correlation between the true genotypic value of genetic treatment and that estimated or predicted from the information from the experiments. As a correlation, it ranges from 0 to 1, and the appropriate accuracy values are those close to the unit or 100% (Henderson, 1984).

Therefore, for all evaluated characteristics in the present experiment, the observed values for accuracy are considered very high, as they are above 0.90. High accuracy variables indicate small absolute deviations between true genotypic values and those estimated from experimental information. Resende and Duarte (2007) emphasize the importance of achieving optimal selective accuracy greater than 0.90 for safe statistical inference.

Correlation between traits and path analysis

Correlation estimates indicate good signal agreement between phenotypic and genotypic correlations (Table 4). In general, genotypic correlations present values higher than their corresponding phenotypic and environmental correlations. Similar results were obtained by Andrade *et al.* (2010), Correa *et al*. (2015), Almeida *et al.* (2014), Gerrano *et al*. (2015), Teixeira *et al.* (2007) and Manggoel *et al.* (2012) in studies conducted with cowpea, evaluating yield components.

There was a significant ($p \leq 0.01$) and high magnitude positive phenotypic correlation (Υ_P) between the traits pod grain mass (PGM) and pod mass (PM), which was already expected, insofar that pod grain mass increase happens, it should also increase the pod mass, or vice versa. However, the traits grain index and seeds per pod presented negative phenotypic correlation at 1% probability (Table 4). For the other pairs of characteristics there were no significant phenotypic correlations.

Genotypic correlations (Υ_G) showed the same sign and, in most cases, values higher than their corresponding phenotypic correlations, indicating that the phenotypic expression is decreased because of environmental influences. Although the yield components were positively correlated with yield, the Υ_P and Υ_G estimates showed low magnitude and they

Table 4 - Estimates of the correlation coefficients phenotypic (Υ_P), genotypic (Υ_G) and environmental (Υ_E) between the traits plant height (PH), pod length (PL), pod mass (PM), pod grain mass (PGM), grain index (GI), seeds per pod (SPP) and Yield in 20 cowpea genotypes evaluated in Cerrado/Amazon Rainforest ecotone region, Brazil, 2019

Characteristics	Υ	PH	PL	PM	PGM	GI	SPP	Yield
PH	P	1	-0.47*	-0.14 NS	-0.06 NS	0.15 NS	-0.35 NS	0.18 NS
	G	1	-0.52*	-0.14 NS	-0.05 NS	0.18 NS	-0.37 NS	0.20 NS
	E	1	-0.04 NS	-0.07 NS	-0.09 NS	-0.16 NS	-0.02 NS	-0.07NS
PL	P		1	0.06 NS	0.14 NS	0.11 NS	-0.02 NS	0.05 NS
	G		1	0.07 NS	0.14 NS	0.12 NS	-0.00 NS	0.04 NS
	E		1	0.04 NS	0.14 NS	0.06 NS	0.21 NS	0.07 NS
PM	P			1	0.90 **	-0.64 **	0.32 NS	-0.14 NS
	G			1	0.91 **	-0.66 **	0.34 NS	-0.16 NS
	E			1	0.44 **	-0.47 **	0.10 NS	0.10 NS
PGM	P				1	-0.23 NS	0.18 NS	-0.03 NS
	G				1	-0.31 NS	0.19 NS	-0.04 NS
	E				1	0.55 **	0.04 NS	0.04 NS
GM	P					1	-0.39 NS	0.26 NS
	G					1	-0.43 NS	0.33 NS
	E					1	-0.12 NS	-0.12 NS
SPP	P						1	0.12 NS
	G						1	0.12 NS
	E						1	0.11 NS
Yield	P							1
	G							1
	E							1

NS= not significant; (*), (**) significant at 5% and 1%, respectively, by the t test.

were, mostly, non-significant.

Cruz *et al.* (2012) attribute the genetic correlations occurrence, mainly to the pleiotropy or to the genetic links between traits pairs, in the latter case, transient causes. In any case, genetic correlations favor the simultaneous selection of two or more traits by selecting only one of these. On the other hand, according to these authors, the selection of one trait may lead to an undesirable selection of another.

The negative estimates of correlation between pairs of traits indicate that improving one trait will decrease the other, and in these cases, the selection based on this one is not recommended. The characteristic plant height was phenotypically and genetically negatively correlated with pod length, indicating that the smaller the plant, the longer the pod length, which directly influences the yield. According to Falconer and Mackay (1996), genotypic and environment correlations of exchanged signals, as can be observed in some characteristics pairs (Table 4), reveal that the causes of genetic and environmental variation influenced the traits through different physiological mechanisms.

Given the complexity among the yield components that contribute to yield, the selection of cowpea genotypes is difficult. Thus, it is evident the need to unfold the correlations in direct and indirect effects, evaluating the importance degree of each of the explanatory variables in relation to the main or basic variable (Daros *et al*., 2004).

Cruz *et al*. (2014) report that the parameter estimates under multicollinearity may assume absurd values or with no consistency to the studied biological phenomena. Thus, for greater reliability of the path analysis results, the phenotypic correlation matrix between characteristics was tested for multicollinearity by the condition number proposed by Montgomery *et al.* (2012).

The correlation matrix had a condition number equal to 993.97, that is, collinearity between the characters considered moderate to strong, presenting no problem for the path coefficients estimates. The coefficient of determination (R^2) and the residual effect indicate how much the explanatory variables determine the yield. The coefficient of determination was 0.2025 and the residual effect was 0.8930 (Table 5).

The direct effects magnitudes of the traits analyzed on yield were higher than the estimates magnitudes of their respective simple correlations with

Table 5 - Estimates of direct and indirect effects involving the main variable, Yield in kg ha^{-1}, and the explanatory variables: plant height, pod length, pod mass, pod grain mass, grain index, seeds per pod concerning to 20 cowpea genotypes evaluated in Cerrado/Amazon Rainforest ecotone region, Brazil, 2019

Characteristics	Association effects	Path coefficients
Plant height	Direct on Yield	0.3671
	Indirect via PL	-0.0805
	Indirect via PM	-0.1327
	Indirect via PGM	0.0434
	Indirect via GI	0.1162
	Indirect via SPP	-0.1302
	Total	0.1833
Pod length	Direct on Yield	0.1711
	Indirect via PH	-0.1727
	Indirect via PM	0.0612
	Indirect via PGM	-0.1058
	Indirect via GI	0.0845
	Indirect via SPP	0.0082
	Total	0.0466
Pod mass	Direct on Yield	0.9628
	Indirect via PH	-0.0506
	Indirect via PL	0.0109
	Indirect via PGM	-0.7015
	Indirect via GI	-0.4831
	Indirect via SPP	0.1191
	Total	-0.1425
Pod grain mass	Direct on Yield	0.7835
	Indirect via PH	-0.0203
	Indirect via PL	0.0231
	Indirect via PM	0.8621
	Indirect via GI	-0.1774
	Indirect via SPP	0.0664
	Total	-0.0295
Grain index	Direct on Yield	0.7593
	Indirect via PH	0.0561
	Indirect via PL	0.0190
	Indirect via PM	-0.6126
	Indirect via PGM	0.1831
	Indirect via SPP	-0.1444
	Total	0.2605
Seeds per pod	Direct on Yield	0.3702
	Indireto via PH	-0.1291
	Indirect via CV	0.0038
	Indirect via PM	0.3097
	Indirect via PGM	-0.1407
	Indirect via GI	-0.2963
	Total	0.1177
Coefficient of determination		0.2025
Residual variable effect		0.8930

yield (Table 5). Based on this information, it is possible to infer there are other traits influencing both the magnitude and the correlation direction between the yield components.

Considering the direct effects on yield, included in Table 5, the trait pod mass (0.9628) has the greatest effect, indicating a major contribution to the yield increase, surpassing the pod grain mass, which also had a high direct effect (0.7835). In contrast, pod length (0.1711) was the trait with the lowest effect. Important to mention there was no negative direct effect of any trait on yield.

Still in Table 5, it can be seen that although the character PM had a high direct effect on yield, in general, the indirect effects via PM on yield were low. Indicating that indirect truncation selection in the auxiliary character may not provide satisfactory gains in the main variable (yield). In these cases, the best strategy is the multi-trait selection (Cruz *et al.*, 2012).

Indirect effects on yield were relatively low, except for the trait PGM via PM, which pointed to an estimate of 0.8621. This result is indicative of the indirect selection viability via pod mass to obtain gains on the most important character. The trait PH had negative indirect effect via all the characteristics, except GI, which indicates that the plant height reduction induces the increase in the other characteristics, which is very important in this crop production system, considering that plants very high hinder crop handling and harvesting.

Considering the total effect, the traits have had the greatest effect on yield were as follows grain index (0.2605), plant height (0.1833), seeds per pod (0.1177) and pod length (0.0466) (Table 5). This result of the total effect in relation to the direct effects on yield was owing to the negative indirect effects via the other characteristics, which confirms the need to apply a multi-trait selection.

Considering that the existence of genetic variability in population is a determining factor for any breeding program (Ramalho *et al.*, 2012), the germplasm under study is, initially, promising for selection or hybridization work with potential for the new cultivars development.

4. Conclusions

The study concluded there is a considerable degree of genotypic variation between important agronomic traits in cowpea. Genotypic variation contributed most of the phenotypic variation. Result corroborated by the high estimates of genotypic determination coefficient.

Thus, the genetic parameters estimates obtained for yield and agronomic traits, in the present study, will provide a basis for selection in order to obtain gains in the breeding for cowpea yield.

The path analysis indicated the pod mass and pod grain mass had the greatest favorable effect on yield in cowpea, and could also be used for indirect selection aiming at the development of new genotypes with high yield potential.

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