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# Estimation of genetic parameters in white seed cowpea (Vigna unguiculata (L) Walp)

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### Abstract

The objective of this research was to estimate genetic parameters of characteristics associated with yield in 42 genotypes of white colored cowpea. The experimental design was Federer's augmented blocks, with five replications. Ten quantitative characters were recorded. Analysis of variance detected significant and highly significant differences between genotypes, in nine of the ten characters. The coefficients of phenotypic variation were greater than those of genotypic variation, due to the influence of the environment. High broad-sense heritability was revealed for peduncle length, 97.05%, number of pods per plant, 95.48% and weight of 100 seeds, 98.51%; the expected genetic progress varied between 0.07 (seed width) and 17.04 (seed yield per plant), while the genetic advance as a percentage of the average ranged from 2.80 (days to harvest) to 87.07 (seed yield per plant). The first four principal components explained 80.66% of the total variability; the length and width of the seed, and the weight of 100 seeds contributed to PC1; and the number of days, both for maturity of the first pod and for harvest, and the length of the pod, contributed to a greater degree to PC2. It was concluded that the number of pods per plant, the weight of 100 seeds and the yield of seed per plant are selection criteria for future breeding programs

Keywords: Crop yield, genetic advances, genetic variability, heritability, yield components.

**Abbreviations**: Anova\_ variance analysis; PV\_ Phenotypic variance; GV\_ Genotypic variance; EV\_ Environmental variance; GCV\_ Coefficient of genotypic variation; PCV\_ Coefficient of phenotypic variation; b\_Quotient between the coefficient of genetic variation and the coefficient of environmental variation; h2\_Heritability broad sense; GA\_Genetic advances; GAM\_Genetic advance as percent of mean lines;  $\sigma_p$ \_Standar desviation K\_ Selection differential; PCA\_ Principal component analysis

### Introduction

The cowpea (Vigna unguiculata (L.) Walp) is a legume of social and economic importance, especially in countries of Africa, Asia and America, for the use of its grain (seed) and leaves in human food. Also their leaves are used as green manure or as animal feed or silage crop (Magulu and Kabambe, 2015). It contains high levels of protein, iron and zinc (Lazaridi et al., 2017). Its commercialization as green pod and white and dry seed in the Colombian Caribbean, generates income in the short term because its cycle does not exceed 60 days. Cowpea seeds, marketed for human consumption as grain, have a market value, according to size and color: between US \$ 0.0289 and US \$ 0.0337 per kilogram for large seeds, and US \$ 0.0289- 0.0363 per kilogram, for smooth seed, black hilum and white color (Mishili et al., 2009). In Colombia, cowpea is produced by small farmers in the seven departments of the Atlantic coast, due to their adaptation to their climate and soil conditions, as in other tropical and subtropical areas of the

world, but their yields are considered low (600 kg ha<sup>-1</sup>) compared to those in the United States and Peru, which yielded 1.790 and 1.376 kg ha<sup>-1</sup> in 2014 (FAO, 2017). Low yields are attributed to the use of obsolete varieties and to susceptibility to biotic and abiotic factors, especially drought and high temperatures (Kumar and Kumar, 2015). For Ribeiro et al. (2014), the genetic improvement by programs of public entities has allowed to increase the yields and the adaptation to different systems of production. The development of new cultivars according to the demand of producers and the satisfaction of a growing population was proposed by Singh (2007), who highlights the new generation of improved cowpea cultivars must combine high grain yield, erect growth habit, determinate growth pattern, an early to medium maturity cycle and branches with pods located above the plant canopy. Studies of genetic parameters for different plant characters have been reported in several agricultural species



(Kumar et al., 2013, Raturi et al., 2015, Ali et al., 2016). In *Vigna unguiculata*, estimates of the most important parameters such as genetic variability, heritability and genetic progress, by direct and indirect selection, have contributed to significant genetic progress in characters of interest for its use in the conservation and development of cultivars with greater adaptation, Production and productivity, according to the needs, conditions and requirements of the producers, processors and final consumers (Andrade et al., 2010, Manggoel et al., 2012, Ribeiro et al. 2014, Silva et al., 2014, Agyeman et al., 2015 and Rambabu et al., 2016).

Genetic analyses dealing with traits related to the yield of cowpea have been reported in the literature, providing estimates of genetic parameters for characteristics related to a more efficient plant. For example, Ribeiro et al. (2014) estimated genetic parameters for branch length; secondary vegetative branch length; number of secondary vegetative branches; number of nodes, and number of days to grain maturity, concluding that the minimum number of genes controlling the five traits ranged from two to 17 and broad and narrow sense heritability estimates were either close to or above 50% for all traits under evaluation. Andrade et al. (2010), estimated genetic parameters in traits associated with the production of fresh southern pea in 14 cowpea genotypes of purple pod and white grains, highlighting there is a high genetic component in the phenotypic expression of all the traits studied, with a high probability of genetic gains in additional cycles of selection based on phenotype.

The estimation of genetic and phenotypic parameters like heritability, correlations and expected gains from selection has a prime role in genetic breeding programs. These parameters enable the breeders to make decisions about the appropriate methods to handle the populations and select the characteristics to be considered in initial and advanced steps of the breeding program. High heritability indicates a greater better chance of success in selection and genetic advancement in the improvement of a trait (Ali et al., 2016).

The study and identification of genetic parameters such as the coefficient of genetic variation, heritability and correlation between characters are of sum importance, because through these we can know the genetic variability, the degree of expression character from one generation to another and the possibility of earnings through direct selection or indirect (Rocha et al., 2003).

The objective of this study was to estimate genetic parameters of characteristics associated with yield in 42 genotypes of white seeds cowpea, to improve the selection criteria of plants.

## **Results and Discussion**

# ANOVA assessments

The results of the analysis of variance are recorded in Table 1. Significant differences (p < 0.05) and (p < 0.01) were detected between the lines for all variables except for seed length; while for check varieties the differences were found for pod length, seed length, pods per plant, peduncle length and weight of 100 seeds, as a consequence of the genetic differences between said genotypes, which is desired in obtaining of new cultivars

that respond to the needs of a breeding program. The existence of these statistical differences between lines and check varieties, indicate the presence of genetic variability, which have been reported by Manggoel et al. (2012); Kumar et al. (2013); Silva et al. (2014) and Rambabu et al. (2016) in investigations in the same species.

#### **Genetic parameters**

The coefficients of phenotypic variation in lines, check varieties and general, were less than 10.0% for all the characteristics studied, except for yield per plant that ranged from 17.56 to 20.47% (Table 1), which indicates reliability in these records, high accuracy and valid conclusions (Correa et al., 2012), being comparable to those of Silva et al. (2014) and Agyeman et al. (2015) and lower than those reported by Raturi et al. (2015) in cultivars of *Vigna unguiculata* and *Vigna radiata*.

The coefficient of variance i.e GCV and PCV give information about the nature and magnitude of variation. It clarifies either the variations are due to genetic causes or environmental causes. Usually the PCV is greater than the GCV. If the differences between PCV and GCV are larger, then the environmental effects on the character will be more visible. In the present study, most characters exhibited moderate GCV and PCV with smaller differences, except days to harvest (Table 2).

The coefficient of variance genetic (GCV) oscillates between 2.35% for days to first pod maturity to 45.32% for day to harvest (Table2). The highest estimates (GCV) were recorded for pods per plant (17.92%), peduncle length (23.49%), pods per peduncle (29.22%), 100 seed weight (41.14%) and days to first pod maturity (45.32%), Indicating that these characters offer greater selection prospects to obtain genotypes much more in line with what was proposed (Singh, 2007), since they are cultivars of erect type and determined growth. These results are consistent with those found by Andrade et al. (2010) for weight of 100 grains and yield per plant; Silva et al. (2014) for number of pods per plant and peduncle length and Manggoel et al. (2012) for weight of 100 seeds, number of pods per plant and yield per plant in this species. The characteristics days to first pod maturity, yield per plant, seed length, seed width and pod length, registered lower GCV and therefore greater difficulties in the process of selection and expected genetic advance, a fact that agrees with Correa et al. (2012) and Silva et al. (2014), since it is an indicator of how much of the genetic variability is affected by the environment in its phenotypic expression as Subbiah et al. (2013).

Estimates of the values of b (Table 2) > to 1.0 show that most of the phenotypic variance is genetic in nature and there are possibilities for selection, especially in those with higher values, such as 100 seed weight, peduncle length, pods per plant, pods per peduncle and days to harvest, but not for days to first pod maturity, which resulted from 0.71; What is not favorable to direct the selection to early cultivars, to have an average cycle of 57 days and reduce this time would be to sacrifice yield.

According to Verma and Agarwal (1982), heritability values > 50% are considered as high, whereas values less than 20% are considered to be low and between 20 and 50% are moderate.

| Name               | Accesión number | Origin   | Pedigree          |
|--------------------|-----------------|----------|-------------------|
| Caupicor 50        | 2015-55         | Colombia | Criollo - Córdoba |
| ICA Betancí        | 2004-06         | Colombia | Germoplasm bank   |
| LC-009-016         | 2016-09         | Colombia | IT 86 x LCPM-35   |
| LC-013-016         | 2016-13         | Colombia | IT 86 x LCPM-35   |
| LC-018-016         | 2016-18         | Colombia | IT 86 x LCPM-35   |
| LC-022-016         | 2016-22         | Colombia | IT 86 x LCPM-35   |
| LC-029-016         | 2016-29         | Colombia | IT 86 x LCPM-35   |
| LC-006-016         | 2016-06         | Colombia | IT 86 x LCPM-35   |
| LC-016-016         | 2016-16         | Colombia | IT 86 x LCPM-35   |
| LC-002-016         | 2016-02         | Colombia | IT 86 x LCPM-35   |
| LC-041-016         | 2016-41         | Colombia | IT 86 x LCPM-35   |
| LC-021-016         | 2016-21         | Colombia | IT 86 x LCPM-35   |
| LC-036-016         | 2016-36         | Colombia | IT 86 x LCPM-35   |
| LC-014-016         | 2016-14         | Colombia | IT 86 x LCPM-35   |
| FRIJOL DESCONOCIDO | 2015-01         | Perú     | Germoplasm bank   |
| LC-012-016         | 2016-12         | Colombia | IT 86 x LCPM-35   |
| LC-026-016         | 2016-26         | Colombia | IT 86 x LCPM-35   |
| LC-003-016         | 2016-03         | Colombia | IT 86 x LCPM-35   |
| LC-039-016         | 2016-39         | Colombia | IT 86 x LCPM-35   |
| LC-025-016         | 2016-25         | Colombia | IT 86 x LCPM-35   |
| LC-032-016         | 2016-32         | Colombia | IT 86 x LCPM-35   |
| LC-038-016         | 2016-38         | Colombia | IT 86 x LCPM-35   |
| L-034              | 2014-34         | Colombia | Criollo - Córdoba |
| LC-030-016         | 2016-30         | Colombia | IT 86 x LCPM-35   |
| LCPM-37            | 2007-09         | Colombia | Germoplasm bank   |
| LC-033-016         | 2016-33         | Colombia | IT 86 x LCPM-35   |
| LC-017-016         | 2017-17         | Colombia | IT 86 x LCPM-35   |
| LC-040-016         | 2016-40         | Colombia | IT 86 x LCPM-35   |
| L- 019             | 2014-19         | Colombia | Criollo - Córdoba |
| LC-024-016         | 2016-24         | Colombia | IT 86 x LCPM-35   |
| LC-010-016         | 2016-10         | Colombia | IT 86 x LCPM-35   |
| LC-042-016         | 2016-42         | Colombia | IT 86 x LCPM-35   |
| LCPM-35            | 2007-08         | Colombia | Germoplasm bank   |
| LC-005-016         | 2016-05         | Colombia | IT 86 x LCPM-35   |
| LC-008-016         | 2016-08         | Colombia | IT 86 x LCPM-35   |
| LC-011-016         | 2016-11         | Colombia | IT 86 x LCPM-35   |
| LC-027-016         | 2016-27         | Colombia | IT 86 x LCPM-35   |
| L – 047            | 2014-47         | Colombia | Criollo - Córdoba |
| LC-007-016         | 2016-07         | Colombia | IT 86 x LCPM-35   |
| L-020              | 2014-20         | Colombia | Criollo - Córdoba |
| LC-015-016         | 2016-15         | Colombia | IT 86 x LCPM-35   |
| LC-034-016         | 2016-34         | Colombia | IT 86 x LCPM-35   |

Table 2. Mean squares for 10 quantitative traits of 42 genotypes of cowpea (Vigna unguiculata (L.).

| · · · · · ·                       |                     | 0 /1                 | 1 . 5          | 5                              |         |  |  |
|-----------------------------------|---------------------|----------------------|----------------|--------------------------------|---------|--|--|
| Traits                            | Mean squares        | 5                    | Coefficient of | Coefficient of variability (%) |         |  |  |
|                                   | Lines               | Check                | Lines          | Check                          | General |  |  |
| Pod length (cm)                   | 1.54 <sup>*</sup>   | 77.21**              | 3.26           | 2.72                           | 3.13    |  |  |
| Seed length (cm)                  | 0.003 <sup>NS</sup> | 0.009*               | 3.11           | 3.00                           | 3.09    |  |  |
| Seed width (cm)                   | 0.003*              | 0.0001 <sup>NS</sup> | 3.69           | 3.71                           | 3.69    |  |  |
| Pods per plant (#)                | 40.73**             | 714.15**             | 5.04           | 6.07                           | 5.37    |  |  |
| Pods per peduncle (#)             | 0.25*               | 0.02 <sup>NS</sup>   | 8.52           | 8.77                           | 8.50    |  |  |
| Peduncle length (cm)              | 45.68 <sup>*</sup>  | 229.94**             | 3.89           | 4.46                           | 3.99    |  |  |
| 100 seed weight (g)               | 4.80*               | 12.49**              | 5.04           | 4.93                           | 5.02    |  |  |
| Yield per plant (g)               | 76.93 <sup>*</sup>  | 62.03 <sup>NS</sup>  | 17.56          | 20.47                          | 18.07   |  |  |
| Days to first pod maturity (days) | 9.94*               | 0.005 <sup>NS</sup>  | 3.91           | 3.88                           | 3.90    |  |  |
| Days to harvest (days)            | 4.16*               | 0.45 <sup>NS</sup>   | 3.28           | 3.30                           | 3.29    |  |  |

\*, \*\* and <sup>NS</sup> = significant (p<0.05), highly significant (p<0.01) and non-significant, respectively.

**Table 3**. Phenotypic variance (PV), genotypic variance (GV), environmental variance (EV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), variability index (b), heritability in the broad sense (h<sup>2</sup>), genetic advance (GA) and genetic advance as percent of mean (GAM) for 10 quantitative traits of cowpea (*Vigna unquiculata* (L.) Walp).

| Traits                     | PV     | GV     | EV     | GCV (%) | PCV(%) | b    | h²(%) | GA    | GAM(%) |
|----------------------------|--------|--------|--------|---------|--------|------|-------|-------|--------|
| Pod length                 | 1.52   | 1.25   | 0.25   | 7.17    | 7.57   | 2.22 | 82.23 | 2.09  | 13.36  |
| Seed length                | 0.0039 | 0.0031 | 0.0008 | 6.14    | 6.93   | 1.96 | 79.48 | 0.10  | 11.11  |
| Seed width                 | 0.0024 | 0.0018 | 0.0006 | 6.20    | 7.20   | 1.68 | 75.00 | 0.07  | 10.14  |
| Pods per plant             | 60.84  | 58.09  | 2.74   | 17.92   | 18.81  | 4.59 | 95.48 | 15.34 | 36.06  |
| Pods per peduncle          | 0.31   | 0.28   | 0.02   | 29.22   | 30.59  | 3.42 | 90.32 | 1.03  | 6.28   |
| Peduncle length            | 47.92  | 46.51  | 1.41   | 23.49   | 25.51  | 5.73 | 97.05 | 13.83 | 47.65  |
| 100 seed weight            | 35.73  | 35.20  | 0.52   | 41.14   | 41.28  | 8.15 | 98.51 | 12.13 | 84.11  |
| Yield per plant            | 11.95  | 7.80   | 4.51   | 5.36    | 6.63   | 1.37 | 65.27 | 4.64  | 8.91   |
| Days to first pod maturity | 5.44   | 1.84   | 3.60   | 2.35    | 4.04   | 0.71 | 33.82 | 1.62  | 2.80   |
| Days to harvest            | 90.54  | 78.72  | 11.82  | 45.32   | 50.05  | 2.58 | 86.94 | 17.04 | 87.07  |

Table 4. Eigen values and percentage explained variation by the first four principal components for ten agronomic traits associated with 42 genotypes of cowpea.

| Component                 | PC1     | PC2     | PC3     | PC4     |  |
|---------------------------|---------|---------|---------|---------|--|
| Eigen value               | 3.36    | 2.31    | 1.24    | 1.13    |  |
| Variance (%)              | 33.66   | 23.19   | 12.43   | 11.39   |  |
| Cumulative variance (%)   | 33.66   | 56.85   | 69.28   | 80.66   |  |
| Agronomic traits          |         |         |         |         |  |
| Pod length                | 0.2082  | 0.3003  | 0.0659  | -0.6939 |  |
| Seed length               | 0.3328  | 0.2469  | 0.3764  | 0.1988  |  |
| Seed width                | 0.4373  | -0.0314 | 0.1298  | 0.4120  |  |
| Pods per plant            | -0.3649 | -0.2808 | 0.2533  | 0.3700  |  |
| Pods per peduncle         | 0.2057  | -0.4820 | -0.1152 | -0.2273 |  |
| Peduncle length           | -0.3419 | -0.1618 | -0.0905 | -0.0632 |  |
| 100 seed weight           | 0.4100  | 0.2506  | -0.2410 | 0.2662  |  |
| Yield per plant           | -0.1311 | 0.1226  | 0.8023  | -0.1339 |  |
| Day to first pod maturity | -0.2978 | 0.4469  | -0.1660 | 0.1389  |  |
| Day to harvest            | -0.2967 | 0.4824  | -0.1482 | 0.0911  |  |

Heritability accounted for higher values for 65.27% for all evaluated characteristics, except for days to first pod maturity, which presented a moderate register of 33.82% (Table 2) and is consistent with that reported by Mohammed et al. (2010), which is due to the genetic differences between the genotypes studied, since each contributes with a different genetic identity as Andrade et al. (2010) and this allows a better selection margin for the evaluated characters (Ali et al., 2016), especially for pod length and pods per peduncle for fresh consumption, pods per plant, peduncle length, 100 seed weight, which presented values of 82.23; 90.32, 95.48, 97.05 and 98.51%, respectively, and also the selection of plants with a shorter peduncle length, for the sake of assimilates, to revert to the seeds, since the yield is associated with the length of pods, number of pods by plant and weight of 100 seeds (Mohammed et al., 2010, Manggoel et al., 2012, Silva et al., 2014).

The efficacy of selection depends on the existence and magnitude of genetic variability for yield and yield traits in the breeding material (Adewale et al., 2010; Andrade et al., 2010; Raturi et al., 2015). Considering that the genetic control of quantitative traits as yield and its components is due to additive, dominant and epistatic genetic effects (Singh et al., 2016), heritability in conjunction with genetic advance alone is much better than the inheritance itself in the prediction of the best genotypes (Johnson et al., 1955, Ali et al., 2016). According to Johnson et al. (1955), genetic advance the percentage of the mean was high ( $\geq 20\%$ ), moderate (10-20%) and low (0-10%); In this sense, pods per plant, peduncle length, 100 seed weight and days to harvest, accounted for the highest genetic gain GAM (%), with values of 36.06; 47.65; 84.11 and 87.07%, respectively (Table 2). Adewale et al. (2010) and Raturi et al. (2015) have reported significant advances with these characters.

# Principal component analysis (PCA)

The principal components analysis is important for the breeder because it allows identifying characteristics that contribute with significant genetic variability among genotypes and selecting agronomically desirable parents for hybridizations (Gerrano et al., 2015) .The results obtained from the analysis revealed that the four first components explain 80.66% of the total variability and have eigenvalues higher than 1.0 (Table 3), very similar to those reported by Gerrano et al. (2015) and Adewale et al. (2011). The first principal component retains 33.66% of the total variability, due to the width and length of the seed and weight of 100 seeds, characters that contrast in greater degree with the number of pods per plant, length of the peduncle, days to first mature pod and days to harvest, that is to say, when increasing the first three, the four second ones decrease and, vice versa, a performance similar to that reported by Jonah et al. (2014) in Vigna subterranea.

The second main component retains 23.19% of the total variability and is indicative of plant phenology in terms of the duration of the plant cycle, days at first mature pod and days to harvest. These characters are contrasted mainly with the number of pods per peduncle and number of pods per plant, so that an increase in the days required for maturation of pods

and harvest, is associated with a decrease in the number of pods per peduncle and number of pods per plant.

The third principal component retains 12.43% of the total variability, due to the yield per plant which, at the same time, is positively associated with the length of the seed and number of pods per plant and contrasts with the weight of 100 seeds. A lower weight of seeds, higher yield per plant, associated simultaneously with a greater length of seed and greater number of pods per plant.

The fourth main component retains 11.39% of the total variability and is indicative of the length of the pod that contrasts with the width of the seeds, number of pods per plant and the weight of 100 seeds; when the length of the pod increases, the three mentioned characters decrease.

# Materials and methods

#### Description of the study area and experimental materials

The experiment was conducted at the Universidad de Córdoba – Colombia, during 2013. Forty cowpea lines obtained for Tropical Climate Crops Research Group from the Universidad de Córdoba and two check varieties Caupicor 50 and ICA Betancí were used. The total rainfall received between mid-October and mid-December was 312 mm.

# Experimental design

The experiment was designed as incomplete blocks (Federer, 1956). Seeds were sown with spacing of 30 cm between rows and 10 cm between plants. Each genotype was sowed in a row of 5.2 m. It was used 26 plants per experimental unit, 260 plants per block and 2600 plants in the five augmented blocks. The experimental area was 380.8  $m^2$ .

# Data collection and measured characters

Peduncle length, number of pods per peduncle, number of pods per plant, pod length, 100 seed weight and yield per plant (adjusted at 12% moisture content) were taken from five randomly selected plants per genotype. Both the length and width of seeds were measured on 10 seeds taken at random per genotype. In addition, the number of days to first mature pod and to harvest was registered for each genotype.

## Statistical analysis

Analysis of variance was performed on data; phenotypic variance (PV), genotypic variance (GV), environmental variance (EV), coefficient of genotypic variation (CGV), coefficient of phenotypic variation (CPV) in percentage, index of variability b (quotient between the coefficient of genetic variation and the coefficient of environmental variation) and heritability broad sense ( $h^2$ ) were estimated with the GENES program [GENES V.2016.6.0 developed by Cruz (2016)]. Also, the general lineal model of the SAS software (SAS Institute Inc.) was used to evaluate differences between lines and check varieties. Genetic advances (GA) was computed according to the formula given by Johnson et al. (1955). Genetic advance as percent of

mean lines (GAM) expressed in percentage was also computed according to Robinson et al. (1949). Genetic advance as percent of mean was classified as low, moderate and high (Johnson et al., 1955).

$$GA = k\sigma_p h^2$$

(GA: Genetic Advance, k: Selection differential, it is a constant for a given selection intensity (2.06 at 5%);  $\sigma_p$ : Standard deviation and  $h^2$ : Heritability).

To obtain more reliable information about relationships among the ten traits, data were evaluated by principal component analysis (PCA), as a multivariate data analysis technique

# Conclusions

There is genetic variability among the evaluated genotypes, corroborated by the coefficient of genetic variation and index of variability b in the weight of 100 seeds, length of the peduncle, pods per plant and pods per peduncle, which are desired in plant genetic improvement. The magnitude of the heritability, coefficient of genetic variation, index of variability, allow achieving genetic advances significant with respect to the average in the reduction of the peduncle length and increases in the pods per plant, weight of 100 seeds and days to harvest.

**Conflict of interest**: The manuscript was prepared and reviewed with the participation of all authors, who declare that there is no conflict of interests that jeopardizes the validity of the presented results

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