Heritability, genetic gain, and correlations in cowpea beans (*Vigna unguiculata* [L.] (Walp.))

Heredabilidad, ganancia genética y correlaciones en fríjol caupí (*Vigna unguiculata* [L.] (Walp.))

**ABSTRACT**

Cowpea beans are the most important legume in the Caribbean region of Colombia. This grain is produced mainly by small farmers in rural agriculture but is becoming more important every year for commercial agriculture. The objective of this study was to estimate heritability, genetic gain and correlations between agronomic characteristics and the nutritional content of 30 cowpea bean cultivars. The number of days to flowering (NDF), number of pods per plant (NPP), number of pods per peduncle (NPPE), peduncle length (PEL), number of nodes on main stem (NNMS), grain length (GL), grain width (GW), weight of 100 seeds (W100S), iron content (FeC), zinc content (ZnC), protein content in percentage (PROT) and YIELD were evaluated. Likewise, the genetic parameters: phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), variability index (b), heritability (*\( h^2 \) (%)), genetic gain (GG) and genetic progress (%), together with phenotypic correlations and genetic correlations, were determined. Genetic variability was evidenced in the population (*\( P < 0.05 \)*), except for PEL. The highest heritability was in W100S, ZnC and FeC (*\( h^2 > 96\% \)*). The greatest advance was achieved in ZnC, FeC, W100S and YIELD, with values higher than 30%, indicating the potential use of the evaluated genotypes for improving this species and positive and significant phenotypic and genotypic correlations between YIELD and PROT. Therefore, cultivars with higher yields and protein contents can be obtained.

**Additional key words:** grain legumes; micronutrients; genetic parameters; genetic variability; variability index.
The cowpea bean (Vigna unguiculata (L.) Walp) is the second most cultivated legume in the world after common beans and had an area of 12,496,305 ha in 2018, with an average yield of 578 kg ha\(^{-1}\), which makes it important in tropical and subtropical areas because of its protein content (20-25%), iron (48-69 mg kg\(^{-1}\)) and zinc (29.9-41.8 mg kg\(^{-1}\)), mitigating the problems of hidden hunger in vulnerable families (Da Silva et al., 2017; Faostat, 2020). Also, it has the ability to adapt to water stress, high temperatures, soils with low fertility, such as with green manure, and crop rotation, especially with cereals, managing to fix between 40 to 80 kg of nitrogen per ha (Mafakheri et al., 2017).

In Colombia, it is cultivated in departments of the Caribbean region, where fresh or dry grain is consumed in various ways because of its rapid cooking, especially in recipes for rice with beans, soups, fritters, and stews, etc. (Araméndiz-Tatis et al., 2019).

The success of a genetic improvement program depends on the magnitude of the variability present in the available resources. In this way, the determination of the yield and its components is of vital importance, to know the genetic differences between the accessions and to plan the activities of a genetic improvement program in order to make a selection of parents with desirable genes. Then, hybridization can be used to obtain segregating populations and generational advancement with the selection of plants with excellent agronomic attributes that achieve planned objectives (Devi and Janamami, 2018). Nkoana et al. (2019) argued that morphological diversity plays an important role in the genetic improvement of plants since it satisfies the needs of farmers and consumers, especially for proteins, vitamins and minerals for vulnerable populations in rural and urban areas instead of meat, and complements diets rich in carbohydrates, such as cereals.

According to Weldemichael et al. (2017), genetic parameters such as the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) are fundamental to understanding variability in a germplasm collection; while, heritability is associated with the efficiency of the selection on the phenotypic behavior of cultivars. However, this alone does not provide information for individual genotype selection, which is why the heritability associated with genetic advancement predicts the effect of selecting the best genotypes with respect to performance and nutritional contents.
Studies on this species by Kumar et al. (2013) and Silva et al. (2014) reported that the studied populations had a potential for selection and gains from crosses in terms of the studied phenotypes in the evaluated characteristics.

The objective of the present research was to estimate the heritability, genetic advancement and correlations of the cowpea bean collection under the conditions of the Sinu Valley of Colombia to identify parents with desirable agronomic characteristics that significantly contribute to the improvement of yield and nutrient contents.

MATERIALS AND METHODS

This research was carried out in 2018 in Cerete-Colombia, at 8°54’45” N and 75°48’33” W, altitude of 12 m a.s.l., with an average annual temperature of 27°C and average rainfall of 1,500 mm. The soil has a loamy texture, with a slightly acidic pH, CEC of 22.85±4.36 cmol(+) kg⁻¹, CE of 0.52±0.48 dS cm⁻¹ and OM of 2.72 ± 0.81% (Contreras-Santos et al., 2020).

The 30 genotypes are listed in table 1, identified according to their origin.

The experiment was carried out according to the recommendations for the agronomic management of cowpea beans in the Colombian Caribbean (Araméndiz-Tatis et al., 2019). The experiment design was randomized complete blocks, with 30 cultivars and four replications. The size of the experiment unit was two rows of 4 m in length, separated by a distance of 1.0 m between rows and 0.4 m between plants. The experiment area was 960 m².

The measurement of response variables was carried out based on the descriptors proposed by IBPGR (1983). The registered characteristics were: number of days to flowering (NDF), number of pods per plant (NPP), number of pods per peduncle (NPPE), peduncle length (PEL), number of nodes on main stem (NNMS), grain length (GL), grain width (GW), weight of 100 seeds (W100S), iron content (FeC), zinc content (ZnC), protein content in percentage (PROT) and YIELD.

Analysis of variance was performed for all traits, using the GENES program version 2016, 6.0, developed by Cruz (2016), with which the genetic parameters were estimated.

Heritability in the broad sense (h²ₐ) was estimated for each variable with the classic method, as described below:

\[ h^2_a = \left( \sigma^2_Y / \sigma^2_F \right) \times 100 \]  

where, \( \sigma^2_Y \) was the mean genetic variance, and \( \sigma^2_F \) was the mean phenotypic variance.

The genetic gain (GG) was estimated for each variable according to Johnson et al. (1955):

\[ GG = K \sigma h^2 \]  

Table 1. Name and origin of cultivars.

| No. | Name       | Origin   |
|-----|------------|----------|
| 1   | Caupí Negro| Colombia |
| 2   | Caupí Calamari | Colombia |
| 3   | Caupica M-11 | Colombia |
| 4   | Caupí Cuarentano | Colombia |
| 5   | Caupí Provinciano | Colombia |
| 6   | Caupí Betancí | Colombia |
| 7   | Criollo Córdoba | Colombia |
| 8   | L-CP-M-35  | Nigeria  |
| 9   | L-CP-M-37  | Nigeria  |
| 10  | BRS Milenium| Brasil   |
| 11  | IT 86      | Brasil   |
| 12  | TVU 382    | Brasil   |
| 13  | Gurgueia   | Brasil   |
| 14  | BRS Guariba| Brasil   |
| 15  | BRS Potengi| Brasil   |
| 16  | BRS Tumucumaque| Brasil |
| 17  | BRS Jurua  | Brasil   |
| 18  | Caupí Brasil-2016 | Brasil |
| 19  | MNC05-828C-3-15 | Brasil |
| 20  | Judío Blanco| México   |
| 21  | 24135      | UNK      |
| 22  | Caupicor 50| Colombia |
| 23  | L 019      | Colombia |
| 24  | LC 006-016 | Colombia |
| 25  | Momposino  | Colombia |
| 26  | Mono Largo | Colombia |
| 27  | Mono de Tigre| Colombia |
| 28  | Guajiro    | Colombia |
| 29  | Capisuna   | Colombia |
| 30  | “Nuevo”    | Colombia |
where, \( k \) was the selection differential at 5% selection intensity, equivalent to 2.06; \( \sigma_f \) was the phenotypic standard deviation; and \( h^2 \) was the heritability.

The genetic progress (GP) was also expressed as a percentage, according to Robinson et al. (1949), and classified as low, moderate and high (Johnson et al., 1955).

RESULTS AND DISCUSSION

Analysis of variance

The results of the analysis of variance are shown in table 2. The genotypes showed highly significant differences (\( P<0.01 \) and \( P<0.05 \)), except PEL, which showed genetic variability, which is interesting for genetic improvement programs since it selects the best genotypes according to the agronomic characteristics of interest; these results agree with those of Nkoana et al. (2019) and Ribeiro et al. (2019).

The coefficients of variation were less than 20%, except for NPP, PEL and YIELD, without affecting the experiment precision, as noted by Silva and Neves (2011).

Table 2. Mean squares and statistical significance of the sources of variation for the characteristics in the 30 genotypes of cowpea beans.

| Characteristics                  | Mean squares        | CV (%) |
|----------------------------------|---------------------|--------|
|                                  | Genotypes | Replications | Error |        |
| Number of days to flowering (NDF) | 27.53**     | 5.9      | 4.61  | 5.89   |
| Number of pods per plant (NPP)   | 24.15**     | 30.32    | 10.88 | 24.65  |
| Number of pods per peduncle (NPPE) | 0.20*      | 0.05     | 0.12  | 18.77  |
| Peduncle length (PEL) (cm)       | 0.27NS      | 0.21     | 4.35  | 27.81  |
| Number of nodes on main stem (NNMS) | 2.66**     | 5.47     | 0.77  | 13.70  |
| Grain length (GL) (mm)           | 2.70**     | 0.12     | 0.14  | 4.19   |
| Grain width (GW) (mm)            | 0.62**     | 0.01     | 0.02  | 3.34   |
| Weight of 100 seeds (W100S) (g)  | 77.64**    | 5.43     | 1.55  | 6.42   |
| Yield (YIELD) (kg ha\(^{-1}\))   | 1506482*** | 2502903  | 522426 | 40.53 |
| Iron content (FeC) (mg kg\(^{-1}\)) | 356.17**  | 5.23     | 12.14 | 6.14   |
| Zinc content (ZnC) (mg kg\(^{-1}\)) | 253.58** | 12.54    | 5.86  | 4.59   |
| Protein (PROT) (%)               | 13.18**    | 10.47    | 1.75  | 6.28   |
| Degrees of freedom               | 29         | 3        | 87    |        |

** significant at \( P<0.01 \), * significant at \( P<0.05 \), NS not significant, CV (%), coefficient of variation.

Genetic parameters

Table 3 shows the results for the parameters. The genetic variance (GV) was higher than the environmental variance (EV), which corroborates the results of the ANOVA and supports the usefulness of genetic improvement for plants and the fact that the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged between <10%, 10 to 20% and > 20%, considered low, medium and high, respectively (Getachew et al., 2015).

The PCVs had a greater magnitude than the GCVs, which means that the existing variation was not only due to genetic differences between the cultivars but also to environmental effects given the polygenic inheritance of these characteristics, as has been indicated by Nkoana et al. (2019) in cowpea beans.

Since genetic improvement is a function of the quantification of exploitable genetic variability (Keneni et al., 2011), genetic variance with a greater magnitude than the environmental variance in the studied traits (Tab. 3) means that the differences with a genetic origin, which was observed in the variation indices b, with values ≥ 1.0 in NDF, GL, GW, W100S, FeC, ZnC and PROT, favorable for the selection (Mofokeng et al., 2020).
The characteristics with a high and moderate PCV and GCV included NPP, NNMS, W100S, YIELD, FeC and ZnC (Tab. 3), similar to that obtained by Gerrano et al. (2015) and Mofokeng et al. (2020), suggesting they can be significantly improved through selection, as argued by Mendonça et al. (2018).

The heritability estimates in the broad sense ranged between 19.56 and 97.99%, with more than 80% for NDF, GL, GW, W100S, FeC, ZnC and PROT and lower values (50 to 70%) for NPP, NNMS and YIELD, indicating the existence of genetic variability between cultivars. According to Nkoana et al. (2019) and Mofokeng et al. (2020), these heritability values mean the phenotype exhibited a high expression in the genotype, indicating good efficiency of selection and genetic gain, which must be demonstrated with the selection of the best genotypes.

The genetic progress (GPM) percentage showed values of 5.33% for PEL, a low value, with 45.81 for W100S and 46.34% for YIELD, high values. According to Ubi et al. (2001), high heritability values associated with higher percentages of genetic progress indicate the predominance of genes with additive action and much easier selection.

Low heritability and genetic gain were observed in PEL and NPPE, while high heritability and moderate genetic gain were estimated for PROT. Combinations of genetic parameters can be attributed to genes with non-additive gene action (Ara et al., 2009). Therefore, a cross between parents with complementary characteristics will obtain progenies with better grain yields and micronutrient contents.

Correlations

The study of the interrelation between several characters in the form of correlation is one of the very important aspects in the genetic improvement of plants, so that the breeder is very efficient in selections based on correlation and uncorrelated responses (Agrawal et al., 2018).

The values of the genotypic correlations (rG) had the same tendency and superior to the phenotypic correlations (rF) (Tab. 4), which indicated that the relationship between the variables was based on additive genetic effects. Preliminary results have been reported by Andrade et al. (2010) and Silva et al. (2014) in cowpea beans and by Agrawal et al. (2018) in chickpeas, who argued that phenotypic selection can be efficient.

There were negative phenotypic and genotypic correlations (P<0.01) between NDF and NNMS, that is, as phylochron decreased, NDF increased, indicating that early cultivars form leaves more quickly than

### 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 (h²), genetic gain (GG) and genetic progress as percentage of mean (GPM).

| Characteristics | Mean | PV  | GV  | EV  | PCV (%) | GCV (%) | b     | h² (%) | GA   | GAM (%) |
|-----------------|------|-----|-----|-----|---------|---------|-------|--------|------|---------|
| NDF             | 36.48| 6.88| 5.72| 1.15| 7.19    | 6.56    | 6.56  | 83.22  | 4.48 | 12.29   |
| NPP             | 13.38| 6.03| 3.32| 2.72| 18.36   | 13.60   | 0.55  | 54.92  | 2.77 | 20.76   |
| NPPE            | 1.85 | 0.05| 0.03| 0.02| 12.31   | 7.59    | 0.40  | 39.56  | 0.18 | 9.85    |
| PEL (cm)        | 1.68 | 0.068| 0.013| 0.054| 15.52   | 6.78    | 0.24  | 19.56  | 0.09 | 5.33    |
| NNMS            | 6.44 | 0.666| 0.471| 0.194| 12.67   | 10.66   | 0.77  | 70.76  | 1.18 | 18.47   |
| GL (mm)         | 9.02 | 0.675| 0.639| 0.035| 9.11    | 8.86    | 2.11  | 94.69  | 1.60 | 17.77   |
| GW (mm)         | 5.16 | 0.156| 0.149| 0.007| 7.66    | 7.48    | 2.23  | 95.24  | 0.77 | 15.04   |
| W100S (g)       | 19.41| 19.41| 19.02| 0.38| 22.69   | 22.47   | 3.49  | 97.99  | 8.89 | 45.81   |
| YIELD (kg)      | 1782 | 376620.56| 246013.93| 130606.63| 34.42   | 27.81   | 0.68  | 65.32  | 8.25 | 46.34   |
| FeC (mg kg⁻¹)   | 56.71| 89.04| 86.00| 3.03| 16.63   | 16.35   | 2.66  | 96.58  | 18.77| 33.10   |
| ZnC (mg kg⁻¹)   | 52.73| 63.39| 61.92| 1.46| 15.09   | 14.92   | 3.24  | 97.68  | 16.02| 30.38   |
| PROT (%)        | 21.08| 3.29 | 2.85| 0.43| 8.61    | 8.01    | 1.27  | 86.55  | 3.24 | 15.37   |

NDF = number of days to flowering; NPP = number of pods per plant; NPPE = number of pods per peduncle; PEL = peduncle length; NNMS: number of nodes on main stem; GL = grain length; GW = grain width; W100S = weight of 100 seeds; FeC = Iron content; ZnC = Zinc content; PROT = protein content.
late ones. In addition, NDF had positive phenotypic and genotypic correlations with YIELD ($P<0.05$), i.e., later cultivars have the potential of generating higher yields because of an increased number of branches, which favors the development of a greater number of pods per plant (Ferrari et al., 2018; Meena et al., 2015).

NPP correlated phenotypically ($P<0.05$), genotypically ($P<0.01$) and positively with NNMS because pods are produced from the differentiation of flower buds in the stem nodes. However, the phenotypic ($P<0.05$) and genotypic ($P<0.01$) correlations of NPP with GW were negative, which was due to the fact that a higher NPP means GW decreases, along with PEL and W100S. The plants distribute photo-assimilates to the organs in formation, in proportion to demand, which depends on the number of organs in development. Similar results were found by Mendonça et al. (2018). The lack of significance of the correlation between NPP and YIELD could have been overshadowed by phenotypic plasticity in the face of environmental effects on polygenic characteristics (Ferrari et al., 2018).

NPPE registered positive phenotypic and genotypic correlations ($P<0.01$) and ($P<0.05$) with NNMS and FeC. The increase in NPPE was associated with an increase in NNMS and, simultaneously, with an increase in FeC in the seeds. The higher the rate of leaf emission, the greater the accumulation of iron in the seed by translocation despite the fact that it is not very mobile element in the plant. Furthermore, a higher NNMS could lead to the formation of a greater number of productive branches (Kinhöegbè et al., 2020). On the other hand, the negative phenotypic and genotypic correlations ($P<0.01$) between NPPE

### Table 4. Estimates of the phenotypic and genotypic correlation matrix in cowpea bean characteristics.

| VAR'S     | r's NPP | NPPE | PEL | NNMS | GL | GW | YIELD | W100S | FeC | ZnC | PROT |
|-----------|---------|------|-----|------|----|----|-------|-------|-----|-----|------|
| NDF rF    | -0.15   | -0.24| 0.32| -0.53**| 0.03| -0.06| 0.40* | -0.13 | 0.07| -0.11| 0.12 |
|          | rG      | -0.19| -0.47**| 0.73**| -0.60**| 0.04| -0.08| 0.52**| -0.13| 0.08| -0.11| 0.14 |
| NPP rF    | 0.23    | -0.07| 0.45* | -0.07  | -0.42* | 0.16| 0.16  | 0.06  | 0.05| 0.24 | 0.13 |
|          | rG      | -0.51**| 0.60**| -0.10  | -0.60**| 0.03| -0.40*| -0.06 | 0.32| 0.16 |
| NPPE rF   | -0.36* | 0.62**| -0.45*| -0.37* | 0.21 | -0.47**| 0.43* | 0.09 | 0.16 |
|          | rG      | -1.00**| 1.00**| -0.73**| -0.56**| 0.34| -0.77**| 0.72**| 0.13| 0.34 |
| PEL rF    | -0.35  | 0.19 | 0.05 | 0.03  | 0.13 | -0.03 | -0.07 | -0.06 |
|          | rG      | -0.98**| 0.41* | 0.04  | 0.01 | 0.31 | -0.13 | -0.21 | -0.23 |
| NNMS rF   | -0.24  | -0.22| 0.15 | -0.21 | -0.06 | 0.18 | 0.30  |
|          | rG      | -0.30 | -0.25| 0.11 | -0.26 | -0.08 | 0.22 | 0.43* |
| GL rF     | 0.59** | -0.22| 0.86**| -0.39* | -0.24 | 0.04 |
|          | rG      | 0.60**| -0.29| 0.88**| -0.41| -0.25 | 0.06  |
| GW rF     | -0.35 | 0.83**| -0.34| -0.13 | -0.25 |
|          | rG      | -0.43 | 0.85* | -0.36 | -0.14 | -0.27 |
| YIELD rF  | -0.33  | -0.14| -0.23 | 0.49**|
|          | rG      | -0.43*| -0.19| -0.29 | 0.70**|
| W100S rF  | -0.46*| -0.19| -0.13 |
|          | rG      | -0.48**| -0.19| -0.13 |
| FeC rF    | 0.21   | -0.08 |
|          | rG      | 0.21 | -0.08 |
| ZnC rF    | 0.10   |
|          | rG      | 0.11 |

VAR'S = variables; r's = correlations; rF = phenotypic correlations; rG = genotypic correlations; NDF = number of days to flowering; NPP = number of pods per plant; NPPE = number of pods per peduncle; PEL = peduncle length; NNMS: number of nods on main stem; GL = grain length; GW = grain width; W100S = weight of 100 seeds; YIELD; FeC = Iron content; ZnC = Zinc content; PROT = protein content; * significant at $P<0.05$; **: significant at $P<0.01$. 

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and PEL, GL, GW and W100S showed that, when NPPE is increased, along with NPP, the supply of photoassimilates to the seeds increases. This competition reduces the agronomic value of characteristics that could be used as selection criteria (MathosFilho et al., 2009).

PEL had a negative genotypic correlation ($P<0.01$) with NNMS but a positive one with GL ($P<0.05$). This indicates that a higher GL is associated with a higher PEL, but the latter characteristic is associated with a lower NPP and NPPE. In addition, the selection of a higher PEL would compromise commercial performance since a higher PEL, together with the weight of the pods, would lead to greater contact with the soil, with a consequent deterioration because of the influence of the microclimate on the lower part of the plant.

NNMS was only genotypically correlated with PROT ($P<0.05$). This indicates that as more knots originate, the rate of leaf formation increases and therefore protein accumulates in the seeds, which suggests that it is possible to select plants with higher NNMSs, with greater accumulation of protein in the seeds.

GL and GW registered positive phenotypic and genotypic correlations ($P<0.01$) with W100S, that is, the heavier seeds were larger, as expected because of their allometry. On the other hand, the negative correlation between GL and FeC ($P<0.05$) showed that longer grains have decreased iron contents, possibly because, when the size of the organ longitudinally increases, the accumulation of iron decreases because of the low mobility of iron.

YIELD did not have a correlation with FeC and ZnC, which agreed with the results obtained by Singh et al. (2018). For the development of cultivars with higher yields and high micronutrient and protein contents, cultivars should be submitted to genetic studies to find quantitative trait loci (QTL) for Fe, Zn, protein and high yield contents (Gerrano et al., 2018; Gondwe et al., 2019). In this study, YIELD presented positive phenotypic and genotypic correlations ($P<0.01$) with PROT, indicating that it is possible to find high yield and protein contents simultaneously. This contradicts the results of Moura et al. (2012), who reported a negative correlation between yield and protein contents. On the other hand, YIELD presented a negative correlation with W100S ($P<0.05$), coinciding with the result of Silva and Neves (2011), so an improvement in performance through P100S is not possible.

CONCLUSIONS

There is genetic variability in the population of 30 cowpea bean cultivars that can be exploited in genetic improvement for characteristics of agronomic interest and for nutritional contents.

A high heritability was observed in the characteristics NDF, GL, GW, W100S, FeC, ZnC and PROT, while a high genetic advancement was seen in YIELD, W100S, FeC and ZnC, along with positive phenotypic and genotypic correlations between YIELD and PROT, which allow for the parallel improvement of yield and protein percentage, which are associated with iron and zinc contents.

Conflict of interests: The manuscript was prepared and reviewed with the participation of the authors, who declare that there exists no conflict of interest that puts the validity of the presented results at risk.

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