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Scientific Article

Selection of cowpea genotypes for the black specialty grain market

Seleção de genótipos de feijão-caupi com potencial para o mercado de grãos especiais do tipo preto

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ABSTRACT - Cowpea grain in the black commercial class is part of the specialty grain market, and cultivar development for this market may contribute to diversifying and expanding the cowpea market and increasing cowpea consumption in Brazil. The objective of this study was to evaluate and select cowpea genotypes with potential for the black specialty grain market. Sixteen genotypes were evaluated in a randomized complete block design with three replications in Teresina, Piauí, Brazil, during the 2023–2024 growing season. The following traits were evaluated: number of days to flowering onset, pod length, number of grains per pod, 100-grain weight, grain index, and grain yield. Data were analyzed using mixed models and the restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) procedure. Genotypes were selected based on empirical best linear unbiased predictions (eBLUPs)/genetic values and the multi-trait genotype-ideotype distance index (MGIDI). Genetic variability was detected, especially for 100-grain weight, grain index, and grain yield. Selection for earlier flowering and greater pod length and grain index can increase grain yield, while selection for larger grains can reduce the number of grains per pod. Based on the eBLUP estimates and MGIDI, the cowpea genotypes with the greatest potential for the black specialty grain market were BRS Tapaihum, BRS Guirá, MNC10-998B-8-1, Pretinho-PA, MNC09-981B-6, MNC09-988B-20, and MNC10-982B-3-7.

Keywords: *Vigna unguiculata*. Agronomic traits. Plant breeding. Genetic parameters. Selection index. Genotype–ideotype distance.

RESUMO – Os grãos de feijão-caupi da classe comercial preto integram o mercado de grãos especiais, e o desenvolvimento de cultivares destinadas a esse mercado pode contribuir para diversificar e ampliar o mercado do feijão-caupi e aumentar seu consumo no Brasil. O objetivo deste estudo foi avaliar e selecionar genótipos de feijão-caupi com potencial para o mercado de grãos especiais do tipo preto. Dezesseis genótipos foram avaliados em delineamento em blocos completos casualizados, com três repetições, em Teresina, Piauí, Brasil, durante a safra 2023–2024. Foram avaliados os seguintes caracteres: número de dias até o início da floração, comprimento de vagem, número de grãos por vagem, peso de 100 grãos, índice de grãos e produtividade de grãos. Os dados foram analisados por meio de modelos mistos e do procedimento de máxima verossimilhança restrita/melhor preditor linear não viesado (REML/BLUP). A seleção dos genótipos baseou-se nos valores empíricos do melhor preditor linear não viesado (eBLUPs)/valores genéticos e no índice de distância genótipo-ideótipo multicaráter (MGIDI). Foi detectada variabilidade genética, especialmente para peso de 100 grãos, índice de grãos e produtividade de grãos. A seleção para precocidade de floração e maior comprimento da vagem e índice de grãos pode aumentar a produtividade de grãos, enquanto a seleção para grãos maiores pode reduzir o número de grãos por vagem. Com base nas estimativas de eBLUPs e no MGIDI, os genótipos de feijão-caupi com maior potencial para o mercado de grãos especiais do tipo preto foram BRS Tapaihum, BRS Guirá, MNC10-998B-8-1, Pretinho-PA, MNC09-981B-6, MNC09-988B-20 e MNC10-982B-3-7.

Palavras-chave: *Vigna unguiculata*. Caracteres agronômicos. Melhoramento de plantas. Parâmetros genéticos. Índice de seleção. Distância genótipo–ideótipo.

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INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is consumed by millions of people and is an important staple food in low-income communities in developing countries. Several characteristics favor cowpea cultivation in different regions worldwide, including a short crop cycle, low water and fertilizer requirements, and the capacity for biological nitrogen fixation through symbiotic association with soil bacteria, which can improve soil quality (SPRIGGS et al., 2018; BOUKAR et al., 2019).

Cowpea originated in Africa and was introduced into Brazil by Portuguese colonizers in the state of Bahia during the second half of the 16th century (FREIRE FILHO et al., 2017). In Brazil, cowpea is cultivated predominantly in the North, Northeast, and Central-West regions for the dry-grain and pod or immature-grain markets (ROCHA et al., 2017). In the 2023–2024 growing season, the cultivated area, production, and grain yield were 1,287,300 ha, 631,400 Mg, and 491 kg ha^{-1}, respectively (BRASIL, 2024).

Black beans are widely consumed in Brazilian cuisine, primarily in feijoada, a dish prepared throughout the country. However, the black bean most used for this purpose in northeastern Brazil is common bean (*Phaseolus vulgaris* L.), which is produced mainly in the South and Southeast regions of Brazil and is

marketed in the Northeast at higher prices (LUZ et al., 2025). The black commercial class of cowpea is part of the specialty grain market; however, few cultivars in this class are available (SANTOS, 2011; FREIRE FILHO et al., 2022).

The objective in cowpea breeding is to select superior genotypes for multiple traits simultaneously. One of the most effective breeding strategies for simultaneous selection of multiple traits is the use of selection indexes. Several selection indexes based on univariate analyses of variance, including the classical indexes of Smith (1936) and Hazel (1943), the Williams (1962) base index, and the Mulamba and Mock (1978) rank-sum index, have been used for this purpose in cowpea (ARAGÃO et al., 2022; ALVINO et al., 2023; LOPES et al., 2023; PESSOA et al., 2023).

Selection indexes based on multivariate approaches using mixed models and graphical interpretation have been used less frequently in cowpea breeding; however, they can provide more accurate estimates of genetic parameters and facilitate interpretation and are not based on the assumptions of conventional analysis of variance. One of these indexes is the multi-trait genotype–ideotype distance index (MGIDI) proposed by Olivoto and Nardino (2021).

The development of new cowpea cultivars in the black commercial class may contribute to market expansion and increased crop competitiveness in response to current consumption and export trends. Thus, the objective of this study was to evaluate and select cowpea genotypes with potential for the black specialty grain market.

MATERIAL AND METHODS

Sixteen cowpea genotypes from the black commercial class were selected from the Brazilian Agricultural Research Corporation (Embrapa Meio-Norte) germplasm bank and evaluated (Table 1).

Table 1. Identification number (N), name/code, genealogy, and commercial subclass of the evaluated cowpea genotypes in the black commercial class.

N	Name/Code	Genealogy	Commercial subclass
1	MNC08-937C-6-1	Pretinho × TE97-309G-9	Opaque black
2	MNC09-981B-1	{[BRS Guariba × (Pretinho × TE97-309G-9)] × BRS Guariba} × BRS Guariba	Slightly glossy black
3	MNC09-981B-3	{[BRS Guariba × (Pretinho × TE97-309G-9)] × BRS Guariba} × BRS Guariba	Slightly glossy black
4	MNC09-981B-6	{[BRS Guariba × (Pretinho × TE97-309G-9)] × BRS Guariba} × BRS Guariba	Slightly glossy black
5	MNC09-981B-9	{[BRS Guariba × (Pretinho × TE97-309G-9)] × BRS Guariba} × BRS Guariba	Slightly glossy black
6	MNC09-988B-3	IT85F-1045 × MNC01-689F-11	Opaque black
7	MNC09-988B-3-20	IT85F-1045 × MNC01-689F-11	Opaque black
8	MNC09-988B-20	IT85F-1045 × MNC01-689F-11	Opaque black
9	MNC10-982B-3-7	{[BRS Guariba × (Pretinho × TE97-309G-9)] × Pretinho} × Pretinho	Slightly glossy black
10	MNC10-982B-11-1	{[BRS Guariba × (Pretinho × TE97-309G-9)] × Pretinho} × Pretinho	Slightly glossy black
11	MNC10-998B-8-1	{F3RC1[(Pretinho × TE97-309G-9) × Pretinho]} × Pretinho	Slightly glossy black
12	MNC10-998B-20-3	{F3RC1[(Pretinho × TE97-309G-9) × Pretinho]} × Pretinho	Slightly glossy black
13	Pretinho-PA	Landrace Pretinho Pará	Glossy black
14	Pretinho-THE	Landrace Pretinho Teresina, Piauí	Glossy black
15	BRS Tapaihum	Epace 11 × 293588	Glossy black
16	BRS Guirá	{[BRS Guariba × (Pretinho × TE97-309G-9)] × Guariba} × Guariba	Slightly glossy black

The field experiment was conducted at the Embrapa Meio-Norte experimental station (5°02′17″S, 42°47′54″W; altitude 74 m) in Teresina, Piauí, Brazil, during the 2023–2024 growing season. The soil at the experimental site ranged in texture from sandy clay loam to clay, with pH (H_2O) ranging from 5.14 to 6.89. The mean annual temperature in the region is approximately 27.2 °C.

The experiment was conducted in a randomized complete block design with three replications. Each experimental unit (plot) measured 10 m² (2 × 5 m) and consisted of four rows, with a net plot area of 5 m² (1.0 × 5 m) comprising the two central rows, from which data were collected. Rows were spaced 0.50 m apart, with a final stand of 40 plants per row.

Seeds were sown at a rate of 12 seeds m^{-1}. Plants were thinned 15 days after sowing to a density of 8 plants m^{-1}. Manual weeding was performed 20 and 35 days after sowing. Insect pests and diseases were controlled with pesticides as needed, with preference given to biological control products in accordance with crop recommendations to maintain the plant stand. Sprinkler irrigation was used throughout the experiment. No rainfall occurred during the experimental period. Plants were harvested manually 70–75 days after sowing (January 22, 2024).

The following traits were evaluated: number of days to flowering onset (NDF; day), pod length (PL; cm), number of grains per pod (NGP), 100-grain weight (W100G; g), grain index (GI; %), and grain yield (GY; kg ha^{-1}). Grain index (GI) was calculated as *GI (%) = (grain weight/pod weight) × 100*. Grain weight was defined as the mass of grains obtained from each pod, whereas pod weight was defined as the total pod mass. Statistical analyses were performed using restricted maximum likelihood (REML) and empirical best linear unbiased prediction (eBLUP). Variance component estimates were used to estimate broad-sense heritability based on genotype means and to calculate the genetic and experimental coefficients of variation.

Variance components were estimated by REML, and

genetic values were predicted by eBLUP using the following mixed model:

$$Y = Xr + Zg + e$$

where Y is the vector of observed data; r is the vector of replication effects, treated as fixed and added to the overall mean; g is the vector of genotypic effects, treated as random; and e is the vector of residuals, also treated as random. X and Z are the incidence matrices associated with the fixed and random effects, respectively.

The following variance components were estimated by REML: phenotypic variance (σ_f^2), residual variance (σ_e^2), and genotypic variance (σ_g^2); broad-sense heritability based on genotype means $[h^2 = (\frac{\sigma_g^2}{\sigma_f^2})]$; genetic coefficient of variation $[CV_g = 100(\sqrt{QM_g/m})]$, where (σ_g^2) is the genotypic variance and m is the overall trait mean; experimental coefficient of variation $[CV_e = 100(\sqrt{QM_e/m})]$, where QM_e is the residual mean square; quotient b ($b = CV_g/CV_e$); and selective accuracy of genotypes $\{Acs = [1/(1 + (\sigma_e^2/r)/\sigma_g^2)]^{0.5}\}$, according to Resende (2007), where r is the number of blocks, (σ_e^2) is the residual variance, and (σ_g^2) is the genotypic variance.

The significance of random effects was assessed using the likelihood ratio test (LRT) by comparing models with and without the tested effect, with significance evaluated against a chi-square distribution with 1 degree of freedom.

Genetic values were predicted using eBLUP, and Pearson genotypic correlations between traits were calculated according to Falconer (1987) as follows:

$$r_{g\,(xy)} = \frac{COV_{g(xy)}}{\sqrt{\sigma_{gx}^2 \sigma_{gy}^2}},$$

where r_g (x,y) is the genotypic correlation between x and y traits; $Cov_{g(xy)}$ is the genotypic covariance between x and y traits; σ_{gx}^2 is the genotypic variances of x trait; and σ_{gy}^2 is the genotypic variance of y trait.

Superior genotypes were selected using the multi-trait genotype-ideotype distance index (MGIDI) described by Olivoto and Nardino (2021), which enables simultaneous selection for multiple traits. The distance between the genotypic scores and the ideotype was calculated as follows:

$$MGIDI_i = \left[\sum_{j=1}^{f}(\gamma_{ij} - \gamma_j)^2\right]^{0.5}$$

where Y_{ij} is the score of i genotype for j factor, γ_j is the ideotype score for j factor, and f is the number of retained factors.

The genotype with the lowest MGIDI value is closest to the ideotype and has trait values closest to the desired values for all evaluated traits. Selection differentials were calculated for all traits using a selection intensity of 30%, with the following economic weights: NDF (0.7), PL (0.6), NGP (0.6), W100G (0.7), and GY (1.0).

Statistical analyses were performed using R version 4.4.2 (R CORE TEAM, 2024). Mixed-model analyses and MGIDI calculations were performed using the "metan" package (OLIVOTO; LÚCIO, 2020).

RESULTS AND DISCUSSION

Summaries of the deviance analyses for all traits evaluated in cowpea genotypes of the black commercial class are provided in Table 2. The genotype effect was significant (p<0.001) for all evaluated traits, indicating genetic variability and the potential for genetic gain through selection. These results are consistent with those reported by Aragão et al. (2022), who also detected genetic variability for most traits, except number of days to flowering onset (NDF). Similar genetic variability for all evaluated traits was reported by Lopes et al. (2023) in cowpea genotypes grown in the semiarid region of Piauí, Brazil.

Table 2. Summary of deviance analyses for number of days to flowering onset (NDF), pod length (PL), number of grains per pod (NGP), 100-grain weight (W100G), grain index (GI), and grain yield (GY) in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class evaluated in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Trait	Deviance	LRT	Pr (> χ^2)
NDF	160.37	21.30	3.94×10^{-6}
PL	124.17	17.30	3.24×10^{-5}
NGP	153.89	22.30	2.34×10^{-6}
W100G	237.65	49.00	2.54×10^{-12}
GI	301.62	37.30	1.00×10^{-9}
GY	680.09	80.40	2.99×10^{-19}

LRT: likelihood ratio test; Pr: probability; χ^2: chi-square.

Estimates of the genetic parameters indicate that genetic variance was the main contributor to phenotypic expression, suggesting that selection should be effective, especially for W100G, GI, and GY, which showed greater genetic variability (Table 3).

Table 3. Estimates of genetic parameters for number of days to flowering onset (NDF), pod length (PL), number of grains per pod (NGP), 100-grain weight (W100G), grain index (GI), and grain yield (GY) in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class evaluated in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Parameter*	NDF	PL	NGP	W100G	GI	GY
σ_f^2	1.72	0.77	1.49	9.57	39.60	178,174.00
σ_g^2	1.17	0.48	1.03	8.45	32.60	171,036.00
σ_e^2	0.55	0.29	0.46	1.12	7.02	7,138.00
h^2_{mg}	0.86	0.83	0.87	0.90	0.89	0.94
Ac_s	0.93	0.91	0.93	0.94	0.92	0.95
CV_g	2.98	3.74	7.53	17.2	7.74	53.60
CV_e	2.04	2.90	5.02	6.26	3.59	10.90
CV_g/CV_e	1.46	1.29	1.50	2.74	2.15	2.89

* σ_f^2: phenotypic variance; σ_g^2: genotypic variance; σ_e^2: residual variance; h^2_{mg}: broad-sense heritability based on genotype means; *Acs*: selective accuracy of genotypes; CV_g: genotypic coefficient of variation; CV_e: experimental coefficient of variation.

High estimates of selective accuracy indicate high reliability of selection, and CV_g/CV_e values greater than 1 support the effectiveness of selection for the evaluated traits. These estimates were higher than those reported by Aragão et al. (2022) and Lopes et al. (2023) for cowpea genotypes analyzed using mixed linear models.

Estimated genetic values for traits evaluated in cowpea genotypes of the black commercial class indicated that NDF ranged from 33 to 39 d, with an overall mean of 36.27 d (Figure 1). Among the evaluated genotypes, 50% had mean NDF values below 36.27 d and were therefore considered superior for earliness, including genotypes 15 (BRS Tapaihum), 9 (MNC10-982B-3-7), and 10 (MNC10-982B-11-1). Genotype 15 (BRS Tapaihum) had the lowest NDF and was therefore the earliest, whereas genotype 14 (Pretinho-THE) had the highest NDF and was the latest to reach flowering onset. Previous studies have reported a significant positive correlation between NDF and days to maturity (PESSOA et al., 2023; ABHA; MEENA, 2024), indicating that early-maturing genotypes may be selected indirectly based on NDF.

Early maturity is advantageous in regions with short growing seasons because it may reduce exposure to stress, terminal drought, crop-management constraints, and diseases. Early maturity also enables more efficient crop rotation and production of up to three crops per year and can meet the increasing demand for early cultivars in off-season production systems in the Brazilian Cerrado while reducing costs and risks associated with insufficient rainfall.

Pod length (PL) in cowpea genotypes of the black commercial class ranged from 16.62 to 21.00 cm, with an overall mean of 18.51 cm. This mean was lower than the 19.93 cm reported by Lopes et al. (2023) for cowpea genotypes of the colored commercial class. Among the 16 evaluated genotypes of the black commercial class, 56.25% had PL values above the overall mean of 18.51 cm. Genotypes with PL values above the overall mean included 11 (MNC10-998B-8-1), 7 (MNC09-988B-3-20), 16 (BRS Guirá), 13 (Pretinho-PA), 3 (MNC09-981B-3), 10 (MNC10-982B-11-1), 12 (MNC10-998B-20-3), 8 (MNC09-988B-20), and 4 (MNC09-981B-6). Genotype 11 (MNC10-998B-8-1) had the highest PL, whereas genotype 14 (Pretinho-THE) had the lowest. Cultivars with larger pods are preferred by family farmers, while cultivars with medium and small pods are more suitable for large-scale commercial farmers who carry out mechanized harvesting, as they provide greater harvesting efficiency.

The number of grains per pod (NGP) ranged from 11.00 to 16.40, with an overall mean of 13.47 grains per pod. This mean was higher than that reported by Aragão et al. (2022) and lower than that reported by Lopes et al. (2023). Among the evaluated genotypes, 50% had NGP values above the overall mean, including genotypes 13 (Pretinho-PA), 12 (MNC10-998B-20-3), 7 (MNC09-988B-3-20), 6 (MNC09-988B-3), 8 (MNC09-988B-20), 14 (Pretinho-THE), 4 (MNC09-981B-6), and 9 (MNC10-982B-3-7). Genotype 13 (Pretinho-PA) had the highest NGP, whereas genotype 15 (BRS Tapaihum) had the lowest.

Number of grains per pod is an important yield component and, because it is positively correlated with grain yield, may allow indirect gains in grain yield through selection. This trait also generally has lower environmental sensitivity and higher heritability than grain yield (ROCHA et al., 2017; PESSOA et al., 2023).

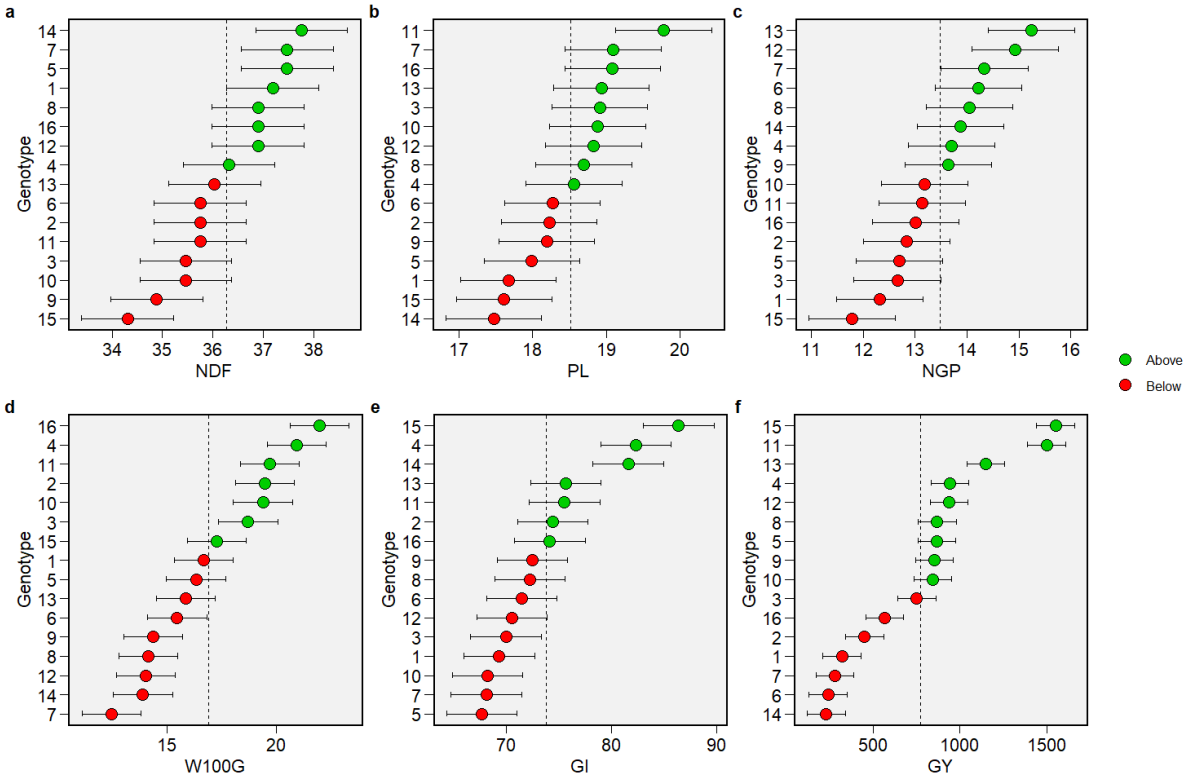


Figure 1. Empirical best linear unbiased predictions (eBLUPs) of genetic values for six traits evaluated in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class in Teresina, State of Piauí, Brazil, during the 2023–2024 growing season. The traits and corresponding panels are: (a) NDF, number of days to flowering onset; (b) PL, pod length; (c) NGP, number of grains per pod; (d) W100G, 100-grain weight; (e) GI, grain index; and (f) GY, grain yield.

The overall mean W100G in this study was 16.92 g, which was lower than the mean of 19.93 g reported by Lopes et al. (2023) for the semiarid region of Piauí. Among the evaluated genotypes, 43.75% had W100G values above the overall mean, including genotypes 16 (BRS Guirá), 4 (MNC09-981B-6), 11 (MNC10-998B-8-1), 2 (MNC09-981B-1), 10 (MNC10-982B-11-1), 3 (MNC09-981B-3), and 15 (BRS Tapaihum). Genotype 16 (BRS Guirá) had the highest W100G, exceeding 20 g, whereas genotype 7 (MNC09-988B-3-20) had the lowest value.

According to Freire Filho et al. (2017), producers, buyers, and packers prefer cowpea grain with a 100-grain weight greater than 20 g. This market preference is reported to reflect consumer preference for larger grains. Larger grains also command higher prices in the Brazilian cowpea market.

Grain index (GI) in cowpea genotypes of the black commercial class ranged from 62.90% to 90.95%, with an overall mean of 73.75%. This mean was lower than the 78.00% reported by Públio Júnior et al. (2017) for cowpea genotypes evaluated in Vitória da Conquista, Bahia, Brazil. Among the 16 evaluated cowpea genotypes of the black commercial class, 43.75% had GI values above the overall mean of 73.75%, including genotypes 15 (BRS Tapaihum), 4 (MNC09-981B-6), 13 (Pretinho-PA), 11 (MNC10-998B-8-1), 2 (MNC09-981B-1), and 16 (BRS Guirá). Genotype 15 (BRS Tapaihum) had the highest GI and therefore the highest grain-to-pod weight ratio, whereas genotype 5 (MNC09-981B-9) had the lowest GI.

Cultivars with GI values between 70% and 95% are considered suitable for efficient manual or mechanical threshing, which may reduce grain losses and problems associated with pod dehiscence. Higher GI values are also considered desirable because they indicate greater allocation to grain production relative to pod wall biomass (PÚBLIO JÚNIOR et al., 2017; OLIVEIRA et al., 2024).

Grain yield (GY) in cowpea genotypes of the black commercial class ranged from 195.45 to 1,686.60 kg ha^{-1}, with an overall mean of 779.09 kg ha^{-1}. This mean grain yield was higher than the national mean of 497 kg ha^{-1} (BRASIL, 2024). Among the 16 evaluated cowpea genotypes of the black commercial class, 56.25% had GY values above the overall mean of 779.09 kg ha^{-1}. Genotypes with GY values above the overall mean included 15 (BRS Tapaihum), 11 (MNC10-998B-8-1), 13 (Pretinho-PA), 4 (MNC09-981B-6), 12 (MNC10-998B-20-3), 8 (MNC09-988B-20), 5 (MNC09-981B-9), 9 (MNC10-982B-3-7), and 10 (MNC10-982B-11-1). Among the evaluated genotypes, genotype 15 (BRS Tapaihum) had the highest GY, whereas genotype 14 (Pretinho-THE) had the lowest.

Increasing grain yield is a primary objective of cowpea breeding programs (ROCHA; DAMASCENO-SILVA; MENEZES JÚNIOR, 2017), given the demand for increasingly high-yielding cultivars that can provide greater economic returns to farmers. Genetic improvement of cowpea is an effective approach for increasing mean grain yield and developing higher-yielding cultivars. Value for cultivation

and use (VCU) trials allow high-yielding genotypes adapted to different soil and climatic conditions in Brazil to be selected.

Studies in cowpea breeding have shown that grain yield is strongly correlated with yield components, particularly number of pods per plant, number of grains per pod, and W100G, indicating the potential for indirect gains in grain yield through selection for these components because they generally have lower environmental sensitivity and higher heritability than grain yield.

Estimates of Pearson genotypic correlations among the evaluated traits in cowpea genotypes of the black commercial class are shown in Figure 2. Significant negative correlations were observed between NDF and GY (-0.49; p<0.001) and between NGP and W100G (-0.36; p<0.05), suggesting that selection for earlier flowering may be associated with increased GY and that increased NGP may be associated with reduced grain size, possibly because of competition for photoassimilates during grain filling. This inverse association is particularly relevant to the cowpea market because larger grains are generally preferred by consumers and buyers.

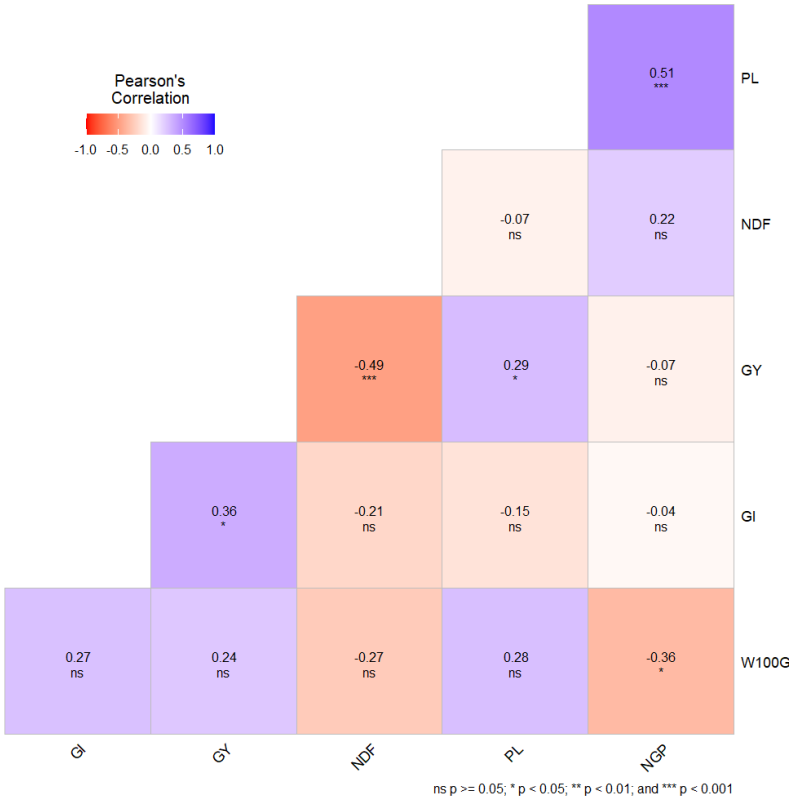


Figure 2. Pearson genotypic correlations among number of days to flowering onset (NDF), pod length (PL), number of grains per pod (NGP), 100-grain weight (W100G), grain index (GI), and grain yield (GY) in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class evaluated in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Significant positive correlations were observed between PL and NGP (0.51; p<0.001), GI and GY (0.36; p<0.05), and PL and GY (0.29; p<0.05), suggesting that selection for greater PL may be associated with increased NGP and GY and that a higher grain-to-pod weight ratio (GI) may be associated with increased GY. The remaining correlations were low and nonsignificant, suggesting limited associations among these traits for selection. These correlations are consistent with those reported by Pessoa et al. (2022), who also observed significant correlations among pod, grain, and physiological traits that may be useful for indirect selection.

Correlations among traits can support indirect selection and may reduce the time required for selection when the same genetic factors influence the expression of multiple traits (SANTOS et al., 2019). Defining the desired cultivar traits and breeding objectives is an essential step in plant breeding. The eigenvalues quantify the variance explained by each of the six principal components, and the cumulative percentages summarize the variance explained across successive components; these results were used to characterize the ideotype profile (Table 4).

This profile can be used to select black cowpea genotypes with earlier flowering, larger pods and grains, greater NGP, higher grain-to-pod weight ratio (GI), and higher grain yield. Only the first three principal components had eigenvalues greater than 1 and were therefore retained according to Kaiser's criteria (KAISER, 1958).

Table 4. Eigenvalues and proportions of variance explained by six principal components (PCs) based on six traits - number of days to flowering onset (NDF), pod length (PL), number of grains per pod (NGP), 100-grain weight (W100G), grain index (GI), and grain yield (GY) - evaluated in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Eigenvalue	Variance (%)	Cumulative variance (%)
2.27	37.80	37.80
1.46	24.40	62.10
1.08	18.00	80.10
0.66	11.10	91.20
0.41	6.75	98.00
0.12	2.05	100.00

The six-trait data set was therefore reduced to three dimensions. The first three principal components jointly explained 80.10% of the total variance, indicating that these components captured most of the variability in the six traits. This cumulative proportion was greater than the 68.29% reported by Sá (2024) for components with eigenvalues greater than 1 in an evaluation of six traits in 28 cowpea genotypes. The six traits were subsequently grouped into three factors by factor analysis (FA) (Table 5).

FA1 included NDF, GI, and GY; FA2 included PL; and FA3 included NGP and W100G. The grouping in FA1 indicates that NDF, GI, and GY shared a common underlying dimension, whereas NGP and W100G shared a common dimension in FA3. PL loaded primarily on FA2, indicating that its variation was represented separately from the traits grouped in FA1 and FA3. The mean communality of 0.80 indicates that, on average, 80% of the variance in the six traits was accounted for by the three retained factors. PL, NGP, W100G, and GY had the highest communalities and were therefore more strongly represented by the retained factor structure than the other traits.

Table 5. Factor loadings after varimax rotation and communalities obtained by factor analysis (FA) of six traits evaluated in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Trait	FA1	FA2	FA3	Commonality
NDF	**-0.73**	0.04	-0.31	0.62
PL	-0.10	**0.97**	0.03	0.95
NGP	0.08	0.35	**0.87**	0.88
W100G	-0.24	0.28	**-0.82**	0.81
GI	**-0.71**	-0.48	-0.02	0.74
GY	**-0.86**	0.26	-0.08	0.81
Mean commonality				0.80

NDF: number of days to flowering onset; PL: pod length; NGP: number of grains per pod; W100G: 100-grain weight; GI: grain index; GY: grain yield. Bold values indicate the traits grouped within each factor.

The mean communality obtained in this study (0.80) was higher than the 68% reported by Sá (2024) in an evaluation of 28 genotypes and 10 cowpea traits.

The multi-trait genotype-ideotype distance index (MGIDI) provided satisfactory estimates of the selection differential (Sd) for most evaluated traits (Table 6), particularly GY and GI.

Heritability estimates ranged from 0.82 for NDF to 0.99 for W100G, suggesting favorable expected gains from selection, especially for traits with higher h^2 values, such as PL (0.97), GI (0.97), GY (0.97), and W100G (0.99).

Overall, the MGIDI index provided satisfactory predicted genetic gains (Gs) for all traits evaluated in the black commercial class genotypes, enabling efficient selection of genotypes close to the ideotype, particularly for GY, for which total Gs was 34.27%. NDF and PL had the lowest Gs values, reflecting their lower Sd estimates relative to those of the other traits. The predefined selection goals (increase or decrease) were achieved for all traits.

Based on the MGIDI index and a selection intensity of 30%, the five selected genotypes were 4 (MNC09-981B-6), 8 (MNC09-988B-20), 9 (MNC10-982B-3-7), 11 (MNC10-998B -8-1), and 13 (Pretinho-PA). The strengths and weaknesses of the selected genotypes are shown in Figure 3.

A lower proportion of a factor contributing to the MGIDI indicates that the traits within that factor are closer to the ideotype and are plotted nearer the outer edge of the corresponding sector (OLIVOTO; NARDINO, 2021).

Table 6. Selection differential (Sd), heritability (h^2_{mg}), and predicted selection gain (Gs) based on the MGIDI index for six traits evaluated in 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class in Teresina, State of Piauí, Brazil, during the 2023–2024 growing season.

Trait[1]	Factor	X_o	X_s	Sd	h^2_{mg}	Gs	Gs(%)	Goal
NDF	FA1	36.30	37.20	0.90	0.82	0.74	2.04	0
GY	FA1	651.00	881.00	230.00	0.97	223.10	34.27	100
PL	FA2	18.90	18.60	-0.30	0.97	-0.29	-1.53	0
W100G	FA2	18.30	19.10	0.80	0.99	0.79	4.32	100
NGP	FA3	11.30	11.70	0.40	0.95	0.38	3.36	100
GI	FA3	83.00	86.70	3.70	0.97	3.59	4.32	100
Total Gs (increase)						227.57	44.74	
Total Gs (decrease)						0.74	2.04	

[1]NDF: number of days to flowering onset; PL: pod length; NGP: number of grains per pod; W100G: 100-grain weight; GI: grain index; GY: grain yield. X_o: mean of the trait in the original population; X_s: mean of the trait in the selected genotypes at a selection intensity of 30%; Gs: predicted genetic gain from selection of the five best genotypes; Goal: whether the predicted selection gain matches the desired selection direction (100 = yes; 0 = no).

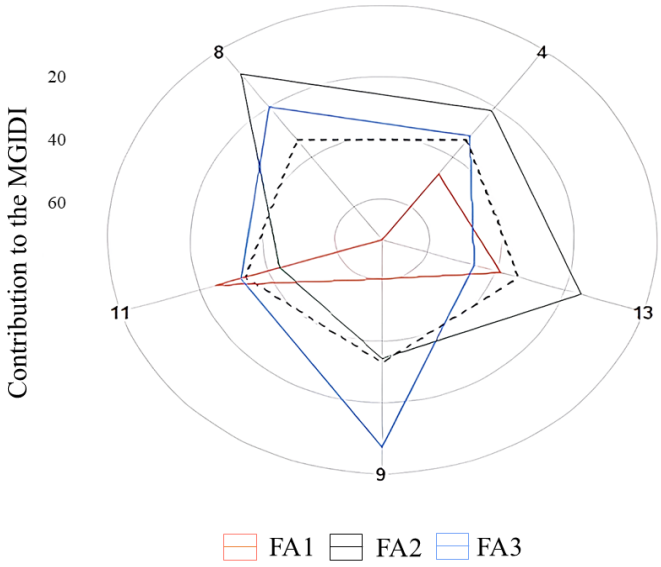


Figure 3. Visualization of the strengths and weaknesses of 16 cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class selected by MGIDI in Teresina, State of Piauí, Brazil, during the 2023-2024 growing season.

Genotype 11 (MNC10-998B-8-1) had the lowest contribution to FA1, indicating greater proximity to the ideotype for NDF, GI, and GY and therefore earlier flowering, a higher grain-to-pod weight ratio (GI), and higher grain yield. This combination of traits indicates that genotype 11 may be suitable for cultivation under off-season and irrigated conditions because of its favorable agronomic performance.

Genotypes 4 (MNC09-981B-6), 8 (MNC09-988B-20), and 13 (Pretinho-PA) had low contributions to FA2, which was associated with PL, indicating greater proximity to the ideotype for this trait and larger pod size. Larger pods are preferred by family farmers who select cultivars with this characteristic.

Genotype 9 (MNC10-982B-3-7) had a low contribution to FA3, which included NGP and W100G, and was described as having high NGP and large grain size, both of which are associated with GY. Preference for large grains has been reported particularly in the North and in some states of the Northeast region of Brazil, including Ceará (ROCHA; DAMASCENO-SILVA; MENEZES JÚNIOR, 2017).

Selection based on the MGIDI index was largely consistent with selection based on empirical best linear unbiased predictions (eBLUPs) of genetic values, indicating that the two approaches identified several of the same superior genotypes despite considering traits differently. Selection based on eBLUPs was more directly focused on GY, whereas the MGIDI index considered all evaluated traits and allowed greater weight to be assigned to components considered more important for the breeding objective, enabling more targeted selection for specific traits.

The selected cowpea genotypes of the black commercial class may be useful for developing recombinant populations and may contribute to sustainable and efficient cowpea breeding strategies, as also discussed by Sá (2024). These genotypes combine favorable agronomic traits and may allow simultaneous improvement of multiple traits, supporting their potential use in future cowpea breeding programs.

The applicability of MGIDI to simultaneous multi-trait selection has been reported for several crops, including oat, rice, and cowpea, for which Klein et al. (2023), Pallavi et al. (2024), and Sá (2024), respectively, reported effective selection of superior genotypes with desirable simultaneous gains across multiple traits.

CONCLUSIONS

The evaluated cowpea (*Vigna unguiculata* (L.) Walp.) genotypes of the black commercial class showed genetic variability and potential genetic gains from selection, particularly for 100-grain weight, grain index, and grain yield. Selection for earlier flowering and greater pod length and grain index can increase grain yield, while selection for larger grains can reduce the number of grains per pod. Based on empirical best linear unbiased predictions (eBLUPs) of genetic values, the genotypes with the greatest potential for the black specialty grain market were BRS Tapaihum (earlier flowering and high grain index and grain yield), MNC10-998B-8-1 (greater pod length), Pretinho-PA (greater number of grains per pod), and BRS Guirá (greater 100-grain weight). Based on the multi-trait genotype-ideotype distance index (MGIDI), MNC09-981B-6, MNC09-988B-20, MNC10-982B-3-7, MNC10-998B-8-1, and Pretinho-PA were selected as the genotypes with the greatest potential for the black specialty grain market.

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