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Genetics/ Original Article

Selection of superior cowpea lines derived from local cultivars for the Brazilian semiarid region

Abstract – The objective of this work was to select superior cowpea lines derived from local cultivars for the semiarid region of southeastern Piauí, Brazil. A total of 38 genotypes (36 lines and two commercial cultivars) were evaluated in a randomized complete block design, with two replicates, in the municipality of Ipiranga do Piauí, in the state of Piauí. The following traits were evaluated: number of days to the onset of flowering, pod length, number of grains per pod, weight of 100 grains, commercial grain quality, and grain yield. Deviance analyzes were performed using the restricted maximum likelihood and best unbiased predictor approach, the parameters and genetic values were estimated, and simultaneous selection was carried out via the sum of ranks index. The likelihood ratio test showed a significant difference between the evaluated genotypes. Lines 36, 5, 24, 8, 2, 23, 29, 28, 34, 6, 19, 11, 7, and 20 are superior for the set of evaluated traits and, therefore, are the most promising to compose the advanced trial of the cowpea breeding program and to generate cultivars for family farmers in the semiarid region of southeastern Piauí.

Index terms: *Vigna unguiculata*, genetic parameters, REML/BLUP, simultaneous selection.

Seleção de linhagens superiores de feijão-caupi derivadas de cultivares locais para a região semiárida brasileira

Resumo – O objetivo deste trabalho foi selecionar linhagens superiores de feijão-caupi derivadas de cultivares locais para a região semiárida do sudeste do Piauí, Brasil. Foram avaliados 38 genótipos (36 linhagens e duas cultivares comercias) em um ensaio conduzido em delineamento de blocos ao acaso, com duas repetições, no município de Ipiranga do Piauí, no estado do Piauí. Foram avaliados os seguintes caracteres: número de dias para o início do florescimento, comprimento de vagem, número de grãos por vagem, peso de 100 grãos, qualidade comercial do grão e produtividade de grãos. Análises de deviance foram realizadas pela abordagem da máxima verossimilhança restrita e do melhor preditor não viesado, os parâmetros e os valores genéticos foram estimados, e a seleção simultânea foi realizada via índice de soma de postos. O teste da razão de verossimilhança mostrou diferença significativa entre os genótipos avaliados. As linhagens 36, 5, 24, 8, 2, 23, 29, 28, 34, 6, 19, 11, 7 e 20 são superiores para o conjunto de caracteres avaliados e, portanto, são as mais promissoras para compor o ensaio avançado do programa de melhoramento genético de feijão-caupi e gerar cultivares para os agricultores familiares da região semiárida do sudeste piauiense.

Termos para indexação: *Vigna unguiculata*, parâmetros genéticos, REML/BLUP, seleção simultânea.

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Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is a protein-rich food of high nutritional value used for human consumption worldwide, especially in tropical and subtropical regions, with a satisfactory adaptation to dry regions, where it has an important socioeconomic role and contributes to the food security of thousands of people (Gondwe et al., 2019).

In Brazil, the crop is an excellent source of proteins and minerals, mainly for the poorest populations from the Northeastern region of the country (Araújo et al., 2021). Brazil is the fourth largest producer of cowpea in the world (FAO, 2020; Acompanhamento…, 2022), with an average harvested area of 1,287,300 ha, production of 631,400 tons, and yield of 491 kg ha^{-1} in the 2021/2022 season, of which 65.88, 19.61, and 13.29% were produced by the Northeastern, Northern, and Midwestern regions, respectively (Acompanhamento…, 2022).

In the Brazilian semiarid region, the area with the highest cowpea production is located in the state of Piauí, an environment with the greatest risk for the cultivation of the crop due to scarce and poorly distributed rainfall, with long periods of drought (Meira et al., 2020). To obtain a higher yield, based on the importance of the cowpea crop for the Northeastern region of Brazil, it is essential to carry out studies analyzing the production of genotypes under limited biotic and abiotic conditions, including climatic and phytosanitary factors, associated with genetic parameter estimates and correlations.

Specifically in the state of Piauí, there is currently a low availability, in the market, of cowpea cultivars of the *sempre-verde* and *canapu* commercial subclasses with more competitive characteristics, since local farmers use cultivars with a low yield and inferior commercial grain quality (Rocha et al., 2008). In addition, among the cultivars of these subclasses, only BRS Acauã of *canapu* is registered in Registro Nacional de Cultivares of Ministério de Agricultura, Pecuária e Abastecimento (Santos, 2011).

Researches have been carried out for the selection of cowpea genotypes taking advantage of the variability of landrace cultivars and using analysis of variance models for data analysis (Miqueloni et al., 2018; Gomes et al., 2020), but are scare in the semiarid region of Piauí (Rocha et al., 2008, 2011). Barroso Neto et al. (2017) highlighted that, together with the variability present in landrace cultivars, the use of methods with a better genetic prediction and accuracy can contribute to increasing the efficiency and genetic gain from selection.

The estimation of important genetic parameters, such as genetic variance and heritability of agronomically important traits, has guided cowpea breeders in the choice of the best breeding strategies (Ongom et al., 2021; Pessoa et al., 2023). Restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) are considered the most efficient methods for estimating variance components and predicting genetic values, respectively (Resende, 2016). Therefore, these methods have been used by cowpea breeders to investigate the effect of the genotype by environment interaction and the adaptability and stability of genotypes (Torres Filho et al., 2017; Sousa et al., 2019; Cruz et al., 2021), as well as in intermediate selection stages (Barroso Neto et al., 2017; Oliveira et al., 2017; Aragão et al., 2022).

The objective of this work was to select superior cowpea lines derived from local cultivars for the semiarid region of southeastern Piauí, Brazil.

Materials and Methods

The used genetic material consisted of 38 cowpea genotypes, comprising 36 lines and two commercial cultivars, used as controls (Table 1). The lines were originated from 100 plants of the local cowpea lines Bico de Ouro and Pingo de Ouro, which were selected, in 2017, in a family farm area, located in the municipality of Ipiranga do Piauí, in the semiarid of the southeast of the state of Piauí, Brazil (06º49'42"S, 41º44'26"W, at an altitude of 424 m). According to Köppen-Geiger's classification, the climate of the region is As, hot and humid tropical rainy, with an average annual precipitation of 821 mm.

The breeding method of selecting individual plants through progeny testing was used. In 2019, the 100 derived lines were evaluated in a preliminary trial in the municipality of Teresina, in the state of Piauí, Brazil (06º49'42"S, 41º44'26"W, at an altitude of 424 m). To compose the intermediate trial, a total of 36 lines were selected based on grain yield, plant architecture, maturation cycle, and grain size.

This study corresponded to the intermediate trial and was performed under rainfed conditions in the municipality of Ipiranga do Piauí, in the state of Piauí, Brazil. Planting was carried out from January to March 2020 using 20 seeds per meter. In a 10 m^2 (2.0x5.0 m) plot, composed of four rows spaced at 0.50 m, two seeds were sown per hole, resulting in 20 plants per row. Data were collected from an useful area of 5.0 m^2 (1.0x5.0 m), consisting of the two central rows. The experimental design was a randomized complete block with 38 treatments (genotypes) and two replicates.

Fifteen days after sowing, plant thinning was performed to standardize the stand. Manual weeding was carried out 20 and 35 days after sowing. For pest and disease control, agricultural pesticides were applied when necessary according to the

Table 1. Number, name/code, origin, AND commercial subclass of the evaluated cowpea (*Vigna unguiculata*) genotypes.

Nº	Name/Code	Origin[(1)]	Commercial subclass
1	Bico de Ouro-17-10	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
2	Pingo de Ouro-17-18	Pingo de Ouro from Ipiranga-PI	*Canapu*
3	Bico de Ouro-17-19	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
4	Bico de Ouro-17-20	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
5	Bico de Ouro-17-21	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
6	Bico de Ouro-17-23	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
7	Bico de Ouro-17-24	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
8	Bico de Ouro-17-33	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
9	Bico de Ouro-17-35	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
10	Bico de Ouro-17-37	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
11	Bico de Ouro-17-38	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
12	Bico de Ouro-17-43	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
13	Bico de Ouro-17-44	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
14	Bico de Ouro-17-45	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
15	Bico de Ouro-17-46	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
16	Bico de Ouro-17-47	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
17	Bico de Ouro-17-48	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
18	Bico de Ouro-17-53	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
19	Pingo de Ouro-17-61	Pingo de Ouro from Ipiranga-PI	*Canapu*
20	Pingo de Ouro-17-62	Pingo de Ouro from Ipiranga-PI	*Canapu*
21	Bico de Ouro-17-64	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
22	Bico de Ouro-17-65	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
23	Pingo de Ouro-17-68	Pingo de Ouro from Ipiranga-PI	*Canapu*
24	Pingo de Ouro-17-69	Pingo de Ouro from Ipiranga-PI	*Canapu*
25	Pingo de Ouro-17-70	Pingo de Ouro from Ipiranga-PI	*Canapu*
26	Pingo de Ouro-17-72	Pingo de Ouro from Ipiranga-PI	*Canapu*
27	Pingo de Ouro-17-75	Pingo de Ouro from Ipiranga-PI	*Canapu*
28	Bico de Ouro-17-80	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
29	Bico de Ouro-17-81	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
30	Bico de Ouro-17-82	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
31	Bico de Ouro-17-83	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
32	Bico de Ouro-17-86	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
33	Bico de Ouro-17-87	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
34	Bico de Ouro-17-89	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
35	Bico de Ouro-17-92	Bico de Ouro from Ipiranga-PI	*Sempre-verde*
36	Pingo de Ouro-17-96	Pingo de Ouro from Ipiranga-PI	*Canapu*
37	'BRS Inhuma'	Inhuma	*Canapu*
38	'BRS Pajeu'	CNCx405-17F x TE94-268-3D	*Mulato*

(1)Ipiranga-PI, municipality of Ipiranga do Piauí, in the state of Piauí, Brazil.

recommendations for the crop (Freire Filho, 2011). Harvesting was performed manually around 65 to 75 days after cowpea was planted.

The agronomic and commercial traits evaluated were: number of days to the onset of flowering (DOF), corresponding to the number of days from planting to the stage when 50% of the plants in the useful area of the plot showed flowers; pod length (cm), the average length of five pods randomly selected in the useful area of the plot; number of grains per pod (NGP), the average number of grains obtained from five pods randomly selected in the useful area of the plot; weight of 100 grains (W100G), the average weight of 100 grains (g) randomly selected in the useful area of the plot; commercial grain quality, evaluated according to a visual score scale (Aragão et al., 2022), based on grain color, shape, size, and hilum aspect, as well as on the presence/absence of defects (Table 2); and grain yield of the Bico de Ouro and Pingo de Ouro lines, based on the useful area of the plot, expressed in g m^{-2} and extrapolated to kg ha^{-1}. The data related to the visual score scale were transformed by $(x + 0.5)^{0.5}$ for the statistical analysis.

The data were preliminarily analyzed for normality of residues, performed using the SAS software (SAS Institute Inc., Cary, NC, USA). The data with absence of normality were replaced by their respective predicted phenotypic values.

The REML/BLUP method was used since it is the standard for estimating variance components and genetic parameters, preferably when there are a low number of replicates (Resende, 2016). This analysis was performed with the aid of the SELEGEN – REML/BLUP statistical software (Resende, 2016), addressing the 21 model, which consists of the following estimator: $Y = Xr + Zg + e$, where Y is the data vector, r is the replicate effects vector (assumed as fixed) added to the overall mean, g is the genotypic effects vector (assumed as random), e is the error or residue vector (assumed as random), and X and Z are the incidence matrices for the mentioned effects.

The variance components obtained via REML were subsequently used to estimate the following genetic parameters: phenotypic variance (σ^2_f), environmental variance (σ^2_e), genotypic variance (σ^2_g), broad-sense heritability (h^2_g), broad-sense heritability at the level of genotype means (h^2_{mg}), genetic coefficient of variation (CV_g), experimental coefficient of variation (CV_e), relative coefficient of variation (CV_r) obtained as the ratio between the genotypic coefficient of variation and the experimental coefficient of variation, and genotype accuracy or selective accuracy ($\hat{r}_{\hat{g}g}$).

The likelihood ratio test (LRT) was performed to evaluate the significance of the random effects in the mixed linear model, established by the difference between the deviances for the model with and without the effects being tested, where significance was compared with the chi-square test, with one degree of freedom. Therefore, the genetic values were estimated using the BLUPs generated for each individual and trait evaluated. With these values, the traits that showed significant differences via the LRT test were simultaneously subjected to selection by the sum of ranks index (IMM) proposed by Mulamba & Mock (1978), using the following equation: $I_{MM} = Rxu$, where R is the v x n matrix of ranks associated with the adjusted genotypic means of v genotypes relative to n traits, and u is the n x 1 vector of economic weights. Selection was based on the classification or ordering of the lines for multiple traits. The calculation depended only on genotypic means, without assigning economic

Table 2. Visual scoring scale used to classify the commercial grain quality of the evaluated cowpea (*Vigna unguiculata*) genotypes.

Grade	Commercial grain quality
1	Very bad: grain with a high postharvest color loss, non-reniform shape, number of grains per 100 grams below 400 or above 500, and presence of defects (cracks in the tegument and/or fish bill).
2	Bad: grain with a high postharvest color loss, non-reniform shape, number of grains per 100 grams below 400 or above 500, and no defects.
3	Regular: grain with a low postharvest color loss, non-reniform shape, number of grains per 100 grams between 400 to 500, and no defects.
4	Good: grain with a low postharvest color loss, reniform shape, number of grains per 100 grams between 400 and 500, and no defects.
5	Excellent: grain with no or a low postharvest color loss, reniform shape, and number of grains per 100 grams between 400 to 500, and no defects.

Source: Aragão et al. (2022).

weights to the traits. The selection intensity adopted for the index was 38.8%, i.e., 14 lines.

Results and Discussion

According to the deviance analysis (Table 3), a significant difference was observed between genotypes by the chi-square test for the traits DOF, pod length, NGP, W100G, and grain yield; however, there was no significant difference for commercial grain quality. The occurrence of significance for these traits indicates that, despite the several cycles of selection performed previously, there is still a genetic variability that allows of breeders to practice selection and obtain selection gains, and, consequently, superior genotypes for these traits.

The absence of significant differences for the trait commercial grain quality is probably due to the low genetic variability among the evaluated cowpea lines, related to the several cycles of selection performed in previous generations of inbreeding (Cobb et al., 2019). The obtained results show that the evaluated genotypes have the same behavior for this trait, indicating that the practice of selection will not bring more genetic gains. This stagnation is considered beneficial since a fixed average value in individuals is an indicative that the grains have most of the commercial characteristics desired by the market.

The highest estimates of σ^2_f were observed for grain yield, W100G, pod length, and NGP. Among these traits, all presented a σ^2_f greater than σ^2_g, except grain yield. Regarding phenotype expression, the environmental component influenced pod length the most, whereas DOF and grain yield were the only traits that presented a greater genetic component, meaning that they show the greatest probability of success with selection. Therefore, the heritability estimates indicate that DOF and grain yield have a stronger genetic component in their phenotypic expression. The heritability value obtained for grain yield was higher than that of 0.11 found by Cruz et al. (2021). According to Teixeira et al. (2007), high h^2 estimates could be attributed to an inherent genetic variability among the tested genotypes, each with a unique genetic identity. Furthermore, Correa et al. (2012) suggested that high h^2 estimates for yield components, combined with direct and strong correlations with grain yield, may indicate the potential for indirect selection via yield components to increase grain yield. This trait is, therefore, strongly influenced by the environment and

Table 3. Deviance analysis, chi-square test, and variance component estimates for the traits number of days to the onset of flowering (DOF), pod length (PLNT), number of grains per pod (NGP), 100-grain weight (W100G), grain yield, and commercial grain quality (CGQ) of 38 cowpea (*Vigna unguiculata*) genotypes evaluated in 2021 in the municipality of Ipiranga do Piauí, in the state of Piauí, Brazil.

Effects	DOF	PLNT	NGP	W100G	Grain yield	CGQ(1)
Complete model	161.00	247.53	188.65	232.78	925.69	-199.11
Genotypes	173.38	251.53	193.02	240.00	937.40	-196.65
LRT (χ^2)(2)	12.38**	4.17*	4.37*	7.22**	11.71**	2.46^{ns}
Parameter(3)						
σ^2_g	1.85	3.25	1.51	3.59	55,089.18	0.0060
σ^2_e	1.62	6.72	3.01	4.94	50,699.87	0.0175
σ^2_f	3.47	9.98	4.52	8.54	105,789.06	0.0224
h^2_g	0.53	0.32	0.33	0.42	0.52	0.2538
h^2_{mg}	0.69	0.49	0.50	0.59	0.68	0.4048
$\hat{r}_{\hat{g}g}$	0.83	0.70	0.70	0.76	0.82	0.6363
CV_r	1.06	0.69	0.70	0.85	1.04	0.5832
Overall average	40.62	19.65	14.74	19.93	987.34	1.9542
Initial average(4)	-	-	-	-	-	4.0

(1)Data transformed to $(x + 0.5)^{0.5}$. (2)LRT, likelihood ratio test. * and ** represent the chi-square test at 5 and 1% probability, respectively. (3)σ^2_g, genotypic variance; σ^2_e, environmental variance; σ^2_f, phenotypic variance; h^2_g, broad-sense individual heritability; h^2_{mg}, broad-sense heritability at the level genotype means; $\hat{r}_{\hat{g}g}$, genotype/selective accuracy; and CV_r, relative coefficient of variation. (4)Original average obtained before data transformation and genotype selection.

has a low heritability, leading to a low efficiency in direct selection, but, possibly, to greater gains through simultaneous selection.

The highest estimates of heritability at the individual (h^2_g) and mean (h^2_{mg}) levels were observed for the traits DOF, pod length, NGP, W100G, and grain yield. The lower values obtained for these parameters when the variable did not show genetic variability in the analysis of deviance reaffirm that all changes found for commercial grain quality are of environmental nature and that the environmental variance cannot be transmitted after successive selection cycles (Ramalho et al., 2012).

The CV_r is another crucial genetic parameter that is the result of the ratio between the genotypic coefficient of variation and the experimental coefficient of variation. In the literature, this ratio indicates the viability of selecting a trait under study if its result is equal to or greater than 1 (Meira et al., 2020). The CV_r estimates were above 1 only for DOF and grain yield, indicating a weaker influence of the environment, which translates into a greater selection efficiency for these traits.

Aragão et al. (2022), studying compound-inflorescence cowpea genotypes, obtained higher CV_r estimates of 1.51, 1.18, 1.76, and 1.90 for NGP, W100P, grain yield, and commercial grain quality, respectively. According to Resende & Duarte (2007), a certain $\hat{r}_{\hat{g}g}$ and the value of this coefficient are directly related to the number of replicates used in the experiment, i.e., in order to obtain a $\hat{r}_{\hat{g}g}$ with an interval classified as high in an experiment with two replicates, the CV_r should be between 1.0 and 1.25, the interval in which DOF and grain yield fit for this parameter.

Therefore, $\hat{r}_{\hat{g}g}$ is one of the most important genetic parameters and is linked to the true genetic value of each genotype when the genotype effect in the model is mixed, that is, contains fixed and random effects. This parameter is based on phenotypic experimental data, ranging from 0 to 1, where values closer to unity are desirable (Resende & Duarte, 2007). In general, the accuracy values achieved in the present study ranged from moderate to high according to the classification proposed by Resende & Alves (2020). The lowest estimate for this parameter was 0.63 for commercial grain quality, whereas the highest values were 0.83, 0.83, 0.70, 0.70, and 0.76 for DOF, grain yield, pod length, NGP, and W100G, respectively.

For the trait grain yield, Rocha et al. (2017) obtained an accuracy of 85%, similar to that observed in the present work, revealing a good experimental quality, attributing security and credibility to select superior genotypes for this trait. In contrast, in other regions in Brazil, low accuracy estimates of 20 and 33% were reported by Torres Filho et al. (2017), when studying the grain yield of immature cowpea genotypes in the municipality of Mossoró, in the state of Rio Grande do Norte, and Cruz et al. (2021), when evaluating cowpea genotypes in the northwest of the state of Rio de Janeiro, respectively.

Based on the individual classification of the 38 cowpea genotypes determined by the IMM index (Table 4), the 14 best lines were selected. The genetic gain values obtained for the evaluated traits (Table 5) were similar to those found by Oliveira et al. (2017), who evaluated 14 traits simultaneously in F_4 cowpea progenies, and by Aragão et al. (2022), who analyzed compound-inflorescence cowpea lines. The overall mean genetic gain based on the simultaneous selection of all these traits was 21.89%, suggesting that the joint selection of DOF, pod length, NGP, W100G, and grain yield can be an effective strategy to improve cowpea yield. According to Rocha et al. (2017), the increase in yield is one of the main objectives of cowpea genetic breeding programs.

The following 14 cowpea lines were selected to be part of the advanced trial of the cowpea breeding program: 36, 5, 24, 8, 2, 23, 29, 28, 34, 6, 19, 11, 7, and 20 (Table 5). Cowpea lines 36 (Pingo de Ouro-17-96), 5 (Bico de Ouro-17-21), and 24 (Pingo de Ouro-17-69), belonging to the commercial class *cores* and subclasses *canapu*, *sempre-verde*, and *canapu*, respectively, stand out for presenting superiority for the set of evaluated traits, mainly W100G and grain yield, when compared with 'BRS Pajeu', the best control (Table 6). Lines 36 and 24 showed a superior pod length and NGP, respectively. Regarding precocity in DOF, lines 5 and 36 were similar, whereas line 24 showed later flowering in comparison with the controls.

The evaluated cowpea lines, derived from the local lines Bico de Ouro and Pingo de Ouro, represent a better option for farmers who traditionally cultivate and consume cowpea from the *cores* class and *canapu* and *sempre-verde* subclasses in the semiarid of southeastern Piauí.

Table 4. Individual classification of 38 cowpea (*Vigna unguiculata*) genotypes based on the simultaneous selection of five traits using the sum of ranks index of Mulamba & Mock (1978), carried out in 2021 in the municipality of Ipiranga do Piauí, in the state of Piauí, Brazil.

Mulamba & Mock's sum of ranks index						
Genotype	DOF	PLNT	NGP	W100G	Grain yield	Sum of ranks[1]
1	24	34	17	35	6	116
2	1	14	10	21	19	65
3	4	27	29	32	17	109
4	27	25	20	27	27	126
5	6	4	18	4	10	42
6	7	28	21	7	20	83
7	10	23	13	37	8	91
8	2	13	27	6	13	61
9	21	20	24	36	34	135
10	11	38	37	22	32	140
11	12	21	28	12	14	87
12	13	29	33	19	5	99
13	8	31	36	25	28	128
14	14	37	26	26	33	136
15	5	36	31	33	2	107
16	15	33	34	30	23	135
17	9	19	22	20	26	96
18	16	30	23	24	3	96
19	28	10	4	8	36	86
20	36	5	6	9	35	91
21	25	24	32	29	31	141
22	30	15	14	13	22	94
23	32	6	7	5	16	66
24	31	3	1	1	9	45
25	38	1	11	15	37	102
26	33	7	2	11	38	91
27	29	17	25	23	24	118
28	26	11	30	3	1	71
29	17	12	19	16	4	68
30	18	35	38	28	12	131
31	22	16	9	17	29	93
32	37	22	3	38	18	118
33	34	32	35	31	30	162
34	23	8	12	18	15	76
35	35	18	15	34	21	123
36	19	2	5	2	7	35
37	20	26	16	10	11	83
38	3	9	8	14	25	59

[1] Sum of the ranks of individuals in relation to each evaluated trait.

Table 5. General and specific selection gains for the traits number of days to the onset of flowering (DOF), pod length (PLNT), number of seeds per pod (NGP), 100-seed weight (W100G), and grain yield (GY) obtained through the sum of ranks index of Mulamba & Mock (1978) for the 14 best cowpea (*Vigna unguiculata*) genotypes evaluated in 2021 in the municipality of Ipiranga do Piauí, in the state of Piauí, Brazil.

Genotype	Rank index	DOF (day)	PLNT (cm)	NGP	W100G (g)	GY (kg ha^{-1})
		Specific gain (%)[1]				
36	1	-0.90	10.12	-8.63	13.24	17.69
5	2	-2.61	7.37	7.33	10.77	11.65
24	3	2.52	9.37	13.78	14.75	14.67
38	4	-4.33	3.86	4.27	2.25	-5.15
8	5	-6.04	0.86	-3.54	10.09	7.75
2	6	-6.04	0.11	3.25	-2.86	3.47
23	7	3.38	5.62	6.31	10.47	5.65
29	8	-0.90	1.11	-0.14	1.67	23.52
28	9	0.81	2.36	-4.56	12.85	55.50
34	10	-0.05	5.62	3.25	-0.25	7.20
6	11	-1.76	-3.90	-1.16	6.58	2.03
37	12	-0.90	-3.02	2.06	4.91	9.30
19	13	-1.67	6.61	7.33	6.50	-32.08
11	14	-0.90	-2.14	-3.88	4.12	7.42
General gain[2]		-1.15	2.93	1.83	6.79	9.19

[1] Specific gain of a genotype for a specific trait. [2] General gain obtained by the genotypes selected by the selection index.

Table 6. General average for the traits number of days to the onset of flowering (DOF), pod length (PLNT), number of seeds per pod (NGP), 100-seed weight (W100G), and grain yield (GY) of the three best cowpea (*Vigna unguiculata*) lines based on the simultaneous selection of these traits using the sum of ranks index of Mulamba & Mock (1978), carried out in 2021 in the municipality of Ipiranga do Piauí, in the state of Piauí, Brazil.

Genotype[1]	DOF (day)	PLNT (cm)	NGP	W100G (g)	GY (kg ha^{-1})
36	40.99	23.22	16.13	22.72	1,255.60
5	40.81	22.26	15.49	22.65	1,216.10
24	42.05	22.65	16.77	22.87	1,228.70
37	40.96	20.16	15.55	21.84	1,203.70
38	40.66	21.40	15.93	21.51	1,096.30

[1] 36, Pingo de Ouro-17-96; 5, Bico de Ouro-17-21; 24, Pingo de Ouro-17-69; 37, 'BRS Inhuma' (control); and 38, 'BRS Pajeu' (control).

Conclusions

1. Cowpea lines 36, 5, 24, 8, 2, 23, 29, 28, 34, 6, 19, 11, 7, and 20 show the greatest agronomic potential to be part of the advanced cowpea breeding trial.

2. Cowpea lines 36 (Pingo de Ouro-17-96), 5 (Bico de Ouro-17-21), and 24 (Pingo de Ouro-17-69) have potential to generate cowpea cultivars of the *canapu* and *sempre-verde* commercial subclasses for family farmers in the semiarid of southeastern Piauí, Brazil.

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