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Genetic parameters and selection indices of cowpea genotypes for green grain production

Parâmetros genéticos e índices de seleção de genótipos de feijão-caupi para produção de grãos verdes

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ABSTRACT - Cowpea is a legume that is grown worldwide and used for different purposes, especially as green grains. However, considering the low availability of cowpea cultivars for green grain production, selecting genotypes that have better traits for this purpose is necessary. In this context, the objective of this study was to estimate genetic parameters and evaluate different selection indices for identifying superior cowpea genotypes and subsidizing cowpea breeding programs focused on green grain production. A field experiment was conducted at the Center of Agricultural Sciences of the Federal University of Ceará (UFC), Ceará, Brazil. The treatments consisted of 42 cowpea genotypes from the Active Germplasm Bank of the UFC. Fourteen traits were used for characterization. The experiment was conducted in an augmented block design with four controls. The data obtained were subjected to analysis of variance, and genetic parameters, correlations, and selection indices were determined. The traits days to flowering (DFL), days to fruiting (DFR), green pod weight (GPW), green pod width (GW), green pod length (GPL), green pod thickness (GPT), number of grains per pod (NGP), and green grain thickness (GGT) showed heritability higher than 70%, indicating that selection in an early generation is favorable. The genetic correlations between the trait pairs DFL×DFR, GPW×GPL, and GW×GGT were higher than the phenotypic and environmental correlations. Genotypes CE-228, CE-688, CE-994, CE-165, CE-796, and BRS-Paraguaçu showed simultaneous superiority for the evaluated traits and are the most appropriate for green grain production.

Keywords: Plant breeding. Genetic variability. *Vigna unguiculata*.

RESUMO - O feijão-caupi é uma das leguminosas mais cultivadas no mundo, sendo comercializado para diversas finalidades, como o feijão verde. Considerando a reduzida disponibilidade de cultivares de feijão-caupi para o mercado de feijão verde, é necessário selecionar genótipos que ofereçam características intrínsecas para este fim. Assim, objetivou-se estimar parâmetros genéticos e índice de seleção na identificação de genótipos superiores de feijão-caupi, fornecendo subsídios para programas de melhoramento visando a produção de grãos verdes. O experimento foi conduzido em campo, no Centro de Ciências Agrárias da Universidade Federal do Ceará (UFC), Ceará, Brasil. Os tratamentos consistiram de 42 genótipos de feijão-caupi do Banco Ativo de Germoplasma da UFC. Quatorze descritores foram utilizados para a caracterização. O experimento foi montado em um delineamento de blocos aumentados, com quatro testemunhas adicionais. Foi realizada análise de variância, parâmetros genéticos, correlação e índices de seleção. As características de dias para floração, dias para frutificação, peso da vagem verde, largura da vagem verde, comprimento da vagem verde, espessura da vagem verde, número de grãos por vagem e espessura do grão verde apresentaram valores de herdabilidade acima de 70%, indicando que a seleção em geração precoce com base nestas características é favorável. As correlações genéticas entre os pares de caracteres DFL×DFR, GPW×GPL, e GW×GGT foram superiores às correlações fenotípicas e ambientais. Os genótipos CE-228, CE-688, CE-994, CE-165, CE-796 e BRS-Paraguaçu apresentam superioridade simultânea para as características avaliadas e os mais adequados para o mercado de grãos e vagens verdes.

Palavras-chave: Melhoramento de plantas. Variabilidade genética. *Vigna unguiculata*.

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INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is a legume that is grown worldwide and has high protein and nutrient contents; it can be marketed as dry grains, immature grains, and seeds (SILVA et al., 2018a).

Brazil is one of the three major cowpea-producing countries, with an estimated production of 701,100 Mg in 2020 (CONAB, 2021). The Northeast is the main producing region in Brazil, even though this species is grown in all Brazilian states (SILVA et al., 2018b; VALERIANO et al., 2019).

Cowpea green grains are highly appreciated by the Northeastern population of Brazil and are an ingredient in several traditional dishes (MELO et al., 2020). The term green grain refers to the stage in which the pod is harvested (SOUSA et al., 2015), usually coinciding with the beginning of the grain physiological maturity (ALMEIDA; TOMAZ; ARAÚJO, 2020). In this sense, farmers have used genotypes with grains of various colors for this specific grain markets, e.g., the cowpea cultivars Sempre-Verde, Azulão, and Corujinha (SOUSA et al., 2015).

Considering the low availability of cowpea cultivars with desirable traits for green grain production in the Brazilian market, selecting genotypes that have better traits for this purpose is essential (SOUZA et al., 2019). In that regard, the information obtained with plant characterization in germplasm banks is a valuable tool to identify genotypes focused on increasing grain yield (SANTANA et al., 2019) and developing new cultivars. However, evaluating large numbers of genotypes from such banks requires the use of an augmented block design when there is area restriction (PETERNELLI et al., 2009); this procedure is viable for selecting families in initial stages of breeding programs (SOUZA; GERALDO; RAMALHO et al., 2000).

Simultaneous selection based on a set of traits increases the likelihood of success of a breeding program (VASCONCELOS et al., 2010). However, an increasingly accurate selection, based on estimates of genetic parameters and information on the degree of association, is required to appropriately assess the genetic variability of a population, due to the complexity of most traits. Therefore, measuring genetic variability and knowing the correlations between traits of interest for selection are essential for plant breeding (LEITE et al., 2015).

Simultaneous evaluation of a set of traits can also be performed through the selection index. This parameter allows the establishment of an additional trait to simultaneously select several attributes of interest through the linear combination of several traits (CRUZ, 2013). Selection indices are useful tools for plant breeding, enabling the efficient selection of superior genotypes, serving as a theoretical trait to combine previously selected specific traits for which simultaneous selection is desired (CREVELARI et al., 2019). Bertini et al. (2010) recommended selecting superior cowpea genotypes using a selection index to form segregating populations. In this context, the objective of this study was to estimate genetic parameters and the selection index to identify superior cowpea genotypes and subsidize breeding programs focused on green grain production.

MATERIAL AND METHODS

The experiment was conducted at the experimental area of the Horticulture Sector of the Plant Science Department of the Center of Agricultural Sciences of the Federal University of Ceará (CCA/UFC), Pici Campus, Fortaleza, Ceará, Brazil (3°44'24.4"S, 38°34'32.0"W). The experiment was conducted in a rainfed farming system; the cumulative rainfall depth was 1,111.8 mm and the mean temperature was 27.3 °C during the experimental period, February to May 2020 (FUNCEME, 2020).

The treatments consisted of 38 cowpea genotypes, named with a CE prefix as: 24, 61, 68, 70, 114, 123, 151, 164, 165, 172, 189, 199, 201, 205, 206, 207, 228, 243, 244, 248, 253, 313, 337, 542, 685, 686, 688, 689, 925, 957, 958, 964, 986, 994, 997, 999, 1002, and 1007; and four commercial cultivars: BRS-Guariba, BRS-Tumucumaque, BRS-Paraguaçu, and Paulistinha. All these genotypes belong to the Active Germplasm Bank (BAG) of the Plant Science Department of the CCA/UFC and are listed in Table 1.

The total area of the experiment was 52 m²; each block had 13 m² and consisting of five 11-m long central rows. The spacing used was 2 m between blocks; 1.0 m between rows; and 0.50 m between plants in the rows, with two rows forming the border in each block.

Three seeds were sown per hole; seedlings were thinned to two plants per hole at 15 days after sowing. The soil of the experimental area was prepared using plowing and harrowing. Fertilizers were applied based on the soil chemical analysis and considering the crop requirements (CRAVO; VIÉGAS; BRASIL, 2007). The cultural management practices applied consisted of weed control by manual hoeing during seedling emergence and close to the flowering stage; and insecticide application for pest control during plant development, according to conventional recommendations for cowpea crops.

Fourteen quantitative variables were considered for the morpho-agronomic characterization, as described by IPGRI (2007): plant height, measured with a tape ruler from the plant base to the apex; days to flowering, determined by counting the number of days from sowing to flowering in each treatment; days to fruiting, determined by counting the number of days from sowing to the beginning of harvest in each treatment; stem diameter, measured with a digital caliper; number of main-stem nodes, determined by counting the number of nodes in the main stem of the plant; green pod length, determined by the mean of ten pods per plant, measured with a ruler; green pod weight, determined by the mean of 10 pods; number of locules per pod; green pod width, measured with a digital caliper based on 10 pods; green pod thickness, measured with a digital caliper based on 10 pods; green grain thickness, measured with a digital caliper based on 10 pods; grain weight per pod, determined by weighing based on 10 pods; and number of grains per pod, determined by counting the mean number of marketable grains based on 10 pods.

Table 1. Name in the active germplasm bank, common name, class, and subclass of cowpea genotypes.

ID BAG	COMMON ID	CLASS	SUBCLASS
CE0002	Bengala	colors	butter
CE0024	Cowpea-535	mixed	mixed
CE0061	_	colors	vinegar
CE0068	Lampião	colors	rajado
CE0070	Quarenta dias - 1	colors	mulatto
CE0114	Texas Purple Hull - 49	mixed	mixed
CE0151	1304	colors	mulatto
CE0155	1571	brown	mulatto
CE0164	2380	white	blackeye
CE0165	2381	black	black
CE0172	4280 (*V. sesquipedales*)	black	black
CE0189	Costa Rica V-10	colors	mulatto
CE0199	Coleção Pernambuco V-8	white	blackeye
CE0205	V-24	white	blackeye
CE0206	V-33	white	blackeye
CE0207	V-34	colors	mulatto
CE0228	Guerreiro 105	mixed	mixed
CE0243	Malhado Preto	colors	owl
CE0244	Tvu 2000	black	black
CE0248	Tvu 91	colors	vinegar
CE0253	TVu191	colors	mulatto
CE0313	Tvu 2000	colors	mulatto
CE0337	Tvu 4538	colors	mulatto
CE0398	TVu 200	colors	mulatto
CE0542	ER-7	white	blackeye
CE0685	CNCx666-21E	black	black
CE0686	CNCx666-26E	black	black
CE0688	CNCx666-26E	black	black
CE0689	CNCx666-31E	black	black
CE0796	CNCx251-60E	colors	mulatto
CE0925	Tvu 4552	white	brown
CE0957	MNC-01627D-65-1	white	Plain white
CE0958	IT 91K-118-2	colors	butter
CE0964	MNC-06-887B-561	white	blackeye
CE0986	IT 81D-1032	colors	vinegar
CE0997	IT 81D-1073	colors	mulatto
CE0999	MNC 03-720-C-31	white	blackeye
CE1002	MNC 01-627F-14-5	white	white
CE1007	MNC-01-625D	white	plain white
CE939	Paulistinha	colors	canapu
CE0978	BRS-Tumucumaque	white	plain white
CE0934	BRS-Guariba	white	plain white
CE938	BRS-Paraguaçu	white	white

The genotype effect was considered random for each response variable. The data were subjected to analysis of variance based on the augmented block design to obtain the residual variance-covariance matrix (PIMENTEL-GOMES, 2009). The heritability and the coefficients of genetic and environmental variations were estimated according to Vencovsky and Barriga (1992) and Cruz, Regazzi, and Carneiro (2012):

$$h^2 = \frac{\sigma_g^2}{\sigma^2}$$

where: h^2 is the heritability, σ^2g is the genotypic variance, and σ^2 is the environmental variance.

$$CV_g = \left(\frac{\sqrt{\sigma_g^2}}{m}\right) \times 100$$

where: CVg is the coefficient of genetic variation, σ^2g is the genotypic variance, and m is the mean of the trait.

$$CV_e = \left(\frac{\sqrt{\sigma^2}}{m}\right) \times 100$$

where: CVe is the coefficient of environmental variation, σ^2 is the environmental variance, and m is the mean of the trait.

The residual correlations were subjected to the Student's t-test at a nominal level of 5% of significance.

The selection indexes used were:

Base index (WILLIAMS, 1962),

$$I = \sum_{i=1}^{n} a_i y_i = y' a$$

where: n is the number of characters evaluated, y is the mean, and a is the economic weight for the analyzed traits.

Classic index (HAZEL, 1943; SMITH, 1936; SUBANDI; COMPTON; EMPIG, 1973),

$$H = \sum_{i-1}^{n} a_i g_i = a' g$$

where: n is the number of characters evaluated, g is the population effect for the n traits, a is the effect of previously established economic weights, which can vary from 0 to 1, according to the selection.

Sum of ranks (MULAMBA; MOCK, 1978),

$$I_{MM(i)} = \sum_{k=1}^{n} u_k r_{ik}$$

where: u_k is the economic weight of the trait k, rik = ranks associated with the genotypic mean of the population i relative to the trait k.

Desired gains (PESEK; BAKER, 1969),

$$I = \hat{b}' y$$

where: $\hat{b}$ is the vector of desired grains of the n traits, and y is the column vector of phenotypic values.

The genotype-ideotype distance index (CRUZ, 2013) considers that X_{ij} is the average phenotypic value of the *i*-th genotype in relation to the *j*-th characteristic, Y_{ij} represents the standardized average phenotypic value, and C_j is a constant related to the depreciation of the average of the genotype, for not being within the standards desired by the breeder. The Euclidean distance between the genotype and this ideotype was estimated through the estimator:

$$d_{jI} = \sqrt{\sum_{i=1}^{42} (X_{ij} - X_{Ii})^2} \quad j$$

where: d_{jI} is the Euclidean distance between genotype j and ideotype I (j=1, ..., 42), Xij is the measure of character i in genotype j, XIi is the value defined for ideotype I referring to character i. All statistical analyses were performed using the software GENES (CRUZ, 2013).

RESULTS AND DISCUSSION

The treatments had significant effect ($p \leq 0.01$) on days to flowering, days to fruiting, green pod weight, green pod width, green pod length, green pod thickness, and green grain thickness; and on number of grains per pod and grain weight per pod ($p \leq 0.05$) (Table 2). It indicates variability among the cowpea genotypes, enabling the selection of superior genotypes for green grain production. Genetic variability is a key aspect of breeding programs, as it facilitates identifying promising parental individuals to produce hybrids and provide subsequent gains in segregating populations.

The means found for number of days to flowering and fruiting were 42.82 and 58.82, respectively (Table 2). Rocha et al. (2017) reported that early cowpea genotypes with this cycle length reach maturity at 60 days after sowing. In addition, Oliveira et al. (2015) found 45 days for number of days to flowering in cowpea genotypes, a similar result to those found in the present study. Earliness is a strategic aspect for cowpea crops grown in semi-arid regions, especially due to the characteristic rainfall instability of rainfed farming; it also enables the growth of cowpea crops in three cycles during the same year.

Table 2. Summary of the analysis of variance: mean squares, coefficient of variation (CV%), heritability [(h^2 (%)], and ratio between genetic and environmental coefficients of variation (CVg/CVe) of cowpea.

Source of variation	Traits / Mean squares						
	PH	NMSN	SD	DFL	DFR	GPW	GW
Treatment	91.97^{ns}	3.90^{ns}	0.19^{ns}	21.79**	19.34**	6.74**	0.19**
Mean	36.12	8.72	0.49	42.82	58.82	6.24	0.91
CV%	30.64	20.58	20.70	4.54	2.03	14.49	3.43
	Genetic parameters						
h²	0.00	30.86	48.93	82.09	93.00	88.09	94.86
CVg/CVe	0.00	0.81	0.97	2.14	3.64	2.71	4.30

Source of variation	Traits / Mean squares					
	GPL	GPT	NLP	NGP	GWP	GGT
Treatment	35.77**	0.02**	4.76^{ns}	8.08*	1.99*	0.01**
Mean	17.51	0.80	15.22	11.59	3.77	0.65
CV%	6.77	4.82	8.97	12.37	18.73	3.86
	Genetic parameters					
h²	96.55	93.35	65.44	76.69	65.01	91.81
CVg/CVe	5.29	3.74	1.37	1.81	1.36	3.34

** = significant at 1%, * = significant and 5%, and $^{ns =}$ not significant by the F-test. Plant height (PH), number of main stem nodes (NMSN), stem diameter (SD), days to flowering (DFL), days to fruiting (DFR), green pod weight (GPW), green pod width (GW), green pod length (GPL), green pod thickness (GPT), number of locules per pod (NLP), number of grains per pod (NGP), grain weight per green pod (GWP), and green grain thickness (GGT).

The green pod weight, width, length, and thickness presented means of 6.24, 0.91, 17.51, and 0.80, respectively (Table 2). Silva et al. (2016) found pods with similar results and stressed that these features are desirable for manual harvest. Moreover, large pods are considered attractive by consumers, since these structures contain large numbers of grains.

The grain-related traits number of grains per pod, grain weight per pod, and green grain thickness presented means of 11.59, 3.77, and 0.65, respectively (Table 2). The genotypes showed desirable traits for commercialization, with large and heavy grains. The green bean market is significant in the Northeast region and several capitals of the North, Southeast, and Central-West regions of Brazil (SOUSA et al., 2015), denoting the need for identification of new promising genotypes for breeding programs focused on green bean production.

The coefficient of experimental variation (EV) ranged from 2.03% (days for fruiting) to 36.98% (green grain width) (Table 2). Some studies report that CV values vary according to the studied species (ALMEIDA et al., 2014; WERNER et al., 2012), although not interfering with the experimental accuracy. These oscillations may also be due to the phenotypic variability inherent to the genotypes tested, since each genotype contributes to a different genetic identity (BURATTO; MODA-CIRINO, 2017; TEIXEIRA et al., 2007).

The estimates of genetic parameters for the studied traits are shown in Table 1. Days to flowering (DFL), days to fruiting (DFR), green pod weight (GPW), green pod width (GW), green pod length (GPL), green pod thickness (GPT), number of grains per pod (NGP), and green grain thickness (GGT) showed heritability higher than 70%, indicating little effect of the environment and control by genetic variability components, denoting potential for selection (KAMPA et al., 2020). Heritability (h^2) expresses the proportion of genetic variance over phenotypic variance (SANTOS et al., 2018).

The ratio between coefficients of genetic and environmental variations (CVg/CVe) were higher than 1 for the same traits (DFL, DFR, GPW, GW, GPL, GPT, NGP, and GGT), with high heritability values (Table 2). This result indicates that selection in an early generation is favorable since the environmental variation is lower than the genetic variation, confirming that these traits should be used to select plants for genetic improvement in breeding programs (PÚBLIO JÚNIOR et al., 2018).

Phenotypic, genotypic, and environmental correlations showed significant values ($p \leq 0.01$ and $p \leq 0.05$) and coincident positive signs between the cowpea traits related to green grains (Table 3). In this context, three aspects should be considered when interpreting correlations: magnitude, direction, and significance (LEITE et al., 2016). Information about relationships between characters, as estimated by correlations, has been essential for plant breeding, as it assists in the selection process (NOGUEIRA et al., 2012).

The correlation between variables is an important parameter that can be used as an indirect selection tool and for saving time, occurring when a gene interferes with the expression of other traits (SANTOS et al., 2019). Positive correlations indicate that the correlated traits vary towards the same direction. Therefore, the higher the correlation value, the greater the association between the traits. The sign of *r* expresses the direction of the correlation, whereas its intensity is represented by a numerical value that ranges from –1 to 1 (SILVA et al., 2014).

Table 3. Estimates of phenotypic (rF), genotypic (rG), and environmental correlation coefficients (rA) between morpho-agronomic traits evaluated in cowpea genotypes.

Variable		DFR	GPW	GW	GPL	GPT	NGP	GWP	GGT
DFL	rF	0.84^{**}	0.26^{ns}	0.15^{ns}	0.11^{ns}	0.69^{*}	0.18^{ns}	0.25^{ns}	0.04^{ns}
	rG	0.86^{**}	0.23^{ns}	0.14^{ns}	0.09^{ns}	0.07^{ns}	0.14^{ns}	0.12^{ns}	0.03^{ns}
	rA	0.79^{**}	0.43^{ns}	0.26^{ns}	0.38^{ns}	0.03^{ns}	0.33^{ns}	0.62^{*}	0.11^{ns}
DFR	rF		0.42^{ns}	0.33^{ns}	0.22^{ns}	0.22^{ns}	0.15^{ns}	0.37^{ns}	0.14^{ns}
	rG		0.45^{ns}	0.35^{ns}	0.20^{ns}	0.27^{ns}	0.09^{ns}	0.39^{ns}	0.18^{ns}
	rA		0.22^{ns}	-0.02^{ns}	0.49^{ns}	-0.41^{ns}	0.60^{ns}	0.42^{ns}	-0.29^{ns}
GPW	rF			0.50^{ns}	0.82^{**}	0.74^{**}	0.31^{ns}	0.66^{*}	0.23^{ns}
	rG			0.49^{ns}	0.85^{**}	0.76^{**}	0.30^{ns}	0.62^{*}	0.18^{ns}
	rA			0.70^{**}	0.62^{*}	0.53^{ns}	0.38^{ns}	0.96^{**}	0.60^{ns}
GW	rF				0.21^{ns}	0.62^{*}	-0.14^{ns}	0.52^{ns}	0.73^{*}
	rG				0.20^{ns}	0.61^{*}	-0.14^{ns}	0.54^{ns}	0.74^{**}
	rA				0.49^{ns}	0.71^{*}	-0.21^{ns}	0.67^{*}	0.62^{*}
GPL	rF					0.43^{ns}	0.37^{ns}	0.41^{ns}	-0.20^{ns}
	rG					0.45^{ns}	0.36^{ns}	0.42^{ns}	-0.21^{ns}
	rA					0.04^{ns}	0.64^{*}	0.69^{*}	-0.06^{ns}
GPT	rF						-0.28^{ns}	0.31^{ns}	0.55^{ns}
	rG						-0.28^{ns}	0.32^{ns}	0.53^{ns}
	rA						-0.32^{ns}	0.40^{ns}	0.79^{**}
NGP	rF							0.57^{ns}	-0.28^{ns}
	rG							0.62*	-0.29^{ns}
	rA							0.45^{ns}	-0.23^{ns}
GWP	rF								0.50^{ns}
	rG								0.53^{ns}
	rA								0.53^{ns}

** = significant at 1%, * = significant and 5%, and ^{ns} = not significant by the F-test. Days to flowering (DFL), days to fruiting (DFR), green pod weight (GPW), green pod width (GW), green pod length (GPL), green pod thickness (GPT), number of grains per pod (NGP), grain weight per pod (GWP), and green grain thickness (GGT).

The traits that showed non-significant estimates for the coefficients of genotypic, phenotypic, and environmental correlations (Table 3) were independent, despite their low correlation. Information on the degree of association between traits of interest is essential for plant breeding, since it assists in the selection (LEITE et al., 2015).

The genetic correlations between pairs of traits DFL×DFR (rG = 0.86**), GPW×GPL (rG = 0.85**), and GW×GGT (rG = 0.74**) were higher than the phenotypic and environmental correlations (Table 3). These traits also showed high heritability, confirming that they were little affected by the environment and enabling the selection of promising genotypes based on these traits. When genotypic correlations are higher than phenotypic correlations, there are greater contributions of genetic factors in relation to environmental factors regarding trait correlations (LEITE et al., 2016). Pessoa et al. (2022) also reported a significant correlation among pod variables, grains, and physiological aspects in cowpea genotypes, which can be directly or indirectly used to assist in selection.

The association between GW×GPT (rA = 0.71*) and GPW×GWP (rA = 0.96**) showed higher positive environmental correlations than the phenotypic and genotypic correlations (Table 3). These findings denote that the environment favored one trait to the detriment of the other and that the causes of genetic and environmental variation showed differences that complicate indirect selection (SILVA et al., 2014).

The correlation DFL×GPT (rF = 0.69*) showed a significant phenotypic correlation. However, GPW×GPT (rG = 0.76**) and NGP×GWP (rG = 0.62*) showed positive and significant genetic correlations (Table 2), indicating that the higher the value of one trait, the higher the value of the other. If one trait has a low heritability value, e.g., GWP, indirect selection can be used, based on the NGP, as this trait shows high heritability. Therefore, information on the correlation between traits of interest indicates the degree of association between economically important traits (FOLLMANN et al., 2017).

There was similarity between the following pairs of traits: DFL×GWP (rA = 0.62*), GPW×GW (rA = 0.70**), GW×GWP (rA = 0.67*), GPL×NGP (rA = 0.64*), GPL×GWP (rA = 0.69*), and GPT×GGT (rA = 0.79**) (Table 3) regarding sign, magnitude, and significance level, highlighting the greater contribution of environmental factors over genetic factors for these traits. Correa et al. (2015) analyzed genetic variability and correlations between cowpea genotypes and reported the occurrence of environmental correlations between traits, indicating that the environment favored one trait to the detriment of the other and indirectly complicates the selection, since the phenotypic expression increases due to environmental effects.

According to the estimates of genetic gains obtained using different selection indices, all indices showed positive values for number of days to fruiting, green pod weight, green pod width, green pod length, green pod thickness, number of grains per pod, grain weight per pod, and green grain thickness (Table 4). The values observed in the selection indices indicate positive gains for all these traits (SILVA et al., 2014).

Table 4. Estimates of expected genetic gains with simultaneous selection for 14 traits obtained by selecting 42 cowpea genotypes.

Genetic gains (%)	Selection index					
	Willians	Smith and Hazel	Subandi, Compton and Empig	Mulamba and Mock	Pesek and Baker	Genotype-ideotype distance
DFL	7.8	2.7	4.6	-1.2	4.6	6.6
DFR	6.0	3.0	3.8	1.1	3.8	6.3
GPW	38.8	24.6	44.0	27.8	44.0	45.0
GW	4.3	8.1	9.3	14.1	9.1	10.8
GPL	23.4	26.5	24.4	7.8	24.4	23.6
GPT	8.2	3.7	12.9	8.8	12.9	13.4
NGP	15.0	10.4	12.2	7.3	12.2	12.5
GWP	26.0	17.6	30.0	31.7	30.0	24.6
GGT	4.1	3.6	8.7	14.0	8.7	6.3

Days to flowering (DFL), days to fruiting (DFR), green pod weight (GPW), green pod width (GW), green pod length (GPL), green pod thickness (GPT), number of grains per pod (NGP), grain weight per green pod (GWP), and green grain thickness (GGT).

The highest individual gains were found for GPW (38.85), GWP (26.0), and GPL (23.4%), which is interesting since they provide genotypes with larger and heavier pods and higher number of grains, which are essential traits for increasing production. Similar results were reported by Rodrigues et al. (2017) when using different selection indices for water-tolerant cowpea genotypes, with pod weight standing out as an important trait to increase cowpea production components.

The Mulamba and Mock index (1978) showed negative gains for number of days to flowering (Table 4), with a reduction in this trait, which is a desirable aspect since genotypes with earlier cycles result in faster flowering. According to Lessa, Ledo, and Santos (2017), a negative shift means that the value attributed to the ideotype is higher than the mean. This result denotes that the Mulamba and Mock index (1978) is appropriate for selecting genotypes with faster flowering among the genotypes evaluated.

The Mulamba and Mock (1978) and Williams (1962) indices and the genotype-ideotype distance showed the best results for the evaluated traits (Table 4), providing expressive genetic gains through genotype selection due to the high values of some traits. Pedrozo, Benites, and Barbosa (2009) reported that the higher the coefficient of agreement between selection indices, the more efficient the section results. However, the genotype-ideotype distance index showed to be more efficient than the other indices, highlighting its potential to indicate cowpea genotypes with promising genetic gains.

The selected genotypes can be indicated after identifying the indices that provided the highest genetic gain estimates. In this context, the selection index showed a different dynamic in the choice of most individuals (Table 5). According to Silva and Viana (2012), the use of selection indices is a good alternative to obtain selection gains for more than one character, simultaneously, allowing for faster obtaining of genotype responses with adequate patterns for several characteristics.

Table 5. Cowpea genotypes selected by the indices Williams (1962), Mulamba and Mock (1978), and genotype-ideotype distance among the 42 genotypes evaluated.

Order of the selected genotypes	Selection index		
	Willians	Mulamba and Mock	Genotype-ideotype distance
1	CV 938	CE-205	CE-994
2	CE-994	CE-688	CE-688
3	CE-24	CE-994	CV-938
4	CE-165	CE-206	CE-165
5	CE-228	CE-228	CE-228
6	CE-313	CE-172	CE-796
7	CE-688	CE-997	CE-688
8	CE-796	CE-123	CE-164

The genotypes CE-228, CE-688, and CE-994 were similar and are recommended for selection based on the indices Williams (1962), Mulamba and Mock (1978), and the genotype-ideotype distance, with 37.5% coincidence. Carneiro et al. (2021) used the Mulamba and Mock (1978) index in soybean populations and reported that it provided the best results, identifying promising soybean genotypes. Bertini et al. (2010) recommended selecting cowpea genotypes using the Mulamba and Mock (1978) index for simultaneous evaluation of traits. Therefore, using selection indices facilitates the breeder's decision-making and makes selection more efficient by combining several traits (CRUZ, 2013).

Based on the Williams (1962) index and the genotype-ideotype distance, the CV-938, CE-796, and BRS-Paraguaçu genotypes showed similarities (Table 5), although in different orders. These genotypes can be selected and used as parents in cowpea breeding programs to produce new green grain cultivars. Unlike direct selection, the studied indices allow the simultaneous selection of several characters (BIZARI et al., 2017; PEIXOTO et al., 2021), increasing the likelihood of success in the selection process. Melo et al. (2020) also recommended the selection of cowpea genotypes based on selection indices for identifying promising genotypes to be recommended for green bean production.

CONCLUSIONS

Selection based on number of days to flowering, days to fruiting, green pod weight, green pod width, green pod length, green pod thickness, number of grains per pod, and green grain thickness is efficient in cowpea genotypes grown for green grain production.

The trait grain weight per pod can be used to indirectly select the variables days to flowering, green pod width, and green pod length, since they are highly and positively correlated.

The indices Williams (1962), Mulamba and Mock (1978), and genotype-ideotype distance provide greater genetic gains in the selection of superior cowpea genotypes when compared to the other methods used.

The genotypes CE-228, CE-688, CE-994, CE-165, CE-796, and BRS-Paraguaçu show simultaneous superiority for the evaluated traits and are the most appropriate genotypes for green grain production.

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