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Selection indexes and economic weights applied to runner-peanut breeding[1]

Índices de seleção e pesos econômicos aplicados ao melhoramento do amendoim rasteiro

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HIGHLIGHTS:

The selection index based on the Mulamba & Mock method provides gains close to the maximum limits via direct selection.
Earliness traits do not aid in the selection of genotypes of runner peanuts suitable for pod production.
Traits associated with pod production have high heritability and contribute to the genetic progress of runner peanuts.

ABSTRACT: Runner peanuts are known for their high pod yields, but are late to flowering and pod maturation, and the optimal combination of these traits with pod yield is widely desired for peanut improvement. Selection indexes are useful tools for crop breeding. In this study, seven selection indexes combined with economic weights were used in a peanut population to estimate the superior and balanced genetic gains. Eleven runner genotypes were grown in three environments in the Northeast region of Brazil under a randomized block design with five replicates. The following indices were used: Smith and Hazel, Pesek and Baker, Williams, Elston, Subandi, Cruz, and Mulamba & Mock, in combination with the following economic weights: weight 1 for all evaluated traits, primary and secondary traits, genetic variation coefficient, genetic standard deviation, and b coefficient, obtained via multivariate regression. Although the population is genetically uniform, statistical differences were found, indicating sufficient genetic variability to generate selection progress. The combinations involving earliness traits were not satisfactory for production gains. The index based on the Mulamba & Mock rankings combined with weight 1 for all traits proved the optimal combination, as indicated by the most balanced gains. The cultivars Florunner, Cavalo, LGoPE-06, and LViPE-06 are promising germplasm for ensuring satisfactory selection gains based on production means and high heritability of the most evaluated traits.

Key words: *Arachis hypogaea* L., genetic gain, selection methods

RESUMO: O amendoim rasteiro é conhecido pela alta produtividade, porém as plantas são tardias para florar e maturar as vagens, A combinação desses caracteres e produção de vagens é largamente almejada no melhoramento dessa oleaginosa. Índices de seleção são ferramentas úteis para auxiliar no melhoramento da cultura. Neste trabalho foram usados sete índices de seleção combinados com pesos econômicos, com objetivo de estimar ganhos genéticos superiores e equilibrados em uma população de amendoim runner. Onze genótipos foram cultivados em três ambientes na região Nordeste sob o delineamento de blocos ao acaso com cinco repetições. Foram utilizados os seguintes índices: Smith e Hazel (SH), Pesek e Baker (PB), Williams (W), Elston (E), Subandi (S), índice de Cruz (GI) e Mulamba e Mock (MM), que foram combinados com os pesos econômicos: W1- peso 1 para todas as características avaliadas; PT - traços primários e secundários; CGv - coeficiente de variação genética; SDg - desvio padrão genético e coeficiente b, obtido por meio de regressão multivariada. Embora a população seja geneticamente uniforme, diferenças estatísticas foram encontradas indicando variabilidade genética suficiente para gerar progresso na seleção. As combinações envolvendo os caracteres de precocidade (B e FPM) não foram satisfatórias para ganhos de produção. O índice baseado no ranks de MM combinado com W1 para todas as características foi o melhor por indicar ganhos mais equilibrados. As cultivares Florunner, Cavalo, LGoPE-06 e LViPE-06 são germoplasma promissores para garantir satisfatórios ganhos de seleção, baseando-se nas medias de produção e alta herdabilidade dos caracteres avaliados.

Palavras-chave: *Arachis hypogaea* L., ganho genético, métodos de seleção

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Introduction

Selection indices are valuable genetic tools to assist in routine breeding procedures, especially for estimating genetic progress to predict the success of modified populations.

The selection indexes available in the literature are divided into parametric and nonparametric categories. The parametric indexes reveal genetic gains by maximizing the genotypic value × index correlation, thereby aiming to maximize the phenotypic selection and gradually increase the frequency of favorable alleles related to relevant traits. These include the Smith (1936), Hazel (1943), Pesek & Baker (1969), and Williams (1962) indexes. Non-parametric indexes are based on a more simplistic classification of genotypes, such as those of Elston (1963), Subandi et al. (1973), Cruz (Cruz et al., 2012), and Mulamba & Mock (1978).

In addition to choosing the appropriate method, there remains the challenge of defining the economic weights that will be assigned to each trait. In the literature, the definitions proposed by Hazel (1943), Pesek & Baker (1969), and Cruz et al. (2012) have been widely adopted. This combination of the selection index and economic weight enhances the benefits of the tool in the selection procedure.

Peanuts are an important oilseed worldwide. Brazil produces over 516 000 tons of grains, the majority of which are from runner cultivars (*Arachis hypogaea* subsp. hypogaea) (CONAB, 2020). Runner types have late cycles and high yields, and widely depend on favorable weather conditions (Vasconcelos et al., 2015). The identification of earliness and productive accessions would be advantageous to further indicate cultivars that are adaptable to less favorable environments (Dutra et al., 2018). In this study, seven selection indexes were tested in combination with economic weights to estimate maximum genetic gains in a runner peanut population.

Material and Methods

The experiments were conducted in three environments in Northeast Brazil: Barbalha, CE (07° 17' 29" S; 39° 16' 12" W; 415 m, Vertisols), Campina Grande, PB (07° 13' 11" S; 35° 52' 31" W; 552 m, Psamments), and Abreu e Lima, PE (07° 54' 37" S; 34° 54' 12" W; 19 m, Entisols), during the rainy season (May-Sept 2015). The soil of the experimental areas was previously limed (2 tons ha^{-1} dolomitic limestone) and fertilized (NPK, 20:60:30, ammonium sulfate, single superphosphate, and potassium chloride).

Eleven runner peanut genotypes (Table 1) were obtained from Embrapa Algodão (Campina Grande, PB). The seeds of each genotype were cultivated on May 17, 2015 in rows (5 m length) and spaced 80 cm apart. After emergence, the density was maintained at 8 plants m^{-1} per row. The plot consisted of three rows (12 m^2), and measurements were collected in plants from the central row. A randomized complete block design was adopted, with three repetitions. Standard agronomic practices were applied according to the recommendations described by Ramos et al. (2020). After harvesting, the plants were dried under natural conditions for further data collection.

Table 1. Origin, genealogy, and certain agronomical traits of runner genotypes

Genotype	Origin	Genealogy	Seed Size	Seed Color	NSP	PMP (dae)
BRA 02179201	DF, Brazil	Accession	M	T	2	118-120
BRS Pérola Branca	PB, Brazil	Cultivar	L	W	3-4	110-115
Florunner	USA	Cultivar	L	T	2-3	125-130
M407.F(B)	PB, Brazil	Top line	M	T	2	115-120
F.M424(B)	PB, Brazil	Top line	L	T	2-3	115-120
IAC Caiapó	SP, Brazil	Cultivar	L	T	2	125-130
Porto Alegre	PR, Brazil	Accession	M	T	2	118-120
Cavalo	RB, Brazil	Accession	EL	T	2	130-135
LGoPE-06	PE, Brazil	Top line	EL	T	2	125-130
BR1xAnonV	PE, Brazil	Top line	G	R	2-3	110-115
LViPE-06	PE, Brazil	Top line	EL	T	2-3	125-130

Seed size: M, Mid; L, Large; EL, Extra-large; Seed color, T-Tan; W-White, R-Red; NSP, Number of seeds per pod; dae, days after emergence; PMP, physiological maturation of pods

Nine traits were evaluated: main stem height (MSH), harvest index (HI), 100 pod weight (100PW), 100 seed weight (100SW), number of pods per plant (NPP), pod length (PL), oil concentration (OC), blooming (B), and full pod maturation (FPM). Blooming was recorded when 50% of the plants started flowering in the central rows of each plot. The records ranged from 29-32 (early) to 38-40 (late) dae. The MSH and NPP were documented from 15 plants randomly chosen from the central rows of each plot. The harvest began when genotypes reached full pod maturation, ranging from 110-115 (BRS Pérola Branca) to 130-135 (Cavalo) dae.

The oil concentration was estimated using a nuclear magnetic resonance spectrometer (H1 Oxford MQA 7005) with 20 g of seeds of each genotype (AOCS, 2004). The readings were performed with three biological replicates and five experimental repetitions The GENES software, version 2013.5.1. (2013) was used for statistical analyses, and the F and Tukey tests were adopted for analysis of variance (ANOVA) and mean classification, respectively. ANOVA was based on the following statistical model (Eq. 1):

$$Y_{ijk} = m + G_i + \frac{B}{E_{jk}} + E_j + GE_{ij} + E_{ijk} \qquad (1)$$

where:

Y_{ijk} - phenotype observed in individual i, in environment j, and repetition k;
m - general mean;
G_i - effect of the i^{th} genotype (i = 1, 2, ..., g);
B/E_{jk} - effect of the k^{th} block within the j^{th} environment;
E_j - effect of the i^{th} environment (j = 1, 2, ..., e);
GE_{ij} - effect of i^{th} G × j^{th} E interaction; and
E_{ijk} - random error.

All effects were considered random, except the general mean.

The phenotypic mean matrices, phenotypic and genotypic variances, and covariance were obtained from ANOVA, and later used in correlations and selection procedures. The genetic correlation was estimated according to the following expression (Eq. 2):

$$r_g = \frac{\hat{\sigma}_{gxy}}{\sqrt{\hat{\sigma}^2_{gx}\hat{\sigma}^2_{gy}}} \qquad (2)$$

where:

r_g - genetic correlation;

σ_{gxy} - estimator of the genotypic covariance between X and Y traits; and

σ^2_{gx} and σ^2_{gy} - estimators of the genotypic variances of the X and Y traits, respectively.

For HI, 100PW, 100SW, NPP, PL, OC, and MSH, the selection of traits was based on the highest means, whereas for B and FPM, the selection was based on the lowest values.

The economic weights adopted for the different traits were determined considering the following parameters: a) primary and secondary traits (PT) - primary: HI, 100PW, 100SW, and NPP (weight 1), B and FPM (weight -1), secondary: PL, OC, and MSH (weight 0); b) weight 1 for all traits, regardless of their importance; c) coefficient of genetic variation (CGv) of each trait; d) genetic standard deviation (SDg) of each trait; and e) b coefficient of each trait, estimated through multiple regression analysis. Pod production was adopted as the dependent variable and the other traits were considered independent. Direct and indirect selections were based on the identification of the main genotypes for the i^{-th} trait, where direct gain is estimated based on statistics (Eq. 3):

$$GS_i = \left(\bar{X}_{si} - \bar{X}_{oi}\right)h_i^2 = DS_i h_i^2 \tag{3}$$

where:

GS_i - gain of selection to trait i;

DS_i - differential of selection to trait i;

X_{si} - mean of materials selected for trait i;

X_{oi} - original mean of population to trait i; and

h^2i - trait i heritability.

The indirect gain in trait j for direct selection in trait i, was estimated using Eq. 4:

$$GS_j(i) = DS_j(i)h_j^2 \tag{4}$$

where:

$GS_j(i)$ - gain of indirect selection to trait j when selection is practiced for trait i;

$DS_j(i)$ - indirect selection differential to trait j, obtained through the difference between the means of selected and original populations, to trait i; and

h_j^2 - heritability of trait j.

For selection based on the classical index (Smith, 1936; Hazel, 1943), the indexes were estimated through a linear combination of traits weighted by the respective b coefficients. These coefficients, which maximize the correlation between the index and genotype aggregate, are estimated using the following equations:

$$H = a_1g_1 + a_2g_2 + \ldots + a_ng_n = ni = 1a_ig_i = a'g \tag{5}$$

$$I = b_1y_1 + b_2y_2 + \ldots + b_ny_n = ni = 1b_iy_i = b'y \tag{6}$$

where:

H - genotype aggregate;

I - selection index;

g - vector (1 × n) of genetic values of n traits;

y - vector (1 × n) of phenotypic means;

a' - vector (n × 1) of economic weights of different traits established by breeder;

n - number of traits adopted to estimate the index; and

b' - vector (n × 1) of weighting coefficients of the index estimated by Eq. 7:

$$b = P - 1Ga \tag{7}$$

where:

P - matrix (n × n) of the phenotypic variance and covariance; and

G - matrix (n × n) of the genotypic variance and covariance.

For selection based on the sum of ranks (Mulamba & Mock, 1978), the index is based on an equation that adjusts the genotype classification in an order favorable for crop improvement. The equation is as follows (Eq. 8):

$$I = p_1r_1 + p_2r_2 + \ldots + p_nr_n = nj - 1p_jr_j \tag{8}$$

where:

p_j - economic weight attributed by breeder to the j^{-th} trait; and

r_j - rank of genotype in relation to j^{-th} trait.

The base index (Williams, 1962) is based on a linear combination of phenotypic trait means, directly determined through their economic weights, as follows (Eq. 9):

$$I = a_1y_1 + a_2y_2 + \ldots + a_ny_n \tag{9}$$

where:

a_j - economic weight to the j^{-th} trait; and

y_j - mean of the j^{th} trait for a given genotype.

For selection proposed by Subandi et al. (1973), the index is based on the product of the phenotypic means of traits, considering the sense of the selection. The equation is as follows (Eq. 10):

$$I = y_1k_1y_2k_2 \ldots y_nk_n \tag{10}$$

where:

y_j - mean of the j^{-th} trait;

k_j - 1, if we consider a direct relationship between index and j trait; and

k_j- -1, if consider an inverse relationship between index and trait j.

In relation to the free index of weights and parameters (Elston, 1963), the index was estimated using Eq. 11:

$$I = w_1w_2 \ldots w_j \tag{11}$$

where:

$w_j = y_j - k_j$, and w_j is the deviation of the j-th trait in relation to the minimum (or maximum) j-th pre-established value;

y_j - mean of genotype in relation to j trait; and

k_j - minimum (or maximum) pre-established for trait j; w_j will be null if the y_j values are below the minimum or above the maximum.

In the method based on desired gains (Pesek & Baker, 1969), we replace the expected gain (Δg) with the desired gain (Δg_d) by adopting Eq. 12:

$$b = G - 1gd \qquad (12)$$

The economic weights were then estimated (Eq. 13):

$$\hat{a} = G - 1P\hat{e} \qquad (13)$$

where:

$\hat{a}$ - vector (n ×1) of economic weights for the different traits;

G^{-1} - inverse matrix (n × n) of genotypic variances and covariance;

P -matrix of genotypic variances and covariance; and

$\hat{e}$ - vector (n × 1) of the index weighting coefficients.

Finally, the index proposed by Cruz (Cruz et al., 2012), which is based on the distance between genotype and ideotype shows the graphic dispersion of genotypes in the 2D plane based on the mean of the i-th genotype in relation to the j-th trait (Xij).

Dissimilarity analysis was performed to estimate the agreement of the classifications involving genotypes and index/economic weight combinations. The order of selection, from the first to the last individual, was considered as a category and evaluated in terms of agreement and disagreement, as described in Eq. 14:

$$dii' = \frac{D}{C} + D \qquad (14)$$

where:

$d_{ii'}$ - dissimilarity between observation i (here considered economic index/weight combinations) and i';

D - total disagreements between genotype classifications; and

C - total agreements between genotype classifications.

Lower dissimilarities indicate more concordant combinations. A hierarchical multivariate method was then adopted, using the unweighted pair group method with arithmetic mean (UPGMA), with 5000 bootstrap replicates. Statistical analyses were performed using the GENES software, version 2016.6.0 (Cruz, 2013).

RESULTS AND DISCUSSION

Significant statistical effects were found for genotypes in all traits (Table 2), indicating variability between germplasm and the contribution of selection techniques to assist in the identification of genotypes with favorable alleles. The absence of a significant effect from the environment was observed for most traits, demonstrating that, in general, the environments were representative for trait expression. The G × E interaction was significant for HI, 100SW, NPP, PL, B, MSH, and 100PW, indicating that the genotypes had different behaviors due to changes in the environment, as the mean ranking altered depending on growth location.

The experimental precision of the assays was adequate, based on the low CE (≤ 7.65). In general, the σ^2_g values were higher than σ^2_{gxe} and σ^2_e, indicating a predominance of genetic factors, corroborated by high estimates of h^2 (above 85%), suggesting the possibility of genetic progress with the selection procedures.

Higher CGv estimates for MSH, NPP, 100PW, and 100SW were observed, indicating a wide variation in these traits. OC and B recorded lower CGv values, signifying little variation, resulting in limited contribution to the selection procedures. Based on the values found for the CGv/CEv ratio, this runner-peanut population appears to have a high probability of producing a satisfactory genetic gain, since high values for this relationship

Table 2. Analysis of variance of nine peanut traits and genetic parameters. HI - Harvest index; 100PW - 100 pod weight; 100SW - 100 seed weight; NPP - Number of pods per plant; PL - Pod length; OC - Oil concentration; B - Blooming; FPM - Full pod maturation; MSH - Main stem height (MSH)

SV	DF	Mean square								
		HI (%)	100PW	100SW	NPP	PL (cm)	OC (%)	B	FPM	MSH (cm)
			(g)					(dae)		
B/E	6	3.55	70.46	4.57	10.22	0.36	0.99	0.27	6.86	0.63
G	10	208.28**	1400.4**	527.09**	838.28**	109.93**	19.36**	57.68**	673.48**	439.01**
E	2	602.71**	38.33	34.48	440.12**	6.71	2.03**	4.31	12.74	18.44
G x E	20	27.74**	25.4*	11.59**	21.86**	3.21**	0.76	2.99**	4.6	7.82**
Error (σ^2_e)	60	2.8	13.79	4.47	4.34	0.75	0.83	0.89	5.79	2.53
Mean		45.66	98.67	60.86	34.20	30.21	49,97	35.35	122.99	20.81
CEv (%)		3.67	3.76	3.47	6.09	2.88	1.83	2.68	1.96	7.65
		Genetic parameters								
σ^2_g		20.06	152.78	57.28	90.71	11.86	2.07	6.08	74.32	47.91
σ^2_{gxe}		8.31	3.87	2.37	5.84	0.81	-0.02	0.69	-0.39	1.76
h^2 (%)		86.68	98.19	97.8	97.39	97.08	96.06	94.82	99.32	98.22
CGv (%)		9.81	12.53	12.43	27.85	11.4	2.88	6.97	7.01	33.26
CGv/CEv		2.68	3.33	3.5	4.57	3.96	1.57	2.61	3.58	4.35

**,* - Significant by F test ($p \leq 0.01$ and 0.05, respectively; SV - Source of variation; DF - Degree of freedom; B/E - Block/environment; G - Genotype; E - Environment; G × E - Genotype × environment interaction; σ^2_e - Environmental variation; CEv (%) - Coefficient of environmental variation; σ^2_g - Genotypic variance; σ^2_{gxe} - Variance attributed to G × E; h^2 (%) - Heritability (mean); CG_v (%) - Coefficient of genotypic variation (%); dae - Days after emergence

(CG_V/CE_V) indicate that the existing phenotypic variability is mostly composed of genetic factors.

Similar results have been reported by other authors (Kukanur et al., 2014; Silva et al., 2016; Rathod & Toprope, 2018; Ramos et al., 2020). The study by Kukanur et al. (2014) is expressive because those authors estimated the genetic variability, heritability, and genetic gain of 13 traits in a mini core peanut collection, containing 225 fastigiata, vulgaris, hypogaea, peruviana, and aequatoriana accessions. That study documented high CGvs for NPP, pod yield, seed yield, and 100SW, suggesting the presence of considerable variability. The smallest CGv values were observed for B and OC, as also seen in this study. Broad-sense heritability estimates were high for most traits (≥ 83%), corroborating the means displayed in Table 2, indicating that these traits can be improved by selection.

The genetic correlations involving the agronomical traits obtained from the 11 runner genotypes are shown in Table 3. Significant positive correlations of high to medium magnitudes were found for most traits, corroborating the findings of Luz et al. (2014) and Yol et al. (2018).

Significant negative correlations were revealed in only four combinations, all of which involved MSH. Based on the growth of runner plants, it is prudent for the breeder to focus on selection sense in order to avoid discarding promising germplasm. Thus, the main contributory combinations for peanut breeding based on MSH are B × MSH and FPM × MSH, because both B and FPM are associated with earliness and reproductive efficiency (Luz et al., 2014). Late cycle materials are more decumbent, and their canopy facilitates the entrance and elongation of pegs in the soil, ensuring the formation of pods (Vasconcelos et al., 2015). Kotzamanidis et al. (2006) conducted a correlation study using 21 peanut lines from Virginia × Virginia, Valencia × Valencia, Virginia × Spanish, and Virginia × Valencia genotypes. The correlation between MSH and pod yield was positive only in Virginia × Virginia lines because of the proximity of the canopy to the soil, often below 20 cm. To improve runner genotypes in environments with regular rainfall, the selection was focused on decumbent and late flowering plants, which can contribute to the identification of more productive genotypes, due to the greater viability of the flowers (Vasconcelos et al., 2015).

Table 4 displays the estimates of genetic gains through direct and indirect selection of peanut traits. The combination of these estimates with heritability values is useful for predicting the effects of selection. Considering the path of direct selection, we found six traits whose effort can ensure gains in the range of 9.46 to 34.71%, which is relevant in pure populations of autogamous plants: HI, 100PW, 100SW, NPP, PL, and MSH. In the literature, gains in the range of 10 to 12% have been reported for NPP and 100PW in hypogaea genotypes, indicating that improvement in these traits may lead to high yields (Luz et al., 2014; Patil et al., 2018).

In the indirect path, selection based on 100PW benefited other traits responsible for seed and oil production, such as 100SW, PL, OC, and HI, allowing gains equal or close to the gains obtained via direct selection. From the vegetative aspect, selection based on plant height will result in indirect gains for flowering (6.09%) and pod maturation (6.25%), indicating gains in precocity, but an insignificant response for most other reproductive traits associated with production. This has been reported in other studies and corroborates the correlation magnitudes shown in Table 3 (Patil et al., 2018; Yol et al., 2018). Based on these results, the genotypes Florunner, Cavalo, LGoPE-06, and LViPE-06 were selected, considering the higher means of each trait.

Table 3. Genetic correlations of agronomical traits from runner peanut genotypes. HI - Harvest index; 100PW - 100 pod weight; 100SW - 100 seed weight; NPP - Number of pods per plant; PL - Pod length; OC - Oil concentration; B - Blooming; FPM - Full pod maturation; MSH - Main stem height

Trait	100PW	100SW	NPP	PL	OC	B	FPM	MSH
HI	0.79**	0.88**	0.34	0.54	0.64*	0.99**	0.69*	-0.61*
100PW		0.92**	0.36	0.70**	0.81**	0.84**	0.71*	-0.59*
100SW			0.52	0.83**	0.71*	0.86**	0.66*	-0.46
NPP				0.57*	0.50	0.13	-0.16	0.18
PL					0.59*	0.58*	0.34	-0.11
OC						0.63*	0.52*	-0.52
B							0.82**	-0.62*
FPM								-0,59*

**,* - Significant: $p \leq 0.01$ and 0.05, respectively

Table 4. Estimates of genetic gains (%) through direct and indirect selection of peanut traits evaluated in runner genotypes grown in three environments of the Brazilian Northeast. HI - Harvest index; 100PW - 100 pod weight; 100SW - 100 seed weight; NPP - Number of pods per plant; PL - Pod length; OC - Oil concentration; B - Blooming; FPM - Full pod maturation and MSH - Main stem height (MSH)

Trait	HI	100PW	100SW	NPP	PL	OC	B	FPM	MSH
HI	9.46	13.59	12.52	12.04	9.26	2.73	7.02	4.52	-24.65
100PW	9.46	13.59	12.52	12.04	9.26	2.73	7.02	4.52	-24.65
100SW	7.61	12.04	12.78	11.33	9.41	2.35	6.8	6.74	-23.16
NPP	2.87	2.24	4.77	31.10	5.24	0.91	0.62	-2.71	8.86
PL	2.34	11.7	9.09	13.78	9.47	2.57	3.07	2.72	-17.73
OC	9.46	13.59	12.52	12.04	9.26	2.73	7.02	4.52	-24.65
B	-6.47	-7.35	-8.43	7.3	-8.03	-0.74	-6.54	-5.51	15.02
FPM	-8.26	-8.47	-9.12	6.19	-3.74	-1.28	-6.09	-6.25	34.70
MSH	-8.26	-8.47	-9.12	6.19	-3.74	-1.28	-6.09	-6.25	34.71

The simultaneous selection of traits was performed from all selection indexes with different economic weights, and gains were estimated for all 27 combinations (Table 5). Similar to that with direct selection, a block of accessions was indicated as the most promising for more than one combination (index × weight).

SH-PT, SH-W1, SH-SDg, W-W1, and W-SDg were the main combinations and indicated the same genotypes, which resulted in equal gains for the traits, followed by maximum gains via direct selection, for HI, 100PW, 100SW, NPP, and OC. Therefore, these combinations allow the selection of genotypes with a high level of production at the expense of those related to earliness, since the gains in B and FPM (4.79 and 2.57%, respectively) were unsatisfactory because they increased the phenotypic means. Despite the high SDg values found for FPM, NPP, and MSH, the SH and W methods were not able to balance genetic gains, resulting in the selection of materials with the same principles as those attributed to W1 for all traits.

MM-PT, MM-CGv, MM-SDg, GI-PT, GI-W1, GI-CGv, GI-SDg, and E were also consistent in the selection of genotypes, leading to the same gain estimates. This block of combinations was more promising because it indicated an improvement in earliness, reducing FPM by almost one day, and maintained satisfactory gains for the other traits. For SH-CGg, SH-b, W-CGv, W-b, and S, we found maximum gains for NPP and a reduction in FPM by 2.71%; however, these groups did not maintain gains for the majority of the other traits.

In general, the gains obtained through the Pesek & Baker (1969) index were unsatisfactory for most traits; therefore, they were not considered suitable to provide an increase in favorable alleles. The Mulamba & Mock index was promising because the gains were balanced to the maximum limits for most traits via direct selection, except for HI. This index also reduced B and FMP. As this method is non-parametric and focuses on the selection of top genotypes via classification (or ranking) of means, this method is a feasible option for breeding, based on the results found here.

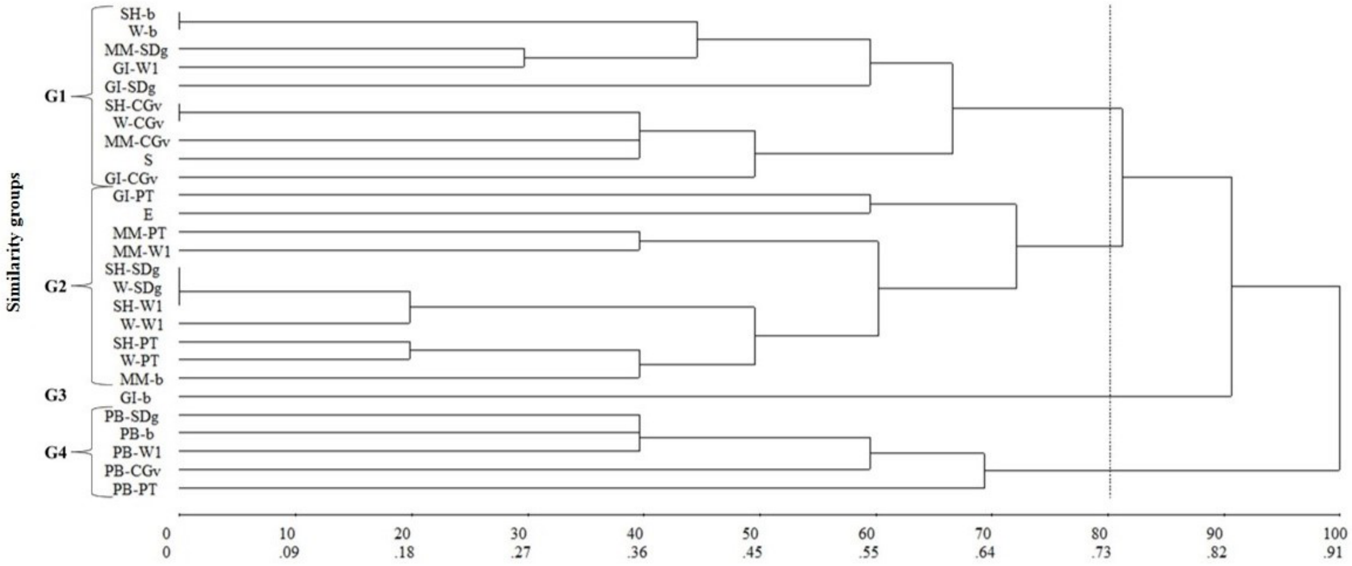
In the literature, other breeders have recommended this method for breeding programs. In soybean, Bizari et al. (2017) compared different selection indexes by segregating populations, using economic weightings to obtain higher gains. According to Mulamba & Mock (1978), the index provides the most favorable gains. Gomes et al. (2018) tested Smith (1936) and Hazel (1943), Williams (1962), Pesek & Baker (1969), and Mulamba & Mock (1978) selection indexes and the REML/BLUP methodology in beans to predict genetic gains in breed lines. According to those authors, the Mulamba & Mock (1978) method provided the best gain distribution and higher coincidence coefficients, resulting in a 62% increase in seed and pod yields.

Figure 1 displays the classification of genotypes based on 27 combinations (indexes/economic weights) represented by the UPGMA dendrogram. Four similarity groups were identified. Among them, GII (GI-PT, E, MM-PT, MM-W1, SH-SDg, W-SPg, SH-W1, W-W1, SH-PT, W-PT, and MM-b) gathered the combinations that provided the greatest gains for production traits, followed by GI (SH-b, W-b, MM-SDg, GI-W1, GI-SDg, SH-CGv, W-CGv, MM-CGv, S, and GI-CGv). Group III, which contained only GI-b, estimated unsatisfactory gains for most traits, and GIV represented all combinations involving the index based on desired gains proposed by Pesek & Baker (1969). The dendrogram results are consistent with those presented in Table 5.

Table 5. Gain estimates (%) involving selection indexes × economic weights in runner peanut genotypes. EW - Economic weight; HI - Harvest index; 100PW - 100 pod weight; 100SW - 100 seed weight; NPP - Number of pods per plant; PL - Pod length; OC - Oil concentration; B - Blooming; FPM - Full pod maturation and MSH - Main stem height (MSH)

Index	EW	HI	100PW	100SW	NPP	PL	OC	B	FPM	MSH
SH	PT	6.19	12.03	12.11	23.43	9	1.66	4.79	2.57	-9.1
	W1	6.19	12.03	12.11	23.43	9	1.66	4.79	2.57	-9.1
	CGv	2.87	2.24	4.77	31.1	5.24	0.91	0.62	-2.71	8.8
	SDg	6.19	12.03	12.11	23.43	9	1.66	4.79	2.57	-9.1
	b	2.87	2.24	4.77	31.1	5.24	0.91	0.62	-2.71	8.8
W	PT	7.61	12.04	12.78	11.33	9.41	2.35	6.8	6.74	-23.1
	W1	6.19	12.03	12.11	23.43	9	1.66	4.79	2.57	-9.1
	CGv	2.87	2.24	4.77	31.1	5.24	0.91	0.62	-2.71	8.8
	SDg	6.19	12.03	12.11	23.43	9	1.66	4.79	2.57	-9.1
	b	2.87	2.24	4.77	31.1	5.24	0.91	0.62	-2.71	8.86
PB	PT	4.24	9.17	7.4	5.48	7.41	1.23	5.09	2.81	-15.0
	W1	0.92	-0.62	0.06	13.15	3.65	0.49	0.91	-2.46	2.87
	CGv	0.92	-0.62	0.06	13.15	3.65	0.49	0.91	-2.46	2.87
	SDg	1.13	2.34	-0.06	3.63	0.67	0.38	1.36	1	2.09
	b	1.13	2.34	-0.06	3.63	0.67	0.38	1.36	1	2.09
MM	PT	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	W1	-0.4	4.95	6.29	26.31	8.83	1.07	-0.65	-2.71	4.66
	CGv	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	SDg	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	b	-0.4	4.95	6.29	26.31	8.83	1.07	-0.65	-2.71	4.66
GI	PT	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	W1	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	CGv	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	SDg	6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
	b	2.87	6.51	6.69	14.92	9.09	2.14	1.58	-0.75	-10.8
E		6.72	6.84	9.72	24.57	8.62	1.23	3.3	-0.91	-2.25
S		2.87	2.24	4.77	31.1	5.24	0.91	0.62	-2.71	8.86

SH - Smith (1936) and Hazel (1943); W - Williams (1962); PB - Pesek & Baker (1969); MM - Mulamba & Mock (1978); GI - Genotype-ideotype distance; E- Elston (1963); S - Subandi et al. (1973); PT - Principal traits; W1 - Weight 1; CGv - Coefficient of genetic variation; SDg - Genetic standard deviation; b - Coefficients estimated by analysis of multiple regression



Similarity index above 60% (p ≤ 0.01, F test)

Figure 1. Dendrogram obtained by hierarchical clustering method UPGMA, from a matrix generated with 11 peanut genotypes

CONCLUSIONS

1. The index based on the Mulamba & Mock method, combined with weight 1 for all traits, provides balanced gains for most traits, and is therefore a potential tool for estimating genetic progress in improvement programs.

2. The cultivars Florunner, Cavalo, LGoPE-06, and LViPE-06 are promising germplasm to ensure satisfactory selection gains, based on production means and high heritability of the most evaluated traits.

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