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Genetic parameters and selection strategies for soybean progenies aiming at precocity and grain productivity

Parâmetros genéticos e estratégias de seleção de progênies de soja visando precocidade e produtividade de grãos

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ABSTRACT

Genetic parameters and correlations are useful tools in breeding programs, helping to make decisions about the most efficient method of selecting soybean progenies. The objective was to determine genetic parameters and correlations between characters in 52 soybean genotypes, from 4 populations and to select the superior progenies for early cycle and grain productivity. The experiment was carried out in a randomized block design consisting of 52 RCF$_{3:4}$ progenies and three controls (UFUS7010, TMG801, BRSGO7560). Agronomic and yield traits were evaluated. For the number of days to flowering and maturity, plant height at maturity and number of nodes at maturity, a high heritability estimate and favorable conditions for selection were observed. The existence of correlations between the characters was verified with the predominance of genetic causes, which allows the success in the indirect selection. By the Mulamba and Mock method, the highest selection gain was obtained, however, for the genotype-ideotype distance index method, greater gains were obtained for production components, therefore, 15 early cycle and productive superior RCF$_{3:4}$ progenies were selected with a cycle between 79.0 and 105.0 days and production of 302.5 to 463.0 g plot^{-1}.

Index terms: Segregating population; selection indices; soy breeding.

RESUMO

Os parâmetros genéticos e as correlações são ferramentas úteis em programas de melhoramento, auxiliando na tomada de decisões sobre o método mais eficiente de seleção de progênies de soja. Objetivou-se determinar parâmetros genéticos e correlações entre caracteres em 52 genótipos de soja, provenientes de 4 populações e selecionar as progênies superiores para precocidade e produtividade. O experimento foi conduzido em delineamento em blocos casualizados composto por 52 progênies RCF$_{3:4}$ e três testemunhas (UFUS7010, TMG801, BRSGO7560). Foram avaliados caracteres agronômicos e de produtividade. Para número de dias para florescimento e maturidade, altura de planta na maturidade e número de nós na maturidade foi observada estimativa de herdabilidade alta e condição favorável à seleção. Foi constatada a existência de correlações entre os caracteres com predominância de causas genéticas, o que permite o sucesso na seleção indireta. Pelo método de Mulamba e Mock foi obtido o maior ganho de seleção, porém para método de índice da distância genótipo-ideótipo foram obtidos maiores ganhos para componentes de produção, portanto, foram selecionadas 15 progênies RCF$_{3:4}$ superiores precoces e produtivas com ciclo entre 79,0 a 105,0 dias e produção de 302,5 a 463,0 g parcela^{-1}.

Termos para indexação: População segregante; índices de seleção; melhoramento de soja.

INTRODUCTION

The success of genetic improvement depends on the existence of genetic variability, which allows the selection of superior soybean genotypes in relation to cultivars (Carneiro et al., 2021). These new genotypes must simultaneously present favorable characters that provide a significant increase in grain yield (Vianna et al., 2019).

Assessing the genetic variability in a given population is important to guide the breeder, since it allows expanding and exposing the gene pool, while information on the dimension of genetic control of a given character is given through heritability (Onwubiko; Uguru; Chimdi, 2019). Furthermore, it allows selection to be carried out in the first generations, saving time and physical and financial resources by allowing the removal of descendants of low genetic potential (Silva et al., 2021).

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In the soybean breeding process, it is common to evaluate progenies resulting from inbred plants based on appearance or phenotypic score for advancement in replicated tests and eventual release of cultivars (Smallwood et al., 2019). This method has resulted in an average increase of 1.5 to 2.0% in soybean productivity from the 1980s to the present (Leite et al., 2015).

The selection process of superior soybean genotypes is complex, most of the characters are quantitative and correlated with each other (Leite et al., 2018), which makes it necessary to analyze the characters simultaneously during the selection process (Silva et al., 2018). This can be done by estimating genetic parameters, which allow the identification and study of the characters of interest, while the analysis of the correlation between agronomic characters allows verifying whether the variation observed in one character can influence the variation observed in another character (Gesteira et al., 2018).

This allows choosing the most suitable method of selection. Selection indices allow efficient simultaneous selection of characters (Silva et al., 2021), and some of the most used are based on the sum of ranks index by Mulamba and Mock (1978) and on the genotype-ideotype distance index (Cruz, 2006).

Soybean breeding programs have sought to develop earlier cultivars, to anticipate the harvest and enable the sowing of the off-season in succession, in addition to providing better disease management (Bezerra et al., 2017). However, precocity has a negative impact on productivity, as there is a positive correlation of great magnitude between grain productivity and absolute soybean maturity (Gesteira et al., 2018). Thus, the objective of this work was to determine genetic parameters and correlations between characters in 52 soybean genotypes, from 4 populations and to select the superior progenies for early cycle and grain yield.

MATERIAL AND METHODS

The experiment was carried out between February and May/21 at the Experimental Farm Capim Branco (18º 52' S, 48º 20' W and 835 m altitude) in the municipality of Uberlândia-MG. The predominant climate in the region is Aw with an average temperature of 22.6 °C and an average annual rainfall of 1487 mm (Petrucci; Oliveira, 2019). The soil was classified as Dystrophic Dark Red Latosol (Santos, H. G. et al., 2018).

52 $RCF_{3:4}$ progenies originated from artificial hybridization between UFUS 7010♀ × TMG 801♂ (C1) and UFUS 7010♀ × BRSGO 7560♂ (C2) plus the three parents were evaluated. Each F_1 hybrid combination was back crossed to its respective parents, yielding 4 segregating populations: C1 × TMG 801 with 10 progenies; C1 × UFUS 7010 with 11 progenies; C2 × BRSG 7560 with 16 progenies and C2 × UFUS 7010 with 15 progenies. The experiment was carried out in a randomized complete block design, with two replications. Each plot consisted of 1 row with 5 meters long.

The soil was prepared by the conventional method. Then, the area was fertilized with 400 kg ha^{-1} of the NPK 08-28-16 formula. The seeds were treated with Much 600 FS, Rancona T and the Brandt® Genesis rooter and inoculated with the strains SEMIA 5079 and SEMIA 5080 of *Bradyrhizobium japonicum*. The sowing took place on February 1st, 2021.

Whenever necessary, weed control was carried out by manual weeding. Pulverization with insecticides and fungicides indicated for the crop were carried out to control pests and diseases that occurred during the experiment. In the phenological stage V_4, a commercial fertilizer composed of cobalt (12.5 g L^{-1}) and molybdenum (62.5 g L^{-1}) was applied via foliar at a dose of 100 mL ha^{-1}. Also, topdressing was carried out with potassium chloride (KCl) (60% K_2O) at a rate of 150 kg ha^{-1}.

The evaluations were carried out at stages R_1 and R_8, according to the scale of Fehr and Caviness (1977). The 5 phenotypically superior plants were sampled. The characters obtained were: a) number of days to flowering (NDF) and maturity (NDM): number of days from the VE stage to the first flower on the main stem and to maturity; b) plant height at flowering (PHF) and maturity (PHM): measurement (cm) from the soil surface to the last node of the main stem; c) height of insertion of the first pod (HIP): distance (cm) from the soil surface to the insertion of the first pod; d) number of nodes at flowering (NNF) and maturity (NNM): the number of nodes on the main stem at flowering and maturity; e) number of productive nodes at maturity (NPN) and branched (NBN): count of the number of nodes on the main stem or branches that have pods; f) number of pods with 1 grain (NP1G), 2 grains (NP2G) and 3 grains (NP3G): counting the number of pods with one, two or three grains per plant; g) total number of pods (TNP): count of the total number of pods on the main stem at maturity; h) number of seeds per pod (NSP): the ratio between the total number of grains and the TNP; j) Grain yield (PROD): total weight of soybeans produced per plot.

The data obtained were submitted to analysis of variance (ANOVA). The statistical model was followed: $Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij}$, where: Y_{ij}: value of each character in a parcel comprising the i-th genotype in the j-th block; μ: overall character average; G_i: effect of the genotype considered random i; B_j: block effect considered random j; ε_{ij}: error effect considered random.

The genotype means were submitted to the Scott-Knott cluster test at a 5% probability level by the R statistical software version 3.6.2 (R Core Team, 2019), with scripts developed for the ExpDes.pt data package version 1.2 (Ferreira; Cavalcanti; Nogueira, 2010). Genetic-statistical analyzes were performed using the computer program GENES (Cruz, 2016).

The estimated genetic parameters were: the CVg/CVe ratio was given by $\mathrm{CVg/CVe} = \frac{\mathrm{CVg}}{\mathrm{CVe}}$, where: CVg: genotypic variation coefficient; CVe: coefficient of environmental variation. Heritability in the broad sense through $h_a^2 = \frac{\sigma_g^2}{\frac{MST}{r}}$, where: h_a^2: heritability in the broad sense; σ_g^2: genetic variance; MST: mean square of treatment in ANOVA; r: number of repetitions.

The phenotypic and genotypic correlations were estimated using the expressions $r_f = \frac{PMG_{xy}}{\sqrt{SGM_x SGM_y}}$ e $r_g = \frac{\sigma_{g(xy)}}{\sqrt{\sigma^2_{g(x)}\sigma^2_{g(y)}}}$ (Cruz; Regazzi; Carneiro, 2012), where: r_f: phenotypic correlation estimator; PMG_{xy}: average product between genotypes for characters X and Y; SGM_x: mean square between genotypes for character X; SGM_y: mean square between genotypes for character Y; rg: genotypic correlation estimator; $\sigma_{g(xy)}$: genotypic covariance estimator; $\sigma_{g(x)}$ e $\sigma_{g(y)}$: estimator of the genotypic variances of characters X and Y, respectively.

Estimates of selection gains were obtained by different selection strategies: a) direct and indirect selection (Cruz et al., 2017); b) index of the sum of "ranks" by Mulamba and Mock (1978) and; genotype-ideotype distance index (Cruz, 2006). Thus, to carry out the selection of superior progenies, it was established as selection criteria the reduction of cycle characters and increase of the other study characters. To determine the selection gains (SG), the proportion of 29% of the best progenies was adopted, with the SG for indirect and direct selection based on the selection differential by the expression $SG_i = \left(X_{si} - X_{oi}\right) h_a^2 = DS_i h_i^2$, where: SG_i: direct selection gain on the i-th character; X_{si}: average of the progenies selected for character i; X_{oi}: original population means for character i; h_a^2: heritability of character i; DS_i: selection differential practiced in the population.

RESULTS AND DISCUSSION

Significant differences were verified by the Snedecor F test at the level of 1% and 0.1% of probability for the characters NDF, NDM, PHF, HIP, PHM, NNF, NNM, NSP and PROD. This demonstrated the existence of genetic variability among the 52 $RCF_{3:4}$ progenies, which allows the selection of promising progenies based on these characters (Table 1).

For breeding programs, a prerequisite is the existence of genetic variability to analyze the feasibility of the selection process (Soares et al., 2020). In turn, for the characters of NBN, NPN, NP1G, NP2G, NP3G and TNP, no genetic variance was observed (Table 1).

It was found that the estimate of heritability in the broad sense ranged from 0.00 to 92.21% (Table 1). According to the classification proposed by Falconer and Mackay (1996), the characters NP1G, NP2G and TNP had a low heritability coefficient, while the characters NBN, NPN and NP3G had a medium heritability coefficient, however the characters NDF, NDM, PHF, HIP, PHM, NNF, NNM, NSP and PROD were classified as having a high heritability coefficient.

The traits NDF, NDM. PHM and NNM showed heritability values greater than 70%, which according to Cruz, Regazzi and Carneiro (2012) indicates that they obtained high estimates, so the phenotype can be considered fully determined by the genotype. These results indicate the probability of success in the selection of genotypes with superiority in early generations in the four populations studied. However, for the other characters with low heritability, the selection must be carried out in advanced generations, when they will present greater homozygosity.

The $F_{3:4}$ and $F_{3:5}$ segregating progenies, from the cross P 98Y11 RR × BRS Favorita RR, were sown in three locations (Lavras-MG, Itutinga-MG and Ijaci-MG) in the 2016/17 and 2017/18 harvests, and provided high heritability estimates for the characters of NDF (94%), NDM (94%), HIP (62%), PHM (86%) and lodging (75%) and average estimate for grain yield (33%) (Bianchi et al. al., 2020), results similar to those obtained in the present study.

The observed CVg/CVe ratios were equal to or greater than 1.0 for the characters NDF, NDM, PHM and NNM, evidencing a favorable situation for selection (Table 1). In the same way, favorable conditions for selection were verified in $F_{3:4}$ progenies of two segregating populations of soybean, originated from the cross between BRSMG 790A x BRSMG 810C, sown in Jaboticabal-SP in the 2015/16 harvest, since they presented a CVg/ CVe equal to or greater than 1.0 for the characters NDM (1.82 and

1.58 for populations A and B, respectively) and NNM (1.01 and 1.04 for populations A and B, respectively). The PHM (0.48 and 0.52 for populations A and B, respectively) of the same progenies, however, presented values lower than 1.0, unlike the present study (Azevedo et al., 2021).

The formation of different groups was verified by the Scott-Knott cluster test at a probability of 5% for most agronomic traits evaluated. The range of means of each of the groups within the characters is shown in Table 2.

Three groups were formed for the NDF, and the one with the best performance was composed of 28 $RCF_{3:4}$ progenies (33.0 to 36.5 days), followed by the second best with 21 $RCF_{3:4}$ progenies (38.0 to 39, 5 days) and the group with the worst performance composed of 6 $RCF_{3:4}$ progenies (44.0 to 46.0 days). Likewise, the formation of three clusters for the NDM was verified, in which the group consisting of 37 $RCF_{3:4}$ progenies (79.0 to 83.0 days) presented the best result, followed by the grouping of 9 $RCF_{3:4}$ progenies (93.0 to 95.0 days) and, finally, by the group with lower performance than the others with 9 $RCF_{3:4}$ progenies (100.0 to 105.0 days) (Table 2).

The Brazilian market has demanded early cultivars (Daronch et al., 2019), however, it is worth noting that the selection of genotypes with earlier flowering can result in lower productivity (Almeida; Peluzio; Afferi, 2010). For normal growing conditions, soybean cultivars are classified as early (111 days), semi-early (112 to 124 days) and late (over 125 days) (Almeida et al., 2013). All genotypes evaluated in the present study were classified as an early cycle.

It was verified for 20 soybean cultivars sown on January 5th, 2017 in Uberlândia-MG that the NDF character ranged from 33.25 to 46.25 days and the NDM from 98.75 to 121.25 days, with similar values of NDF and higher for NDM obtained in the present study (Mattos et al., 2020). In F_2 progenies (UFUS 7415 × TMG 7161 RR) sown in Uberlândia-MG, NDM values were obtained between 76.0 and 108.0 days, like the present study (Silva et al., 2021).

It is worth mentioning that the progenies of group “a”, if sown in October, will probably have a cycle close to 100 days, since late sowing is responsible for shortening the cycle (Mattos et al., 2020). Furthermore, progenies that result in early cultivars allow the use of the crop succession system, which

Table 1: Genetic parameters of agronomic characters of $RCF_{3:4}$ progenies of 4 segregating soybean populations conducted in the municipality of Uberlândia (MG), 2020/2021 harvest.

Characters	Genetic parameters			
	SGM	CV (%)	h^2_b (%)	CVg/CVe
NDF	21.40***	6.49	72.37	1.14
NDM	144.36***	3.85	92.21	2.43
PHF	78.97**	11.74	54.64	0.78
HIP	22.25***	22.37	64.97	0.96
PHM	193.72***	11.47	79.07	1.37
NNF	1.01**	7.00	55.07	0.78
NNM	5.40***	7.58	80.08	1.42
NBN	3.55^{ns}	40.33	23.19	0.39
NPN	3.41^{ns}	14.78	27.90	0.44
NP1G	8.46^{ns}	35.26	0.00	0.00
NP2G	40.66^{ns}	30.64	9.27	0.23
NP3G	66.64^{ns}	37.27	23.29	0.39
TNP	134.34^{ns}	29.10	0.00	0.00
NSP	0.02***	4.13	65.02	0.96
PROD	12032.11***	21.55	59.67	0.86

***Significant at the 0.1% probability level for Snedecor’s F test. **Significant at 1% probability level for Snedecor’s F test. ^{ns}: Not significant. Abbreviations: NDF and NDM: number of days to flowering and maturity, respectively; PHF and PHM: plant height at flowering and maturity, respectively; HIP: Height of insertion of the first pod; NNF, NNM, NBN and NPN: number of nodes at flowering, at maturity, branched and productive, respectively; NP1G, NP2G and NP3G: number of pods with, 1, 2 and 3 grains, respectively; TNP: total number of pods; NSP: number of seeds per pod; PROD: grain productivity per plot.

allows the cultivation of a second crop after the soybean harvest in the main cereal-producing states of the country, in addition to being an alternative to avoid foliar diseases and end of the cycle (Bezerra et al., 2017; Hartman; Sikora; Rupe, 2015).

Table 2: Grouping of means of agronomic traits of $RCF_{3:4}$ progenies from 4 segregating populations of soybean and their controls.

Characters	Number of progenies	Range of averages	Group
NDF (days)	6	44.0-46.0	c[1]
	21	38.0-39.5	b
	28	33.0-36.5	a
NDM (days)	9	100.0-105.0	c
	9	93.0-95.0	b
	37	79.0-83.0	a
PHF (cm plant^{-1})	40	49.1-66.0	a
	15	34.3-48.0	b
HIP (cm plant^{-1})	19	13.6-20.4	a
	36	6.9-13.0	b
PHM (cm plant^{-1})	33	54.2-70.9	a
	10	46.1-53.6	b
	12	33.4-45.2	c
NNF (nodes plant^{-1})	22	9.8-11.0	a
	33	7.8-9.7	b
NNM (nodes plant^{-1})	37	13.2-16.9	a
	18	10.1-12.9	b
NBN (nodes plant^{-1})	55	0.0-7.2	-
NPN (nodes plant^{-1})	55	7.9-13.9	-
NP1G (pods plant^{-1})	55	3.6-13.6	-
NP2G (pods plant^{-1})	55	11.5-32.0	-
NP3G (pods plant^{-1})	55	8.0-42.5	-
TNP (pods plant^{-1})	55	29.5-72.9	-
NSP (seeds pod^{-1})	55	1.9-2.54	-
PROD (g plot^{-1})	26	328.5-463.0	a
	29	118.75-324.0	b

[1]Averages followed by similar letters belong to the same group by the Scott-Knott test at the 5% probability level.

For the PHF character, two groups were formed, in which the group with the highest PHF was composed of 40 $RCF_{3:4}$ progenies (49.1 to 66.0 cm plant^{-1}), followed by the group with the lowest PHF consisting of 15 RCF_{3} progenies (34.3 to 48.0 cm plant^{-1}). Regarding the PHM character, three clusters were generated, one with the highest PHM formed by 33 $RCF_{3:4}$ progenies (54.2 to 70.9 cm plant^{-1}), another with intermediate values composed of 10 $RCF_{3:4}$ progenies (46.1 to 53.6 cm plant^{-1}) and, finally, the group with the lowest PHM constituted by 12 $RCF_{3:4}$ progenies (33.4 to 45.2 cm plant^{-1}) (Table 2).

The PHF and PHM characters are extremely important, as they directly influence mechanized harvesting. In general, plants with 50.0 to 60.0 cm are recommended for soils with flat topography and 70.0 to 80.0 cm for uneven topography, plants with heights greater than 90.0 cm favor lodging (Bezerra et al., 2017). The progenies of group "a" (54.2 to 70.9 cm plant^{-1}) meet these requirements, while the others are smaller than 53.6 cm plant^{-1}, thus, the smaller stature gives the plants a smaller size, number of nodes and a lower number of pods, which interferes with the productive potential of the plant (Vianna et al., 2019).

For the HIP character, two groups were formed, in which the group with the highest HIP was composed of 19 $RCF_{3:4}$ progenies (13.6 to 20.4 cm plant^{-1}), while the group with the lowest HIP was constituted by 36 $RCF_{3:4}$ progenies (6.9 to 13.0 cm plant^{-1}) (Table 2). It is recommended that soybean cultivars have HIP ranging from 10.0 to 15.0 cm plant^{-1} (Bezerra et al., 2017), to obtain maximum efficiency in the harvest, with most of the evaluated progenies being situated in this range. It was verified in Uberlândia-MG that 127 F_2 plants (UFUS 7010 × MG/BR 446 Conquista) conducted in a greenhouse had HIP ranging from 10.0 to 44.0 cm plant^{-1} (Teixeira et al., 2017).

Two groups were formed for the NNF character, where the one with the highest NNF value was constituted by 22 $RCF_{3:4}$ progenies (9.8 to 11.0 plant^{-1} nodes), and the group with the lowest NNF was composed of 33 $RCF_{3:4}$ progenies (7.8 to 9.7 nodes plant^{-1}). Likewise, for the NNM character, two clusters were generated, in which the highest value was constituted by 37 $RCF_{3:4}$ progenies (13.2 to 16.9 nodes plant^{-1}) and the smallest by 18 $RCF_{3:4}$ progenies (10.1 to 12.9 nodes plant^{-1}) (Table 2).

It is recommended that soybean cultivars have between 17 and 18 nodes on the main stem to provide good yields (Sediyama; Silva; Borém, 2015). The evaluated progenies had the number of nodes below this range. A justification for the results found is that sowing carried out out of season tends to reduce the final number of nodes, due to the lower height of the plants (Mattos et al., 2020).

Only one cluster was formed for the characters of NBN (0.0 to 7.2 nodes plant^{-1}), NPN (7.9 to 13.9 nodes plant^{-1}), NP1G (3.6 to 13.6 pods plant $^{-1}$), NP2G (11.5 to 32.0 pods plant^{-1}), NP3G (8.0 to 42.5 pods plant^{-1}), TNP (29.5 to 72.9 pods plant^{-1}) and NSP (1.9 to 2.54 seed pod^{-1}) (Table 2).

Regarding the character of TNP, the national soybean cultivars have, on average, a maximum value of 80 pods plant^{-1} (Matsuo; Ferreira; Sediyama, 2015). The TNP found in the present study was lower than 72.9 pods plant^{-1}. A superior result was obtained in Anhumas-SP, TNP was obtained ranging from 74.53 to 261.83 pods plant^{-1} for $F_{2:3}$ progenies (IAC-100 × CD215) sown in the 2008/09 crop (Santos, M. F. et al., 2018).

For the PROD character, two groups were formed, in which the group with the highest grain yield was composed of 26 $RCF_{3:4}$ progenies (328.5 to 463.0 g plot^{-1}), while the smallest group consisted of 29 $RCF_{3:4}$ progenies (118.75 to 324.0 g portion^{-1}) (Table 2).

It is extremely important to know the correlations in a breeding program, since they are responsible for quantifying the possibility of indirect gains by selection in correlated traits, in addition, it allows the selection of low heritability traits to be efficient when performed on traits that are correlated. The phenotypic (r_f) and genotypic (r_g) correlations between the agronomic traits of 52 $RCF_{3:4}$ progenies are shown in Table 3. The correlation between traits makes it possible to measure the degree of interference of one trait over another of interest, as well as how to practice indirect selection (Zuffo et al., 2018).

It is worth noting that the interpretation of the results must consider the magnitude, which is high above 0.7 (Souza et al., 2016), however, characters with correlations with values greater than 0.5 have been valued for allowing the indirect selection (Cruz; Regazzi; Carneiro, 2012). Other aspects that must be considered are the direction, which can be positive, indicating the tendency of one variable to increase when the other increases, or negative, which indicates the tendency of one variable to increase when the other decreases; and significance (Nogueira et al., 2012).

Thus, it was verified by the t test at 1% and 5% probability that 20 phenotypic correlations were significant. Estimates ranged from 0.28 to 0.78, which shows that there was a high degree of correlation between some evaluated characters (Table 3). For these characters it was also observed that they showed high genotypic correlation and values higher than the phenotypic correlation, indicating that genetic factors were responsible for the correlation and not the environment (Almeida; Peluzio; Afferri, 2010). Similar results were also found for the agronomic characters of 28 soybean lines evaluated in Currais-PI (Leite et al., 2015) and 71 F_6 progenies in the municipality of Uberlândia-MG (Sousa et al., 2015).

Table 3: Phenotypic (r_f) and genotypic (r_g) correlations of agronomic characters of $RCF_{3:4}$ progenies from 4 segregating soybean populations conducted in Uberlândia (MG).

Character	r	NDM	PHF	HIP	PHM	NNF	NNM	NSP	PROD
NDF	r_f	0.60**	0.21	0.57**	0.32*	0.19	0.39**	0.12	-0.14
	r_g	0.72	0.41	0.78	0.38	0.41	0.50	0.11	-0.36
NDM	r_f		0.16	0.63**	0.37**	0.30*	0.50**	0.07	-0.13
	r_g		0.21	0.79	0.41	0.37	0.58	0.11	-0.26
PHF	r_f			0.46**	0.72**	0.56**	0.44**	0.04	0.28*
	r_g			0.68	0.97	0.64	0.57	0.11	0.45
HIP	r_f				0.62**	0.37**	0.59**	-0.06	-0.05
	r_g				0.65	0.75	0.71	0.05	-0.10
PHM	r_f					0.64**	0.78**	-0.01	0.09
	r_g					0.99	0.82	0.08	0.06
NNF	r_f						0.62**	0.10	0.16
	r_g						0.91	0.15	0.26
NNM	r_f							-0.05	-0.03
	r_g							-0.09	-0.10
NSP	r_f								0.32*
	r_g								0.53

** and * are significant at the 1 and 5% level, respectively, of probability by the t test.

The occurrence of pleiotropism, a property in which a gene simultaneously affects two or more traits, may be the main factor that contributes to the achievement of high magnitude of genetic correlations. In soybean, correlation studies have focused on the evaluations of the characters collected from flowering to maturation, with emphasis on productivity and its components (Carneiro et al., 2021; Silva et al., 2021; Smiderle et al., 2019; Zuffo et al., 2018).

Significant, high magnitude and positive phenotypic correlations were obtained for the following combinations: NDF × NDM (0.60), NDF × HIP (0.57), NDM × HIP (0.63), NDM × NNM (0, 50). The results are different from those obtained for the phenotypic correlation of NDF and NDM with the other characters of 22 $F_{2:3}$ progenies (Silva et al., 2021). The other main phenotypic correlations were PHF × PHM (0.72), PHF × NNF (0.56), HIP × PHM (0.62), HIP × NNM (0.59), PHM × NNF (0.64), PHM × NNM (0.78), NNF × NNM (0.62).

The character of PROD, for being of a quantitative nature, that is, governed by several genes, makes the selection difficult, being essential the studies of correlations in this character. These are the medium and high-magnitude characters considered in the selection (Vale et al., 2014).

In breeding programs, the identification and selection of superior genotypes are one of the biggest challenges for breeders, especially since breeding targets are predominantly quantitative in nature (Xiong et al., 2018). In this context, using information from correlations and phenotypic means allows the analysis of selection strategies aiming at greater gains in the selection process. When practicing direct selection, high gains are achieved for the target character (Table 4).

It was verified that the direct selection gain (SG) ranged between -7.83 and 22.84 for NDM and HIP, respectively. For the characters NDF and NDM, it was verified that the direct selection provided the reduction of the cycle of the $RCF_{3:4}$ progenies. Direct selection obtained the best SG for all evaluated characters, and SG greater than 10% were obtained for HIP, PHM, NNM and PROD characters, that is, direct selection provides increases in the studied characteristics (Table 4).

When directly selecting the character NDF and NDM, there was a reduction of SG by the indirect selection for all study characters, except for PROD, which had a gain of 3.61% when selecting directly for NDM, which indicates that the selection of early genotypes may result in more productive genotypes. Almeida, Peluzio and Afferri (2010) stated that the selection of genotypes with early flowering results in less productive plants, as the plants had lower height and number of nodes, which are essential for grain production. However, performing selection by the PHF character is what presented the best results for the indirect selection for the characters NSP and PROD (Table 4).

In addition to the NDM character, the indirect selection performed for the NSP, PHF, NNF, and HIP characters resulted in indirect SG for PROD of 7.48%, 5.33%, 2.68% and 0.62%, respectively. However, the direct selection for PROD provided the highest SG, not negatively affecting secondary characters, in some cases their gains were insignificant, tending to zero (NDF, NDM and NNM) (Table 4).

Table 4: Selection gain estimates obtained for the evaluated traits, by direct and indirect selection in $RCF_{3:4}$ progenies from 4 segregating soybean populations.

Character	Selection gain (%)								
	NDF	NDM	PHF	HIP	PHM	NNF	NNM	NSP	PROD
NDF	-6.26[1]	-4.58	-3.65	-7.95	-8.77	-1.62	-4.31	-0.83	-0.04
NDM	-3.10	-7.83	-2.40	-11.11	-8.79	-1.24	-7.67	-0.62	3.61
PHF	0.76	-0.34	6.96	5.10	9.43	3.46	2.79	0.52	5.33
HIP	4.37	6.62	3.18	22.84	9.67	1.09	4.98	-0.47	0.62
PHM	3.79	6.23	5.02	13.22	14.60	3.12	6.46	-0.62	-0.57
NNF	0.57	3.51	4.46	7.25	10.81	4.99	6.70	0.97	2.68
NNM	4.37	4.96	2.18	10.10	9.15	3.27	10.48	-0.25	-5.14
NSP	0.70	1.04	1.25	-2.60	-0.40	-0.59	-2.63	3.83	7.48
PROD	-0.33	-0.73	3.17	2.60	4.16	1.09	1.00	1.70	17.00

[1] Highlight corresponds to the character›s direct selection gain.

The application of direct selection in 145 $F_{2:3}$ progenies (UFUS 7415 × TMG 7161 RR) in Uberlândia-MG gave the lowest SG of NDF (-5.34) and NDM (-4.22%), while the highest SG were obtained for PROD (16.19%), PHF (12.21%) and PHM (16.45%), a result close to the present study (Silva et al., 2021). In 123 $F_{3:4}$ progenies of soybean (BRS 256 RR × TMG 1179 RR) direct SG of -2.32% for NDF, 7.22% for PHF, 12.93% for HIP, 18.06% for NNM were observed and 9.12% for PROD (Carneiro et al., 2021).

However, as there is a need to simultaneously select earlier and more productive progenies, direct and indirect selection may not result in expressive results, so the most viable alternative is to apply selection indices that effectively select by combining several characters (Rosado et al., 2012).

The selection gains obtained by the rank sum index of Mulamba and Mock (1978) and the genotype-ideotype distance index are shown in Table 5. 15 genotypes were selected for both indices. The rank sum index of Mulamba and Mock (1978) resulted in higher total gain value (36.51%) than in relation to the genotype-ideotype distance index. The latter provided an increase of 2.34% for the PROD character and 63.09% more for NSP than the one given by the sum of ranks index by Mulamba and Mock (1978). However, the latter gave SG of 1.07%, 42.37%, 6.28% and 2.03% more than the genotype-ideotype distance index for the characters PHF, HIP, PHM and NNF, respectively (Table 5).

The indices of genotype-ideotype distance and sum of ranks by Mulamba and Mock (1978) have been the most recommended as a selection strategy in soybean, providing more favorable results for selection. The rank sum index by Mulamba and Mock (1978) has provided higher total SG and a balanced distribution of SG among the characters, while the genotype-ideotype distance index gives higher SG in some characters than the other indices used (Rosado et al., 2012; Bizari et al., 2017; Teixeira et al., 2017 Silva et al., 2021). These circumstances were observed in the present study (Table 5).

In 386 F_5 progenies from seven segregating populations sown in Jaboticabal-SP, a total of 36.04% SG was obtained for the sum of ranks index by Mulamba and Mock (1978) while for the genotype-ideotype distance index it was obtained 29.85% of total SG (Bizari et al., 2017). In turn, similar total SG were obtained for 123 $F_{3:4}$ soybean progenies (BRS 256 RR × TMG 1179 RR), in which total SG of 37.11% was obtained for the sum index of "ranks" of Mulamba and Mock (1978), while for the genotype-ideotype distance index a total of 36.95% SG was obtained, with the PROD in the latter being 4.42% and for the sum of "ranks" 3.55% (Carneiro et al., 2021). Fifteen superior $RCF_{3:4}$ progenies were selected from 4 segregating soybean populations that showed greater selection gains through the applied selection indices. These genotypes are candidates for generation advancement because they are superior in the analyzed characters: G2, G6, G13, G15, G20, G21, G29, G33, G36, G38, G39, G42, G48, G51 and G52. The characters for these genotypes ranged from 33.0 to 39.0 days for NDF, 79.0 to 105.0 days for NDM, 52.3 to 66.2 cm $plant^{-1}$ for PHF, 10.0 to 17, 8 cm $plant^{-1}$ for HIP, 54.2 to 70.9 cm $plant^{-1}$ for PHM, 9.1 to 11.0 nodes $plant^{-1}$ for NNF, 13.3 to 16.9 nodes $plant^{-1}$ for NNM, 2.2 to 2.4 seeds pod^{-1} for NSP and 302.5 to 463.0 g $plot^{-1}$ for PROD.

Table 5: Estimates of selection gains (SG%) for characters by selection by the Genotype-Ideotype distance index and rank sum index by Mulamba and Mock (1978) for $RCF_{3:4}$ progenies from 4 segregating populations $RCF_{3:4}$ of Soy.

Characters	Selection gain (%)	
	Mulamba and Mock (1978)	Genotype-Ideotype Distance
NDF	-2.12	-2.12
NDM	-1.38	-1.38
PHF	5.64	5.58
HIP	6.35	4.46
PHM	10.14	9.54
NNF	3.10	3.03
NNM	4.97	4.97
NSP	0.84	1.37
PROD	8.97	9.18
Total Gain	36.51	34.63

CONCLUSIONS

Heritability was high and the CVg/CVe ratio was favorable for selection for NDF, NDM, PHM and NNM characters in 52 soybean progenies. The direct selection for NDM provided genetic gains for the PROD character, however, the direct selection for the PROD character provided better SG for the secondary characters, such as those related to precocity. The selection indices provided the greatest genetic gains for early cycle and grain yield when compared to the direct selection, in addition, they were more efficient, since they allow the simultaneous selection of different agronomic characters.

AUTHOR CONTRIBUTION

Conceptual Idea: Hamawaki, O. T.; Nogueira, A. P. O.; Gastl Filho, J. Methodology design: Gastl Filho, J.; Nogueira , A. P. O.; Silva, C. O. Data collection: Gastl Filho, J.; Silva, C. O.; Hamawaki, C. D. L. Data analysis and interpretation: Gastl Filho, J.; Nogueira, A. P. O.; Hamawaki, R. L. Writing and editing: Gastl Filho, J.; Nogueira , A. P. O.; Hamawaki, O. T.

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