

Comparison of non-parametric indexes to select soybean genotypes obtained by recurrent selection

Comparação de índices não paramétricos na seleção de genótipos de soja obtidos por seleção recorrente

Gustavo Henrique Freiria^{1*}; Luiz Júnior Perini¹; Douglas Mariani Zeffa²; Paulo Sérgio Novais³; Wilmar Ferreira Lima⁴; Leandro Simões Azeredo Gonçalves⁵; Cássio Egídio Cavenaghi Prete⁵

Abstract

In the final steps of a breeding program, it is necessary to evaluate several traits, which makes it difficult to select the superior genotypes. This study aimed to compare nonlinear indexes in the selection of superior soybean inbred lines obtained by recurrent selection. The experiment was carried out in Londrina, Paraná State, Brazil. During the 2010/11 and 2011/12 seasons, 67 soybean inbred lines and two commercial controls (BMX Potência RR and NK 7059 RR) were evaluated. The experimental design was a randomized complete block with three replicates. The evaluated traits were: days to maturity, agronomic value, lodging, first pod insertion height, and grain yield. A combined analysis of variance for seasons was performed and the sum of ranks index, ideotype distance index, and cultivars selection index were applied. All traits were significant for the genotypic source of variation and showed complex genotype \times environment interactions. The selection indexes were consistent with each other. The ideotype and cultivar selection index showed higher concordance on indication of 15 superior inbred lines with a coefficient of coincidence of 80%. The inbred lines SR-03, SR-12, SR-22, SR-41, SR-49, SR-55, SR-61, and SR-62 were indicated for all indexes and are therefore considered superior to other inbred lines.

Key words: *Glycine max*. Agronomic traits. Cultivar selection. Grain yield. Non-linear indexes.

Resumo

Nas etapas finais de um programa de melhoramento é necessário a avaliação de diversos caracteres, o que gera dificuldade na escolha dos melhores genótipos. O presente trabalho teve como objetivo comparar índices não lineares na seleção de linhagens superiores de soja, obtidas por seleção recorrente. Os experimentos foram conduzidos em Londrina, Paraná, Brasil. Durante as safras 2010/11 e 2011/12 foram avaliados sessenta e sete linhagens de soja e duas testemunhas comerciais ((BMX Potência RR e NK 7059 RR). O delineamento experimental adotado foi em blocos completos ao acaso, com três

¹ Discentes, Pós-Graduação em Agronomia, Universidade Estadual de Londrina, UEL, Londrina, PR, Brasil. E-mail: gustavo-freiria@hotmail.com; luizperini50@hotmail.com

² Discente, Pós-Graduação em Genética e Melhoramento, Universidade Estadual de Maringá, UEM, Maringá, PR, Brasil. E-mail: douglas.mz@hotmail.com

³ Eng^o Agr^o, GDM Genética do Brasil LTDA, GDM, Cambé, PR, Brasil. E-mail: pnovais@gdmseeds.com

⁴ Pesquisador, Instituto Agronômico do Paraná, IAPAR, Londrina, PR, Brasil. E-mail: wilmar@iapar.br

⁵ Profs. Drs., Departamento de Agronomia, Centro de Ciências Agrárias, UEL, Londrina, PR, Brasil. E-mail: leandrosag@uel.br; cassio@uel.br

* Autor for correspondence

repetições. As características avaliadas foram: dias para maturação, valor agrônomico, acamamento, inserção da primeira vagem e produtividade de grãos. Realizou-se a análise de variância conjunta para anos agrícolas e empregaram-se os índices de soma de ranks, de distância ao ideótipo e de seleção de cultivares. Todas características para a fonte de variação genótipo foram significativas e apresentaram predomínio da interação complexa na interação genótipo x ambiente. Os índices de seleção se mostraram concordantes entre si. O índice de distância ao ideótipo e o índice de seleção de cultivar apresentaram maior concordância na indicação das 15 melhores linhagens com coeficiente de coincidência de 80%. As linhagens SR-03, SR-12, SR-22, SR-41, SR-49, SR-55, SR-61 e SR-62 foram indicadas em todos os índices e, portanto, consideradas superiores às demais.

Palavras-chave: *Glycine max*. Características agrônomicas. Seleção de cultivares. Produtividade de grãos. Índices não lineares.

Introduction

Among plant breeding methods, recurrent selection is a technique that aims to gradually increase the frequency of favorable alleles for quantitative traits through repeated cycles of selection and recombination without any reduction in the variability of the genetic population (BORÉM et al., 2017). Information about this method has largely been obtained in studies on allogamous species, particularly in corn crop. However, this method has also been applied to autogamous species, such as rice (GRENIER et al., 2015; MORAIS JÚNIOR et al., 2015), oats (HOLLAND et al., 2002), wheat (RAMYA et al., 2016), common bean (PIRES et al., 2014), and soybean (POSADAS et al., 2014).

After recombination cycles, promising families can be selected and self-fertilized to participate in new trials that evaluate inbred lines to launch new cultivars. In recurrent selection, and in the final steps of genetic breeding programs, it is necessary to evaluate several agronomic traits, which make it difficult to select the best genotypes. Therefore, an alternative method combining information on several traits in a single value would be the utilization of selection indexes, which would facilitate the comparison and rating of individuals based on traits set of interest (CRUZ et al., 2014).

Selection indexes can be classified as linear and non-linear. Linear indexes, which are obtained by the linear function of genotype values, aim to improve population means, and genotypes with traits below acceptable commercial levels

can be selected whereas concentrate reasonable number of alleles to other traits. In this way, these indexes are indicated just for situation that after the selection cycle the recombination step is done. Conversely, the non-linear indexes, also known as non-parametric indexes, do not require estimates of genetics parameters, which allows the simple rating of genotypes and the use of indexes in the selection of inbred lines during the final steps of a breeding program (GARCIA; SOUZA JÚNIOR, 1999).

There are several notable non-parametric indexes: the multiplicative index proposed by Elston (1963), the use of distance to classify genotypes in the function of an ideal genotype (ideotype), described by Schwarzbach (1972) and cited by Wricke and Weber (1986), and the sum of ranks index described by Mulamba and Mock (1978). These indexes have been applied to the selection of superior inbred lines of cowpea (BERTINI et al., 2010), snap bean (MARINHO et al., 2014), common bean (MAZIERO et al., 2015), popcorn (VITTORAZZI et al., 2013), and soybean (BÁRBARO et al., 2007).

A possible limitation to the use of these methods is that it is not possible to apply acceptable minimum values to each trait, or use means tests to give higher statistical precision to the results (MARINHO et al., 2014). Such parameters are applied to the cultivar selection index method proposed by Garcia (1998), where the main steps are average grouping (each genotype is represented by the average of its group), definition of minimum acceptable levels for each trait, definition of ideotype and Euclidean distance

means, and the ranking and selection of superior genotypes.

Therefore, this study aimed to compare non-parametric indexes (sum of ranks, ideotype distance, and cultivar selection), with the aim of selecting superior soybean inbred lines obtained by recurrent selection.

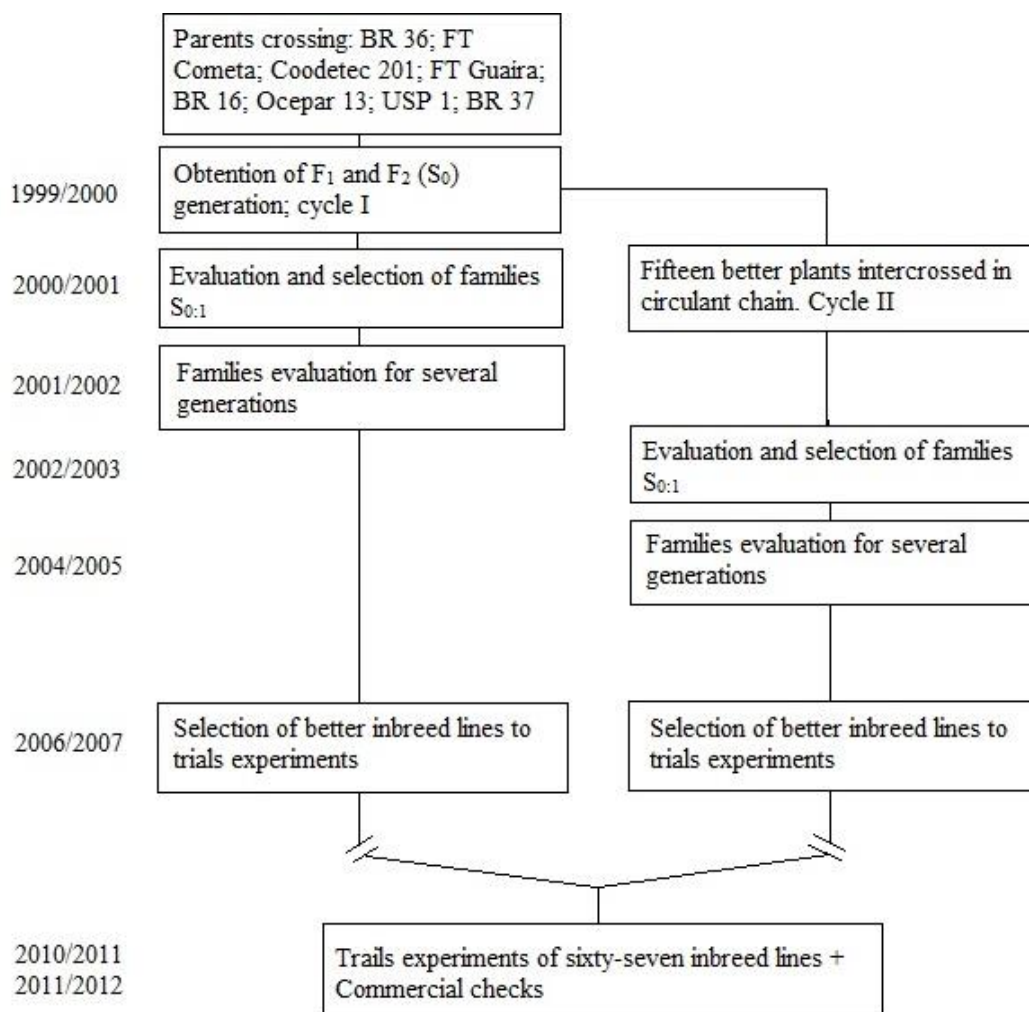
Material and Methods

The experiments were performed during the 2010/2011 and 2011/2012 seasons in Londrina city, Paraná, Brazil (latitude: 23° 20' 23.45" S, longitude: 51° 12' 32.38" W and altitude: 532 m). The climate

of this region is classified as Cfa, described as wet subtropical with hot summer according to the Köppen classification.

Sixty-seven inbred lines were evaluated in advanced self-fertilized generations obtained through recurrent selection and two commercial controls (BMX Potência RR and NK 7059 RR) (Figure 1). Sowing was performed in 10/20/2010 and 10/07/2011 in a random blocks experimental design with three replicates. The plots were composed of two rows, each 4 m long with row spacings of 0.45 and 12 plants/meter. Measurements of 0.5 m were discarded from both extremities.

Figure 1. Scheme of procedure adopted in the application of recurrent selection on soybean breeding to grain yield improvement. Londrina, Paraná State, Brazil, 2012.



At sowing, seeds were inoculated with *Bradyrhizobium japonicum* strains SEMIA 5079 and 5080 at a concentration of 5.0×10^9 colony-forming units per milliliter of the commercial product at a dose of 100 mL for 50 kg of seeds.

The measured traits were: days to maturity (DTM), assessed as the number of days from sowing to physiological maturation; agronomic value (AV), which was a visual rating from 1 to 5, with 1 corresponding to no agronomic value and 5 corresponding to high agronomic value (high number of pods and no lodging, no green stem, no threshing, and no diseases) (LOPES et al., 2002); lodging (LOD), ranging from 1 to 5, where 1 is low and susceptible to lodging and 5 is complete lodging; first pod insertion height (PIH), measured as the distance in centimeters from the soil surface to the first pod measured in six plants from the useful area in the plots and; grain yield (GY), obtained by trashing the plants from the useful plot area and adjusting the humidity to 13%, expressed in kg ha⁻¹. AV, LOD, and PIH were measured at physiology maturation of the grain.

Individual analysis of variance was performed for all traits in each season, and after variance homogeneity was confirmed through the Hartley test, a grouped analysis was performed for seasons. Participation of the complex genotype \times season interaction was evaluated using the methods described by Robertson (1959) and Cruz and Castoldi (1991). Additionally, the Pearson correlation was estimated among evaluated traits.

The genotypes were classified by the following indexes:

Sum of ranks index

The sum of ranks index (MULAMBA; MOCK, 1978) classifies genotypes in relation to each favorable trait in a breeding program. Thus, it sums the sequence of each genotype resulting in a selection index as follows: $I = r_1 + r_2 + \dots + r_n$, where,

I is the index value to some individual or family; r_j is the classification (or “rank”) of one genotype in relation to the j -th trait; and n is the number of traits considered by index.

This strategy allows different weights to be specified in the ranking of traits. Thus, it has: $I = p_1r_1 + p_2r_2 + \dots + p_nr_n$ being p_j = economic weight assigned by the researcher to the j -th trait. In the present study, the grain yield trait was considered the primary trait and received an economic weight value of 2. Other traits were considered as secondary and received a value of 1.

Ideotype distance index

The ideotype distance index (SCHWARZBACH, 1972 *apud* WRICKE; WEBER, 1986) allows an optimum to be adopted for each trait. For this, the distance of each individual to an ideal genotype defined for the traits DTM, AV, LOD, PIH, and GY is calculated from the phenotypic means. The ideotype is defined as the genotype with high values for the AV and GY traits, low values for the DTM and LOD, and 15 cm to the PIH.

Next, the phenotype means were standardized and the Euclidean distances for each genotype were calculated in relation to the proposed ideotype through the following formula:

$d_{jI} = \sqrt{\sum_{i=1}^n (x_{ij} - x_{Ii})^2}$, where, d_{jI} = Euclidean distance between genotype j and ideotype I ($j = 1, \dots, 69$); x_{ij} = measure of trait i in genotype j ($i = 1, \dots, 5$); x_{Ii} = value defined to the ideotype I , referring to trait i . The genotypes were ranked based on the distance of, with lower distances considered better.

Cultivar selection index

The cultivar selection index (GARCIA, 1998) requires parameter estimates and prioritizes fixing the discarded values and applying a means test, attending cultivar selection. The steps to obtain this index are as following:

1) Means grouping (Scott–Knott test) and obtaining reciprocals, lower values are the target of the selection;

2) Definition of minimum and maximum levels, depending of the pattern acceptable for each trait. In this study, the minimum acceptable levels were the statistical values inferior to the mean DTM and LOD, statistical superior to means of AV and GY, and statistical superior to 10 cm for PIH;

3) Data transformation by the equation:

$$y_{tij}^m = \frac{y_{ij}^m - y_{ij}^{Nm}}{S_m}$$
 where, y_{tij}^m is the transformed means of trait m; y_{ij}^m is the trait m means after grouping; y_{ij}^{Nm} is the minimum or maximum level acceptable to the means of trait m; and S_m is the standard deviation of trait m;

4) Ideotype definition (fixed as ideotype with low values for DTM and LOD, high values for AV and GY, and a 15 cm PIH);

5) Calculation of Euclidean distance in relation to the ideotype (according to the equation presented for the previous index, ideotype distance index); and

6) Superior genotype classification, whereby genotypes of lower distance to the ideotype were considered best.

The selection indexes were compared based on the coefficient of coincidence in the classification of 15 better inbred lines. Statistical analyses were performed using Genes program (CRUZ, 2016) and Microsoft Excel®.

Results and Discussion

Through grouped analysis of variance (Table 1), sources of variation in genotype (G) and genotype × environment (GE) were significant for all evaluated traits, indicating that genotypes showed genetic variability and different performance due to environmental variation. Several authors have verified a significant interaction of GE in phytometric traits and in yield compounds in soybean, which is explained by environmental conditions such as temperature and precipitation (BARBOSA et al.; 2013, FREIRIA et al., 2016; FREIRIA et al., 2018).

The presence of a GE interaction may be a complicating factor in breeding programs, when there is a lack of correlation among genotypes in distinct environments; this is classified as a complex interaction. Thus, when this changes the genotypes ranking, it makes it difficult to select and recommend the best genotypes (ROBERTSON, 1959).

Table 1. Means square values to traits of days to maturity (DTM), agronomic value (AV), lodging (LOD), first pod insertion height (PIH) and grain yield (GY) of 67 soybean inbred lines obtained by recurrent selection and two commercial checks (BMX Potência RR and NK 7059 RR). Londrina, Paraná State, Brazil, 2012.

Sources of Variation	Means Square					
	F.D.	DTM	AV	LOD	PIH _(cm)	GY _(kg ha⁻¹)
Block (Environment)	4	5.63	0.11	0.06	9.15	983172.95
Genotypes (G)	68	185.39**	0.69**	0.97**	36.41**	796897.33**
Environment (E)	1	22440.35**	86.83**	41.93**	3484.82**	2521210.19
G x E	68	91.89**	0.34**	0.55**	25.52**	785315.54**
Error	272	3.21	0.06	0.13	8.593	325858.93
Means		127.62	3.35	1.61	10.93	2785.58
C.V. (%)		4.33	7.11	22.46	26.82	17.74
%PCGA ¹		99.36	92.45	97.67	99.19	90.19
%PCGA ²		80.80	73.86	82.80	90.74	88.25

** Significant at the $p < 0.01$ and * Significant at the $p < 0.05$ by test F.

¹ e ² %PCGA: Complex interaction participation, on genotype x environment interaction according to methods proposed by Robertson (1959) and Cruz and Castoldi (1991), respectively.

Regarding the interaction, a predominance of complex interactions for all traits was found, with percentages ranging from 92.45 (AV) to 99.36% (DTM) with the Robertson (1959) method, and 73.86 (AV) to 90.74% (PIH) with the Cruz and Castoldi (1991) method (Table 1). According to Silva et al. (2013) and Elias et al. (2016), high percentage for the complex interaction makes it necessary to reduce the effects of this interaction, through measurements obtained during local, season, and seeding season. Therefore, to apply selection indexes, the means of genotypes for each season were used instead of considering only the means of genotypes from two seasons.

Pearson linear correlation analysis of the five traits evaluated (Table 2) revealed a negative correlation between LOD \times AV and DTM \times AV, and a positive correlation between GY \times AV. These results corroborate the capacity of the agronomic value to indicate genotypes with desirable agronomic traits, as reported by Lopes et al. (2002). A positive correlation was observed for days to maturity \times lodging trait; however, this was of lower magnitude. According to Perini et al. (2012) and Maziero et al. (2015), when there is no correlation or a weak correlation among traits of interest, it is possible to select genotypes that combine all favorable traits, since those of interest participate in selecting the best genotypes.

Table 2. Pearson correlation among traits days to maturity (DTM), agronomic value (AV), lodging (LOD), first pod insertion height (PIH) and grain yield (GY) of sixty-seven soybean inbred lines obtained by recurrent selection and two commercial checks (BMX Potência RR and NK 7059 RR). Londrina, Paraná State, Brazil, 2012.

Traits	AV	LOD	PIH	GY
DTM	- 0.42**	0.29*	- 0.24	- 0.11
AV		- 0.45**	0.17	0.50**
LOD			- 0.4	- 0.08
PIH				- 0.01

*, **: Significant at the 5 and 1 % probability level by test t, respectively.

The 15 inbred lines with the best ranking were those with a low sum of ranks index (I): RS-03, RS-62, RS-41, RS-05, RS-56, RS-55, RS-61, RS-53, RS-63, RS-49, RS-22, RS-12, RS-04, RS-17, and RS-67 (Table 3). This group obtained means of 126.72 days, 3.67, 1.38, 11.99 cm, and 3100.85 kg ha⁻¹, respectively, for DTM, AV, LOD, PIH, and GY, with values ranging from 207 to 301. Selection of these individuals would represent a yield gain of 315.27 kg ha⁻¹ in relation to the general mean.

Garcia and Souza Júnior (1999) classified this index as easy to apply, because it does not use the phenotypic values obtained but the ranking number attributed to it, which generates the same variance for all traits, avoiding data transformation.

According to Bárbaro et al. (2007), the sum of ranks index enabled the larger yield gains of soybean in an F₅ population selection without impacting the phytometric traits. However, in the final steps of breeding, in which no recombination cycle will occur, the selection must not aim for populational genetic gain but for individual selection of genotypes that combine required traits to obtain a new cultivar, without any restrictive trait to its launch (CRUZ et al., 2014).

From the evaluated inbred lines, only RS-03 (I = 207), RS-62 (I = 213), and RS-41 (I = 216) presented values of I lower than the commercial controls NK 7059 RR (I = 223) and BMX Potência RR (I = 235). According to Bertini et al. (2010), a lower value of

I indicates the most favorable combinations among all traits in the study; conversely, a higher value indicates an unfavorable combination of traits with values below those required by breeding.

High LOD values and low PIH values (in general less than 10 cm) would result in losses by mechanical harvesting (CHIODEROLI et al., 2012). Therefore, the three inbred lines with a lower sum of I obtained satisfactory results for the LOD and PIH traits, except for the inbred line RS-62, which obtained a PIH value of 7.67 cm in the 2010/11 season (Table 3).

The ideotype distance index (d_{ji}) showed a coincidence coefficient of 80% in relation to the values of I upon ranking the 15 inbred lines of lower value d_{ji} , which presented a lower Euclidean distance regarding the established ideotype. A strong relationship between these two indexes was reported by Marinho et al. (2014) and Buzzello et al. (2015).

The inbred lines RS-53, RS-17 and RS-67 it was classified among the 15 better by values of I were

replaced to RS-59, RS-21 and RS-15 that summed to RS-62, RS-03, RS-41, RS-55, RS-56, RS-63, RS-22, RS-49, RS-05, RS-12, RS-61 and RS-04 make up the group of lower values of d_{ji} , ranging from 4.03 to 5.81 (Table 3). Therefore, the inbred lines RS-62 ($d_{ji} = 4.03$) and RS-03 ($d_{ji} = 4.18$) presented a lower ideotype distance than the commercial controls (NK 7059 RR = 4.67 and BMX Potência RR = 4.83).

The main criticism of the sum of ranks and the ideotype distance indexes is the difference among the means of each trait, since these indexes doesn't expect to perform multiple comparison test. Consequently, differences among the phenotypic means of each trait may not be statistically significant, which would result in errors (GARCIA; SOUZA JÚNIOR, 1999; MARINHO et al., 2014). This would not be a problem for the cultivar selection index, as described by Garcia (1998), which requires the application of a means grouping test and the replacement of observed phenotypic means with the means of the group in which the genotype was inserted by a statistical test.

Table 3. Sum of ranks index (I), ideotype distance index (d_{ij}) and cultivars selection index (Isc) applied to traits of days to maturity (DTM), agronomic value (AV), lodging (LOD), first pod insertion height (PIH) and grain yield (GY) of 67 soybean inbred lines obtained by recurrent selection and two commercial checks (BMX Potência RR and NK 7059 RR). Londrina, Paraná State, Brazil, 2012.

Genotypes	Season 10/11					Season 11/12					I	d_{ij}	Isc
	DTM	AV	LOD	PIH (cm)	GY (kg ha ⁻¹)	DTM	AV	LOD	PIH (cm)	GY (kg ha ⁻¹)			
RS-01	131.0 c	3.7 d	1.6 c	12.8 a	2776 b	131.0 c	2.5 c	2.2 b	18.6 a	2185 b	486 (50)	7.63 (46)	6.37 (52)
RS-02	120.0 f	3.7 d	1.1 c	7.0 b	2706 b	120.0 g	2.9 c	2.7 a	13.0 b	2519 b	427 (41)	7.12 (37)	5.88 (37)
RS-03	123.3 e	4.3 b	1.4 c	10.1 a	3079 a	129.0 d	3.4 a	1.6 c	17.7 a	3785 a	207 (1)	4.18 (2)	3.74 (6)
RS-04	125.0 e	4.3 b	1.0 c	8.3 b	2878 b	133.0 c	3.0 b	1.6 c	15.2 b	2819 b	292 (15)	5.70 (14)	4.95 (18)
RS-05	123.3 e	4.0 c	1.0 c	4.8 b	3970 a	131.7 c	3.2 b	1.7 c	18.9 a	3104 a	226 (5)	5.39 (11)	5.28 (26)
RS-06	120.0 f	3.8 d	1.0 c	12.9 a	2789 b	133.7 b	2.8 c	2.3 b	13.3 b	3548 a	318 (20)	6.06 (20)	5.34 (28)
RS-07	120.0 f	3.7 d	1.0 c	5.3 b	2444 b	122.0 f	2.7 c	1.7 c	17.0 a	2252 b	419 (38)	7.38 (38)	5.99 (39)
RS-08	123.3 e	3.7 d	1.4 c	11.8 a	3069 a	136.0 a	2.5 c	2.3 b	14.6 b	1815 c	482 (48)	7.66 (47)	5.99 (39)
RS-09	123.3 e	2.8 e	1.0 c	8.1 b	1862 b	122.0 f	2.4 c	2.1 b	11.4 c	2507 b	524 (60)	9.19 (65)	6.32 (50)
RS-10	123.3 e	3.7 d	1.4 c	10.3 a	2661 b	131.3 c	2.6 c	2.0 c	15.0 b	1811 c	503 (55)	7.54 (42)	5.74 (36)
RS-11	123.3 e	3.3 e	2.1 b	11.9 a	2469 b	132.3 c	2.7 c	2.0 c	14.9 b	2400 b	512 (56)	7.75 (50)	6.31 (49)
RS-12	126.7 d	4.2 c	1.3 c	13.7 a	3138 a	131.0 c	3.0 b	1.8 c	20.4 a	2726 b	284 (14)	5.55 (12)	4.86 (17)
RS-13	131.3 c	3.2 e	2.4 b	5.5 b	2757 b	129.0 d	2.5 c	2.8 a	11.1 c	1974 c	645 (68)	9.46 (68)	7.66 (67)
RS-14	131.7 c	4.2 c	1.0 c	5.0 b	3359 a	122.0 f	3.0 b	1.7 c	12.0 b	2444 b	327 (23)	5.98 (18)	5.02 (19)
RS-15	125.0 e	4.5 b	1.0 c	8.6 b	3493 a	134.7 b	2.8 c	1.6 c	14.4 b	2281 b	304 (18)	5.81 (17)	5.28 (26)
RS-16	125.0 e	4.5 b	1.0 c	9.4 a	2846 b	133.7 b	2.4 c	1.3 c	6.3 c	2056 c	440 (44)	7.56 (44)	5.15 (23)
RS-17	138.0 b	4.0 c	1.0 c	5.3 b	3152 a	132.3 c	3.1 b	1.6 c	15.2 b	3148 a	294 (16)	6.43 (25)	5.55 (33)
RS-18	138.0 b	4.0 c	1.7 c	8.1 b	3386 a	131.0 c	2.7 c	2.4 b	18.1 a	2248 b	443 (46)	7.49 (40)	6.69 (58)
RS-19	129.7 c	3.3 e	1.4 c	2.4 b	2680 b	132.0 c	2.8 c	2.5 b	12.0 b	3085 a	544 (63)	8.26 (58)	6.86 (58)
RS-20	134.0 c	3.5 d	1.5 c	4.3 b	2820 b	131.0 c	2.7 c	2.4 b	13.3 b	3370 a	487 (51)	7.78 (51)	6.39 (53)
RS-21	120.0 f	3.7 d	1.1 c	5.6 b	2537 b	117.7 g	3.7 a	1.9 c	12.2 b	4181 a	326 (22)	5.80 (16)	4.72 (15)
RS-22	120.0 f	4.5 b	1.0 c	6.3 b	3108 a	122.0 f	3.2 b	1.8 c	12.6 b	2644 b	268 (13)	5.07 (9)	4.01 (8)
RS-23	125.0 e	3.0 e	2.5 b	13.6 a	3112 a	122.0 f	2.5 c	3.1 a	23.1 a	2822 b	402 (34)	8.72 (63)	6.54 (55)
RS-24	133.0 c	3.0 e	1.1 c	6.3 b	2527 b	127.0 d	2.9 c	2.0 c	14.8 b	1996 c	548 (64)	8.32 (60)	7.05 (64)

continue

continuation

RS - 25	133.0 c	3.7 d	1.0 c	3.3 b	2584 b	129.0 d	2.6 c	2.4 b	13.7 b	2363 b	530 (62)	8.39 (61)	6.42 (54)
RS - 26	133.0 c	3.5 d	1.1 c	8.6 b	2961 a	132.3 c	2.9 c	2.1 b	14.0 b	1719 c	501 (54)	7.69 (48)	6.69 (57)
RS - 27	138.7 b	3.5 d	1.0 c	8.1 b	3507 a	133.3 b	2.7 c	2.0 c	19.9 a	2189 b	407 (35)	7.70 (49)	7.00 (63)
RS - 28	136.3 b	3.3 e	1.1 c	3.6 b	2425 b	131.0 c	3.5 a	1.4 c	16.6 a	3463 a	422 (39)	7.54 (42)	6.95 (61)
RS - 29	139.7 a	3.5 d	2.0 b	6.9 b	3347 a	136.0 a	2.3 c	2.2 b	11.1 c	1741 c	607 (66)	9.11 (64)	7.70 (68)
RS - 30	120.0 f	4.0 c	1.0 c	12.2 a	2831 b	138.0 a	2.5 c	1.4 c	9.6 c	1752 c	430 (43)	7.52 (41)	5.45 (31)
RS - 31	120.0 f	4.0 c	1.0 c	14.7 a	2408 b	131.0 c	2.5 c	2.0 c	13.0 b	2400 b	418 (36)	7.11 (36)	4.73 (16)
RS - 32	125.0 e	3.5 d	1.0 c	11.0 a	2692 b	132.0 c	3.0 b	1.7 c	13.6 b	2989 a	354 (26)	6.31 (24)	4.69 (14)
RS - 33	125.0 e	3.5 d	1.0 c	8.7 b	2966 a	136.3 a	2.8 c	1.3 c	9.0 c	2741 b	378 (32)	6.99 (34)	6.06 (43)
RS - 34	125.0 e	3.5 d	1.0 c	8.3 b	2204 b	133.0 c	2.7 c	1.4 c	12.1 b	2567 b	465 (47)	7.82 (52)	6.03 (41)
RS - 35	133.0 c	3.5 d	1.1 c	4.1 b	2997 a	133.3 b	3.0 b	1.3 c	17.9 a	2967 a	379 (33)	7.05 (35)	6.22 (46)
RS - 36	133.0 c	4.0 c	1.0 c	5.4 b	2691 b	125.0 e	3.2 b	1.6 c	8.2 c	3509 a	359 (28)	6.44 (26)	5.12 (22)
RS - 37	132.3 c	3.7 d	1.7 c	7.4 b	2428 b	130.7 c	3.1 b	1.6 c	12.0 b	2393 b	516 (58)	7.43 (39)	6.05 (42)
RS - 38	133.0 c	3.8 d	1.0 c	7.0 b	2778 b	131.7 c	3.5 a	1.6 c	13.9 b	2619 b	363 (29)	6.44 (26)	5.94 (38)
RS - 39	140.0 a	3.5 d	1.0 c	4.9 b	3081 a	131.0 c	2.6 c	2.6 a	20.1 a	2663 b	428 (42)	8.49 (62)	7.38 (66)
RS - 40	136.3 b	3.5 d	2.0 b	5.9 b	2610 b	134.3 b	2.7 c	2.6 a	15.3 b	1733 c	633 (67)	9.26 (67)	7.76 (69)
RS - 41	132.7 c	4.2 c	1.0 c	9.4 a	3499 a	123.0 f	2.9 c	1.5 c	13.2 b	3574 a	216 (3)	4.74 (4)	4.42 (11)
RS - 42	137.3 b	3.2 e	1.4 c	4.4 b	3040 a	126.3 e	2.7 c	2.4 b	14.0 b	2522 b	518 (59)	8.27 (59)	6.87 (60)
RS - 43	132.0 c	4.0 c	1.0 c	3.6 b	3248 a	133.0 c	2.5 c	2.4 b	9.9 c	2056 c	496 (53)	8.13 (56)	6.29 (47)
RS - 44	127.3 d	3.7 d	1.2 c	5.4 b	2553 b	120.0 g	2.6 c	2.8 a	13.6 b	2493 b	525 (61)	8.06 (54)	6.13 (45)
RS - 45	120.0 f	3.5 d	1.0 c	5.4 b	2873 b	118.0 g	3.0 b	1.5 c	11.4 c	2733 b	324 (21)	6.29 (23)	5.02 (19)
RS - 46	125.0 e	4.0 c	1.0 c	11.3 a	2873 b	134.7 b	2.7 c	1.6 c	13.4 b	2393 b	376 (31)	6.49 (29)	5.06 (21)
RS - 47	120.0 f	4.0 c	1.0 c	12.3 a	3230 a	135.0 b	2.5 c	1.7 c	12.2 b	2259 b	357 (27)	6.44 (26)	4.62 (13)
RS - 48	132.0 c	3.3 e	4.5 a	1.8 b	3594 a	131.7 c	3.3 a	1.5 c	14.1 b	3656 a	344 (24)	9.20 (66)	6.97 (62)
RS - 49	120.0 f	4.0 c	2.0 b	4.7 b	2936 a	122.0 f	3.7 a	1.4 c	13.4 b	4248 a	263 (12)	5.15 (10)	4.53 (12)
RS - 50	132.0 c	3.5 d	2.4 b	6.8 b	2397 b	137.0 a	2.4 c	3.1 a	11.9 b	2270 b	689 (69)	9.88 (69)	7.35 (65)
RS - 51	134.3 c	3.5 d	1.5 c	4.6 b	2748 b	131.0 c	2.7 c	1.7 c	8.3 c	2415 b	558 (65)	8.17 (57)	6.36 (51)
RS - 52	133.0 c	3.0 e	1.6 c	5.0 b	2877 b	131.0 c	2.7 c	1.9 c	9.6 c	3367 a	493 (52)	7.96 (53)	6.67 (56)
RS - 53	115.0 g	3.7 d	1.0 c	11.1 a	2883 b	118.0 g	2.7 c	1.2 c	18.7 a	2489 b	257 (10)	6.03 (19)	5.19 (25)

continue

continuation

RS - 54	120.0 f	3.3 e	1.1 c	8.7 b	2402 b	122.0 f	3.0 b	2.1 b	11.6 c	2970 a	440 (44)	6.89 (32)	5.64 (34)
RS - 55	120.0 f	4.2 c	1.0 c	11.2 a	2711 b	122.0 f	3.0 b	1.5 c	12.7 b	3400 a	236 (8)	4.85 (6)	3.41 (4)
RS - 56	120.0 f	4.5 b	1.0 c	7.7 b	2667 b	117.0 g	3.4 a	1.4 c	14.2 b	2833 b	234 (6)	4.96 (7)	4.11 (9)
RS - 57	125.0 e	3.2 e	1.2 c	11.2 a	2536 b	121.7 f	2.5 c	1.7 c	10.0 c	2396 b	513 (57)	7.59 (45)	5.49 (32)
RS - 58	125.0 e	4.0 c	1.0 c	6.6 b	3113 a	137.0 a	2.8 c	1.6 c	12.9 b	2448 b	371 (30)	6.73 (31)	5.71 (35)
RS - 59	125.0 e	4.5 b	1.0 c	9.1 a	3100 a	133.0 c	2.9 c	2.1 b	9.0 c	3330 a	312 (19)	5.71 (15)	4.22 (10)
RS - 60	125.0 e	4.5 b	1.0 c	8.8 b	2506 b	131.0 c	2.8 c	1.8 c	11.8 b	2367 b	424 (40)	6.70 (30)	5.37 (29)
RS - 61	115.0 g	4.0 c	1.0 c	12.0 a	2122 b	117.0 g	3.6 a	1.6 c	15.4 b	3244 a	239 (9)	5.64 (13)	3.02 (2)
RS - 62	115.0 g	4.0 c	1.1 c	7.7 b	3328 a	118.3 g	3.5 a	1.8 c	12.7 b	3604 a	213 (2)	4.03 (1)	3.78 (7)
RS - 63	115.0 g	4.5 b	1.0 c	12.3 a	2673 b	117.0 g	3.2 b	1.9 c	13.7 b	2682 b	261 (11)	4.96 (7)	3.12 (3)
RS - 64	128.3 d	4.7 b	1.5 c	5.3 b	2902 b	135.0 b	2.8 c	2.5 b	17.2 a	3130 a	418 (36)	6.95 (33)	6.09 (44)
RS - 65	126.7 d	3.5 d	1.1 c	5.0 b	3369 a	122.3 f	2.7 c	2.8 a	14.1 b	1563 c	482 (48)	8.07 (55)	6.30 (48)
RS - 66	140.7 a	3.8 d	1.4 c	9.8 a	3064 a	117.0 g	3.3 a	2.0 c	14.1 b	2826 b	349 (25)	6.14 (21)	5.16 (24)
RS - 67	143.0 a	4.0 c	1.1 c	6.7 b	3417 a	118.3 g	3.0 b	1.9 c	14.4 b	3163 a	301 (17)	6.22 (22)	5.38 (30)
NK 7059	118.3 f	5.0 a	1.0 c	13.8 a	2453 b	117.0 g	3.4 a	2.0 c	14.0 b	3282 a	223 (4)	4.67 (3)	2.39 (1)
Potência	121.3 f	5.0 a	1.0 c	14.9 a	2345 b	119.0 g	3.3 b	1.7 c	17.8 a	3581 a	235 (7)	4.83 (5)	3.51 (5)

Average followed by the same words in the same column belongs to the same group by Scott-Knott test at the 5 % probability level. Means in bold represent transformed means below acceptable minimum level (N_m). Values among brackets represent the genotype classification arranged by favorable selection ranking.

The inbred lines with lower (I_{sc}) in the method described by Garcia (1998), which combined the more favorable traits were: RS-61, RS-63, RS-55, RS-03, RS-62, RS-22, RS-56, RS-59, RS-41, RS-49, RS-47, RS-32, RS-21, RS-31, and RS-12. These inbred lines had a coincidence coefficient of 66.67 and 80.00% with the sum of ranks indexes and ideotype distance an indication of the 15 best inbred lines, respectively (Table 3). The higher coincidence coefficient index observed between the cultivar selection index and the ideotype distance index can be attributed to the fact that both has on o the criteria to obtain its indexes to the Euclidean distance in relation to the ideotype determined by the breeder, which were equal for both indexes.

According to Garcia (1998), the genotypes to be selected would have a lower I_{sc} and would not present any trait below the minimum acceptable level (N_m) to the selection. In Table 3, the phenotypic means in bold represent the values below the N_m . It can be observed that all fifth inbred lines of lower I_{sc} showed some traits below the fixed value to N_m . However, according to Marinho et al. (2014), discarding these genotypes must be balanced by the global performance and importance of the trait in question. Considering the high importance of environment in the expression of evaluated traits, genotypes with values below the minimum acceptable levels for one trait in a season could not be discarded.

Nevertheless, the inbred lines RS-63, RS-56, and RS-31 with grain yields means below N_m values in the two growth seasons showed a low potential *per se* for grain yield. Due to the importance of yield for commercial cultivars (SANTOS et al., 2016), these inbred lines must not be selected. The inbred line RS-12 with number of days to maturity superior to the means in both seasons, must also not be selected because those who showed others traits, such as early maturity, were prioritized. Based on the I_{sc} values, no inbred line were superior when compared with the commercial controls (NK 7059 RR and BMX Potência RR).

Among the five best inbred lines ranked in the three applied indexes and not -considering those with restrictive values based on minimum acceptable levels, RS-03, RS-12, RS-22, RS-41, RS-49, RS-55, RS-61, and RS-62 showed potential for the selection process. These are necessary for evaluating the agronomic traits under broader environmental conditions, with the objective of verifying the adaptability and stability of these inbred lines to launch a new soybean cultivar in the future.

Conclusion

The selection indexes were consistent for the indication of better inbred lines. The superior inbred lines based on three indexes applied were RS-03, RS-12, RS-22, RS-41, RS-49, RS-55, RS-61, and RS-62. These featured RS-03 and RS-62, which obtained a lower sum of ranks and a lower distance to the ideotype when compared to the commercial controls.

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