AGRONOMY SCIENCE AND BIOTECHNOLOGY

RESEARCH ARTICLE

Selection indexes based on genotypic values applied to Brazilian tropical wheat breeding

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ABSTRACT

Although Brazil is one of the main agricultural countries in the world, it is historically an importer of wheat. For this reason, strategies aimed at the expansion of wheat in the country, to areas that are not traditionally producing (warmer), are of paramount importance. In wheat breeding, phenotypic values are usually used in simultaneous selection, however, they do not always correspond with genetic superiority. Therefore, the objective of this work was to evaluate the efficiency of five selection indexes applied to the genotypic values of wheat, the coincidence between the indexes and to select the most promising lines. For this, we evaluated a panel with 41 genotypes of tropical wheat, for the traits: days for flowering, disease note, plant height, hectoliter weight and grain yield. Data were submitted to REML/BLUP analysis to estimate genetic parameters and genotypic values. We applied on the BLUPs the rank summation index, multiplicative index, genotype- ideotype distance index, additive index and FAI-BLUP index. There is a genotypic variation shown by analysis of deviance for all evaluated traits. We presented different estimates of gains from selection according to the selection index applied. We observed higher estimates of gains from selection for additive and genotype-ideotype distance indexes. High similarity was observed in the selection of genotypes through the coefficient of coincidence between the indexes. Eight lines were selected simultaneously by three or more indexes. Lines VI 14047, VI 14774 and VI 14980 showed the best performance among the eight lines evaluated by the Z index.

Keywords: *Triticum aestivum* L., REML/BLUP, simultaneous selection, grain yield, genetic gain, correlated response.

INTRODUCTION

The Brazilian consumer market for wheat (*Tricitum aestivum* L.) flour is huge. Currently, Brazil is in third place, in the import of wheat, representing about 4.3% of the world import. According to data from the Food and Agriculture Organization of the United Nations (FAO) (2020), the expected world wheat production for 2020 is about 762.6 million tons. If achieved, it will represent the second highest mark ever recorded. The use of wheat for the 2019/20 season is also expected to outperform the previous one by 1.2%. Brazil is highly dependent on import of wheat, mainly from Argentina. Data from the Companhia Nacional de Abastecimento (CONAB) (2020) estimate that the volume of wheat imported for the 2019/20 harvest be 7.2 million tons, which corresponds to more than 50% of the Brazilian demand. These estimates reinforce the need for advances in genetic improvement to releasing more productive cultivars so that Brazil becomes self-sufficient.

In the Brazilian scenario, the institutions that work with wheat breeding are committed to developing cultivars adapted to different growing environments. They must have important traits, such as disease resistance, high grain yield, and a technological quality that meets the industrial demand (Scheeren & Caierão, 2015). It is common in wheat breeding programs to evaluate several genotypes and select promising ones according to the main traits of interest (Candido et al., 2020a). In this context, the use of selection indexes is an essential tool in conducting the selection since there is dependence on genetic association for most agronomic traits.

It is known that truncated selection and indirect selection are efficient only for traits with a high genetic association. This situation is quite limited, as the wheat breeder needs to take many attributes into account simultaneously. By using selection indexes, we seek to obtain simultaneous gains for various traits, significantly facilitating proper selection decisions (Michel et al., 2019; Céron-Rojas & Crossa, 2020). Also, the gains are better distributed among the set of traits considered important for selection in the breeding program.

To obtain more reliable gains with selection, tools that allow inferences about genotypic values should be chosen, which allows the breeder to select genotypes more accurately (Candido et al., 2020b). In this sense, the use of REML/BLUP methodology can be considered an appropriate procedure, since it allows greater accuracy in estimates of genetic parameters and prediction of genotypic values (Resende, 2016).

Studies demonstrating the use of selection indexes for wheat have conducted. Guendouz, Guessoum, and Hafsi (2012) used different selection indexes to identify wheat genotypes tolerant to water deficit. Tyagi et al. (2020) also used indexes to select wheat genotypes tolerant to environments with low nitrogen availability. However, most works carried out until now have focused on simultaneous selection applied to phenotypic values, which can represent high estimates of gains with the selection. However, such gains may not be observed in the next breeding generations.

In this context, the objective of this work is to estimate selection gain by indexes based on BLUPs values of wheat genotypes, evaluate the coincidence coefficient between these indexes, and select graphically by Z index the genotypes identified as promising using selection indexes.

MATERIAL AND METHODS

Plant material and experimental design

A panel of 41 tropical wheat lines was evaluated in a field experiment in randomized block design with three replications in the 2019 winter crop. The evaluated genotypes consisted of 33 lines of tropical wheat in Preliminary Phase (EPL) and of Cultivation and Use Value (VCU) developed by UFV Wheat Breeding Program and eight commercial cultivars widely cultivated in the Center-South and Cerrado of Brazil from different breeders: BRS 394, BRS 264, BRS 254 (EMBRAPA), CD 1303 (COODETEC), TBIO Aton, TBIO Duque, TBIO Ponteiro, TBIO Sintonia, TBIO Sossego (Biotrigo Genética). The trial was conducted in the experimental field Professor Diogo Alves de Mello (20º45'14" S; 42º52'55" W; 648 m of altitude) of the Agronomy Department of the Universidade Federal de Viçosa (UFV), Viçosa, MG, Brazil.

The experimental plot consisted of five rows five meters (m) long, at spacing of 0.20 m between rows, with a population density of 350 seeds m^2. For evaluation purposes, the three central rows were considered as useful plot. The trial was conducted between the months of June and October 2019. The crop management was carried out according to the technical recommendations of the wheat crop (Embrapa, 2018).

Climate data were collected from the meteorological station of the National Institute of Meteorology (INMET), located close to the experimental area (Figure 1). We obtained information on relative humidity (RH%), solar radiation (MJ m^{-2}), and maximum, average, and minimum temperature (ºC). Information on recorded rainfalls were minimal, which made irrigation indispensable.

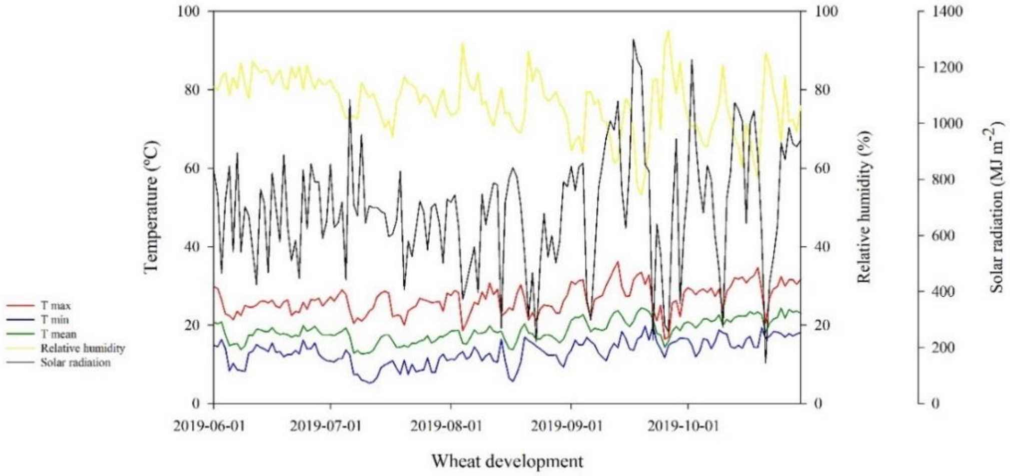

Figure 1. Meteorological data from the station located at the Federal University of Viçosa comprise the period of the growing season of the wheat experiment.

Traits Evaluated

Lines were evaluated for traits: days to flowering (DF), evaluated in days, from phase 10 (first leaf through the coleoptile) to phase 65 of Zadoks, Chang, and Konzak (1974). The disease note (DN) was assigned according to the severity of diseases in leaves and spikes, ranging from 5 (healthy plants without diseases) to 1 (plants with high disease intensity). The plant height (PH) was measured using a ruler graduated in cm measured from the collection to the top of the spike, excluding the awn. The hectoliter weight (HW) was determined according to a specific Dalle Molle scale, measured in kg 100 L^{-1}. Grain yield (GY) was determined in kg ha^{-1}, adjusted to 13% humidity. All data were collected from the useful area of each plot.

Statistical analysis

The data were subjected to analysis of deviance to estimate genetic parameters, genotypic values and confidence intervals using the REML/BLUP method. Thus, the genetic-statistical model 21 was calculated using the software Selegen (Resende, 2016), according to the equation described: $y=XR+ZG+e$, where y is the data vector, R is the vector of repetition effects and the general average (fixed), G is the vector of genotypic effects (random) ($g \sim N(0,\sigma_g^2)$), where σ_g^2 is the matrix of genotypic variances, e is the vector of errors or (random) residuals ($e \sim N(0,\sigma_e^2)$), where σ_g^2 is the residual variance matrix, and X and Z are incidence matrices for the mentioned effects. Using these data, we obtained genotypic values (BLUP) for each trait of each genotype.

Simultaneous selection on genotype values (BLUP) of all the evaluated traits was applied considering the selection of 20% of the superior lines for 5 different selection indexes: ranks summation index (Mulamba & Mock, 1978), multiplicative index (Subandi, Compton, & Empig, 1973), genotype-ideotype distance index (Wricke & Weber, 1986), additive index (Resende, 2007), and FAI-BLUP index (Rocha, Machado, & Carneiro, 2018). We calculated the first three indexes using a Microsoft Excel® Spreadsheet, the additive index using the software Selegen (Resende, 2016), and the FAI-BLUP using the software R, version 3.6.2 (R Core Team, 2019).

For the rank summation index (Mulamba & Mock, 1978), we classified the genotypes as for the traits DF, DN, PH, HW and GY and adopted the criterion of classifying the best genotype for each trait with value 1 and so on, that is, the genotypic value of each trait was transformed into ranks. The genotypes classified as 1 were those with the highest means for the traits DN, HW, and GY, and those with the lowest average for the traits DF and PH, according to the interest of the breeding program in increasing or decreasing the expression of the trait. After obtaining the classification values for each genotype, we calculated the index as follows: $I_{MM(i)}=\sum_{j=1}^{n} r_{ij}$, where $I_{MM(i)}$ is the index for genotype i, r_{ij} is the rank associated with the genotype i value in relation to the trait j. We considered lines with lower $I_{MM(i)}$.

We calculated the multiplicative index (Subandi, Compton, & Empig, 1973) according to the following expression: $I_{S(i)}=\prod_{j=1}^{n} w_i$, where $I_{S(i)}$ is the multiplicative index for the genotype i; $w_i= x_{ij}- k_j$, where x_{ij} is the observed genotype value of genotype i in variable j, k_j is the selection criterion for the variable j assuming $w_i= 0$, if $x_{ij}- k_j > 0$ for the variables DF and PH, and if $w_i= 0$ $x_{ij}- k_j < 0$ for the variables DN, HW and GY. The k_j is defined as the maximum or minimum value established for each trait. In this study, the criterion we adopted was the mean genotypic value of the trait ± genotypic standard deviation. For the traits that satisfy the condition (k_j), the value of the difference $x_{ij}- k_j$ is used in $\prod$. Genotypes that do not meet the criteria conditions receive a value of zero, making $I_{S(i)}$ null, so it cannot be selected.

For the genotype-ideotype distance index (Wricke & Weber, 1986), we adopted the selection criterion (ideotype value) for the maximum genotypic values found in the data set for the traits HW and GY, whereas for the traits DF and PH we considered the minimum values observed as the ideotype. For the trait DN, the ideotype value adopted was 5, which is the theoretical maximum that can be observed (genotypes without symptoms both in leaves and spikes). The index is given by $I_{GI(i)} = D_{ii'} = \sqrt{\sum_{j=1}^{m} d_{ij}^2}$, where $D_{ii''}$ is the Euclidean distance between the genotype i and the ideotype i', and d_{ij} is the standard deviation between the genotypic mean of the trait j measured in the genotype i (x_{ij}), and the value assigned to the ideotype in that trait. The genotypes with the lowest sums of squares $I_{GI(i)}$ are classified as closest to the ideal genotype; therefore, they are selected.

The additive index (Resende, 2007) selects simultaneously based on BLUPs obtained for the traits DF, DN, PH, HW and GY. In addition, it allows the inclusion of economic weights according to the importance and nature of the traits considered. We estimated the index based on the following expression: $I_{A(i)} = \sum_{j=1}^{n} b_j X_j$, where $I_{A(i)}$ is the value of the additive selection index for the genotype i; b_j is the value of economic weight for the trait j; X_j is the genotype value of the trait j. In this study, in order of relevance of traits to the wheat breeding program, the values of 0.1, 0.3, 0.1, null and 0.5 of economic weights were assigned to the traits DF, DN, PH, HW and GY, respectively. The traits DF and PH were selected for the lowest values.

The FAI-BLUP index (Rocha, Machado & Carneiro, 2018) is based on factor analysis and genotype-ideotype distance to classify genotypes considering simultaneous selection. The definition of ideotype values follows the same premise as that described for the method of Wricke and Weber (1986). The steps involved in factor analysis and FAI-BLUP index were carried out using the software R, version 3.6.2 (R Core Team, 2020), metan package (Olivoto & Lúcio, 2020). We defined the number of factors based on the Kaiser (1958) criterion.

The selection gains for each trait (SG%) were calculated according to the expression: $SG_i = (\bar{x}_s - \bar{x}_o) \times \hat{h}^2$, where SG_i is gains with the selection of 20% of the best lines; $\bar{x}_s$ and $\bar{x}_o$ are the mean of selected lines for the trait j and mean of the original population for the trait j (selection differential); $\hat{h}^2$ is heritability for the trait j.

The coincidence in the selection of genotypes between the different indexes was represented by the coefficient of coincidence and the correlation between traits was calculated from the average of the genotypic values and their significance was tested at 5% probability by Student's t test. These analyzes were performed using the software R (R Core Team, 2020).

The gains selection for each trait and for each index were plotted on a radial graph using the software SigmaPlot 14.0. The genotypes selected by three or more indexes were represented by the index Z. The index Z (Mendes, Ramalho & Abreu, 2009) was plotted by the standardized variable Z_{ij}, where Z_{ij} is obtained by the equation $Z_{ij} = ((y_{ij} - \bar{y}_{.j})/s_j)$, where y_{ij} is the genotypic value of trait j of genotype i; $\bar{y}_{.j}$ is the general trait mean; and s_j is the standard deviation of the trait j, Z_{ij} is the standardized genotype value of genotype i for the trait j and can assume positive and negative values to avoid negative values; the value three was added to estimates.

RESULTS AND DISCUSSION

Weather conditions

According to data of the Viçosa Meteorological Station (Figure 1), the average temperature throughout the experiment recorded values slightly below or above 20ºC, which is close to the ideal temperature for wheat (19ºC) (Cristhy et al., 2020). Some values of maximum temperature surpass the limit of optimal range of development. Temperature records close to 30ºC are quite common, especially in the final third of the crop development cycle, as the climate in this region is classified as Cwa (humid temperate climate with dry winters and hot summers), according to the Köppen classification.

Wheat cultivation in regions of Brazil with higher temperatures, although small, has demanded efforts from breeding programs given the regions' potential to contribute to the domestic demand, thus reducing imports (Pasinato et al., 2018). The occurrence of heat stress can become common in these regions. However, recent research has pointed to high variability, which makes the selection promising for this scenario (Pereira, Cunha & Moresco, 2019; Ribeiro et al., 2019).

Analysis of deviance

The analysis of deviance (Table 1) revealed a significant effect of genotypes on all traits evaluated by testing the maximum likelihood ratio test (LRT) at 1% probability. The occurrence of genetic variability for these traits makes it possible to select superior genotypes (Mathew et al., 2018; Abeledo et al., 2019). For all evaluated traits, except for GY, there was a predominance of genetic variance in phenotypic variance. Heritability estimates between the mean of genotypes ranged from 0.63 (GY) to 0.92 (DF), and the selective accuracy ranged from 0.80 to 0.96 for the same traits, respectively. Rapp et al. (2018) conducted a study on simultaneous selection in durum wheat and observed values of h^2 for GY of 0.60 and 0.75 in the agricultural crops of 2014/2015 and 2015/2016.

Table 1. Likelihood ratio test (LTR), variance components and genetic parameters of 41 tropical wheat genotypes for the traits days for flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).

Variance components	DF	DN	PH	HW	GY
Genetic variance ($\hat{\sigma}_g^2$)	12.22	0.98	16.59	4.59	155150.16
Residual variance ($\hat{\sigma}_e^2$)	3.14	0.29	14.24	3.04	269335.18
Phenotypic variance ($\hat{\sigma}_p^2$)	15.36	1.28	30.83	7.62	424485.34
Individual heritability ($\hat{h}^2$)	0.80±0.23	0.77±0.22	0.54±0.19	0.60±0.20	0.37±0.17
Average heritability ($\hat{h}_m^2$)	0.92	0.91	0.78	0.82	0.63
Selective accuracy ($\hat{h}$)	0.96	0.95	0.88	0.91	0.80
Coef. of genotypic variation (CGV %)	5.81	35.83	4.73	2.81	8.97
Coef. of experimental variation (CEV %)	2.94	19.64	4.38	2.28	11.82
Mean	60.20	2.76	86.14	76.28	4391.83
*χ^2	89.01	79.96	32.29	41.87	10.75

$*\chi^2_{1\%} = 6.63 \qquad \chi^2_{5\%} = 3.84$

The values of selective accuracy for the traits HW (0.91), DN (0.95) and DF (0.96) were classified as very high (> 0.90). The traits PH (0.88) and GY (0.80) were classified as high (> 0.70) (Resende & Duarte, 2007). The coefficient of experimental variation (CEV) ranged from 2.28% (HW) to 19.64% (DN), respectively. The main trait GY presented a CEV of 11.82%, which demonstrates an adequate experimental precision. The CGV/CEV ratio was greater than 1 for all traits, except for GY due to its polygenic nature strongly influenced by the environment. Even the trait DN, with the highest CEV value (19.64%), showed a CGV/CEV ratio of 1.82. This result for DN is explained by the existence of high genetic variation among the evaluated wheat genotypes.

Selection indexes

The selection index of Mulamba and Mock (1978) allowed obtaining gains from selection of 10.08% (Table 2) distributed among the five traits evaluated. All gains were favorable towards selection, with negative gains for DF (-2.80%) and PH (-1.57%), in which the objective of breeders is the reduction of these traits for the development of early progenies with a smaller height. Meier et al. (2019) conducted a work on genetic gain among 420 progenies F_5 of wheat resulting from simple crossing between the cultivars Mirante and Abolone and reported positive gains for DF and PH, thus selecting progenies of greater cycle and height of 1.39 and 3.96%, respectively. The gains with selection were 1.83% for GY and 2.07% for DN, values of intermediate magnitude in favor of selection.

For the Subandi et al. (1973) index (Table 2), the total accumulated gains with the selection were 16.11%, higher than those of the previous index. There were gains of 8.29% with the selection of DN, which represented a positive differential in the selection of the lines selected here compared to the original population average (0.25). The gains with the selection for traits in which negative values are targeted were also better than in the previous index: -2.62 and -2.21 for DF and PH, respectively. For GY, the gains were around 1.74%.

Fellahi, Hannachi, and Bouzerzour (2018), in a study evaluating the efficiency of direct and indirect selection and selection indexes in wheat bread, found negative values for GY (-0.93%) in the selection based on the multiplicative index of Subandi et al. (1973). In addition, this same work found a negative sum of gains in the selection of 11 traits simultaneously in 600 F_4 families of wheat. When many traits are considered together, the selection indexes tend to be less efficient. This is due to the high dependence on genetic association that exists between the target characters of selection and the fact that the greater the number of traits, the greater the weighting of total genetic gain.

Therefore, we suggest that, to obtain a greater efficiency in important traits in a wheat breeding program, only the target traits, such as those considered in this work, should be considered. For secondary traits, such as components of production, if not taken into account, the actual gains will be more pronounced among the main traits (Fischer & Rebetzke, 2018; Fellahi et al., 2018; Meier et al., 2019; Fellahi, Hannachi & Bouzerzour 2020).

The Wricke and Weber (1986) index demonstrated the same performance in selection for the trait DN as the Subandi et al. (1973) index, i.e., 8.29%. In addition, it presented the highest estimate of SG% for GY (5.63%). This trait is the main objective of wheat breeding programs. However, the application of this index was not efficient in all traits considered. For DF and PH, the GS% estimates were in the opposite direction (1.37%) or practically null (-0.14%). For HW, this estimate was also modest, as it was for PH. The Wricke and Weber selection index (1986) has been little explored so far in wheat selection. In addition, the research conducted so far on wheat with this index has only considered phenotypic means, differently from what we have done in this research.

Table 2. Estimates of original average ($\bar{X}$o) and average of selected genotypes ($\bar{X}$s), selection differential (SD), heritability ($\hat{h}^2$), selection gain (SG) and selection gain in % (SG%) in the simultaneous selection for eight superior tropical wheat genotypes for the traits days to flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).

Ranks Summation Index (Mulamba & Mock, 1978)								
Trait	$\bar{X}$o	$\bar{X}$s	SD	$\hat{h}^2$	SG	SG%	Selected genotypes	
DF	60.20	58.36	-1.83	0.92	-1.69	-2.80		
DN	2.76	2.83	0.06	0.91	0.06	2.07	CD 1303	VI 14774
PH	86.14	84.39	-1.74	0.78	-1.36	-1.57	BRS 264	VI 131246
HW	76.28	77.97	1.68	0.82	1.38	1.81	BRS 254	VI 131313
GY	4391.83	4518.71	126.88	0.63	80.37	1.83	VI 14980	VI 14047
					∑	**10.08**		
Multiplicative Index (Subandi et al., 1973)								
DF	60.20	58.48	-1.72	0.92	-1.58	-2.62		
DN	2.76	3.02	0.25	0.91	0.23	8.29	BRS 264	VI 14774
PH	86.14	83.69	-2.45	0.78	-1.90	-2.21	VI 14980	VI 131246
HW	76.28	77.44	1.16	0.82	0.95	1.25	VI 14864	VI 131313
GY	4391.83	4512.70	120.87	0.63	76.56	1.74	VI 14867	VI 14047
					∑	**16.11**		
Genotype-Ideotype Distance Index (Wricke & Weber, 1986)								
DF	60.20	61.09	0.90	0.92	0.82	1.37		
DN	2.76	3.02	0.25	0.91	0.23	8.29	TBIO Aton	VI 14980
PH	86.14	85.99	-0.15	0.78	-0.12	-0.14	BRS 254	VI 14668
HW	76.28	76.57	0.29	0.82	0.24	0.31	BRS 394	VI 14867
GY	4391.83	4781.92	390.09	0.63	247.10	5.63	CD 1303	VI 130758
					∑	**15.74**		
Additive Index (Resende, 2007)								
DF	60.20	62.82	2.62	0.92	2.42	4.01		
DN	2.76	3.81	1.05	0.91	0.95	34.45	CD 1303	VI 14864
PH	86.14	85.65	-0.48	0.78	-0.38	-0.44	TBIO Aton	VI 14867
HW	76.28	77.09	0.81	0.82	0.66	0.87	TBIO Ponteiro	VI 14774
GY	4391.83	4706.15	314.32	0.63	199.11	4.53	VI 14980	VI 14668
					∑	**44.3**		
FAI – BLUP (Rocha et al., 2018)								
DF	60.20	57.90	-2.29	0.92	-2.11	-3.51		
DN	2.76	2.79	0.02	0.91	0.02	0.82	BRS 264	VI 131307
PH	86.14	83.92	-2.21	0.82	-1.81	-2.10	VI 14774	VI 14867
HW	76.28	77.59	1.31	0.78	1.02	1.33	VI 131246	VI 14980
GY	4385.77	4527.46	141.69	0.63	89.75	2.05	VI 131313	VI 14047
					∑	**9.81**		

The additive index Resende (2007) presented the highest estimate of SG% for DN, with an increase in genotypic values from 2.76 to 3.81 and 1.05 of selection differential. In addition, we observed a high estimate of SG% for GY. This index was similar as the previous index, since it presented high estimates of GS% for DN and GY and an increase in an unfavorable direction for DF, in addition to low estimates of SG% for PH. The additive index and the Wricke and Weber (1986) index provided the selection of productive and resistant lines compared to the first two indexes above (Subandi et al., 1973; Mulamba & Mock, 1978). However, the lines have a long cycle and a greater plant height. The use of the additive index is reported for other species, but so far, the use of the additive index in wheat has not been found in the literature.

The FAI-BLUP index (Rocha et al., 2018) provided the lowest GS% estimates considering total sum. However, it showed interesting gains for the reduction of the traits DF and PH of -3.51% and -2.10%, respectively. In addition, the GY increase (2.05%) was substantial. The FAI-BLUP index has been used extensively in the application of genotype selection in different crops such as soybean (Woyann et al., 2019), bean (Rocha et al., 2019), and sorghum biomass (Silva et al., 2018). It has the advantage to consider genotypic correlations free from the presence of multicollinearity and without the need to establish economic weights for traits.

Comparative evaluation of genetic gain estimates

According to the analysis in Figure 2, the index that provided the largest sum of SG% estimates was the additive index (Resende, 2007). Of the 44.30% of SG, 34.45% correspond to the increase in DN, followed by 4.53 in GY. However, the selected genotypes presented mean DF genotypic values of 62.82, representing a positive selection differential of 2.62 days, which is unfavorable for wheat breeding programs. However, according to the other traits, we noted that the multiplicative and genotype-ideotype distance indexes are also promising, with a sum of gains of 16.11 and 15.74%, respectively. The rank summation index, together with FAI-BLUP, presented lower SG% estimates, which is evident in the analysis of Table 2 and Figure 2.

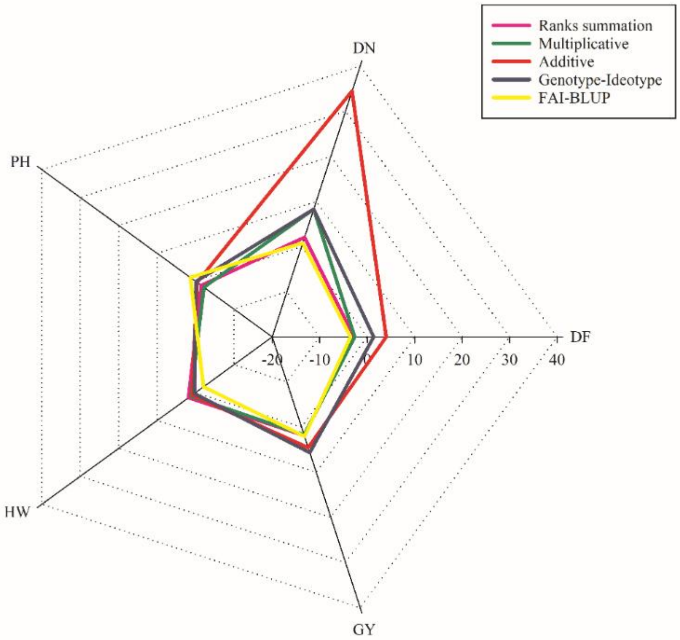

Figure 2. Prediction of genetic gains by selection indexes applied on the genotypic values (BLUPs) for the traits days to flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).

Coefficient of coincidence

Figure 3 shows the coincidence coefficient in the selection of lines among the studied indexes. There was a high level of agreement between the selection indexes rank summation × multiplicative (0.75), rank summation × FAI-BLUP (0.75), multiplicative × FAI-BLUP (0.88), and genotype-ideotype × additive (0.63). The greatest coincidence occurred between the multiplicative × FAI-BLUP selected seven lines concomitantly among the selection of 20% of the best lines (eight selected). Pedrozo et al. (2009) evaluated the efficiency of use of selection indexes using the REML/BLUP procedure in sugarcane and found coefficients of coincidence between the applied indexes lower than those found in this study. A greater agreement between the indexes regarding the selected genotypes indicates a greater accuracy in the selection of superior lines.

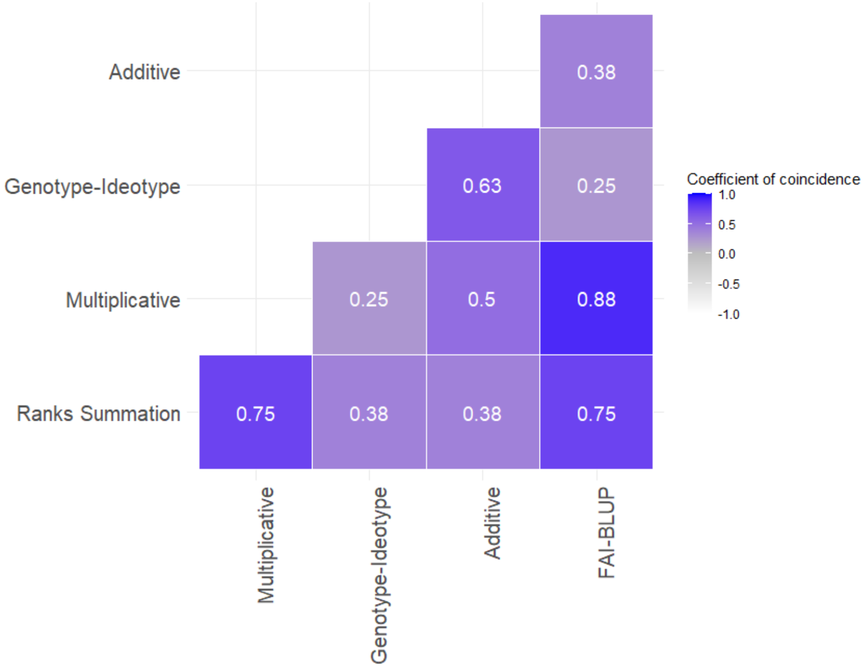

Figure 3. Estimates of the coefficients of coincidence between the selection indexes applied on the genotypic values (BLUPs) for the traits days to flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).

Genotypic correlation

The lack of weighted SG% among all traits in a favorable direction of selection can be explained by the existence of a linear association between traits (Figure 4) evidenced by the genotypic correlation values between DF × DN (0.58), DF × PH (0.34) and DN × GY (0.47). Thus, obtaining higher estimates of GS% for GY and DN will result in lines with higher genotypic values for DF and PH. The association between productive genotypes, high sanity, and greater cycle and height was evident in this panel. If the nature of this association is due to the factorial link, the association may be broken. However, if this nature is due to pleiotropic genes, its cause is permanent (Cruz, Regazzi & Carneiro, 2012).

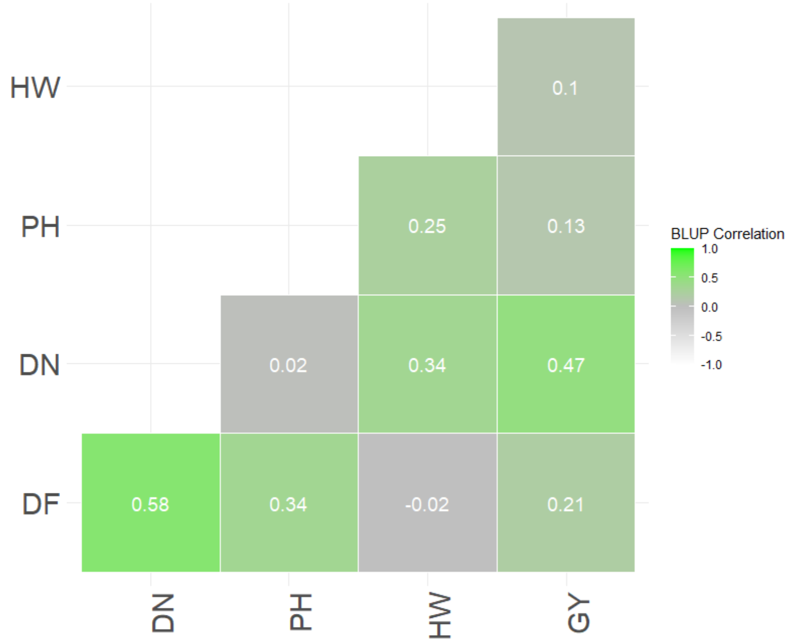

Figure 4. Estimates of the correlation coefficients between genotypic values for the traits days to flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).
**Correlations above 0.3 is significant with 5% probability by Student's t test.*

Z index

The lines CD 1303, BRS 264, VI 14047, VI 14774, VI 131313, VI 131246, VI 14980, and VI 14867 were selected by at least three indexes concurrently (Figure 5). Their performance in relation to genotypic values is represented by the Z index (Mendes et al., 2009). Among the eight lines represented graphically, the lines VI 14047, VI 14774, and VI14980 are genetically superior in relation to the others and will be selected by the breeding program.

Decision-making based on more than one selection index makes selection more accurate. For this reason, the strategy of graphically presenting the genotypes that were selected successively by the indexes is an interesting premise. Line VI 14980 was among the 20% best in all selection indexes applied (Table 2). Through visual analysis by Z index, a high frequency of favorable alleles is perceived for all traits considered in selection. This line has, in addition to high genotypic values for GY and HW, lower genotypic values for DF and PH, which is highly recommended when selecting wheat lines. In the applied selection indexes, consistent gains in GY and DN consequently resulted in late lines with a greater height.

These strategies can be incorporated into the progeny selection steps in recurrent wheat selection programs. Generally, many progenies are evaluated for their performance, each time new parents are incorporated into the crosses to bring about greater variability. Therefore, more accurate identification of highly promising genotypes by selection indexes on BLUPS and their subsequent evaluation of graphic performance, can be very useful.

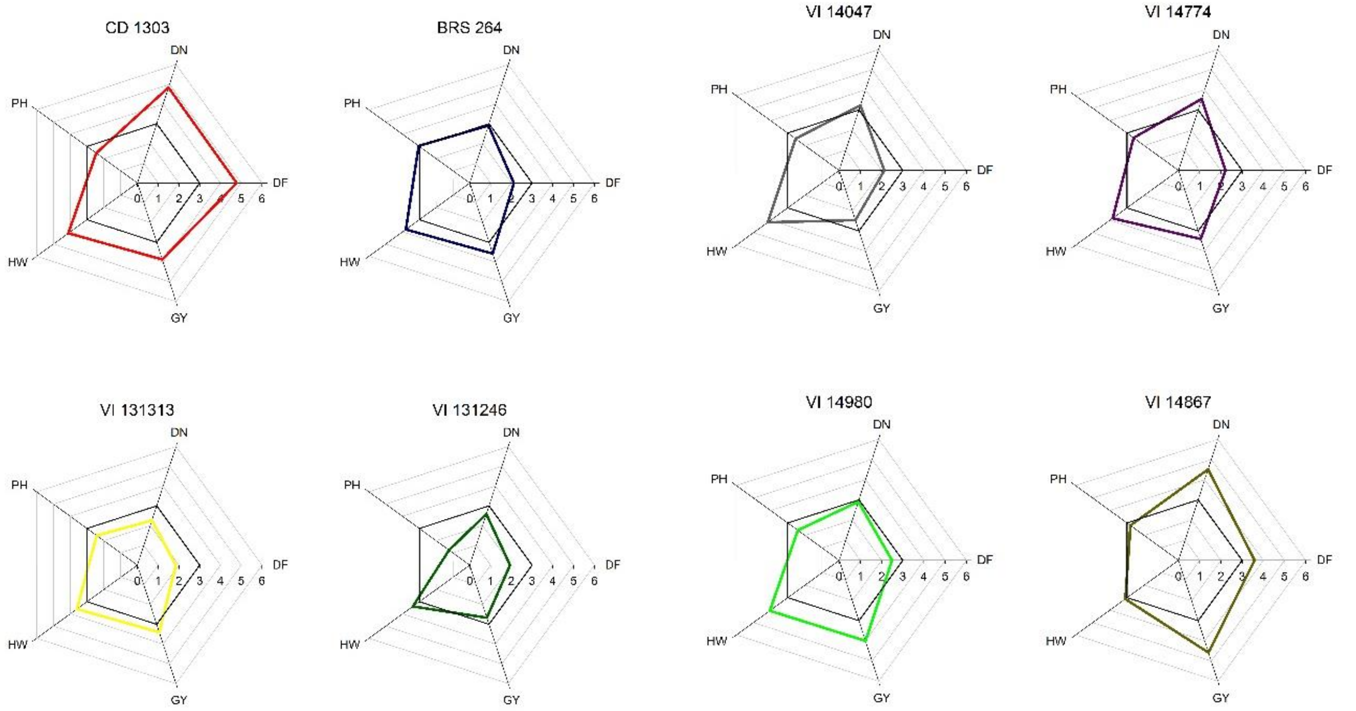

Figure 5. Representation of the Z index from the genetic values of the eight selected lines selected concurrently by three or more selection indexes for the traits days to flowering (days, DF), disease note (scale, DN), plant height (cm, PH), hectoliter weight (kg 100 L^{-1}, HW) and grain yield (kg ha^{-1}, GY).

CONCLUSIONS

There is variability for the traits evaluated in breeding program genotypes.

The additive and genotype-ideotype distance indexes reveal higher estimates of gains to the breeding program with the selection of interest, especially for the traits DN and GY.

The genotypes CD 1303, BRS 264, VI 14047, VI 14774, VI 131313, VI 131246, VI 14980, and VI 14867 will be selected by the breeding program.

The arrangement of the performance of genotypic values for the selected genotypes by selection indexes revealed graphically by Z index, is interesting for the selection of wheat lines.

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