ARTICLE

Selection of superior black oat lines using the MGIDI index

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Abstract: *The objective of this work was to select black oat genotypes using the MGIDI for simultaneous selection, comparing it with the Smith-Hazel index. The experiment was carried out in Frederico Westphalen/RS and Pato Branco/PR, in a randomized block design, with three replications, with 9 genotypes tested. Days from emergence to flowering and maturation; cutting and plant height; number of tillers; panicle length; tiller, plant, panicle, panicle seed mass, green and dry; and seed yield were obtained. MGIDI selected the genotypes UFSMFW 2-01 and UFSMFW 2-04 for Frederico Westphalen and UFSMFW 2-07 and UFSMFW 2-04 for Pato Branco, which varied compared to the Smith-Hazel index in both environments. MGIDI was efficient in selecting the best black oat genotypes, showing desirable selection gains for most traits.*

Keywords: *Productivity, simultaneous selection, selection gains*

INTRODUCTION

Black oats (*Avena strigosa* S.) are one of the main cultivated winter cereals in the world (Meira et al. 2019). In Brazil, the species is widespread to produce forage and has been gaining ground due to the introduction in the no-tillage system for soil cover, also allowing the harvest of grains that serve as an alternative for animal feed (Restle et al. 2009).

The southern region of the country has the best climatic conditions for growing black oats and, therefore, has the largest cultivated areas. In 2020, the states of Paraná and Rio Grande do Sul had, together, about 380,700 hectares of cultivated oats (CONAB 2021). However, it is estimated that the area cultivated with oats is much larger, since cultivation for ground cover and forage production are not accounted for in the statistics.

Despite the extensive area cultivated with black oats, there are few breeding programs, leading to a small number of cultivars available on the market, aligned with dry mass productivity (Silveira et al. 2010). Due to the importance of oats for different cultivation purposes, there is a need to develop new cultivars that combine good dry mass productivity with seed yield.

The genotype that aggregates an ideal combination of traits, both morphological and physiological, can be called an ideotype (Rocha et al. 2018). However, gathering many desirable traits in a single genotype is not a simple

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task. The selection of superior genotypes is often highly complex, since agronomic traits of economic importance have a quantitative inheritance (Nogueira et al. 2012).

To assist in selection, when working with the objective of gathering different traits, using selection indices is an advantageous strategy. Teixeira et al. (2012) report that the first index proposed for the selection of two or more correlated traits was the classic one (Smith 1936, Hazel 1943), which is widely used. The Smith-Hazel index uses phenotypic values and genetic covariances to determine how a vector of weights should be chosen to maximize the correlation of unknown genetic values and phenotypic values (Hazel et al. 1994). However, evaluating several traits simultaneously certainly leads to the presence of correlated traits that can cause multicollinearity problems (Olivoto and Nardino 2021), resulting in biased regression coefficients, which can lead to erroneous conclusions (Purnier et al. 2015). Also, the lack of a procedure to weigh traits of economic importance makes it difficult to apply this index (Stephens et al. 2012).

To overcome the adversities found in traditional indices, Olivoto and Nardino (2021) developed a new simultaneous selection index based on factorial analysis, known as the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). Studies using the MGIDI index have already been reported with the crops of barley (Pour-Aboughadareh et al. 2021), Guar (*Cymopsis tetragonoloba*) (Benakanahalli et al. 2021), wheat (Lima et al. 2022) and corn (Yue et al. 2022). Thus, the objective of this work was to select black oat genotypes using the MGIDI for simultaneous selection, comparing it with the Smith-Hazel index.

MATERIAL AND METHODS

The experiment was conducted in 2020, in two locations in southern Brazil, namely: Federal University of Santa Maria, Campus of Frederico Westphalen/RS (lat 27° 23’ 26” S, long 53° 25’ 43” W, alt 461 m asl) and Federal Technological University of Paraná, in Pato Branco/PR (lat 26° 11’ 54” S, long 52° 41’ 23.2” W, alt 760 m asl). The climate, according to Köppen, for both locations is classified as Cfa, humid subtropical, with average annual precipitation of 2,100 mm for Frederico Westphalen/RS and 1,750 mm for Pato Branco/PR (Alvares et al. 2013).

Five black oat homozygous lines were used: UFSMFW 2-01, UFSMFW 2-02, UFSMFW 2-04, UFSMFW 2-05 and UFSMFW 2-07, together with four cultivars: BRS 139, Agro Esteio, UPFA 21 - Moreninha and IPR Cabocla. To conduct the experiment in both locations, a randomized block design was used, with three replications.

Each experimental unit consisted of 6 rows of 5 m, spaced 0.17 m apart, with a sowing density of 300 suitable seeds per m^2. Sowing was carried out on May 30, 2020, in Frederico Westphalen/RS and on June 25, 2020, in Pato Branco/PR. Fertilization was based soil analysis, and cultural treatments for controlling weeds, pests and diseases followed the technical indications for black oat.

The traits analyzed were days from emergence to flowering (DEF), days from emergence to maturation (DEM), green mass (GRM, kg ha^{-1}), dry mass (DRM, kg ha^{-1}) and cutting height (CUH, cm) measured at full flowering, when 50% of the plants in the plot had produced inflorescences. After physiological maturity, harvest was carried out and 10 plants of each experimental unit were evaluated for plant height (PLH, cm), number of tillers per plant (NTP), tiller seed mass (TSM, g), plant mass (PLM, g), panicle length (PAL, cm), panicle mass (PAM, g) and panicle seed mass (PSM, g). Seed yield (SEY) was obtained from the seed mass of the four central rows of each experimental unit and extrapolated to kg ha^{-1}.

Seeking to identify the presence of interaction between genotypes and environments for the traits studied, based on the experimental design used, a joint analysis of variance and the F test ($p<0.05$) were performed, using the statistical model below, considering balanced data:

$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk}$, where Y_{ijk} is the observation obtained in the plot with i-th genotype in the j-th block, μ is the overall mean of the assay, G_i is the effect of the i-th genotype considered fixed, A_j is the effect of the j-th environment considered fixed, GA_{ij} is the effect of the interaction of the i-th genotype with the j-th environment, B/A_{jk} is the effect of the k-th block within the j-th environment, considered random; and ε_{ijk} is the random error effect.

The MGIDI distance index, proposed by Olivoto and Nardino (2021), was used to identify the genotypes aggregated most of the desired traits within each environment. The MGIDI consists of, first, knowing the ideal genotype, and then rescheduling the variables so that they all fall within a range of 0-100 (Olivoto and Nardino 2021), according to the following equation:

$rX_{ij} = \frac{\eta_{nj} - \varphi_{nj}}{\eta_{oj} - \varphi_{oj}} \times (\theta_{ij} - \eta_{oj}) + \eta_{nj}$, where η_{nj} and φ_{nj} are the new maximum and minimum values for trace *j* after rescheduling, respectively; η_{oj} and φ_{oj} are the original maximum and minimum values for trait *j*, respectively, and θ_{ij} is the original value for the j-th trait of the i-th genotype. For DEF, DEM, CUH and PLH, for which lower values are desired, $\eta_{nj} = 0$ and $\varphi_{nj} = 100$ are assumed. For all other traits, for which larger values are desired, we considered $\eta_{nj} = 100$ and $\varphi_{nj} = 0$. Thus, the ideal treatment would be the one with 100 for all traits after rescheduling.

In the next step, an exploratory factorial analysis was performed with rX_{ij} to group the related traits and reduce the dimensionality of the data, generating factor loadings for each genotype through the following equation (Olivoto and Nardino 2021): $X = \mu + Lf + \varepsilon$, where: *X* is a vector $p \times 1$ of rescaled observations; μ is a vector $p \times 1$ of standardized means; *f* is a vector $p \times 1$ of common factors; and ε is a vector $p \times 1$ of residuals, where *p* and *f* are the number of traits and common factors retained, respectively. The eigenvalues and eigenvectors are obtained from the with rX_{ij} correlation matrix. Only those with eigenvalues greater than one are retained. The scores are obtained by the equation: $F = Z(A^T R^{-1})^T$, where: *F* is a matrix $g \times f$ with the factorial scores; *Z* is a matrix $g \times p$ with standardized (rescaled) means; *A* is a matrix $p \times f$ of canonical loadings, and *R* is a correlation matrix $p \times p$ between traits. *g*, *f* and *p* represent the number of genotypes, retained factors, and analyzed traits, respectively. Then, the Euclidean distance between the genotype scores and the ideal genotypes was estimated, being calculated as the MGIDI index (Olivoto and Nardino 2021), through the equation below: $MGIDI_i = [\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2]^{0.5}$, where γ_{ij} is the score of the i-th genotype/treatment on the j-th factor (i = 1, 2, ..., *g*; j = 1, 2, ..., *f*), where *g* and *f* are the number of genotypes and factors, respectively; and γ_j is the j-th score of the ideotype. The genotype that has the lowest MGIDI is closest to the ideotype, showing desired values for all evaluated traits.

The selection differential for all traits was calculated considering a selection intensity of 25%, and thus, the first two genotypes with the lowest MGIDI, that is, closest to the ideotype, were selected. The proportion of the MGIDI index of the i-th genotype explained by the j-th factor (ω_{ij}) is used to show the strengths and weaknesses of the genotypes, and is calculated by the equation (Olivoto and Nardino 2021): $\omega_{ij} = \sqrt{D_{ij}^2} / \sum_{j=1}^{f} \sqrt{D_{ij}^2}$, where, D_{ij} is the distance between the i-th genotype/treatment and the ideotype for the j-th factor. Low contributions from a factor mean that the traits within it are close to those of the ideotype.

To compare the efficiency of the MGIDI index, the Smith-Hazel (SH) index (Smith 1936, Hazel 1943) was also calculated using the following equation: $I_i = \sum_k b_k \bar{y}_{ik}$, where I_i is the calculated index value for progeny *i*; b_k is the weighting coefficient of the index associated with trait *k*; and $\bar{y}_{ik}$ is the phenotypic mean of progeny *i* relative to trait *k*. The values of b_k were estimated by $b = P^{-1}G \times a$, where: P^{-1} is the inverse of the mean phenotypic covariance matrix between traits; *G* is the matrix of genotypic variances and covariances in the average of progenies among the traits; and *a* is the vector of the economic weights of the traits. The selection intensity used was 25%.

Analysis of variance and calculations to estimate the selection rates were performed in the R software, version 4.0.2 (R Core Team 2020), using the "metan" package (Olivoto and Lúcio 2020).

RESULTS AND DISCUSSION

The result of the joint analysis of variance shows that the genotypes showed significant differences ($p \leq 0.05$) for the thirteen traits studied (Table 1), and the traits CUH, PLH, PLM and PAL did not show a significant effect for the environment. Nine traits showed a significant effect for the genotype x environment interaction, indicating that the genotypes have different responses within each environment. The coefficients of variation ranged from 1.26 to 19.28%, indicating good experimental precision according to Pimentel Gomes (2000).

Since the genotypes show variability, the use of selection indices to search for genotypes of economic interest is justified. The success of plant genetic improvement is based on the existence of genetic variability for the selection of superior genotypes (Neto et al. 2015). As most of the variables showed significant interaction, because of the environment, the MGIDI and SH indices were estimated for the Frederico Westphalen (E1) and Pato Branco (E2) environments, individually.

In plant genetic improvement, one of the most important decisions is to define the cultivar traits to be obtained and their purposes (Bradshaw 2017). Thus, in Table 2, one can observe the design of the ideotype to select black oat genotypes that are short, earlier and with good potential for dry mass and seed yield.

Table 1. Summary of the joint analysis of variance in relation to the traits days from emergence to flowering (DEF), days from emergence to maturation (DEM), cutting height (CUH), plant height (PLH), number of tillers per plant (NTP), tiller seed mass (TSM), plant mass (PLM), panicle length (PAL), panicle mass (PAM), panicle seed mass (PSM), total green mass (GRM), total dry mass (DRM) and seed yield (SEY)

Traits	Mean squares of variation sources					CV (%)
	Block/Environment	**Genotype (G)**	**Environment (E)**	**G x E**	**Residual**	
DEF (days)	5.30	43.504*	4.629.629*	12.340*	1.710	1.66
DEM (days)	3.00	177.811*	2.944.641*	13.653*	2.475	1.26
CUH (cm)	1.79	164.714*	3.16E-30	1.18E-29	14.587	3.15
PLH (cm)	10.90	53.391*	1.682.258*	26.652	13.257	2.73
NTP (n°)	0.05	0.038*	0.054*	0.085*	0.016	6.45
TSM (g)	0.01	0.023*	0.011*	0.016*	0.003	19.28
PLM (g)	0.12	1.050*	0.008	0.150	0.053	7.17
PAL (cm)	2.16	9.016*	27.164*	0.361	1.126	4.73
PAM (g)	0.01	0.066*	0.022*	0.033*	0.013	11.96
PSM (g)	0.01	0.026*	0.029*	0.036*	0.009	13.58
GRM (kg ha^{-1})	2920000.00	44447186.00*	2.76E+08*	18158051.00*	7283608.00	7.50
DRM (kg ha^{-1})	21643.00	2066409.00*	14489638.00*	399223.10*	36886.17	2.74
SEY (kg ha^{-1})	12577.00	765004.80*	6785307.00*	77273.79*	11017.32	5.35
df^1	4	8	1	8	32	

^{1} df: degrees of freedom; * Significant values at 5% probability of error.

Table 2. Eigenvalues, explained variance, factor loadings after *virimax* rotation and commonalities obtained in the factor analysis for the traits days from emergence to flowering (DEF), days from emergence to maturation (DEM), cutting height (CUH), plant height (PLH), number of tillers per plant (NTP), tiller seed mass (TSM), plant mass (PLM), panicle length (PAL), panicle mass (PAM), panicle seed mass (PSM), total green mass (GRM), total dry mass (DRM) and seed yield (SEY)

Traits	Frederico Westphalen/RS				Pato Branco/PR				
	FA1	**FA2**	**FA3**	**Commonality**	**FA1**	**FA2**	**FA3**	**FA4**	**Commonality**
DEF (days)	**-0.94**	0.03	-0.10	0.89	**-0.88**	0.01	0.27	0.21	0.89
DEM (days)	**-0.96**	-0.12	0.07	0.94	**-0.88**	-0.04	-0.02	0.30	0.87
CUH (cm)	-0.33	-0.38	**-0.08**	0.89	-0.19	0.03	-0.13	**0.90**	0.86
PLH (cm)	0.09	**0.93**	-0.03	0.87	-0.51	0.13	**-0.69**	-0.30	0.84
NTP (n°)	**-0.73**	0.46	0.01	0.75	-0.17	0.59	**0.72**	-0.17	0.93
TSM (g)	**-0.80**	0.36	-0.27	0.84	**-0.51**	0.36	0.47	0.15	0.63
PLM (g)	-0.03	**-0.86**	0.10	0.75	-0.06	0.26	**0.93**	0.12	0.95
PAL (cm)	0.27	**-0.78**	-0.27	0.76	0.28	-0.57	0.22	**0.70**	0.94
PAM (g)	**-0.71**	-0.59	-0.18	0.88	-0.14	**-0.89**	-0.22	0.17	0.89
PSM (g)	**-0.67**	-0.55	-0.25	0.81	0.05	**-0.92**	0.03	-0.11	0.86
GRM (kg ha^{-1})	-0.01	-0.10	**0.86**	0.76	-0.27	-0.21	**0.75**	-0.29	0.76
DRM (kg ha^{-1})	-0.23	**-0.74**	-0.53	0.87	-0.28	-0.01	0.05	**0.82**	0.76
SEY (kg ha^{-1})	**-0.85**	-0.44	-0.11	0.93	**-0.97**	0.01	-0.01	-0.05	0.94
Eigenvalues	5.81	3.63	1.50	-	3.90	3.13	2.42	1.67	-
Variance (%)	44.70	27.90	11.50	-	30.00	24.10	18.60	12.80	-
A. variance (%)	44.70	72.60	84.10	-	30.00	54.10	72.70	85.50	-

FA: Factor analysis, A. variance: Accumulated variance.

In the factor analysis, only factors with eigenvalues > 1 were considered, following Kaiser's (1958) criteria. For E1, three factors had eigenvalues > 1, and therefore, the dimensional reduction of the data set must consider three factors (FA), which together explained 84.10% of the variation between traits (Table 3). The traits were grouped into the three factors in E1, as follows: in FA1 those related to the cycle (DEF and DEM) and seed yield (NTP, TSM, PAM, PSM, SEY) were grouped together; in FA2, PLH, PLM, PAL and DRM were grouped, traits related to mass production; in FA3, the traits CUH and GRM were grouped.

Table 3. Factor analysis (FA), original mean (X_0), heritability (h^2), selection differential (SD) and Smith-Hazel selection differential (SH-SD) for the characteristics days from emergence to flowering (DEF), days from emergence to maturation (DEM), cutting height (CUH), plant height (PLH), number of tillers per plant (NTP), tiller seed mass (TSM), plant mass (PLM), panicle length (PAL), panicle mass (PAM), panicle seed mass (PSM), total green mass (GRM), total dry mass (DRM) and seed yield (SEY), in the environments Frederico Westphalen/RS and Pato Branco/PR

Environment	Traits	Factor	Objective	X_0	h^2	SD (%)	SH-SD (%)
Frederico Westphalen/RS	DEF (days)	FA1	Decrease	88.00	0.93	-3.54	2.47
	DEM (days)	FA1	Decrease	132.00	0.95	-2.74	0.73
	CUH (cm)	FA3	Decrease	121.00	0.82	-2.15	2.87
	PLH (cm)	FA2	Decrease	139.00	0.69	-0.66	4.58
	NTP (n°)	FA1	Increase	1.96	0.78	1.78	-0.23
	TSM (g)	FA1	Increase	0.28	0.78	7.89	2.52
	PLM (g)	FA2	Increase	3.18	0.89	3.27	2.33
	PAL (cm)	FA2	Increase	21.70	0.76	-0.79	-0.08
	PAM (g)	FA1	Increase	0.98	0.75	5.64	-2.23
	PSM (g)	FA1	Increase	0.74	0.77	5.90	-16.05
	GRM (kg ha^{-1})	FA3	Increase	33722.00	0.71	-3.71	5.57
	DRM (kg ha^{-1})	FA2	Increase	6471.00	0.93	1.34	9.01
	SEY (kg ha^{-1})	FA1	Increase	1606.00	0.96	17.70	10.61
Pato Branco/PR	DEF (days)	FA1	Decrease	69.50	0.95	-2.27	-2.27
	DEM (days)	FA1	Decrease	118.00	0.98	-6.65	-5.62
	CUH (cm)	FA4	Decrease	121.00	0.82	-1.24	5.31
	PLH (cm)	FA3	Decrease	128.00	0.60	0.24	5.75
	NTP (n°)	FA3	Increase	2.02	0.67	-2.85	-0.09
	TSM (g)	FA1	Increase	0.31	0.91	-5.26	-2.14
	PLM (g)	FA3	Increase	3.21	0.91	-3.61	2.28
	PAL (cm)	FA4	Increase	23.10	0.75	3.63	8.05
	PAM (g)	FA2	Increase	0.95	0.67	9.04	-0.06
	PSM (g)	FA2	Increase	0.69	0.55	5.42	21.29
	GRM (kg ha^{-1})	FA3	Increase	38244.00	0.89	3.86	0.02
	DRM (kg ha^{-1})	FA4	Increase	7507.00	0.98	6.91	7.93
	SEY (kg ha^{-1})	FA1	Increase	2315.00	0.97	14.80	0.23
Total for Frederico Westphalen/RS (Increase)						43.52	40.69
Total for Frederico Westphalen/RS (Decrease)						-13.59	-16.36
Total for Pato Branco/PR (Increase)						43.90	50.86
Total for Pato Branco/PR (Decrease)						-21.88	-10.18

Four factors with eigenvalues > 1 were retained for environment E2 and explained 85.50% of the variance between traits. For E2, the traits were grouped into four factors as follows: in FA1, DEF and DEM were grouped, related to the cycle, in addition to TSM and SEY, related to productivity; in FA2, PAM and PSM were grouped together; in FA3, the traits related to mass production (PLH, NTP, PLM and GRM) were grouped; and in FA4, the traits CUH, PAL and DRM were grouped.

Considering a selection pressure of 25%, the first 2 genotypes of each environment were selected according to the MGIDI index (Figure 1). In E1 the best genotypes were UFSMFW 2-01 and UFSMFW 2-04. The UFSMFW 2-04 genotype was also selected in E2, in addition to UFSMFW 2-07. The selected strains have the potential for new cultivars, showing the desired traits and differentiating themselves from existing cultivars on the market.

The MGIDI index provided the desired selection differential (SD) for 11 of the 13 traits evaluated in the E1 environment and for 9 of the 13 traits in E2 (Table 3). In E1, the two traits with unwanted SD were PAL (-0.79%) and GRM (-3.71%), while in E2 they were TSM (-5.26%), PLH (0.24%), NPF (-2.85%) and PLM (-3.61). High values of broad-sense heritability (h^2) were found, which ranged from 0.55 (PSM) to 0.98 (DEM and DRM), suggesting good prospects for selection gains for the traits studied.

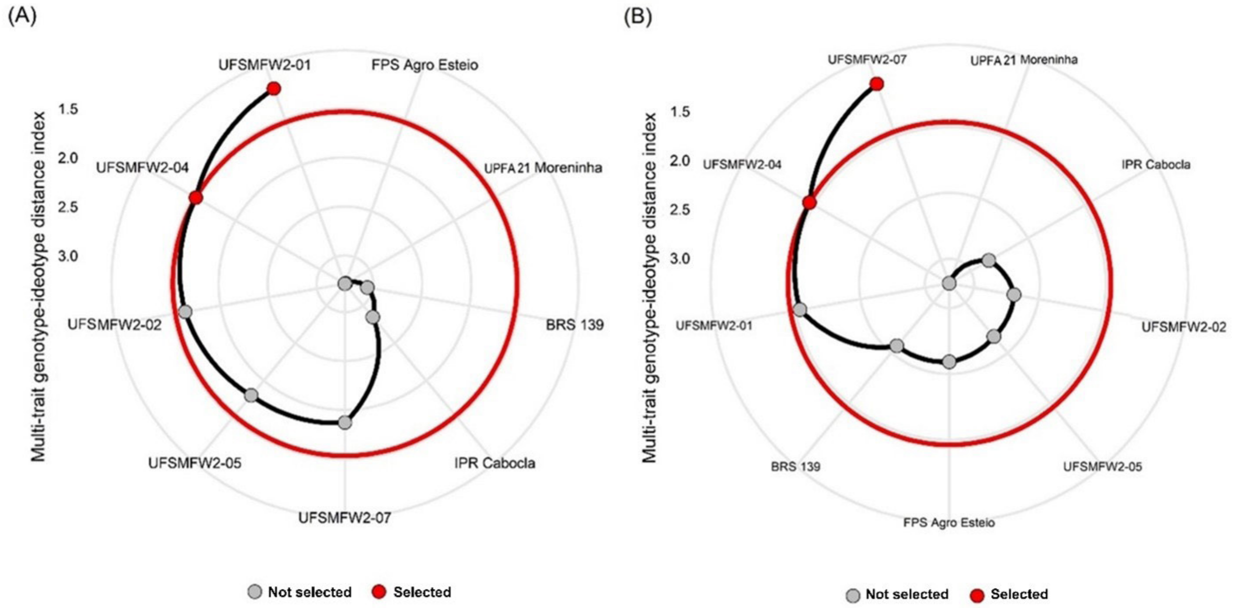

Figure 1. Ranking of genotypes based on the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) for Frederico Westphalen/RS (A) and Pato Branco/PR (B). The red line refers to the selection intensity of 25%, accounting for the selection of 2 genotypes.

The MGIDI index provided satisfactory gains, with good effectiveness when selecting genotypes close to the ideotype in which low height, earliness and higher values of dry mass and seed yield are desired. Negative selection differentials ranged from -2.27% to -6.65% for the DEF and DEM traits, meaning success in using the selection index since cycle reduction was outlined in the ideotype design. For PAM and PSM, in which positive gains were desired, a variation of 5.45% to 9.04% was found. According to Meira et al. (2019), PAM and PSM have high heritability, are correlated, and can be used to select superior genotypes. DRM is important when oats are cultivated for soil cover, for which the index provided positive gains of 1.34% (E1) and 6.91% (E2).

The most significant genetic gains were found for SEY, with SD of 17.7% and 14.80%, for E1 and E2, respectively. The not so significant gains for traits in general can be explained by the simultaneous selection of several traits tending to reduce the genetic gain per trait individually (Almeida et al. 2021). However, for the traits in which the gains were smaller (Zetouni et al. 2017) highlight that this reduction can be balanced by genetic gains in the set of traits. Still, the MGIDI index provided gains of approximately 43.52% and 43.90% (E1 and E2 respectively) for direct selection, simultaneously for traits with desired positive gains and approximately -13.59% and -21.88% for traits with desired negative gains.

A linear correlation matrix among the thirteen characteristics studied revealed the presence of multicollinearity in the data. Generally, in cases like this, it is recommended to exclude the traits that are causing the problem until the condition number is less than 100 (CN < 100) (Olivoto et al. 2017). However, to eliminate the problem, five characteristics of relative economic importance in each environment should be excluded from the analysis, which was not done to preserve the meaning of using the index to evaluate characteristics simultaneously.

For the SH index, considering all traits, the selected genotypes were UFSMFW 2-04 and BRS 139 in E1 and UFSMFW 2-01 and UFSMFW 2-04 in E2 (Table 3). The sum of the SH selection differentials shows good positive gains (40.49% for E1 and 50.86% for E2). The decreased totals were -16.36% and 10.18%, for E1 and E2, respectively. The total SH gains were close to those found for the MGIDI index; however, when analyzing the traits individually and comparing them with the ideotype design, it is noticed in E1 that for the NTP, TSM and PSM traits, for which higher values are desired, the gains were negative and for DEF, DEM and PLH, for which a reduction is desired, the gain was positive. In E2, the gains were more balanced and only PLH and PAL did not show unwanted gains.

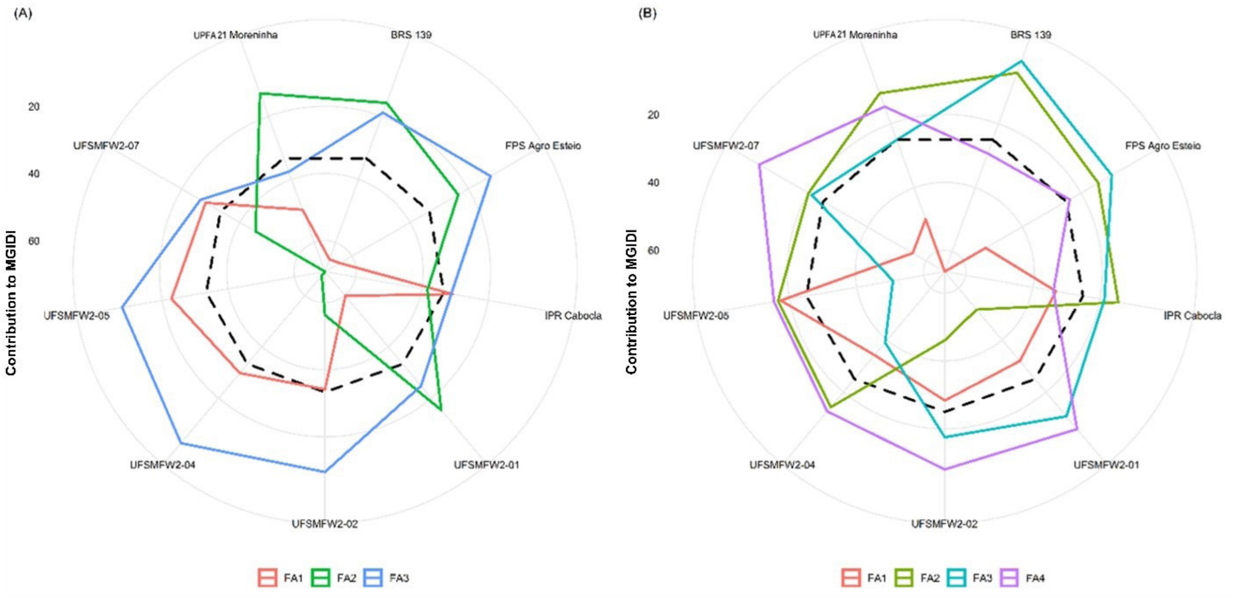

Figure 2. Visualization of the strengths and weaknesses of all genotypes studied for the Frederico Westphalen/RS (A) and Pato Branco/PR (B) environments. The dashed line indicates a theoretical value where all factors would contribute equally.

Rocha et al. (2018) recently proposed the FAI-BLUP multivariate selection index, also based on factor analysis, noting that the difference compared to the classic Smith-Hazel index is that the selected genotypes have the potential to improve all traits simultaneously, bringing as advantages more balanced genetic gains for all traits. Several studies have reported the efficiency of multivariate selection indices for simultaneous selection, for soybean (Woyann et al. 2019, Volpato et al. 2019), for Guar (*Cymopsis tetragonoloba*) (Benakanahalli et al. 2021), for wheat (Meier et al. 2021) and Tahiti acid lime (Peixoto et al. 2021).

The selected genotypes varied between the MGIDI and SH indices, and between the study sites, except for UFSMFW 2-04, common between sites and indices, which demonstrates the potential of this genotype compared to the controls and the other UFSMFW genotypes. The UFSMFW 2-01 genotype was selected by the MGIDI index in E1 and by the SH index in E2.

Figure 2 shows the strengths and weaknesses of the studied genotypes, so that the lower proportion of the factor to explain the MGIDI means that the traits within this factor are close to the ideotype (closer to the outer edge) (Olivoto and Nardino 2021). In E1, the UFSMFW 2-04 genotype, selected by MGIDI, has little contribution from FA3, which indicates good performance of the genotype for the CUH and GRM traits. It is also possible to verify little contribution from FA1, indicating that the UFSMFW 2-04 genotype has desired characteristics such as earliness (lower DEM and DEF) and good seed yield, provided by the higher values found for most of the productivity components (NTP, TSM, PAM and PSM). On the other hand, a high contribution was verified for FA2 and, therefore, it can be observed that in this location the genotype shows as weak points the tall height, which favors lodging, and a lower total dry mass productivity. Leite et al. (2012), when studying white oats, report the preference of producers for earlier cultivars, which allows greater peace of mind in introducing the species in current cultivation systems in which two crops are used per year. On the other hand, shorter cycle cultivars have less time to accumulate total dry mass, which may result in lower productivity.

When cultivated in E2, the UFSMFW 2-04 genotype obtained little contribution from the FA2 and FA4 factors, indicating that for this location the strong points of this genotype are in the traits related to dry mass productivity. The greater contribution from FA1 to this genotype indicates that its strong point is not in seed yield components. However, the selection of this one can be justified by the balance shown between the traits.

The UFSMFW 2-01 genotype, selected in E1, has little contribution from the FA2 and FA3 factors, having as strong points the productivity of dry mass and short height, which promotes less lodging of plants. Seed production can be highlighted as a weakness of this genotype, given the high contribution from FA1.

The UFSMFW 2-07 genotype, selected in E2, has a smaller contribution from FA2, FA3 and FA4 factors. For this material, a greater strength of FA1 was found, indicating that some characteristics within this factor are more distant from those of the ideotype. Thus, it can be noticed that the genotypes UFSMFW 2-01 and UFSMFW 2-07 have mass productivity as a strong point and, therefore, have good suitability for soil cover in a no-tillage system. In addition to the production of grains and fodder for animal feed, the use of oats for green/dead cover protects and improves the physical, chemical, and biological characteristics of the soil (Floss et al. 2007).

Finally, when observing the contribution from the factors provided by the MGIDI for the BRS 139 genotype, in the E1 environment, it is noticed that it only has mass production as a strong point and the longer cycle and low seed production as weak points. The strengths and weaknesses show that the selection of this genotype by the SH index can be wrong, as it has fewer traits close to those of the ideotype planned for the MGIDI. When using MGIDI to select Guar genotypes, Benakanahalli et al. (2021) emphasize that to identify superior genotypes within environments, the index provides a new structure of multivariate techniques and these will optimize the use of resources as well as time, thus contributing to the sustainability of breeding programs.

CONCLUSION

MGIDI was efficient in selecting the best genotypes, showing desirable selection gains for most traits. The UFSMFW 2-04 genotype was selected by both indices, in both cultivation sites. The UFSMFW 2-01 and UFSMFW 2-07 genotypes have as strong points the traits related to dry mass productivity.

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