Scientific Article

Genetic parameter estimates in irrigated barley genotypes in the brazilian savanna of the Federal District

Estimativas de parâmetros genéticos em genótipos de cevada irrigada no cerrado brasileiro do Distrito Federal

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ABSTRACT - Barley is an important crop for Brazil and an advantageous alternative for irrigated cultivation in the Brazilian Savanna. The present study aimed to characterize and estimate genetic, phenotypic, and environmental parameters and select genotypes from the Embrapa Cerrados irrigated barley working collection. The experiment was established in Randomized Blocks with four replications under irrigation in Embrapa Cerrados, Planaltina-DF. The traits evaluated were grain yield, commercial classification of first grains, 1000-seed weight, plant height, lodging, and cycle. The genetic parameters and correlations between the traits evaluated were obtained. High values of heritability, in a broad sense, were verified. The high coefficients of genotypic variance and the high selective accuracy obtained corroborate the favorable environmental condition for the selection of genotypes. It was verified that the genotypic correlations were higher than the phenotypic correlation coefficients, showing a greater contribution of genetic factors in the expression of the traits. Earlier genotypes had higher grain yields, first-class commercial classification, 1000-seed weight, and height. There was a strong positive correlation between the commercial classification of first grains and 1000-seed weight. Genotypes PFC 2005143, PFC 2006134, and PFC 2004212 were selected for use in crossbreeding blocks within the Brazilian irrigated barley breeding program.

Keywords: *Hordeum vulgare* L. Heritability. Genetic improvement.

RESUMO - A cevada é uma importante cultura para o Brasil e uma vantajosa alternativa para o cultivo irrigado no Cerrado. O objetivo deste trabalho foi caracterizar, estimar parâmetros genéticos, fenotípicos e ambientais e realizar a seleção de genótipos da coleção de trabalho de cevada irrigada da Embrapa Cerrados. O experimento foi estabelecido em Blocos casualizados com quatro repetições, sob irrigação, na Embrapa Cerrados, Planaltina-DF. As características avaliadas foram: rendimento de grãos, classificação comercial de primeira, peso de mil sementes, altura de planta, acamamento e ciclo. Foram obtidos os parâmetros genéticos e as correlações entre as características avaliadas. Foram verificados altos valores de herdabilidade, em sentido amplo. Os altos coeficientes de variância genotípica e a alta acurácia seletiva obtida corroboram a condição ambiental favorável para a seleção de genótipos. Verificou-se que as correlações genotípicas foram maiores que os coeficientes de correlação fenotípica, evidenciando uma maior contribuição dos fatores genéticos na expressão dos caracteres. Os genótipos mais precoces apresentaram maiores rendimentos de grãos, classificação comercial de primeira, peso de mil sementes e altura. Houve forte correlação positiva entre classificação comercial de primeira e peso de mil sementes. Os genótipos PFC 2005143, PFC 2006134 e PFC 2004212 foram selecionados para uso em blocos de cruzamento dentro do programa brasileiro de melhoramento de cevada irrigada.

Palavras-chave: *Hordeum vulgare* L. Herdabilidade. Melhoramento genético.

INTRODUCTION

The world barley production in 2021 was around 145 million tons (FAOSTAT, 2023), and Brazil participated only with 425 thousand tons (CONAB, 2023), corresponding to less than 0.30% of the world production. In 2021, Brazil imported 485 thousand tons of barley (FAOSTAT, 2023). In addition to the 425 thousand tons (CONAB, 2023) produced on national territory, domestic consumption was around 910 thousand tons of barley for the year. It is noted that there are two gaps to be filled: the first is to meet the deficit in the trade balance of this commodity in Brazil, and the second is the possibility of export since this grain is the fourth largest cereal consumed worldwide.

Initially, the cultivation of this grain was restricted to areas where climatic conditions were favorable, only in the South of the country whose winter is cold and rainy. With the increase in demand, the cereal became a reality of cultivation in other grain-producing regions, such as the Center-West, and is increasingly present in lower latitudes and geographically located in the Brazilian intertropical zone. This is a reality thanks to the improvement work done on this species, without which production on a commercial scale would not be feasible. Cultivation in the Brazilian Savanna presents several benefits already evidenced, such as healthier seeds, efficient water use by irrigation, and absence or reduced dormancy of the seeds.

Although there are already cultivars recommended for irrigated management in the Brazilian Savanna, such as BRS Sampa, BRS Demeter, BRS Savanna, BRS Manduri, and BRS 195 (AMABILE et al., 2014), there is still a

demand for cultivars better adapted to local soil and climate conditions. In order to exploit the production of this cereal more efficiently, further studies are needed to develop other genotypes better adapted to this specific environment and with high grain yield and quality, resistance to diseases, and lodging, among others.

Selection indexes are used as tools that help breeders simultaneously select for more than one trait of interest using or not genetic parameters or economic weights (SAYD et al., 2017). In search of superior genotypes that have high yield capacity and good morpho-agronomic traits and are better adapted to the conditions of the Brazilian Savanna, seen as the last agricultural frontier in the world and the main biome of the Center-West region, it is necessary to select genotypes for this purpose.

In the continuous search to obtain improved genotypes, there is a need to characterize the genetic resources in germplasm banks to know the available populations. This is done, for example, through studies of the genetic parameters of these populations, which are fundamental in making decisions regarding the use of genotypes in breeding programs. This study contributes to highlighting the genotypes with the desired traits and with quantitative and qualitative gains set by the program.

The present study aimed to characterize and estimate genetic, phenotypic, and environmental parameters and select genotypes from the Embrapa Cerrados irrigated barley working collection.

MATERIAL AND METHODS

We evaluated 17 barley genotypes from the working collection called Class A, a group that has been maintained in the germplasm bank of Embrapa Cerrados. Five cultivars were used as controls: BRS 180, BRS 195, BRS Sampa, BRS Savanna, and BRS Demeter. The experiments were conducted from May to September 2017 under the irrigation system via a center pivot. The conduction site was at Embrapa Cerrados – Centro de Inovação em Genética Vegetal (CIGV), Riacho Fundo II-DF, 15°54'55.4" S and 48°02'16.3" W, at an altitude of 1,100 m, under a typical, clayey, Latossolo Vermelho distrófico. The maximum air temperature recorded in the period covered was 33.3 °C, and the minimum was 7.6 °C. During the period, 13 mm of rain was recorded, with a maximum relative air humidity of 99.2%, a minimum of 11.4%, and an average of 55.3%.

The experimental design used was a randomized block design with four replications, with a density of 300 plants per m^2. In the sowing furrow, 16 kg ha^{-1} of N, 120 kg ha^{-1} of single superphosphate (P_2O_5), 64 kg ha^{-1} of potassium chloride (K_2O), and 40 kg ha^{-1} of N (urea) were applied at the emergence of the fifth fully expanded leaf, according to Amabile et al. (2008). There was no incidence of pests or pathogens during the trials. Weeds were controlled by applying the product pendimethalin. Irrigation was performed based on the Irrigation Monitoring Program in the Cerrado (EMBRAPA, 2023).

Six traits were evaluated: 1. grain yield - estimated grain yield (kg ha^{-1}); 2. CL1 - commercial classification of first grains (>2.5 mm), in percentage (%) (transformed data) (BRASIL, 1996); 3. TSW - 1000-seed weight (g) (BRASIL, 2009); 4. Height - plant height (cm), 30 plants per plot were measured when each genotype was in full head emergence; 5. Cycle - days after emergence to heading (days). 6. Lodging - degree of lodging, in percentage (%). Evaluations of grain yield, commercial classification of first grains, and TSW were made in the Seed Laboratory of Embrapa Cerrados. The other traits were evaluated in the field.

The data obtained were subjected to the Shapiro-Wilk and Bartlett tests in the "R" statistical program 3.6.1 version to verify their normality and homogeneity of variances. The data of CL1, collected in the percentage system, were submitted to a transformation in ARCSENx0,5.100^{-1}, where x = the load value at %, to obtain the normality of the distribution of errors. Subsequently, for all traits, the data were subjected to analysis of variance, and the means were grouped by the Scott-Knott test at 5% by the GENES program (CRUZ, 2013). Also, the coefficient of experimental variation (CV_e), the coefficient of genetic variation (CV_g), and the relative correlation coefficient (CV_r) were estimated for each trait. The phenotypic, genotypic, and environmental correlations were measured from the estimates of variances and covariances between phenotypic, genotypic, and environmental traits two by two, being determined according to Kempthorne (1966).

To perform the analysis of variance, the following statistical model was considered: $Y_{ij} = m + G_i + B_j + e_{ij}$, where: Y_{ij} = the obtained value related to the i-th genotype trait in the j-th block; m = overall average; G_i = effect of the i-th genotype (i = 1,2, …, g); B_j = effect of the j-th block (j = 1,2, ..., r); e_{ij} = random error (uncontrolled factors) and $e_{ij} \sim NID(0)$.

For lodging, as the normality of the data was not achieved, even with the transformation of the original data, the non-parametric Kruskal-Wallis test was used for data analysis.

RESULTS AND DISCUSSION

The analysis of variance of the data obtained for each trait showed the existence of significant effects of genotypes, and these effects were of high magnitude based on statistical analysis ($p \leq 0.05$) for all traits (Table 1). Such effects indicated the existence of genetic variability and differences among the studied accessions regarding the evaluated traits. The F value has often been used to indicate the degree of experimental accuracy. For Resende and Duarte (2007), the F value of genotypic evaluation trials should be greater than 5.26 to achieve the class of "very high" accuracy, which is recommended by Steel and Torre (1980), which provides an accuracy of 90% at least.

Table 1. Genetic and environmental parameters of the 22 barley genotypes of the Class A group for estimated grain yield (Yield), commercial first-grain classification (CL1), 1000-seed weight (TSW), plant height (Height), full head emergence (Cycle).

S.V.	D.F.	F-value				
		Yield	CL1	TSW	Height	Cycle
Blocs	3					
Genotypes	21	606.5334**	10.9428**	25.6054**	7.2257**	93.2829**
Error	63					
MSg		2,537,296.892	0.035038	104.973506	60.61039	47.112554
σ^2_g		633,278.404	0.007959	25.21846	13.055556	11.651876
σ^2_f		634,324.2231	0.008759	26.243377	15.152597	11.778139
σ^2_e		1,045.819039	0.0008	1.024917	2.097042	0.126263
h^2 (%)		99.8351	90.8616	96.0946	86.1605	98.928
CV_e (%)		0.714	4.856	4.616	3.121	1.063
CV_g (%)		8.79	7.656	11.449	3.894	5.105
CV_r		12.304	1.578	2.480	1.248	4.803
$\hat{r}_{\hat{g}g}$		0.999	0.953	0.980	0.928	0.995

*(MSg) mean square of the treatments, (σ^2_g) genotypic variance, (σ^2_f) phenotypic variance, (σ^2_e) environmental variance, (h^2 (%) heritability, (CV_e (%))coefficient of experimental variation, (CV_g (%)) coefficient of genetic variation, (CV_r), CV_g/CV_e ratio, and ($\hat{r}_{\hat{g}g}$) Selective accuracy.

The F-values found were adequate and fit in the very high accuracy class, according to Resende and Duarte (2007), meeting the requirements of the breeders for a selection decision. These authors indicate that observing only the coefficient of variation parameter (CVe) value is insufficient to make inferences about the experimental quality. Observing other statistics, such as the coefficient of genetic variation (CVg) and selective accuracy, is necessary.

All F-values found were greater than 5.26, with the lowest value observed for Height (7.23), followed by CL1 (10.94), TSW (25.61), Cycle (93.28), and Yield (606.53). The selective accuracy ranged from 92.8% for Height, through CL1 with 95.3%, TSW with 98%, Cycle with 99.5%, to 99.9% for Yield, considered high for all traits analyzed (Table 1). Values with the same classification were found in a work on the irrigated Brazilian savannah of Amabile et al. (2015). For the traits studied, the F-values were also higher than 5.26 and significant at 1% probability. For height and CL1, evaluated by Monteiro et al. (2020), in an Irrigated system in the Brazilian savanna, the F values did not exceed the recommended for high accuracy but showed significant differences at 1% probability, as in the study of Amabile et al. (2015).

The coefficient of genetic variation (CVg) is a parameter that allows deducing the magnitude of genetic variability present in populations and for different traits (RESENDE, 2002) and the proportionality of the gain concerning the mean (FALEIRO et al., 2002). All traits studied presented CVg greater than CVe (Table 1). A similar result for the same traits occurred in the studies of Amabile et al. (2015) and Sayd et al. (2017), conducted in the Brazilian savanna under irrigation, and it can be concluded that this is a favorable environment for selection and also favorable for better genotypic expression of this cereal. Table 1 shows that the CVg was higher than the CVe in all traits evaluated.

When analyzing the CVe value, the particularities of each trait and species evaluated should be considered (FERREIRA et al., 2016). The CVe values had a low

magnitude by the criteria of Pimentel-Gomes (2023), 0.71% for Yield, 1.06% for Cycle, 3.12% for Height, 4.62% for TSW, and 4.86% for CL1, indicating a high experimental precision.

Another way to relate the genotypic and environmental coefficients of variation is the ratio between CV$_g$/CV$_e$, called the relative coefficient of variation and presented in Table 1 as CV$_r$, used to quantify the available genotypic variability. According to Steel and Torre (1980), values above unity (>1) for the relative coefficient of variation demonstrate a high possibility of gain with the use of simple strategies such as mass selection. In this sense, the higher the CV$_r$, the more accurate the selection, increasing the probability of gain. Yield showed the highest CV$_r$ (12.30), showing that despite the complexity of genes involving this trait, in the conditions of this study the environment had great control, which allowed visualizing the genetic contribution to this trait. Even with lower CV$_r$ values for height (1.25), cycle (4.8), TSW (2.48), and CL1 (1.58), it was found that all were greater than 1.0, indicating that the genetic variance was greater than the variance due to the environment. This indicates that genetic gain may exist for these traits in the selection of the genotypes studied.

The success of a breeding program can be achieved by selecting traits with high heritability, indicating the possibility of obtaining genetic gains with selection for all traits. High magnitudes of the estimates of the broad-sense heritability indicated the existence of genetic variability. Consequently, the variance and heritability components with the genetic parameters are important for defining strategies for greater efficiency of the breeding program. In Table 1, the broad-sense heritability ranged from 86.16% (Height) to 99.84% (Yield), indicating that there was great genotypic variance in this population. For these traits, the results obtained agree with Amabile et al. (2017) and Sayd et al. (2019). Those authors also verified broad-sense heritability with barley under irrigation in the Brazilian Savanna above 90% for the same traits, indicating a predictive correspondence between

phenotypic and genetic value, as reported by Falconer and Mackay (1996), by Vencovsky and Barriga (1992). This proximity to the integer (100%) shows that environmental control was efficient and that the observed traits closely correlate with the genotypes in the working collection (BORÉM; MIRANDA; FRITSCHE-NETO, 2021). This elevated level of broad-sense heritability in the traits studied allows us to predict that it will be repeated in the next generations, and it is likely that it can also be introduced in new genotypes, with great possibility of success.

Between pairs of traits, it was found that the genotypic correlations for almost all traits, except for Height related to TSW, were in absolute values, higher than the phenotypic correlation coefficients. This shows the greater contribution of genetic factors in the expression of the traits. Similar results were observed by Ebrahim, Shiferaw and Hailu (2015) and Hailu et al. (2016) with clonal soma progenies in Ethiopia, and Amabile et al. (2015) and Sayd et al. (2019) under similar conditions to this study. The signs of the genotypic and phenotypic coefficients had the same sign in the phenotypic and genotypic correlations (Table 2). According to Cruz, Carneiro and Regazzi (2014), this fact is due to the absence of errors in sampling and evaluation. This was further verified between the correlations (Table 2) CL1 x Height, Yield x Cycle, CL1 x Cycle, TSW x Cycle and Height x Cycle. In all correlations, it can be observed that Cycle held a negative sign, meaning that the earlier the genotype is, all its traits have positively intensified expression to a greater or lesser extent. A strong correlation between TSW and CL1 was observed (Table 2). It is noted that the genotypes PFC 2006054 and PFC 2007105 had the best results in both traits, similar to those reported by Amabile et al. (2017). However, for Yield, the correlation with TSW is positive but low, similar to that found in Monteiro et al. (2018) and Sayd et al. (2019), which have negative correlations and low magnitudes.

Table 2. Correlation coefficients (phenotypic and genotypic) for estimated grain yield (Yield), commercial first-grain classification (CL1), 1000-seed weight (TSW), plant height (Height), and full head emergence (Cycle).

Correlation Coefficients (r)		Yield	CL1	TSW	Height	Cycle
Yield	r_f	1				
	r_g					
CL1	r_f	0.0977	1			
	r_g	0.0994				
TSW	r_f	0.1930	0.8479	1		
	r_g	0.1948	0.8924			
Height	r_f	0.4522	-0.0345	0.1049	1	
	r_g	0.4857	-0.0417	0.1017		
Cycle	r_f	-0.3778	-0.3477	-0.4719	-0.3981	1
	r_g	-0.3804	-0.3773	-0.4842	-0.4398	

*According to Dancey and Reidy (2017), correlation coefficients can be classified according to their magnitude, being: null correlation (r=0), weak ($0 < |r| \leq 0.30$), medium ($0.30 < |r| \leq 0.60$), strong ($0.60 < |r| \leq 0.90$), very strong ($0.90 < |r| \leq 1$) and perfect ($|r| = 1$).

The lowest correlations observed for Cycle, both phenotypic and genotypic, were with the trait CL1 with values of -0.3477 and -0.3773, respectively. This correlation was negative for Sayd et al. (2019), but in their work collection, it was much less intense, with rf and rg values of -0.0139 and -0.0141, respectively. Whereas for Amabile et al. (2015), besides being positive this correlation also had low magnitude, 0.0428 and 0.0417. It is inferred that the environment of this experiment allowed better express the genotypic reality of the correlations, which were of greater magnitude. As the working collections differed from this experiment and had more similarities, since both had been selected for high yield, this may explain part of the result obtained. For Cycle, correlations were observed with TSW: r_f -0.4719 and r_g -0.4842. Mean expression, close to 50% inversely proportional, meaning that an earlier genotype has great chances of expressing in this environment high values of TSW and consequently CL1.

In the grouping test among means, for the yield (Table 3), the three genotypes that stood out the most were the genotypes PFC 2005143 (10,737 kg ha^{-1}), PFC 2004212 (10,273 kg ha^{-1}), and PFC 2005142 (10,140 kg ha^{-1}), both had grain yields above 10 tons ha^{-1}, but showed statistical differences among themselves (Table 3). These genotypes had higher yields than the registered and released controls, BRS 180 (9,254 kg ha^{-1}), BRS Savanna (9,197 kg ha^{-1}), BRS Demeter (9,158 kg ha^{-1}), BRS Sampa (8,504 kg ha^{-1}), and BRS 195 (8,069 kg ha^{-1}), all grouped in the same cluster. The estimated grain yield values are higher than the averages found by Amabile et al. (2017) and Sayd et al. (2019) and are higher than the national average of 3.864 kg ha^{-1} in 2023 (CONAB, 2023), so the effect of the positive on the high yields obtained during the year is clear.

Table 3. Averages of the 22 barley genotypes for estimated grain yield (Yield), commercial first-grain classification (CL1), 1000-seed weight (TSW), plant height (Height), full head emergence (Cycle), and percentage of lodged plants (Lodging).

Yield			CL1[*]			TSW		
PFC 2005143	10,737.00	a	PFC 2006054	95.25	a	PFC 2006054	54.45	a
PFC 2004212	10,273.00	b	PFC 2007105	93.25	a	PFC 2007105	54.30	a
PFC 2005142	10,140.25	c	PFC 2006053	92.75	a	PFC 2005138	49.68	b
PFC 2006134	9,749.00	d	PFC 2005143	92.25	a	PFC 2006053	49.13	b
PFC 2005138	9,504.00	e	PFC 2007098	91.75	a	PFC 2007125	48.98	b
98046/MERIT	9,479.50	e	PFC 2005138	88.25	b	PFC 2007098	46.53	c
PFC 2007125	9,453.50	e	PFC 2007125	87	b	PFC 2005143	45.55	c
BRS 180	9,253.75	f	PFC 2004033	84.5	c	PFC 2004033	45.28	c
PFC 2007098	9,234.00	f	BRS Deméter	84	c	PFC 2004212	44.88	c
BRS Savanna	9,196.75	f	PFC 2004216	83.75	c	PFC 2006134	44.43	c
BRS Deméter	9,158.25	f	PFC 2004345	83.5	c	PFC 2005142	44.23	c
PFC 2004345	9,135.75	f	PFC 2003054	83.25	c	BRS Deméter	43.50	d
PFC 2006053	9,063.75	g	PFC 2006134	81.5	c	98046 /MERIT	42.33	d
PFC 2006054	8,997.75	g	BRS 195	81	c	PFC 2005145	42.20	d
PFC 2005145	8,981.25	g	PFC 2004212	80.75	c	PFC 2003054	39.48	e
PFC 2003054	8,508.00	h	PFC 2005142	79.25	d	PFC 2004216	39.40	e
BRS Sampa	8,503.50	h	PFC 2005145	78.75	d	PFC 2004345	39.38	e
PFC 2007105	8,108.50	i	BRS Savanna	78	d	BRS Savanna	39.38	e
BRS 195	8,068.75	i	98046/MERIT	77	d	BRS 195	39.23	e
PFC 2004216	7,904.75	j	BRS Sampa	77	d	PFC 2005141	38.70	e
PFC 2004033	7,882.75	j	PFC 2005141	75.25	d	BRS Sampa	37.90	e
PFC 2005141	7,821.50	j	BRS 180	72.75	d	BRS 180	36.08	e
Height			Cycle			Lodging[**]		
BRS Savanna	98.50	a	BRS Sampa	72.75	a	PFC 2004212	30	a
PFC 2004212	97.25	a	BRS 195	72.00	a	PFC 2005141	20	a
PFC 2007098	96.00	a	BRS Deméter	71.75	a	98046/MERIT	5	ab
PFC 2005141	95.75	a	PFC 2004033	71.25	b	BRS Savanna	5	ab
PFC 2006134	95.50	a	PFC 2003054	71.00	b	BRS 180	0	b
PFC 2006053	95.00	a	PFC 2004345	70.75	b	PFC 2004345	0	b
PFC 2006054	94.75	a	BRS 180	68.75	c	PFC 2005138	0	b
PFC 2004345	94.50	a	PFC 2005138	67.75	d	PFC 2005142	0	b
PFC 2005142	94.25	a	PFC 2004216	67.25	d	PFC 2005143	0	b
PFC 2005138	94.25	a	PFC 2007125	66.75	d	PFC 2005145	0	b
PFC 2007125	93.75	a	PFC 2004212	66.75	d	PFC 2006053	0	b
98046/MERIT	93.50	a	PFC 2005141	66.25	e	PFC 2006054	0	b
BRS 195	93.50	a	PFC 2005143	65.50	e	PFC 2006134	0	b
PFC 2004033	93.25	a	PFC 2006134	64.50	f	PFC 2007105	0	b
BRS 180	92.75	a	PFC 2005145	64.50	f	BRS195	0	b
PFC 2005145	92.50	a	PFC 2007105	64.25	f	PFC 2007125	0	b
BRS Deméter	92.50	a	PFC 2006053	64.00	f	PFC 2007098	0	b
PFC 2005143	92.25	a	BRS Savanna	63.75	f	BRS Sampa	0	b
PFC 2003054	87.00	b	98046/MERIT	63.50	f	BRS Deméter	0	b
PFC 2007105	85.50	b	PFC 2006054	63.50	f	PFC 2003054	0	b
PFC 2004216	85.25	b	PFC 2005142	63.50	f	PFC 2004033	0	b
BRS Sampa	84.00	b	PFC 2007098	61.00	g	PFC 2004216	0	b

Means grouped by the Skott-Knott test at 5% significance. Means followed by the same letter do not differ statistically. *Data collected in percentage system. and submitted to transformation [=ASEN(RAIZ(CL1/100))]. ** The non-parametric Kruskal-Wallis test was used to analyze these data.

As for CL1, four large groups were observed. The first (a), with the commercial classification of first grains higher than 90%, is composed of the genotypes PFC 2006054, PFC 2007105, PFC 2006053, PFC 2005143, and PFC 2007098. This trait is very desired by the industry, and high values as those presented by the genotypes above draw a lot of attention. The second (b) represented by PFC 2005138 and PFC 2007125 and with an average close to 88%, presenting higher averages than the controls when they were launched (BRS Sampa 75%, BRS Savanna 82%, BRS 180 82% and BRS Demeter 85%), similar values found in Amabile et al. (2017) and higher than Sayd et al. (2019). The third Group (c) presents genotypes that are still within the stipulated by ORDINANCE 691 (BRASIL, 1996) and preferred by the industry, with first classification higher than 80%, represented by the genotypes PFC 2004033 (85%), BRS Deméter (84%), PFC 2004216, PFC 2004345, PFC 2003054, PFC 2006134, BRS 195 (81%), and PFC 2004212 (81%). The analysis of Yield and CL1 allows the relation of high-yield genotypes with grain size required by the market. Except for the cultivars BRS 180 and BRS Savanna, the genotypes are two-row and theoretically tend to produce larger grains and achieve higher percentages of grains with the first classification. Except for BRS Sampa, this can be observed in these experimental data, showing the two-row cultivars with more grains in CL1. Therefore, it is necessary to evaluate the grain quality for malting or what the production will be destined for in future work.

For TSW, five groups were ranked, with PFC 2006054 and PFC 2007105 genotypes standing out with no statistical difference and grouped together, with TSW of 54.45 g and 54.3 g, respectively. Amabile et al. (2017) and Sayd et al. (2019) observed values close to these.

Only two statistically distinct groups made up the Height, with only four genotypes (PFC 2003054, PFC 2007105, PFC 2004216, and BRS Sampa) showing values less than 90 cm. According to Amabile et al. (2015), the low height of the genotypes should be explored in breeding programs to avoid lodging.

A positive and median correlation is observed between Height and Yield (Table 2). This makes it difficult to select these genotypes seeking low height since grain yield is an important trait in most breeding programs. Among the genotypes evaluated, those that obtained the highest grain yields were those with the greatest heights (Table 3): [PFC 2005143 (10,737 kg ha^{-1} and 94.5 cm), PFC 2004212 (10,273 kg ha^{-1} and 97.25 cm), and PFC 2005142 (10,140 kg ha^{-1} and 94.25 cm)]. With a view to grain yield, these would be genotypes that can be part of crossbreeding blocks with genotypes of smaller size.

In the Cycle, seven groups were formed. PFC 2007098 is the genotype with the shortest cycle (61 days), followed by a large group composed of PFC 2005142, PFC 2006054, 98046/MERIT, BRS Savanna, PFC 2006053, PFC 2007105, PFC 2005145, PFC 2006134, with a cycle between 63.5 and 64.5 days. BRS Savanna (Control), present in this group, showed an average of 56 days in its release, lower than even the earliest of the genotypes studied. Isolated, BRS 180 (68.75 days) composed the fifth group, much higher than its release in 1999, where it had an average cycle of 58 days. The last two groups have three genotypes each, the sixth group with PFC 2004033, PFC 2003054, and PFC 2004345, and the seventh with BRS Sampa, BRS 195, and BRS Demeter); the last group has the longest cycle, with an average of 72.17 days. The averages of all the controls were above even the release of each cultivar, most likely due to climatic conditions; it is clear that the positions in case of a ranking with absolute numbers for this trait would be maintained, being the six-row earlier and the two-row later. We can observe in Table 2 that for this trait, all correlations were negative and classified as medium. The earlier genotypes tend to have a higher yield, CL1, and TSW.

The Kruskal-Wallis test was used for the statistical study of lodging since the data did not reach normality, a prerequisite for parametric tests. Two groups were defined, and one overlapped due to the test. In the first group, with higher lodging, PFC 2004212 (average of 30%) and PFC 2005141 (average of 20%) did not differ statistically. This was followed by BRS Savanna and 98046/MERIT (with an average of 5%), which overlapped between the two groups (Table 3). The genotypes BRS 180, PFC 2004345, PFC 2005138, PFC 2005142, PFC 2005143, PFC 2005145, PFC 2006053, PFC 2006054, PFC 2006134, PFC 2007105, BRS195, PFC 2007125, PFC 2007098, BRS Sampa, BRS Deméter, PFC 2003054, PFC 2004033, and PFC 2004216 did not lodge, which is a result of an effective selection pressure to avoid this agricultural problem, extremely important for the production system of irrigated barley in the Brazilian Savanna. It can be observed that the cultivars that were used as control either did not lodge or lodged at low values. This demonstrates the selection pressure that they have already undergone for this trait.

CONCLUSIONS

The high values of heritability (h^2) and the low values of the environmental variation coefficients, allow inferring that the genetic variance had more influence on the phenotypic variance observed. The high coefficients of genotypic variance and the high selective accuracy obtained indicate favorable environmental conditions for the selection of genotypes considering the traits studied. For the Cycle, the correlations had a negative sign with all the other traits, demonstrating that earlier genotypes have higher grain yields, commercial classification of first grains, 1000-seed weight, and height. A strong positive correlation was found between commercial first-grain classification and 1000-seed weight. The genotypes PFC 2005143, PFC 2006134, and PFC 2004212 stand out agronomically and have the potential to be used in crossbreeding blocks within the Brazilian irrigated barley breeding program.

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