

Genetic parameters and agronomic characterization of hulless barley accessions under irrigation in the savanna

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ABSTRACT: The purpose of this study was to estimate the genetic parameters and to agronomically characterize 18 accessions of hulless barley and three references of covered barley grains belonging to the Embrapa Recursos Genéticos e Biotecnologia germplasm bank, using ten agronomic quantitative traits. The experiment was performed at two sites in Distrito Federal, in May 2012, using the experimental design of randomized blocks with three replicates. The evaluated characteristics were: estimated grain yield, plumpness kernel, thousand seeds weight, plant height, lodging, days to heading, hectoliter weight, and grain protein content. The obtained data were subjected to the variance analysis and the grouped means by Scott-Knott test. Significant differences at 1% of probability were found among the accessions for all the evaluated traits. It is possible to obtain genetic gains due to the high values of the genotypic coefficient of variation. High heritability in the broad sense was observed for all the characteristics, except for protein content, enabling the effective selection of traits of interest from the parents to the descendants. The accessions CI 13453, CN Cerrado 1, CN Cerrado 2, CN Cerrado 5 and PI356466 stood out positively among the others to Yield and Lodging.

Key words: genetic resources; genetic variability; heritability

Parâmetros genéticos e caracterização agrônômica de acessos de cevada nua sob irrigação no Cerrado

RESUMO: O objetivo deste trabalho foi estimar os parâmetros genéticos e caracterizar agronomicamente 18 acessos de cevada nua, e 3 testemunhas de cevada com grãos cobertos pertencentes ao banco de germoplasma da Embrapa Recursos Genéticos e Biotecnologia, utilizando dez caracteres agrônômicos quantitativos. O experimento foi realizado em dois locais no Distrito Federal, em maio de 2012, utilizando um delineamento experimental de blocos ao acaso com três repetições. As características avaliadas foram: rendimento de grãos, classificação comercial, peso de mil sementes, altura de plantas, acamamento, ciclo de espigamento, peso hectolítrico e teor de proteína no grão. Os dados obtidos foram submetidos à análise de variância e as médias agrupadas pelo teste de Scott-Knott. Foram detectadas diferenças significativas a 1% de probabilidade entre os acessos para todas as características avaliadas. Há possibilidade de se obter ganhos genéticos devido aos elevados valores do coeficiente de variação genotípico. Foi observada alta herdabilidade em sentido amplo para todas as características, exceto para teor de proteína, possibilitando a seleção efetiva de características de interesse dos genitores para seus descendentes. Os acessos CI 13453, CN Cerrado 1, CN Cerrado 2, CN Cerrado 5 e PI356466 destacaram-se positivamente dos demais para rendimento de grãos e acamamento.

Palavras-chave: recursos genéticos; variabilidade genética; herdabilidade

Introduction

Hulless barley (*Hordeum vulgare* L. var. *nudum* Hook. f.) was domesticated about 2.000 years after the covered barley grain, approximately at 6.000 A.C. The main difference between them is that in the hulless barley grain the lemma and palea are non-adherent and presents different nutritional composition. For centuries, hulless barley has been mainly as human food and animal feed (considered as a functional food) and in a lesser scale for malting (Bhatty, 1999).

The use of barley in the nutraceutical industry has recently emerged because of the high content of beta glucans. For malting purposes, the cultivars include hulless and covered varieties, but the hulless barley is usually preferred for its flavor and aids filtering during the brewing process (Sayd et al., 2017).

In Brazil, the hulless barley has been grown only in experimental sites so that researches can study its potentially. In these studies, it is fundamental to perform an economical characterization since the identity of each accession should be known through a series of data allowing the evaluation of its genetic variability in order to avoid the duplication and narrowing of the genetic base of each species. Complementing the accessions characterization, the genetic parameters estimate is the genetic breeding tool used to quantify the existing variability among the collections, which results in a more efficient selection and evaluation process. The genetic gains directly depend on the available variability as well as on the traits of interest that are inherited (Mohammadi & Prassana, 2003).

The purpose of the current study was to agronomically characterize and estimate the genetic parameters of hulless

barley accessions in two environments under irrigation in the savanna located in the Central part of Brazil.

Material and Methods

The experiments were performed from May to September 2012 in two different environments under central pivot irrigation. Environment 1 (CPAC), Planaltina-DF, located at 15°35'30" S latitude and 47°42'30" W longitude and 1.007 m above sea level, in a dystrophic Dark Red Latossol soil with clay texture. On the other hand, Environment 2 (SPM), located at Recanto das Emas - DF at 15°54'53" S latitude and 48°02'14" W, and 1.254 m above sea level, in a typical dystrophic Red Latossol soil with clay texture.

Eighteen hulless barley accessions (two and six-rowed) along with three witnesses of covered barley grain from all over the world from a germplasm bank belonging to Embrapa Recursos Genéticos e Biotecnologia were evaluated (Table 1). The experimental design was random block with three replicates. Five meters long plots with six rows spaced 20 cm apart were used in all trials with a useful area of 4.8 m² for each plot, with a density of 300 plants m². According to the results from the soil analysis, 16 kg ha⁻¹ of N; 120 kg ha⁻¹ of P₂O₅; 64 kg ha⁻¹ of K₂O and 40 kg ha⁻¹ of N were used in the seeding when the fifth leaf was present and totally unfolded.

The following traits were evaluated: 1. EGY - estimated grain yield (kg ha⁻¹); 2. PK- plumpness kernel (%) (grains wider than 2.5 mm); 3. TSW - thousand seed weight (g); 4. PH - plant height (cm); 5. Lodg - lodging degree (zero value for minimum or inexistent lodging and a value of 100 for maximum lodging); 6. DH - days to heading (when silking emergence up to 50% of spikes in the useful area of the parcel

Table 1. Barley accessions characterized in the current study and their respective continent of origin, country of origin, type of heading, type of spikes and type of bark. CPAC/SPM, DF, 2014.

	Accessions	Continent of origin	Country of origin	Types of spike	Types of bark
1	CI 13453	Europe	Romania	Two-rowed	Hulless
2	CI 09976	Africa	Ethiopia	Six-rowed	Hulless
3	CN Cerrado 4	North America	Brazil	Two-rowed	Hulless
4	PI 356474	Africa	Ethiopia	Six-rowed	Hulless
5	CI 12931	Africa	Ethiopia	Six-rowed	Hulless
6	CN Cerrado 1	North America	Brazil	Two-rowed	Hulless
7	CI 14150	Asia	Mongolia	Six-rowed	Hulless
8	CI 09459	Asia	South Korea	Six-rowed	Hulless
9	295418	North America	Brazil	Two-rowed	Covered
10	CN Cerrado 2	North America	Brazil	Two-rowed	Hulless
11	CI 06440	Europe	Poland	Two-rowed	Hulless
12	164321	Africa	Ethiopia	Six-rowed	Covered
13	CI 09977	Africa	Ethiopia	Six-rowed	Hulless
14	CN Cerrado 5	North America	Brazil	Two-rowed	Hulless
15	CN Cerrado 6	North America	Brazil	Two-rowed	Hulless
16	193011	Oceania	Australia	Two-rowed	Covered
17	PI 356466	Africa	Ethiopia	Six-rowed	Hulless
18	CI 07650	Asia	India	Six-rowed	Hulless
19	CI 09969	Africa	Ethiopia	Two-rowed	Hulless
20	CI 09928	Asia	China	Six-rowed	Hulless
21	PI 370799	Europe	Switzerland	Six-rowed	Hulless

was visible) in days; 7. HW - hectoliter weight (kg hL^{-1}); and 8. Protein - total protein content (%) using the Kjeldahl method. Nitrogen analysis to measure the grain protein content was performed in the laboratory, while the evaluations of plant height, lodging degree and days to heading were held in the experimental sites of CPAC and SPM. The studies of EGY, PK, TSW and HW were performed in the laboratory located in Planaltina, Brazil.

Data were analyzed by using analysis of variance and the comparative means through the Scott-Knott (significance level of 1%). The experimental coefficient of variation (eCV), genetic coefficient of variation (gCV) and relative coefficient of variation (rCV) were also estimated for each of the traits with the aid of Genes program (Cruz, 2013). Individual and joint analyses of variance for each trait were performed. The presupposition for the performance of the joint analysis of independence for the residual mean square (RMQ) was evaluated by the relation of RMQ in both sites.

The estimate of heritability at mean level (h^2), coefficients of experimental variance (CEv), coefficient of genetic variation (CGv) and relative variation (CRv) for each of the traits analyzed in the current study was calculated using Genes program (Cruz, 2013).

Results and Discussion

The analysis of joint variance (Table 2) showed the existence of significant differences at 1% ($p = 0.01$) among the genotypes for all traits. Such differences indicate the existence of a high variability among the genotypes of hulless barley. The high variability was expected because the genotypes had different origins. Significant environment effects at 1% were also verified for EGY, TSW, Height and Lodg, while for DH, HW and Protein were significant at 5% ($p = 0.05$). The effect of the interaction genotype x environment was also evidenced for all evaluated traits except for Protein Content (Table 2). This interaction contributes to the highest phenotypic variability of quantitative traits as reported by Molina-Cano et al. (1997).

High values of F for different effects indicate a good experimental accuracy (Resende & Duarte, 2007). Another factor that shows the experimental accuracy is the environmental coefficient of variation (eCV), which showed low magnitudes for all traits except for Lodg (25.66) (Table 2). Žáková & Benková (2006) and Amabile et al. (2015) in their studies have already reported that the trait Lodg is highly affected by the environment, being a trait that is visually evaluated, with a certain degree of subjectivity.

Heritability is directly related to the genotypic variation and experimental accuracy determining how the phenotypic value represents the genotypic value of each evaluated trait. High values for broad sense heritability, that is, based on the average, were found for all traits, except for Protein. The h^2 for EGY was 99.45% (Table 2), being higher than the figures found by Amabile et al. (2015) (96.72%), Marquez-Cedillo et al. (2001) (83%) in covered barley genotypes and by Ajith (2009) who found values close to 60% when researching hulless barley accessions. According to Al-Yassin et al. (2005), the heritability for EGY varies a lot within species because of the genetic difference among accessions and the environment where the study is being held.

Trait "grains wider than 2.5 mm (PK)" showed the greater heritability (99.88%) (Table 2). Values of such magnitude were also reported by Fox (2008), who found out h^2 ranging from 89 to 99% and Amabile et al. (2015) who reported a value of 96.67%. Ajith (2009) and Monteiro et al. (2018) described values for h^2 superior to 80%.

Chand et al. (2008) and Amabile et al. (2015) found high values of h^2 (99.9 and 97.32%, respectively) in elite collections when studying the trait TSW, corroborating with the value observed in the present study (98.75%) (Table 2). Different values ranging from 63.7 to 85.6% were described by Therrien (2006) and Jalata et al. (2011). Therrien (2006) stated that lower values were observed when performing experiments in environments with different climates and water supply. The high values for h^2 might be explained by the climate stability found in the savanna during the dry

Table 2. Analyses of variance and parameters for the traits: estimated grain yield (EGY), plumpness kernel (PK), thousand seed weight (TSW), plant height (Height), plant lodging (Lodg), days to heading (DH), hectoliter weight (HW) and total protein (Protein) evaluated in 21 barley accessions in two different sites. CPAC/SPM, DF, 2014.

VF	G.L.	Values of F							
		EGY	PK	TSW	Height	Lodg	DH	HW	Protein
Blocks/Environment	4								
Blocks	2								
Block X Environment	2								
Genotype	20	180.1**	833.1**	79.8**	11.4**	22.7**	9.2**	24.1**	4.2**
Environment	1	475.6**	133.2**	48.0**	21.8**	520.4**	10.5*	13.1*	15.5*
G X E	20	130.6**	54.8**	24.8**	13.2**	8.6**	2.4**	3.5**	0.6
Residual	80								
h^2 (%)		99.45	99.88	98.75	91.29	95.60	89.17	95.86	76.5
gCV		24.06	68.38	18.43	6.62	48.81	5.44	6.09	8.03
eCV		4.40	5.80	5.08	5.01	25.66	4.64	3.10	10.89
rCv		5.46	11.77	3.62	1.32	1.90	1.17	1.96	0.73

**significant by the F-test, at 1% probability.

* significant by the F-test, at 5% probability.

season, when the crops are planted under irrigation, uniform soil and are get different treatments during the experiments.

The heritability observed for Height was 91.29% (Table 2). Similar numbers (96% and 92.43%, respectively) was described by Amabile et al. (2015). Monteiro et al. (2018) in his study found that the heritability was 44.42%. Most of the values for h^2 are high, being therefore favorable for the direct selection.

When h^2 was 95.6% (Table 2), the selection of genotypes with lower values should contribute for more adjusted lineage, once lodged plants are not harvested at the field, taking into consideration the considerable loss of productivity. A similar value was observed by Monteiro et al. (2018), however other researches have shown a broad sense heritability lower than 53% (Gut et al. 2004; Amabile et al., 2015).

The heritability reported for DH was 89.17%, being relatively high (Table 2). Marquez-Cedillo et al. (2001) and Monteiro et al. (2018) stated values higher than 90% for this trait due to an appropriate environment control. However, other authors reported lower h^2 (Gut et al., 2004) indicating that the accuracy and experimental precision is fundamental for the phenotypic expression and that the selection might not be so effective in determined experimental conditions.

As for the Hectoliter Weight, the h^2 was 95.86% (Table 2), a number that is close to the one found by Marquez-Cedillo et al. (2001) (97%) and the superior limit reported by Fox (2008) (74% to 94%) being higher than the values described by Tinker et al. (1996), which ranged from 37% to 77%.

The high values for heritability observed in the current study might be explained by the irrigation control and other cultural traits and also the absence of other types of stress resulting in a better opportunity for the gene expression in the phenotype, when compared to the expression of genes in sites with different stress indexes and lower environment control (Annicchiarico et al., 2005).

When evaluating all traits, only the Protein Content did not result in high values of heritability ($h^2 = 76\%$) (Table 2) because of the great environment influence on this trait. Amabile & Faleiro (2014) explained that the barley grown in the savanna has high protein index probably due to high temperatures and low humidity that generally are present in the grain filling period. Fox (2008) found that the heritability for protein ranges from 60% to 80%, as opposed to Ajith (2009) who observed a heritability inferior to 40%.

Besides the heritability, another important parameter to analyze the experimental accuracy is the genotypic coefficient of variation (gCV) that quantifies the magnitude of the genetic variability presents at the genotype group evaluated for different traits (Resende & Duarte, 2007). It is important to consider the ratio gCV and eCV, that is, rCV. When the value of gCV is superior to eCV, that means the genotype contribution is higher than the environmental effect in the phenotypic expression, therefore, it is a trait which evaluation in this specific experimental condition is favorable to the breeding processes. Table 2 shows that

the gCV was higher than eCV for all traits, except for Protein Content (0.73%). Therefore, it can suggest a higher genetic contribution in relation to the environmental effect for the selection of accessions based on the phenotype. The highest value for this parameter was found for PK (11.77%) and Lodg (5.46%).

When studying the agronomic performance, the significance of the interaction genotypes x environments for all evaluated traits shows that the effects of the treatments and sites do not explain all the variation observed because of the different behaviors, when using different treatments at the sites where the studies were performed. This result suggests that the analysis of different genotypes in each separate environment is necessary along with a selection of genotypes specific for each site and/or the identification of those that do not present great variations in the two sites evaluated (Table 3 and 4).

As for trait Grain Yield at CPAC, hulless barley genotypes showed an average of 3.576 kg ha⁻¹, being higher than the mean presented by covered genotypes used in the current study (3.358 kg ha⁻¹). Several studies have mentioned a higher EGY in covered barley when compared to hulless (Amabile et al., 2017; Sayd et al., 2017) however, there is certainly a huge genetic variability among the hulless barley accessions, enabling the selection and development of cultivars which productivity is close to covered barley grain accessions. The hulless barley genotype that showed the highest EGY at CPAC was Ethiopian PI 356466 (6.639 kg ha⁻¹), which clustered separated from all other genotypes, and close to the the Brazilian genotype CN Cerrado 4 (5.551 kg ha⁻¹). These values were higher than the ones found by Brooks et al. (2012). The covered barley grain that presented the highest EGY was the Ethiopian six-rowed 164321 (3.649 kg ha⁻¹) and the grain with the lowest EGY was 295418 (3.185 kg ha⁻¹). These results in EGY found for covered barley grain accessions were inferior to the ones observed in elite genotypes developed and selected for a crop grown under irrigation in the savanna (Amabile et al., 2013). This result evidences the importance of performing researches related to genetic selection and breeding to obtain new superior genotypes adjusted to the conditions of the Brazilian savanna. Genotypes that expressed the lowest figures concerning EGY were CI 09977 (2.239 kg ha⁻¹), CI 09459 (2.349 kg ha⁻¹) and PI 356474 (2.381 kg ha⁻¹), being clustered in the same group (Table 3). The high productivity variation evidences the possibility of obtaining genetic gains with the selection of promising genotypes.

The mean for hulless barley genotypes evaluated at SPM was 5.028 kg ha⁻¹, being considered high for hulless barley. As for the covered grain accessions, the mean was 6.928 kg ha⁻¹, which is superior to hulless barley accessions. From a total of 18 hulless barley genotypes, 14 showed a value above 4.000 kg ha⁻¹, indicating the great potential to be grown in the savanna under irrigation. Control 295418 was the genotype that showed the highest EGY (8.500 kg ha⁻¹). As for covered grain accession 164321 that showed a great EGY when studied at CPAC, it presented the lowest

Table 3. Average estimated grain yield (EGY), plumpness kernel (PK), thousand seed weight (TSW) and plant height (Height) in 18 hulless barley accessions and three covered barley witnesses evaluated in experimental sites at Embrapa Cerrados (CPAC) and Embrapa Produtos e Mercado (SPM). CPAC/SPM, DF, 2014.

Genotype	EGY (kg ha ⁻¹)				PK (%)				TSW (g)				Height (cm)			
	CPAC		SPM		CPAC		SPM		CPAC		SPM		CPAC		SPM	
CI 13453	3.805	d	5.520	d	31.0	d	55.7	e	42.0	c	52.3	a	112.3	a	99.0	a
CI 09976	3.527	e	6.226	c	5.0	g	17.7	j	42.2	c	36.5	d	85.3	b	100.7	a
CN Cerrado 4	5.551	b	4.204	f	42.7	c	47.0	f	41.8	c	41.7	c	100.3	a	101.3	a
PI 356474	2.382	h	5.353	d	8.3	g	9.0	k	34.8	d	42.5	c	85.7	b	98.3	a
CI 12931	4.154	c	5.341	d	5.0	g	8.3	k	39.2	d	34.5	d	82.3	b	85.0	b
CN Cerrado 1	3.492	e	5.185	d	85.0	a	90.0	a	50.3	a	51.5	a	89.7	b	82.7	b
CI 14150	3.848	d	3.769	f	29.3	e	53.7	e	35.2	d	22.0	f	85.0	b	90.0	b
CI 09459	2.349	h	2.877	g	7.0	g	9.0	k	32.6	d	14.2	g	72.7	b	104.0	a
295418	3.186	f	8.500	a	82.7	a	84.0	b	41.2	c	46.3	b	79.7	b	97.7	a
CN Cerrado 2	3.332	f	2.204	h	83.3	a	84.0	b	50.8	a	51.8	a	82.3	b	85.3	b
CI 06440	2.643	g	3.959	f	20.0	e	32.0	g	46.3	b	42.0	c	84.0	b	98.0	a
164321	3.649	e	5.127	d	64.3	b	67.0	c	50.7	a	41.8	c	76.7	b	89.0	b
CI 09977	2.239	h	4.191	f	24.0	e	33.0	g	35.7	d	41.2	c	76.7	b	90.3	b
CN Cerrado 5	3.906	d	7.749	b	24.7	e	28.3	h	34.2	d	35.3	d	90.7	b	97.7	a
CN Cerrado 6	2.659	g	7.621	b	63.3	b	62.7	d	36.5	d	40.5	c	92.0	b	85.3	b
193011	3.239	f	7.157	b	25.7	e	33.3	g	31.8	d	30.8	e	107.3	a	83.3	b
PI 356466	6.639	a	7.533	b	35.0	d	10.0	k	36.5	d	38.5	c	83.7	b	98.3	a
CI 07650	4.316	c	4.136	f	25.3	e	24.0	i	52.0	a	31.7	e	111.0	a	96.0	a
CI 09969	3.535	e	4.640	e	34.7	d	54.0	e	46.0	b	53.7	a	83.3	b	102.7	a
CI 09928	2.564	g	5.840	d	15.0	f	53.0	e	34.3	d	35.8	d	77.3	b	99.0	a
PI 370799	3.442	e	4.170	f	14.7	f	2.0	l	32.8	d	32.3	e	84.3	b	95.7	a
Mean CN ¹	3.577		5.029		30.7		37.4		40.2		38.8		87.7		95.0	
Mean (T) ²	3.358		6.928		57.6		61.4		41.2		39.7		87.9		90.0	
General Mean	3.546		5.300		34.6		40.8		40.3		38.9		87.7		94.3	

¹Mean for 18 hulless barley accessions; ²Mean for three covered barley accessions; Scott-Knott test at 1 % significance showed that there was no difference among the means followed by the same capital letter in the line and by the small letter in the column, in each evaluated trait.

Table 4. Average plant lodging (Lodg), days to heading (DH), hectoliter weight (HW) and total protein content (Protein) in 18 hulless barley accessions and three covered barley witnesses evaluated in experimental sites at Embrapa Cerrados (CPAC) and Embrapa Produtos e Mercado (SPM). CPAC/SPM, DF, 2014.

Genotype	Lodg (%)				DH (days)				HW (kg ha ⁻¹)				Protein (%)			
	CPAC		SPM		CPAC		SPM		CPAC		SPM		CPAC		SPM	
CI 13453	100.0	a	100.0	a	63.0	a	67.7	c	71.6	a	73.7	a	17.7	a	15.1	a
CI 09976	100.0	a	100.0	a	64.3	a	63.3	c	73.1	a	74.1	a	18.5	b	16.4	a
CN Cerrado 4	0.0	c	45.0	b	67.7	a	64.7	c	62.3	b	75.0	a	16.7	a	13.7	a
PI 356474	50.3	b	100.0	a	64.3	a	64.7	c	74.2	a	74.7	a	17.7	b	15.3	a
CI 12931	84.0	a	100.0	a	64.3	a	64.0	c	74.3	a	73.4	a	18.4	b	15.7	a
CN Cerrado 1	27.6	c	73.3	a	65.0	a	65.3	c	65.3	b	67.0	b	21.4	b	18.3	a
CI 14150	67.0	b	100.0	a	64.0	a	63.7	c	71.6	a	72.5	a	16.8	b	15.1	a
CI 09459	33.3	c	100.0	a	66.0	a	68.7	b	75.4	a	73.6	a	15.8	b	13.8	a
295418	0.0	c	6.7	c	64.7	a	66.0	c	65.8	b	66.7	b	16.4	b	13.3	a
CN Cerrado 2	0.0	c	0.0	c	64.0	a	65.0	c	72.5	a	70.6	a	20.4	b	19.5	a
CI 06440	0.0	c	100.0	a	64.7	a	65.0	c	72.6	a	73.4	a	17.7	b	16.9	a
164321	50.0	b	100.0	a	53.7	b	54.3	d	64.6	b	59.3	c	17.1	b	13.2	a
CI 09977	50.0	b	100.0	a	64.3	a	64.0	c	72.4	a	71.5	a	18.0	b	15.3	a
CN Cerrado 5	0.0	c	100.0	a	61.3	a	65.0	c	74.9	a	75.9	a	17.8	b	17.4	a
CN Cerrado 6	3.33	c	3.3	c	59.0	b	70.3	b	75.5	a	76.3	a	17.4	b	14.4	a
193011	0.0	c	100.0	a	66.7	a	75.7	a	59.9	b	61.2	c	15.4	a	12.1	a
PI 356466	100.0	a	100.0	a	64.3	a	63.0	c	72.6	a	74.7	a	18.2	b	13.8	a
CI 07650	100.0	a	100.0	a	56.3	b	65.3	c	75.8	a	72.1	a	18.7	a	16.7	a
CI 09969	0.0	c	100.0	a	54.0	b	55.7	d	72.3	a	73.9	a	18.9	b	15.7	a
CI 09928	0.0	c	100.0	a	63.0	a	63.3	c	63.8	b	66.3	b	18.5	b	15.0	a
PI 370799	100.0	a	100.0	a	66.0	a	64.7	c	71.4	a	72.8	a	18.6	b	15.8	a
Mean CN ¹	45.3		84.5		63.1		64.6		71.8		72.9		18.2		15.8	
Mean (T) ²	16.7		68.9		61.7		65.3		63.4		62.4		16.3		12.9	
General Mean	41.2		82.3		62.9		64.7		70.6		71.4		17.9		15.4	

¹Mean for 18 hulless barley accessions; ²Mean for three covered barley accessions; Scott-Knott test at 1 % significance showed that there was no difference among the means followed by the same capital letter in the line and by the small letter in the column, in each evaluated trait.

value at SPM evidencing that two genotypes might present different behaviors due to predictable and unpredictable environmental factors (Borém & Miranda, 2005). Amabile et al. (2015) observed this interaction in the savanna under irrigation evidencing the fact that barley is influenced by the environment. Genotypes CN Cerrado 5 (7.748 kg ha⁻¹), CN Cerrado 6 (7.621 kg ha⁻¹) and PI 356466 (7.532 kg ha⁻¹) presented high EGY and were located in the same cluster, being however statistically different and also presenting superior values than the covered grain accessions 164321 (5.127 kg ha⁻¹) and 193011 (7.156 kg ha⁻¹) (Table 3). These figures found for hulless and covered barley accessions are higher than the world mean for barley, which is 3.000 kg ha⁻¹ (Faostat, 2017), being also higher for values found in the literature concerning the hulless barley (Dickin et al., 2010).

When studying the plumpness kernel, an average of 30.7% of hulless barley accessions grains evaluated at CPAC were classified as first class (grains wider than 2.5 mm) and 37.4% at SPM. The mean values for witnesses were 57.6% for PK at CPAC and 61.4% at SPM (Table 3).

This trait is used to classify the barley in relation to the grains size and according to the rules stated by the Ministry of Agriculture and Food Supply (Brasil, 1996) in order to produce malt at least 70% of the grains should be first class. As for animal feed, the percentage is 40%. In general, hulless barley grains showed grains smaller than the covered barley. However, some genotypes showed a desirable size for this purpose.

Several studies performed in the savanna under irrigation have shown that the PK for barley was over 80%, mainly because of the selection index used in the breeding program at Embrapa Cerrados (Amabile et al., 2017; Sayd et al., 2017). However, this index is inferior for hulless barley grown in the savanna under irrigation as stated by the indexes found by Monteiro et al. (2018), which were up to 2%. However, in this study performed at CPAC, high values for PK were found for genotypes CN Cerrado 1 (85.0%) and CN Cerrado 2 (83.3%), being clustered with the covered grain genotype 295418 (82.7%). At SPM, hulless barley genotypes CN Cerrado 1 and CN Cerrado 2, besides control 295418, showed that more 84% of the grains were PK and six other accessions showed trait PK ranging from 47% to 67% (Table 3). These motivating results might be explained by the initial selection made by Monteiro et al. (2018) for the breeding program at Embrapa Cerrados.

Trait TSW (TSW) showed different ranges in different sites. At CPAC, for instance, the difference between the genotype showing the highest and lowest weight was 20.2 g, while the difference at SPM was 38.1 g, evidencing a high interaction among the genotypes and the environment (Table 3).

At CPAC, the genotype with the highest TSW was CI 07650 (52.0 g) being grouped with the CN Cerrado 2 (50.8 g), witness 164321 (50.7 g) and CN Cerrado 1 (50.3 g). Accessions showing the lowest weight were also similar to one covered accession, however they presented lower values to the ones reported by Amabile et al. (2017) and similar values to the study performed by Sayd et al. (2017) using elite materials in the Savanna.

As for the genotypes studied at SPM, CI 09969 showed the highest value for TSW (53.7 g), being very close to the weight Monteiro et al. (2018) found when studying hulless barley. However, the lowest values (14.2 g for CI 09459 and 22.4 g for CI 14150) showed to be higher when compared to genotypes studied at CPAC and inferior to the means reported by Amabile et al. (2017) and Sayd et al. (2017). Although there was a significant variation of hulless barley genotypes, in average they showed an adequate weight to the expected pattern, which is, being 7% to 13% lighter than the covered barley (Table 3).

As for the Plant Height, genotypes showed different responses in relation to the environments. At CPAC, a higher variation was found among them (from 72.7 cm to 112.3 cm). Some genotypes reached a height above the expected, which was 80 to 90 cm, such as CI 13453 (112.3 cm) and CI 07650 (111.0 cm). This variation at SPM ranged from 82.7 cm (CN Cerrado 1) to 104.0 cm (CI 09459) (Table 3), being also verified by Amabile et al. (2017) and Sayd et al. (2017).

At CPAC, 15 genotypes reached a height that varied from 72.7 to 90 cm, including the highest EGY PI 356466 (83.7 cm). However, seven genotypes evaluated at SPM showed a Height below 90.0 cm. Although accession CN Cerrado 4 showed a height superior to 100.0 cm in both environments, it presented low indexes for Lodg. Ideal values for Height in hulless barley were also reported by Brooks et al. (2012).

The trait "plant lodging" is related to the Height. A high index for Lodg was found in the present study, as it was described by Dickin et al. (2010), showing a higher probability of Lodg in hulless barley compared to covered barleys. Therefore, it can be concluded that the four accessions that did not show a significant Lodg in two sites (CN Cerrado 2, CN Cerrado 6, CN Cerrado 4 and covered grain accession 295418) present a certain degree of resistance. Genotypes CI 09969, CI 09928, CN Cerrado 5, CI 06440 and witness 193011 did not lodge at CPAC as did the ones at SPM (Table 4). All other accessions had high levels of Lodg, being a lot higher than the desired levels and the levels reported by Brooks et al. (2012) and Monteiro et al. (2018). Even with the Lodg found at the current study, no increase of EGY and TSW was observed for genotypes analyzed at both sites.

In relation to the Cycle, the hulless barley accessions showed homogeneous behavior among them and their environment, that is, there was a little interaction between the genotypes and the environment. It is important that the DH is as short as possible without losing its productivity, since it is an irrigated crop. The average DH for the witnesses was 61.7 days (CPAC) and 65.3 days (SPM), while the means for the hulless barley accessions were 63.1 days (CPAC) and 64.6 days (SPM) (Table 4). At CPAC and SPM, 15 out of 21 genotypes had DH ranging from 63.0 and 67.0 days, corroborating with the data presented by Amabile et al. (2017), Sayd et al. (2017) and Monteiro et al. (2018).

The Hectoliter Weight showed a small variation from one environment to the other, although it is a trait influenced by the environment (Molina-Cano et al., 1997). There was a significant variation among the genotypes in each

environment, CPAC (63.8 - 75.8 kg hL⁻¹) and SPM (59.3 - 76.3 kg hL⁻¹), a variation that was superior to the one found to the values stated by Molina-Cano et al. (1997) and Marquez-Cedillo et al. (2001).

The current study observed that the Hectoliter Weight for genotypes evaluated at both sites were inferior to the one reported by Choo et al. (2001) for the hulless barley and higher than the figures observed by Molina-Cano et al. (1997) and Marquez-Cedillo et al. (2001) when studying the covered barley. The means for hulless barley accessions studied at CPAC were 71.8 kg hL⁻¹ and at SPM were 72.9 kg hL⁻¹, being close to the cultivar 'EVE', which HW was 73.8 kg hL⁻¹ (Brooks et al., 2012). They were even higher to the means found for covered grain accessions studied at CPAC (63.4 kg hL⁻¹) and at SPM (62.4 kg hL⁻¹) (Table 4). Choo et al. (2001) described that the hulless barley has a Hectoliter Weight, which is 20 % higher than the covered barley.

The maximum limit of protein levels for beers is 12%. Because the hulless barley in general show higher protein levels, it is used as food and animal feed. The mean protein level for genotypes evaluated at CPAC was 17.9%, being higher than the mean found for genotypes studied at SPM (15.4%), indicating the strong influence of the environment as described by Yalçın et al. (2007), who showed varied Protein Content for identical accessions, possibly because of the genotype-environment interaction.

Accessions CN Cerrado 1 and CN Cerrado 2 showed the highest Protein Content in both environments, with 21.4% and 20.4% at CPAC and 18.3% and 19.5% at SPM, respectively. Another accession with a high Protein Content was CN Cerrado 5 (17.8%) at CPAC and 17.4% at SPM. All these accessions are Brazilians and have a high potential for such trait. Helm & Francisco (2004) have noted figures similar to the average found at SPM while Brooks et al. (2012) reported figures around 10% for a hulless cultivar already launched.

According to Newman & Newman (1991), the Protein in hulless barley might reach up to 20%, however the values for this trait found in the current study ranged from 15.8% to 21.4% (CPAC) and 13.7% to 19.5% (SPM) (Table 4). The controls showed averages lower than the averages found for hulless accessions in both environments. The Protein Content observed by Baik et al. (2011) ranged from 12.1% to 16.6%.

Conclusions

High values of F, heritability or coefficient of genotypic determination, gCV/eCV ratio for several of the traits indicate the possibility of obtaining genetic gains and important advances when performing selection studies.

Accessions CI 13453, CN Cerrado 1, CN Cerrado 2, CN Cerrado 5 and PI356466 were better than the others when comparing traits such as EGY, Plumpness kernel, Lodging degree and Protein Content, being important for the selection programs and genetic improvement of hulless barley grown under irrigation in the Central part of Brazil.

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