Universidade Federal Rural do Semi-Árido
Pró-Reitoria de Pesquisa e Pós-Graduação
https://periodicos.ufersa.edu.br/index.php/caatinga
ISSN 1983-2125 (online)

http://dx.doi.org/10.1590/1983-21252026v3915347rc

Scientific Article

Agronomic characterization and genetic parameters of hulless barley genotypes under irrigation in the Cerrado

Caracterização agronômica e parâmetros genéticos de genótipos de cevada nua sob irrigação no Cerrado

Welinton F. Vieira[1], Renato F. Amabile[1], Juaci V. Malaquias[1], Laís P. da Silva[2]*, José R. Peixoto[3], João V. P. Melo[3], Arlini R. Fialho[3], Bárbara S. A. França[3]

[1]Brazilian Agricultural Research Corporation, Brasília, DF, Brazil. [2]Department of Agronomy, União Pioneira de Integração Social, Brasília, DF, Brazil. [3]Department of Agronomy and Veterinary Medicine, Universidade de Brasília, Brasília, DF, Brazil.

ABSTRACT - This study characterized six hulless barley (*Hordeum vulgare* L.) genotypes selected by the Brazilian Agricultural Research Corporation (Embrapa) barley breeding program and estimated genetic parameters of quantitative traits under irrigation in the Brazilian Cerrado. The experiment was conducted in the Federal District, during the 2020 and 2021 growing seasons, in a randomized block design with four replications. Grain yield, thousand-seed weight, plant height, lodging percentage, and days to heading were evaluated. The data were subjected to joint analysis of variance, and means were compared using Tukey's test. Significant differences were found among genotypes for all traits except lodging, indicating genetic variability in the evaluated set. Genotypic coefficients of variation were low for plant height and days to heading, and high for yield, thousand-seed weight, and lodging, indicating greater variation in these latter traits. High broad-sense heritability was observed for grain yield, thousand-seed weight, and days to heading, suggesting the possibility of significant gains with selection, while lodging showed lower heritability, indicating greater environmental influence. Genotype 295400 combined relatively high grain yield and thousand-seed weight with an intermediate time to heading, making it a promising genotype for irrigated cultivation in the Cerrado. Genotype 299555 had the highest numerical number of days to heading in both years. In general, the earlier genotypes showed greater plant height and higher grain yield.

Keywords: Plant breeding. Heritability. *Hordeum vulgare* L.

RESUMO - Este estudo caracterizou seis genótipos de cevada nua (*Hordeum vulgare* L.), selecionados pelo programa de melhoramento de cevada da Empresa Brasileira de Pesquisa Agropecuária (Embrapa), e estimou parâmetros genéticos de caracteres quantitativos sob irrigação no Cerrado brasileiro. O experimento foi conduzido no Distrito Federal, nos anos agrícolas de 2020 e 2021, em delineamento de blocos ao acaso, com quatro repetições. Foram avaliados rendimento de grãos, massa de mil sementes, altura de plantas, porcentagem de acamamento e número de dias até o espigamento. Os dados foram submetidos à análise de variância conjunta, e as médias foram comparadas pelo teste de Tukey. Foram observadas diferenças significativas entre genótipos para todos os caracteres, exceto acamamento, indicando variabilidade genética no conjunto avaliado. Os coeficientes de variação genotípica foram baixos para altura de plantas e número de dias até o espigamento e elevados para rendimento de grãos, massa de mil sementes e acamamento. Foram observadas elevadas estimativas de herdabilidade em sentido amplo para rendimento de grãos, massa de mil sementes e número de dias até o espigamento, sugerindo a possibilidade de ganhos expressivos com a seleção, enquanto o acamamento apresentou menor herdabilidade, indicando maior influência ambiental. O genótipo 295400 combinou rendimento de grãos e massa de mil sementes relativamente elevados com tempo intermediário até o espigamento, mostrando-se promissor para cultivo irrigado no Cerrado. O genótipo 299555 apresentou, numericamente, o maior número de dias até o espigamento em ambos os anos. Os genótipos mais precoces apresentaram maior altura de plantas e maior rendimento de grãos.

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

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the fourth most produced cereal in the world, behind only maize, wheat, and rice, and has been recognized as an important food ingredient due to the presence of bioactive compounds, especially β-glucans, associated with cholesterol reduction and improved carbohydrate metabolism in humans (MARTÍNEZ-SUBIRÀ et al., 2020; KUMAR et al., 2025; SHAVETA; KAUR, 2019). Within this species, hulless barley (*Hordeum vulgare* L. var. *nudum* Hook. f.) has grains with nonadhering hulls, facilitating processing and increasing flour yield, and is considered a promising raw material for the development of functional foods (SHAVETA; KAUR, 2019; YU et al., 2021).

According to an April 2024 forecast from the Instituto Brasileiro de Geografia e Estatística (IBGE, 2024), Brazilian barley production was estimated at approximately 465 thousand Mg for 2024, with the southern states of Paraná and Rio Grande do Sul accounting for most of the national production. Although the Federal District accounts for a small share of Brazilian barley production, studies have demonstrated the high potential of the Cerrado for irrigated barley cultivation due to favorable winter climatic conditions, high radiation availability,

Conflict of interest: The authors declare no conflict of interest related to the publication of this manuscript.

This work is licensed under a Creative Commons Attribution-CC-BY https://creativecommons.org/licenses/by/4.0/

Received for publication in: March 23, 2026.
Accepted in: September 22, 2026.

Editor in Chief: Aurélio Paes Barros Júnior
Section Editor: Lindomar Maria da Silveira

Data Availability: The data that support the findings of this study can be made available, upon reasonable request, from the corresponding author.

***Corresponding author**:
<silvalaisagro@gmail.com>

and the possibility of achieving high grain yields under irrigation. Recent studies conducted in the Federal District have demosntrated the adaptability, stability, and productive potential of barley genotypes cultivated under irrigated conditions in the Cerrado, reinforcing the strategic importance of this region for the expansion of barley production and breeding programs in tropical environments (THOMÉ et al., 2024a; THOMÉ et al., 2024b; SAYD et al., 2019). Despite its nutritional and technological potential, hulless barley remains little explored in commercial production systems, being mainly maintained in germplasm collections and experimental trials in several countries (LIU et al., 2019; MAANJU et al., 2023). In Brazil, recent studies have focused on the evaluation of barley genotypes under irrigation in the Cerrado (Brazilian Savanna), indicating good adaptation and favorable grain yield in irrigated winter environments (SAYD et al., 2017; SAYD et al., 2018; SAYD et al., 2022). However, most of the evaluated genotypes are still hulled barley, and there is a lack of specific information on hulless barley genotypes under tropical irrigated conditions.

Genetic variability is essential for the success of barley breeding programs, enabling the selection of genotypes with higher yield, better grain quality, and greater stability across different environments (BONMAN et al., 2019; CHEN et al., 2024; MAANJU et al., 2023). Studies on genetic diversity and genetic parameters in barley collections, including hulless barley accessions, have demonstrated wide variability for agronomic and quality traits, reinforcing the potential of these genotypes as sources of favorable alleles (LIU et al., 2019; SAYD et al., 2018).

Estimating genetic parameters, such as genotypic and environmental variances, heritability, and coefficients of variation, helps quantify the genetic control of quantitative traits and support the choice of more efficient selection strategies (CRUZ; REGAZZI; CARNEIRO, 2014; KEMPTHORNE, 1966). Likewise, the study of correlations among traits can identify favorable associations, enabling the indirect selection of traits that are difficult to measure based on others that are simpler and have higher heritability, thus optimizing time and resources in breeding programs (CARVALHO; LORENCETTI; BENIN, 2004; CALLEGARI -JACQUES, 2003).

In the context of the Cerrado, the identification of hulless barley genotypes adapted to irrigated winter cultivation is strategic, as it allows the expansion of crop diversification and provides a distinct raw material for the food industry (MARTÍNEZ-SUBIRÀ et al., 2020; SHAVETA; KAUR, 2019). Earlier genotypes are particularly attractive, as they facilitate succession with summer crops in intensive production systems in the Cerrado (SAYD et al., 2017; SAYD et al., 2018).

This study characterized six hulless barley genotypes under irrigation in the Cerrado and estimated genetic parameters and correlations among quantitative traits to identify promising genotypes for further agronomic evaluation and use in barley breeding programs.

MATERIAL AND METHODS

The experiment was conducted at the Center for Innovation in Plant Genetics of the Brazilian Agricultural Research Corporation (Embrapa Cerrados), in Riacho Fundo II, Federal District, Brazil (15°55′10.7″ S, 48°02′10.4″ W; 1,250 m altitude), on a Latossolo Vermelho Distrófico típico (Typic Hapludox) under a no-tillage system. The trials were conducted during two consecutive growing seasons (2020 and 2021), with sowing in May and harvest in September of each year. The regional climate is classified as Aw according to the Köppen classification, with a dry winter and a rainy summer. During the experimental period (May to September), the 2020 growing season presented a mean temperature of approximately 22.6 °C, cumulative precipitation of 63 mm, and mean relative humidity of 48%, whereas the 2021 season showed a mean temperature of 21.4 °C, cumulative precipitation of 81 mm, and mean relative humidity of 55%. These records indicate that the 2021 growing season had milder and more favorable atmospheric conditions for barley development compared to 2020.

The experimental design was a randomized complete block design with four replications, with six genotypes evaluated in two years. Six hulless barley genotypes were evaluated: 295426, 299555, 295396, 295400, 295442, and the check cultivar CPAC Musa. The plots consisted of four rows, 3 m long, spaced 0.25 m apart, totaling an area of 3.0 m², with a density of 200 plants m^{-2}. Basal fertilization was identical in both years, with the application of 12 kg ha^{-1} of N, 90 kg ha^{-1} of P_2O_5, and 48 kg ha^{-1} of K_2O in the sowing furrow, in addition to 50 kg ha^{-1} of N as topdressing at the stage of the fifth fully expanded leaf.

Irrigation was applied using a center pivot system, following recommendations from the irrigation monitoring system for the Cerrado of Embrapa Cerrados, with a five-day irrigation interval and reported irrigation depths of approximately 25 mm in the first month, 12 mm in the second, 8 mm in the third, and 6 mm in the last month, totaling about 325 mm of water per cycle in each year.

The following morphoagronomic traits were evaluated: grain yield (kg ha^{-1}), obtained by harvesting the assessed plot area and adjusting grain moisture to 13%; thousand-seed weight (g), determined according to the Rules for Seed Analysis (BRASIL, 2009); plant height (cm), measured from the soil surface to the tip of the spike in ten plants per plot; lodging percentage (%), visually estimated as the percentage of lodged plants in the assessed area of each plot; and days to heading, corresponding to the number of days between emergence and heading of 50% of the plants in the plot.

The data for lodging and days to heading were transformed prior to statistical analysis because some variables showed asymmetry. Lodging data was transformed using $arcsin(\sqrt{(x/100)})$, where x is the observed lodging percentage, and days-to-heading data were transformed using $\sqrt{(x + 0.5)}$, where x is the observed number of days to heading, to stabilize variance and approximate normal distribution (VIEIRA, 2017; HADDAD; VENDRAMIM, 2000).

The data were subjected to joint analysis of variance, using a randomized block model with genotype × year interaction, whose analysis of variance scheme, mean squares, and F-test are presented in Table 1: $Yijk=\mu+Bk+Gi+Aj+GAij+Eijk$ where Yijk is the observation in the k-th block, i-th genotype, and j-th year; μ is the overall mean; Bk is the block effect; Gi is the genotype effect; Aj is the year effect; GAij is the genotype × year interaction; and

Єijk is the random error. The effects of genotypes, blocks, environments (years), and genotype × environment interaction were considered fixed. The analyses were performed using R software, version 4.3.0 (R DEVELOPMENT CORE TEAM, 2023).

Table 1. Scheme of the joint analysis of variance for a randomized complete block design with genotype × year interaction, including mean squares and F-test for the sources of variation (SV), considering fixed effects of blocks, genotypes, environment, and genotype × environment interaction.

SV	DF	SS	MS	F
Blocks	r-1	SSB	SSB/DFB	MSB/MSE_a
Genotypes (G)	g-1	SSG	SSG/DFG	MSG/MSE_a
Error a	(r-1)(g-1)	SSE_a	SSE_a/DFE_a	
Years (Y)	a-1	SSY	SSY/DFY	MSY/MSE_b
Interaction (G × Y)	(g-1)(a-1)	SSGY	SQGY/GLGY	$MSGY/MSE_b$
Error b	(gar-1)-[(r-1)+(g-1)+(a-1)]+[(r-1)(g-1)]+[(g-1)(a-1)]	SSE_b	SSE_b/DFE_b	
Total	gar-1			

Based on the mean squares (Table 1), the phenotypic, genotypic, and environmental variances, broad-sense heritability, experimental, genetic, and relative coefficients of variation, as well as selective accuracy, were estimated following procedures described by Cruz, Regazzi and Carneiro (2014) and Carvalho, Lorencetti and Benin (2004). Genotypic correlations between pairs of traits were obtained from genotypic variances and covariances as correlation coefficients as described by Kempthorne (1966), and classified according to the intensity classes proposed by Carvalho, Lorencetti and Benin (2004), where intensities are defined as: perfect ($|r| = 1$); very strong ($0.90 \leq |r| < 1$); strong ($0.60 \leq |r| < 0.90$); moderate ($0.30 \leq |r| < 0.60$); weak ($0.00 < |r| < 0.30$); and null ($r = 0$).

RESULTS AND DISCUSSION

The joint analysis of variance revealed significant differences among genotypes for grain yield, thousand-seed weight, plant height, and days to heading at the 1% probability level, whereas lodging percentage did not differ statistically among the genotypes (Table 2). Significant effects of year and genotype × year interaction were also observed for most traits, indicating that the relative performance of the genotypes varied between the two growing seasons evaluated under irrigation in the Cerrado.

This pattern is consistent with results obtained in irrigated barley collections in the same region, where differences between growing seasons were attributed to variations in temperature and precipitation, even under supplemental irrigation (SAYD et al., 2017; SAYD et al., 2018).

The experimental coefficients of variation (CVe) were low for grain yield, thousand-seed weight, plant height, and days to heading, indicating good experimental precision (Table 2). In contrast, the CVe for lodging percentage was high and the selective accuracy for this trait was low, suggesting a greater influence of environmental factors and subjectivity of visual assessment.

The CVg/CVe ratio was greater than 1 for grain yield, thousand-seed weight, and days to heading, indicating the predominance of genetic over environmental variation in the expression of these traits, a favorable condition for achieving gains through selection (CRUZ; REGAZZI; CARNEIRO, 2014; CARVALHO; LORENCETTI; BENIN, 2004). A similar situation was reported in previous studies on irrigated hulless barley accessions in the Brazilian Cerrado, with high CVg/CVe values for yield and cycle-related traits (SAYD et al., 2018).

Broad-sense heritability estimates were very high for grain yield (99.36%), thousand-seed weight (99.46%), and days to heading (93.71%), high for plant height (73.71%), and moderate for lodging percentage (34.29%) (Table 2). These results indicate an important genetic contribution to the expression of the main agronomic traits evaluated, suggesting potential for selection under irrigated conditions in the Cerrado. However, caution is required when interpreting heritability estimates close to 100% for quantitative traits, since the reduced number of genotypes evaluated and the relatively controlled environmental conditions provided by irrigation may have contributed to inflating these estimates. In this context, the high values observed may reflect the specific experimental conditions and the limited environmental variability among the evaluated genotypes rather than exclusively strong genetic control. Similar trends have been reported in irrigated barley studies conducted under highly controlled environments in the Brazilian Cerrado (SAYD et al., 2017; SAYD et al., 2018; SAYD et al., 2022).

The lower heritability observed for lodging confirms the greater environmental influence on this trait and its strong dependence on climatic and management conditions, as previously described for winter cereals (CALLEGARI-JACQUES, 2003; CARVALHO; LORENCETTI; BENIN, 2004). The mean grain yield of the genotypes was higher in 2021 than in 2020 for all evaluated genotypes (Table 3). This difference may be associated with more favorable environmental conditions during the 2021 growing season, particularly the occurrence of milder temperatures and more stable climate conditions during critical developmental stages such as flowering and grain filling. In contrast, the 2020 season likely exposed the genotypes to greater environmental stress, including higher temperatures and possible fluctuations in atmospheric conditions, which can negatively affect photosynthetic efficiency, assimilate translocation, grain formation, and final yield. Variations in temperature,

radiation, and evaporative demand between years may substantially influence plant metabolism and the expression of agronomic traits, even under a standardized irrigation regime. These environmental differences help explain the marked variation observed not only for grain yield, but also for traits related to plant development and performance, reinforcing the strong influence of genotype × environment interaction on barley cultivation in the Cerrado.

Table 2. Analysis of variance and genetic parameters for the traits grain yield (Yield), thousand-seed weight (TSW), days to heading (DTH), plant height (Height), and lodging percentage (Lodging) of six hulless barley genotypes evaluated in the field of the Center for Innovation in Plant Genetics of Embrapa Cerrados, Riacho Fundo II, Federal District, Brazil, in the years 2020 and 2021.

SV	DF	F Values				
		Yield (kg ha^{-1})	TSW (g)	Height (cm)	Lodging (%)[1]	DTH (days)[2]
Genotype	5	259.564**	127.743**	6.478**	1.0419	30.529**
Blocks	3	1.043	1.369	2.174	0.3228	2.410
Years	1	7711.553**	184.695**	56.298**	1.0330	132.524**
GxY	5	112.996**	34.322**	6.587**	3.5057	11.465**
Residue	18	-	-	-	-	-
CV1		2.1358	2.7384	3.5046	82.6227	0.7164
CV2 = CVe		2.7558	2.2745	4.5733	68.363	0.9924
MSg		2615009.95	145.618	62.083	0.4559	0.1036
Means		4699.5	38.99	88.33	51.25	65.67
σ_f^2		653752.487	36.4044	15.5208	0.114	0.0259
σ_g^2		649559.31	36.2078	11.441	0.0391	0.0243
σ_e^2		4193.177	0.1966	4.0799	0.0749	0.00163
ha^2 (%)		99.36	99.46	73.71	34.29	93.71
CVg (%)		17.1497	15.4331	3.8292	24.6931	1.9161
CVr (%)		12.446	13.570	1.675	0.722	3.861
CVg/CVe		6.223	6.758	0.837	0.361	1.931
?gg		0.998	0.996	0.919	0.20	0.983

Mean square of the genotypes (MSg); estimated phenotypic ($\hat{\sigma}f$ 2), genotypic ($\hat{\sigma}g2$) and environmental ($\hat{\sigma}e2$) variance at the mean level; broad-sense heritability (ha2); genotypic (CVg), experimental (CVe), relative (CVr) coefficients of variation; CVg/CVe; and selective accuracy (r̂gg). ** Significance at 1% probability by F test; [1]Analysis with data transformed to *arcsin(√(x/100))*; [2]Analysis with data transformed to *√(x + 0.5)*.

Table 3. Mean values of grain yield (Yield), thousand-seed weight (TSW), plant height (Height), lodging percentage (Lodging) and days to heading (DTH), of six hulless barley genotypes evaluated in the field of the Center for Innovation in Plant Genetics of Embrapa Cerrados, Riacho Fundo II, Federal District, Brazil, in the years 2020 and 2021.

Genotypes	Yield (kg ha^{-1})		TSW (g)		Height (cm)		Lodging (%)		DTH (days)	
	2020	2021	2020	2021	2020	2021	2020	2021	2020	2021
CPAC Musa	3318.00Bab	6619.75Ab	37.25Acd	33.25Bc	88.75Aa	93.75Aa	37.50Aa	50.00Aa	66.75Abc	59.25Bc
295426	2070.75Bbc	4983.25Ae	35.37Ad	35.50Ab	82.50Ba	93.75Aa	30.00Aa	42.50Aa	69.00Aab	61.00Bc
299555	2998.00Bc	7880.75Aa	38.62Ac	36.62Bb	88.75Aa	88.75Aa	82.50Aa	23.75Ba	69.25Aa	68.00Aa
295396	2366.75Bd	5632.75Ad	38.50Ac	37.12Bb	72.50Bb	93.75Aa	100.00Aa	53.25Aa	65.50Ac	65.00Ab
295400	3054.75Bc	6592.25Ab	43.00Ab	39.75Ba	83.75Ba	93.75Aa	55.00Aa	20.00Aa	68.25Aab	64.00Bb
295442	3539.50Ba	6337.50Ac	51.62Aa	41.25Ba	87.50Aa	92.50Aa	25.00Ba	92.50Aa	68.25Aab	63.75Bb

Within each trait, means followed by different uppercase letters in the rows, or lowercase letters in the columns, differ according to Tukey's test at 5% probability.

Genotype 299555 showed the highest yield in 2021 (7880.75 kg ha^{-1}), whereas 295396 had the lowest yield in 2020 (2366.75 kg ha^{-1}), highlighting a wide productive contrast among genotypes. Some genotypes, especially 295400, maintained comparatively high performance across both years, suggesting greater phenotypic stability and adaptability under contrasting environmental conditions. This stability is particularly desirable in breeding programs, as it indicates greater predictability of performance across growing seasons. However, considering both years, genotype 295400 combined high yield values with relative stability, making it a genotype of interest for future selection stages in irrigated environments of the Cerrado. Studies with barley panels in contrasting environments emphasize that the combination of high mean yield and stability across years and locations is a key criterion for recommending genotypes to farmers (BONMAN et al., 2019; MAANJU et al., 2023).

Regarding thousand-seed weight, a wide range of variation was observed among genotypes and years, with genotype 295442 standing out by presenting the highest values in 2020 (51.62 g) and 2021 (41.25 g), and genotype 295400 also presenting high values, at 43 g in 2020 and 39.75 g in 2021 (Table 3). These results indicate that genotype 295400 had relatively larger grains, which may be desirable in specific market niches for hulless barley intended for human consumption. The literature indicates that hulless barley cultivars usually present lower thousand-seed weight than hulled barley, due to nonadherence of the lemma and palea to the caryopsis and their removal during threshing, which reduces unit mass but increases flour yield (DJELÉL; NABIHA; NOUREDDINE, 2020; CHOO; HO; MARTIN, 2001; SHAVETA; KAUR, 2019). The high heritability estimated for this trait in the present study, combined with the wide variation observed, reinforces its potential as a selection target in breeding programs focused on grain quality and the development of whole-grain products rich in β-glucans (MARTÍNEZ-SUBIRÀ et al., 2020; KUMAR et al., 2025).

Plant height showed significant variation among genotypes mainly in 2020, with genotype 295396 exhibiting the lowest mean height (72.5 cm), whereas in 2021 no statistical differences among genotypes were observed (Table 3). Plant height is directly related to lodging risk and light interception, indirectly influencing grain yield (CARVALHO; LORENCETTI; BENIN, 2004). Although heritability for this trait was relatively high (73.71%), the CVg/CVe ratio lower than 1 indicates that environmental variation had an important contribution to the phenotypic expression of plant height under the evaluated conditions. This suggests that direct selection for plant height may be less efficient when based on a limited number of environments or growing seasons, since climatic factors such as temperature, radiation, and atmospheric demand can substantially affect stem elongation and vegetative growth in barley. Therefore, selection for this trait should preferably be conducted across multiple environments and years to improve the reliability of identifying stable genotypes with desirable plant architecture.

Lodging percentage showed wide variation across years and genotypes, with mean values in 2020 ranging from 25% (295442) to 100% (295396), but without significant differences among genotypes in either year (Table 3). The combination of high environmental variance, low heritability, and low selective accuracy indicates that, under the evaluated conditions, direct selection to reduce lodging would be inefficient. Recent studies in barley and wheat indicate that lodging susceptibility is strongly influenced by stem and root system characteristics, plant density, fertility, and climatic events such as strong winds and heavy rainfall, increasing genotype × environment interaction for this trait (KHOBRA et al., 2019; TAYLOR et al., 2025). In this context, identifying genotypes that combine moderate height with stronger stems and suitable architecture may be a more efficient strategy than selection based on lodging scores obtained in one or a few environments.

Days to heading showed high heritability (93.71%) and significant differences among genotypes and years, with genotype 299555 having the longest cycle in both seasons, while CPAC Musa had the earliest cicle in 2021 (Table 3). In Cerrado production systems, earliness is a desirable trait, as it facilitates barley inclusion in rotation with summer crops and reduces the risk of exposure to end-of-cycle abiotic stresses. Studies with irrigated barley collections in the region also report large variations in cycle among genotypes and years, reinforcing the importance of estimating genetic parameters for this trait to support the recommendation of adapted genotypes (SAYD et al., 2017; MONTEIRO et al., 2018).

The correlogram among traits (Figure 1) showed a strong positive genotypic correlation between grain yield and plant height, indicating that, under the evaluated conditions, taller genotypes tended to be more productive. A moderate positive correlation was also observed between thousand-seed weight and days to heading, suggesting that later genotypes had higher thousand-seed weight. In contrast, days to heading showed negative and significant correlations with yield and height, indicating that earlier genotypes were generally taller and more productive. This relationship may be associated with the environmental conditions of the irrigated Cerrado, where earlier genotypes are able to complete their vegetative and reproductive development under more favorable temperature and radiation conditions, avoiding the exposure to higher temperatures and increased atmospheric demand commonly observed later in the growing season. As a result, these genotypes may exhibit greater biomass accumulation, better resource-use efficiency, and improved grain filling, contributing simultaneously to greater plant height and higher grain yield. In addition, earlier flowering may reduce the impact of terminal stress during grain filling, favoring overall plant performance and grain yield. Weak negative correlations between thousand-seed weight and yield, thousand-seed weight and height, and between height and lodging, as well as the negative correlation between lodging and yield, indicate that increases in lodging tend to reduce grain yield, an effect widely reported in winter cereals (CRUZ; REGAZZI; CARNEIRO, 2014; FEDERIZZI; FANTINI; CARVALHO, 1994).

These association patterns suggest that the selection of earlier genotypes with greater plant height may result in simultaneous gains in grain yield, although there may be a reduction in thousand-seed weight and this trade-off should be considered according to the target market for hulless barley. Similar results, with negative correlations between days to heading and yield and positive correlations between height and yield, have been reported in barley genotypes evaluated under both irrigated and rainfed conditions, indicating that plant architecture and cycle duration are key attributes for adaptation and production efficiency (SAYD et al., 2018; MONTEIRO et al., 2018; CHEN et al., 2024).

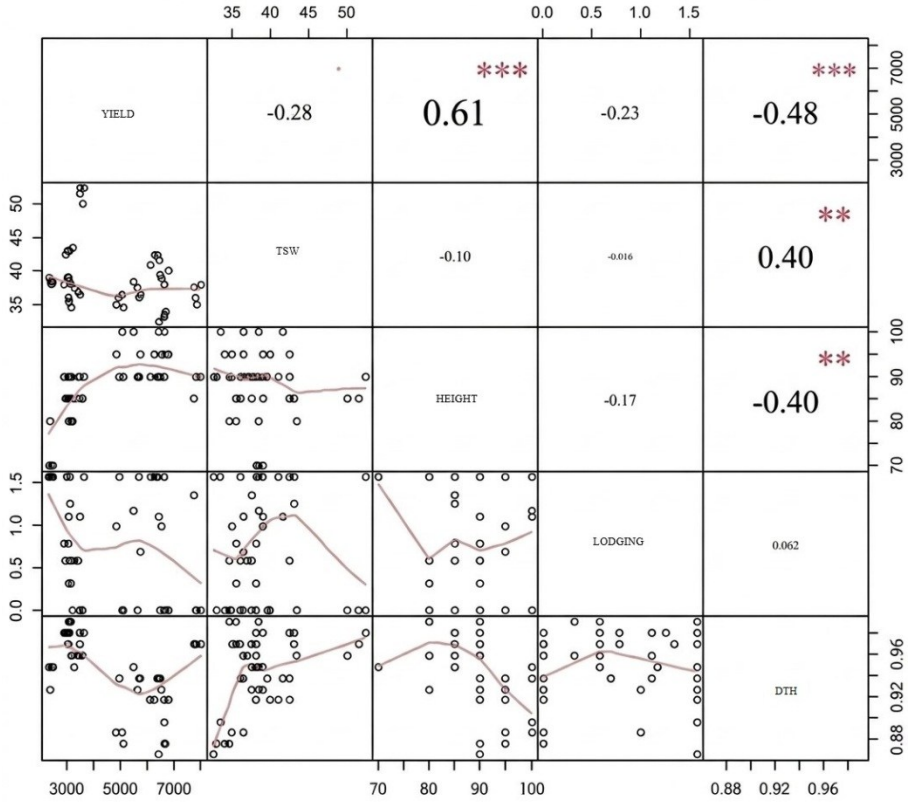


Figure 1. Correlogram of the traits grain yield (Yield), thousand-seed weight (TSW), plant height (Height), lodging percentage (Lodging) and days to heading (DTH), of six hulless barley genotypes evaluated in the field of the Center for Innovation in Plant Genetics of Embrapa Cerrados, Riacho Fundo II, Federal District, Brazil, in the years 2020 and 2021.

In addition, recent studies in grain cereals show that correlation and path analyses remain central tools for identifying indirect selection traits in breeding programs focused on increasing grain yield across different environments (ZUFFO et al., 2023; KUMAR et al., 2025). The positive correlation between thousand-seed weight and days to heading indicates the possibility of fine-tuning the balance between earliness and seed size, enabling the selection of genotypes that combine a cycle suitable for the Cerrado with grain size compatible with specific food uses (MARTÍNEZ-SUBIRÀ et al., 2020; SHAVETA; KAUR, 2019).

Considering the set of traits, genotype 295400 is a promising line for irrigated cultivation in the region, as it combines high grain yield, high thousand-seed weight, and an intermediate number of days to heading, whereas genotype 299555, although productive in one of the years, is less desirable due to its longer cycle and lower suitability to the typical cropping windows of the Cerrado.

CONCLUSION

Genotype 295400 combined high grain yield, high thousand-seed weight, lower relative lodging percentage, and an intermediate number of days to heading, making it a promising genotype for irrigated cultivation in the Cerrado and for use in barley breeding programs. In contrast, genotype 299555 showed a longer cycle in both years, making it less suitable for the predominant cropping windows of the region, despite its good productive performance in one of the growing seasons. Future studies should evaluate the stability and adaptability of these genotypes across different environments and sowing dates in the Cerrado region, focusing on supporting cultivar recommendation and breeding strategies for irrigated barley production.

ACKNOWLEDGMENTS

The authors acknowledge financial support from the Fundação de Apoio à Pesquisa do Distrito Federal (FAPDF), under Edital no. 01/2026 - FAPDF Publica, grant no. 51165.255.63509.09042026.

REFERENCES

BONMAN, J. M. et al. Evaluation of grain β-glucan content in barley accessions from the USDA National Small Grains Collection. **Crop Science**, 59: 2078-2089, 2019.

BRASIL. Ministério da Agricultura, Pecuária e Abastecimento. Secretaria de Defesa Agropecuária. **Regras para análise de sementes**. Brasília, DF: MAPA/ACS, 2009. 399 p.

CALLEGARI-JACQUES, S. M. **Bioestatística: princípios e aplicações**. Porto Alegre,RS: Artmed, 2003. 255 p.

CARVALHO, F. I. F.; LORENCETTI, C.; BENIN, G. **Estimativas e implicações da correlação no melhoramento vegetal**. Pelotas, RS,: Editora UFPEL, 2004. 142 p.

CHEN, G. et al. Genetic diversity and genome-wide association analysis of agronomic traits in barley. **Plants**, 13: 1112, 2024.

CHOO, T. M.; HO, K. M.; MARTIN, R. A. Genetic analysis of a hulless × covered cross of barley using doubled-haploid lines. **Crop Science**, 41: 1021-1026, 2001.

CRUZ, C. D.; REGAZZI, A. J.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 3. ed. Viçosa, MG: UFV, 2014. 668 p.

DJELÉL, R.; NABIHA, B.; NOUREDDINE, Z. Agronomic traits and yield performance variation in hulled and naked barley (*Hordeum vulgare* L.) varieties for adaptation in east Algeria. **Indian Journal of Agricultural Research**, 54: 745-750, 2020.

FEDERIZZI, L. C.; FANTINI, A. C.; CARVALHO, F. I. F. Efeito do acamamento artificial em alguns genótipos de trigo de porte alto e baixo. **Ciência Rural**, 24: 465-469, 1994.

HADDAD, M. L.; VENDRAMIM, J. D. Comparação de porcentagens observadas em casos extremos de 0 a 100%. **Anais da Sociedade Entomológica do Brasil**, 29: 835-837, 2000.

IBGE - Instituto Brasileiro de Geografia e Estatística. **Em abril, IBGE prevê safra de 299,6 milhões de toneladas para 2024**. 2024. Available at: < https:// agenciadenoticias.ibge.gov.br/en/agencia-press-room/2185-news-agency/releases-en/40083-in-april-ibge-forecasts-harvest-of-299-6-million-tonnes-for-2024? > Access on: May. 14, 2026.

KEMPTHORNE, O. **An introduction to genetic statistics**. New York: John Wiley & Sons, 1966. 545 p.

KHOBRA, R. et al. Exploring the traits for lodging tolerance in wheat genotypes: a review**. Physiology and Molecular Biology of Plants**, 25: 589-600, 2019.

KUMAR, A. et al. Barley grain β-glucans: unravelling the biochemistry and functionality for human health. **International Journal of Food Science and Technology**, 60: e.vvaf 109, 2025.

LIU, W. et al. Determining factors for the diversity of hulless barley from the Qinghai–Tibetan Plateau. **Journal of Cereal Science**, 89: 102789, 2019.

MAANJU, S. et al. Deciphering the genetic diversity and population structure of barley using genome-wide SNP markers. **Scientific Reports**, 13: 15542, 2023.

MARTÍNEZ-SUBIRÀ, M. et al. Purple, high β-glucan, hulless barley as valuable raw material for whole-grain products. **Journal of Cereal Science**, 96: 103114, 2020.

MONTEIRO, V. A. et al. Genetic parameters and morpho-agronomic characterization of barley working collection in the Brazilian savannah. **Journal of the Institute of Brewing**, 124: 121-131, 2018.

R DEVELOPMENT CORE TEAM. **R: A language and environment for statistical computing**. Vienna: R Foundation for Statistical Computing. 2022. Available at: < https:// www.R-project.org/ >. Access on: Feb. 10, 2023.

SAYD, R. M. et al. Agronomic characterization of high-yielding irrigated barley accessions in the Cerrado. **Pesquisa Agropecuária Brasileira**, 52: 84-94, 2017.

SAYD, R. M. et al. Genetic parameters and agronomic characterization of hulless barley accessions under irrigation in the savanna. **Revista Brasileira de Ciências Agrárias**, 13: e5567, 2018.

SAYD, R. M. et al. Genetic parameters and agronomic characterization of elite barley accessions under irrigation in the Cerrado. **Acta Scientiarum. Agronomy**, 41: e42630, 2019.

SAYD, R. M. et al. Molecular and agronomic genetic diversity between barley genotypes under irrigation in the Brazilian Cerrado. **Pesquisa Agropecuária Brasileira**, 57: e02731, 2022.

SHAVETA, H. K.; KAUR, S. Hulless barley: a new era of research for food purposes. **Journal of Cereal Research**, 11: 114-124, 2019.

THOMÉ, R. et al. Adaptability and stability of irrigated barley genotypes in the Cerrado of the Federal District. **Agriculture**, 14: 1776, 2024a.

THOMÉ, R. D. et al. Genetic parameter estimates in irrigated barley genotypes in the Brazilian Savanna of the Federal District. **Revista Caatinga**, 37: e12037, 2024b.

VIEIRA, S. **ANOVA: transformação de variáveis**. 2017. Available at: < http://soniavieira.blogspot.com/2017/02/ anovatransformacao-de-variaveis.html >. Access on: Feb. 10, 2023.

WANG, X. et al. Validating the contributions of stem and root traits to barley lodging in western Canada. **Frontiers in Plant Science**, 16: 1547207, 2025.

YU, J. et al. Effect of hulless barley flours on dough rheological properties and bread quality. **Frontiers in Nutrition**, 8: 785847, 2021.

ZUFFO, A. M. et al. Correlations and path analysis of second-crop corn hybrids for grain yield. **Australian Journal of Crop Science**, 17: 639-644, 2023.