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ESTIMATION OF GENETIC PARAMETERS, PHENOTYPIC, GENOTYPIC AND ENVIRONMENTAL CORRELATIONS ON BARLEY (*Hordeum Vulgare* L.) GROWN UNDER IRRIGATION CONDITIONS IN THE BRAZILIAN SAVANNAH

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SUMMARY

The purpose of the present study was to estimate the heritability of traits through phenotypic, genetic and environmental parameters related to the production components and agro-morphological characters: plant height (PHt), days to heading, lodging, grain yield (YLD), thousand kernels weight (TKW), protein content, and commercial classification of grains (CLASS) of an elite collection of 39 barley genotypes grown under irrigated conditions in the savannah of Central Brazil. The experiment was planted under irrigation on May 2009 at Embrapa Cerrados, Federal District, Brazil. A complete randomized block design with four replicates was used. Genetic variability was observed among the tested genotypes. The genotypic correlations (in absolute values) found for

all traits were greater than their corresponding phenotypic and environmental correlations. A significant influence of genetic factors on trait expression was observed. It could be concluded that the phenotypic expression is decreased depending on the environmental conditions. The greatest magnitudes for the genotypic and phenotypic correlations were found for TKW and CLASS. Trait YLD was positively correlated to PHt in terms of genotypic and phenotypic correlation. The selection accuracy was rated high for all traits. The high magnitudes found in the estimation of broad sense heritability indicated the existence of genetic variability, showing the possibility of obtaining genetic gains through the selection for all characters.

 Barley (*Hordeum vulgare* L.), the fourth most grown cereal in the world (Faostat, 2014), is part of the human nutrition, both in its covered and hullless forms, being also considered a functional food (Yalçın *et al.*, 2007) and feed for animals.

Great part of the barley grown in Brazil is used for malt production and afterwards is used as animal feed or seed (Amabile *et al.*, 2007). The national demand for this commodity is increasing and the crop production is far from meeting the market needs. Therefore,

the deficit is solved through the import of the grain, which causes a negative impact in the national trade balance.

Barley was first introduced in the Brazilian savannah to supply the national market of malt and to offer the farmers of Central Brazil an

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alternative to diversify and integrate the irrigated crop production systems. However, more studies are necessary to evaluate the adjustment of barley grown under irrigated conditions in this kind of environment as well as to find more effective agronomical strategies (Amabile *et al.*, 2007).

Cultivars with a better agronomical performance, higher grain yield and better adapted to the irrigated systems are essential for farmers and to help in the development of technological innovation. Breeding programs are dynamic systems, offering new genotypes adapted to the strict requirements of the agricultural systems, contributing to the diversification of these systems and also to the technical and economical system of agricultural commodities. In the case of barley grown under irrigated conditions in the savannah, the present challenge is to obtain cultivars with a better agronomical and industrial quality, with higher yield and adapted to the irrigated system in order to meet the industry's requirements so that barley becomes an economical and agricultural alternative in this area (Amabile *et al.*, 2007).

The estimation of genetic parameters is fundamental to quantify the magnitude of the variability and extension in which the desirable characters are inherited, in order to promote the planning and progress of an effective program of genetic improvement (Vencovsky and Barriga, 1992). Knowing the degree of association between the characters is extremely valuable for the improvement strategies since it clarifies and quantifies the relationship between them, mainly when the selection of a character promotes changes in other correlated traits (Ramalho *et al.*, 2008).

Effective selection necessarily includes the prediction of genetic values of the traits involved and might be obtained by estimating the components of the genetic and phenotypic variance (Smith *et al.*, 2001; Cruz *et al.*, 2004). Information about the nature and importance of genetic variance components for quantitative traits of agronomical and quality relevance are essential when planning a more efficient improvement program. The knowledge of heritability of important traits, its accuracy and its variance components are fundamental when working with traits that are strongly influenced by the environment. When this kind of information is provided, improvement programs may be carried out more effectively and one can predict whether the adopted system will be successful or not, and also to decide, based on scientific facts, which of the alternative selection

techniques will be more efficient (Cruz *et al.*, 2004).

According to Resende and Duarte (2007) the studies performed to evaluate genotypes should address not only the statistical aspect but also the genetic aspect, considering the selection accuracy, since the statistics data take into consideration the ratio between the variations of genetic and residual nature.

Estimation of genetic and statistical parameters in barley in Brazil has been rare. Few studies of genetic estimates are available when using populations, collections of useful accessions for the crop improvement program evaluated in the savannah and on crops grown under irrigated conditions. Therefore, the aim of the present study was to obtain information on the elite barley collection for improvement programs in Brazil through the use of genetic, phenotypic and environmental parameter estimates related to crop components and agromorphological traits of barley grown under irrigated conditions in the savannah.

Material and Methods

A field trial was carried out in Embrapa Cerrados Experiment Station, Planaltina, DF, Brazil, located at 15°35'30"S, 47°42'30"E and 1007masl. It was performed using a conventional irrigation system. The soil was classified as Dystroferic dark red Latossol, clay texture, and the results of chemical and physical analysis of the soil according to Embrapa (1997) indicated the lack of Al, 38.2mmol_c·dm⁻³ Ca; 8.4mmol_c·dm⁻³ Mg; 24.69mg·kg⁻¹ P; 6.8mmol_c·dm⁻³ K; 23.0g·kg⁻¹ OM, and a pH_(water) of 6.07; coarse sand= 60g·kg⁻¹; fine sand= 380g·kg⁻¹; silt= 130g·kg⁻¹ and clay= 430g·kg⁻¹. According to the classification of Köppen, the area is located in a morphoclimatic domain of the savannah, with a tropical seasonal climate (Nimer, 1989), where the weather data during the study included minimum, average and maximum air temperatures of 13.8, 20.7 and 27.9°C, respectively; minimum, average and maximum air humidity of 29.9, 53.5 and 79.3%; air speed of 1.9m·s⁻¹, 444.9cal/cm²/day of solar radiation and lack of rain.

Thirty-nine two and six-rowed barley genotypes from an elite collection of Embrapa Cerrados were planted. They had the following origins: Brazilian (two-rowed genotypes: PFC 2001090, CEV 96046, PFC 213660, PFC 99318, PFC 213106, PFC 2003122, PFC 2005123, PFC 2004345, PFC 2001049, BRS 195, BRS Sampa, PFC 2004216, BRS Elis, BRS Greta, PFC 2004033, PFC

214827-10, Antártica-1, FM 404 and BRS Deméter; six-rowed genotypes: PFC 99324 and PFC 98252); English (two-rowed genotypes: Alliot, Cellar and Prestige); Mexican (six-rowed genotypes: CPAC 20011, CIMMYT 42, CIMMYT 48, CIMMYT 2, CIMMYT 25, CPAC 20020098 and Vicente Morales); North American (two-rowed genotypes: C-70 and M 14; and six-rowed genotypes: Lacey, Foster and BRS 180); German (two-rowed genotypes: Scarlett and Danuta); and Australian (six-rowed genotype: Nandi).

A complete randomized block design with four replicates was used. Five meters long plots with six rows spaced 20cm apart were used in all trials, with a useful area of 4.8m² for each plot, and a density of 300 plants/m². Soil preparation was made by adding soy culture debris, using 32" disk plows, followed by the use of a 20" leveling disk. The herbicide Pendimethalin was used in pre-emergency at a dose of 3.0l·ha⁻¹. According to the results from the soil analysis, 16kg·ha⁻¹ N, 120kg·ha⁻¹ P₂O₅, 64kg·ha⁻¹ K₂O, and 40kg·ha⁻¹ N were used in the seeding when the fifth leaf was present and totally unfolded.

Sprinkler irrigations were made based on the volumetric soil water content (θ), measured by a Profile probe Delta-T placed in the planting line (0.10, 0.20 and 0.30m deep). The irrigations were made when moisture at 0.10m depth was ~0.26cm³·cm⁻³, which corresponds to the consumption of 50% of water, according to the curve related to the water content in the area (Guerra *et al.*, 2003). The amount of irrigation water was calculated based on daily readings of the probe in order to increase moisture in the soil profile from 0 to 0.35m to field capacity (0.35cm³·cm⁻³), with a total of 420mm of net irrigation depth.

The following traits were evaluated: plant height (PHt, cm); heading date (HD, 50% of the plot with 50% of the ears or more outside the boot in days from planting); lodging (LODg, data transformed in arcsen $x^{0.5} \cdot 100^{-1}$, where x = lodging value in %); estimated grain yield (YLD, kg·ha⁻¹); thousand kernel weight (TKW, g) (Brasil, 2009); protein content (PROT, %, using the Kjeldahl method described by Yasuhara and Nokihara (2001); and first commercial classification (CLASS, %, according to Brasil (1996), where the first class represents the healthy and whole grains retained in a 2.5mm wide oblong hole screen). All data were analyzed using analysis of variance with the Genes program (Cruz, 2007).

The estimation of genotypic variance ($\hat{\sigma}_g^2$) was made among the

accessions, phenotypic variance ($\hat{\sigma}_f^2$), environmental average ($\hat{\sigma}_e^2$) and heritability (h^2) at mean level, coefficients of experimental (CVe) and genetic (CVg) variation, coefficient of relative variation (CVr) and the selection accuracy (\hat{r}_{gg}), for each one of the traits analyzed using the Genes program (Cruz, 2007). The phenotypic, genotypic and environmental correlations were determined according to Kempthorne (1966) using the Genes program (Cruz, 2007), where the following equations are employed:

Heritability at mean level:

$$h_a^2(\%) = \frac{\hat{\sigma}_g^2}{\text{QMg}} \times 100$$

Coefficient of genotypic correlation:

$$r_g = \frac{\hat{\text{Cov}}_g(X, Y)}{\sqrt{\hat{\sigma}_g^2(X) \cdot \hat{\sigma}_g^2(Y)}}$$

Coefficient of phenotypic correlation:

$$r_f = \frac{\hat{\text{Cov}}_f(X, Y)}{\sqrt{\hat{\sigma}_f^2(X) \cdot \hat{\sigma}_f^2(Y)}}$$

Coefficient of environmental correlation

$$r_a = \frac{\hat{\text{Cov}}_a(X, Y)}{\sqrt{\hat{\sigma}_a^2(X) \cdot \hat{\sigma}_a^2(Y)}}$$

where $\hat{\text{Cov}}_g(X, Y)$, $\hat{\text{Cov}}_f(X, Y)$ and $\hat{\text{Cov}}_a(X, Y)$: estimators of genotypic, phenotypic and environmental covariance, respectively, between characters X and Y; $\hat{\sigma}_g^2(X)$, $\hat{\sigma}_f^2(X)$ and $\hat{\sigma}_a^2(X)$: estimators of genotypic, phenotypic and environmental covariance, respectively, of the X character; $\hat{\sigma}_g^2(Y)$, $\hat{\sigma}_f^2(Y)$ and $\hat{\sigma}_a^2(Y)$: estimators of genotypic, phenotypic and environmental covariance, respectively, of the Y character.

Results and Discussion

The analysis of variance for each character showed the existence of significant effects of the genotypes, where these effects had an increased value based on the F-statistics ($p \leq 0.01$) for all

characters (Table I). Such effects indicate the existence of genetic variability and differences among the accessions studied concerning the evaluated traits. The value of F has also been used to indicate the degree of experimental precision (Cargnelutti Filho and Storck, 2007, 2009). According to Resende and Duarte (2007), the value of F in essays to evaluate genotypes should be >2.0 . The values of F found in the present study, ranging from 2.008 to 114.748, were adequate and included in the class of precision as high and very high.

The coefficients of environmental variation (CVe) showed a small magnitude, except for the trait lodging (170.70%; Table I). High values for CVe and lodging have been found by several authors (Costa *et al.*, 2002; Žáková and Benková, 2006). This trait is strongly influenced by the environment and difficult to be assessed. When evaluating CVe, the features of each crop studied should be considered, specially the nature of the trait to be approached (Garcia, 1989; Scapim *et al.*, 1995; Costa *et al.*, 2002), so that one might have a better understanding of the results. As for the other traits, the values of CVe ranged from 2.14% for heading date to 5.91% for protein content, being considered low according to the criteria established by Pimentel-Gomes (1990), indicating a high experimental precision.

Resende and Duarte (2007) stated that to focus only on the value of CVe is not enough when evaluating the experiment quality. Even with low

values of CVe, other statistics regarding the genotypic variation, as for instance the coefficient of genetic variation and selection accuracy, are essential to effectively determine the genotypic value of the genetic material resulting from phenotypic evaluations (Resende, 2002). When taking in consideration the outcomes of the present study (Table I), the estimation of the genetic variance was the main component of the phenotypic variance between the genotypes, except lodging. The genetic variance for traits YLD, TKW, CLASS, PHt and HD showed a phenotypic variance greater than 90% and 73.8% for PROT. These results indicate, besides the increased genetic variability, an adequate environmental control, experiment effectiveness and genotypic accuracy, most likely because of the correct agricultural practices used during the research, experiment design including the size of the experiment parcel and number of repetitions, besides a cautious evaluation of the traits. The genetic variability and experimental precision presented are fundamental to plan the improvement program, allowing the precise selection and genetic gains (Allard, 1971; Chapman, 1985; Cruz *et al.*, 2004).

The coefficient of genetic variation (CVg) is a parameter that allows the determination of the magnitude of genetic variability in populations and in different traits (Resende, 2002) and also the proportion of gain in relation to the average (Faleiro *et al.*, 2002). The traits showing more favorable conditions

TABLE I
GENETIC PARAMETERS¹ AND TRAITS² ASSESSED
FOR ALL 39 BARLEY GENOTYPES

Genetic parameters	Traits						
	YLD	TKW	CLASS	PHt	HD	PROT	LODG*
QMg	3.100.108,26	73.83	532.05	279.89	185.21	2.21	0.00101
QMe	101.696,24	1.98	17.74	21.20	1.61	0.58	0.000469
F value	30.48**	37.36**	29.99**	13.21**	114.74**	3.82**	2,16**
σ_f^2	775.027,06	18.46	133.01	69.97	46.30	0.55	0.000252
σ_g^2	25.424,06	0.49	4.44	5.30	0.40	0.14	0.000117
σ_e^2	749.603,00	17.96	128.58	64.67	45.90	0.41	0.00014
$h_a^2(\%)$	96.72	97.32	96.67	92.43	99.13	73.84	53.61
Cve (%)	5.68	3.18	5.04	5.48	2.14	5.91	172.71
CVg (%)	15.42	9.58	13.57	9.56	11.41	4.97	92.83
CVr (%)	2.72	3.02	2.69	1.75	5.33	0.84	0.54
\hat{r}_{gg}	0.98	0.99	0.98	0.96	1.00	0.86	0.73

¹ Genetic parameters are mean squares of the genotypes (QMg) and error (QMe), F value and estimates of the phenotypic (σ_f^2), genotypic (σ_g^2) and environmental (σ_e^2) variance, of heritability at a mean level (h_a^2), experimental (CVe) and genetic (CVg) coefficient of variation, relation between CVr and accuracy (\hat{r}_{gg}) of each trait.

² Traits are YLD: grain yield, TKW: thousand kernel weight, CLASS: first commercial classification, PHt: plant height, HD: days to heading, PROT: protein content, and LODG: lodging.

* Data transformed in $\arcsin x^{0.5} \cdot 100^{-1}$, where x= lodging value in %.

** Significant at 1% of probability by the F test.

concerning the improvement had a superior CVg compared to the CVe. Therefore, Table I shows that there was a significant difference in relation to CVe, similar to the genetic variance when compared to the environmental, for the following traits: YLD (15.42%), TKW (9.58%), CLASS (13.57%), PHt (9.56%) and HD (11.41%). However, it was simultaneously inferior to CVe, for traits PROT and LODG, suggesting a not so favorable condition for the selection of those traits. Faleiro *et al.* (2003) analyzed CVg and CVe through the ratio CVg/CVe to have a real idea of the situation of each trait in relation to the improvement. CVr is a parameter used to quantify the available genotypic variability (Santos, 1985) and to figure out the possibilities of success of the genetic improvement (Vencovsky, 1987). When CVr is >1, it indicates a favorable condition to the selection since the genetic variance overcomes the environmental. The CVr coefficients found were >1, except for traits PROT and LODG (Table I). However, although CVr is <1, when considering trait PROT and the number of repetitions used during the study (4), this additionally ensured a high accuracy and precision, where a CVr of 0.84 and selection accuracy of 0.86 (Table I) are perfectly adjusted to the values established by Resende and Duarte (2007). As for trait lodging, the ratio between the genetic and environmental correlation (CVr) was 0.50. This figure suggests a not so favorable condition for the selection of the character. However, as it was observed for trait PROT, the precision for LODG was 0.732, considered as high. Even though it is not an ideal precision, as stated by Resende and Duarte (2007), values for traits PROT and LODG showed a precision classified as high among the classes provided by those authors, allowing a good statistical inference of the genotype based on the phenotype.

The additional values of selection accuracy (r_{gg}) concerning YLD, TKW, CLASS, PHt, HD (Table I) were classified as very high, according to the accuracy categories provided by Resende and Duarte (2007). As Resende (2002) stated, the greater the accuracy value, the better will be the statistical inference of the genotypic value from the phenotypic value, providing correct information for selection, since it is the main element in the genetic progress that the plant breeders might change when the purpose is to maximize genetic gain.

Another important parameter used to evaluate experimental precision is heritability. Table I shows that estimates of broad sense heritability for traits YLD, TKW, CLASS, PHt and HD had values >90%, indicating a predictive

correspondence between the phenotypic and genetic value, as shown by Falconer and Mackay (1996) and Vencovsky and Barriga (1992). Such statement is evidenced by the greater contribution of the genotypic variation in relation to the environmental one, compared to the phenotypic variance (Searle *et al.*, 1992). High heritability estimates allow a greater efficacy regarding the selection process, so that such traits under the present conditions show the possibility of being inherited from one generation to the other. It is important to highlight that this significant heritability may be explained by the presence of additive genes effects and high degree of homozygosis of genotypes, since they already have more than eight generations of self-pollination.

HD showed the highest heritability (99%). Such high heritability for HD was also found by Marquez-Cedillo *et al.* (2001), and from 92 to 83% by Manzjuk and Barsukov (1974). Frey (1954) described values considered high (47-92%) in different populations, while Delogu *et al.* (1988) showed values of heritability of HD from 65 to 79% and Gut *et al.* (2004) from 63 to 80%. Therefore, it is assumed that in this kind of conditions, there was an effective control in the environment variation, a better expression of genetic differences and consequently, a higher heritability.

For TKW, heritability was high (97%). Chand *et al.* (2008) also found a high heritability (99.9%) for TKW in a collection of elite genotypes in three different environments. Jalata *et al.* (2011) and Kole (2006) found values of broad sense heritability for TKW of 86 and 78%, respectively. Lower values, still considered high, were mentioned by Therrien (2006) when evaluating more than 32 environments and 120 barley genotypes, indicating a broad heritability from 64 to 75%, with an average of 69%. This value was close to data obtained by Delogu *et al.* (1988), 66 and 68% for two populations and also to the value of 97% reported by Manzjuk and Barsukov (1974). However, the value mentioned before was higher than the ones found by Lu *et al.* (1999) which ranged from 27 to 55%, showing a big variation according to the genetic materials and environments used. Tinker *et al.* (1996) confirmed that the heritability estimation for the trait weight of a thousand grains was different depending on the environment used (49 to 82%), with an average of 71%, suggesting that the variation among heritabilities found might be explained by the considerable heteroscedasticity (differences in the quantity of non-genetic variance) among the environments. The high level of heritability observed indicates that the

barley grain weight *per se*, or the components that contribute for this weight, may be introgressed in new genotypes, with a great possibility of success.

Heritability for trait YLD was 97%, being considered significant. Marquez-Cedillo *et al.* (2001) found a high heritability for grain yield (83%) in an average of nine environments, while Hayes *et al.* (1993), when analyzing 16 environments, evidenced a heritability of 77% and Jalata *et al.* (2011) a broad sense heritability of 71%. Gut *et al.* (2004) confirmed values of up to 88%. On the other hand, estimates of lower amplitude have been verified (Rutger, 1966; Delogu *et al.*, 1988; Nadziak *et al.*, 1993). As for Al-Yassin *et al.* (2005), the estimates of broad sense heritability for grain yield, varied considerably in the literature regarding the same species, probably due to differences in the type of genetic material and the environments where the studies were performed. These authors described that the heritability ranged for the same cross due to the ratio genotype \times place and genotype \times year. For a determined cross, the value ranged from 0% to 68%. For a certain barley cross, the average broad sense heritability varied from 17.3% (when the yield was 29kg·ha⁻¹) to 75.8% (when yield 3.923kg·ha⁻¹). Similar variation in heritabilities concerning grain yield were registered by Delogu *et al.* (1988) and Gut *et al.* (2004). Tinker *et al.* (1996) also found out that the estimation of heritability for this trait (0-66%) was different depending on the environment. Similarly, Bouzerzour and Dekhili (1995) observed that the heritability for barley grain yield ranged from 0 to 93%, indicating the significant effect of environment on heritability. They concluded that this fact should be considered to predict a better response and method of selection.

Annicchiarico *et al.* (2005) stated that in order to study heritability, it is necessary to take into consideration the interaction of genotype \times environment, genotype \times location, and genotype \times year. Falconer and Mackay (1996) observed that heritability is not related to only one trait, but also to the genetic variance and environment to which the genotypes are exposed, to the population and environment conditions and circumstances to which the individuals are exposed. The value obtained might be explained by the smaller stress on the environment over the genotypes, corroborating with the proposition made by Frey (1964) who stated that there are higher heritabilities in environments with no stress compared to those under some type of stress. The irrigated environment found in the Brazilian savannah might have influenced this high

heritability, being considered as a favorable environment for a selection based on these statistical data, since according to Johnson and Frey (1967) estimates of heritability might be used as criteria to identify the environments which would result in a more effective selection.

As for trait CLASS (grains ≥ 2.5 mm wide), the heritability was 96.67%, as high as the figures found by Fox (2008) of 88-95% for seeds 2.5-2.8mm and 89-98% for seeds > 2.8 mm. The high heritability indicates a relatively high level of genetic variation regarding the total variation and/or that the environmental conditions were favorable for the selection.

Heritability for trait PHt was high (92.43%). This parameter might be used in the prediction of genotypic values and for the selection of superior genotypes. This outcome reassures the hypothesis that plant height in barley has high heritability and might be inherited from one generation to the other, as previously determined by Frey (1954), who found an index of up to 92%. Similarly, Hayes *et al.* (1993) noted a heritability of 96% in 16 environments evaluated, while Marquez-Cedillo *et al.* (2001) found a value of 95%, Manjuk and Barsukov (1974) 74% and Delogu *et al.* (1988) from 64 to 78%. In general, heritability for this trait in barley is high. Chand *et al.* (1988) obtained a broad sense heritability of up to 95% and Eshghi and Akhundova (2010), when considering the broad sense heritability, found values of 80 and 87%, which were considered as high by the authors.

Heritability of PROT was 74% and was also considered high (Cruz, 2005). Although it was lower than those of the other traits, this estimate might be considered satisfactory for the successful selection of the trait. Similar results for protein were found by Fox (2008) who reported values from 60 to 80%; Olsen (1974) who evidenced an estimate of 73%; Bichoński and Burek (2000) who registered a heritability of 72% and Therrien (2006) who found an estimate from 53 to 94% when he tested about 120 genotypes in 32 environments. It is important to emphasize that Therrien (2003) found a highly inherited protein which is amenable to be genetically improved, even though the heritability he found was 64%.

When studying trait LODG, its heritability (53.61%) was the lowest among all traits evaluated. However, it was greater than those found in the interval set by Tinker *et al.* (1996), 3-52% and the one observed by Gut *et al.* (2004) of 11-54.8%. Even though it was considered a

high heritability (Cruz, 2005), data indicated that there is a small genetic variability in the collection, which affects the genetic advance in the improving program.

In general, the results in the present study show that phenotypic selection is relatively easy to be performed due to the high heritabilities found. Probably, the adequate environmental control, confirmed by statistical parameters, promoted the genotypic variability expression in the traits evaluated.

In terms of estimation of phenotypic, genotypic and environmental correlation among the pairs of traits (Table II), the figures show that in absolute values for all traits, the genotypic correlations were greater than the phenotypic and environmental correlations. This confirms the contribution of genetic factors on the expression of traits compared to the environmental factor and also that the phenotype adequately reflects the genotype. Although there are only few barley genetic correlations estimates found in the literature, similar results were found in studies carried out by Shoufu *et al.* (1996), Bhutta *et al.* (2005) and Kole (2006). It can also be emphasized that genotypic and phenotypic coefficients were identical in sign and that according to Cruz *et al.* (2004), this can be explained by the lack of errors in the sampling and evaluation.

For some pairs of traits, the genotypic and environmental correlations showed different signs (Table II) indicating that the environment positively affected a determined trait in relation to the other. Besides that, these combinations of pairs of traits where the signs are different show that whatever caused the genetic and environmental variation probably affected the traits through dissimilar physiological mechanisms (Falconer and Mackay, 1996). This fact was evidenced when correlating YLD and TKW, YLD and PHt, YLD and PROT, YLD and LODG, TKW and PHt, TKW and HD, TKW and PROT, CLASS and PHt, and finally CLASS and HD.

The greatest magnitudes for the genotypic (0.6076) and phenotypic (0.5677) correlations were found for TKW and CLASS (0.6076), being positive and determining that the selection made with the purpose of developing a trait will cause similar alterations in the other one. Identical signs were found concerning the environmental correlation compared to the respective genetic correlation, showing that the environment did not affect the associated variable, benefiting the indirect selection. Considering that TKW is measured before the trait CLASS, the effectiveness of an indirect selection through the weight of thousand seeds rather than the grain classification is easier to be

TABLE II
ESTIMATES OF THE GENOTYPIC, PHENOTYPIC AND ENVIRONMENTAL CORRELATIONS AMONG SEVEN TRAITS EVALUATED IN 39 BARLEY GENOTYPES

Traits	Correlations	Traits					
		TKW	CLASS	PHt	HD	PROT	LODG
YLD	r_g	-0.2365	0.3119	0.6017**	-0.1182	-0.3104	-0.1028
	r_f	-0.2266	0.3020	0.5677**	-0.1177	-0.2584	-0.0718
	r_a	0.0964	0.0138	-0.0248	-0.1179	0.0424	0.0179
TKW	r_g		0.6076*	-0.1141	0.0172	0.1985	0.1074
	r_f		0.5994**	-0.1061	0.0158	0.1671	0.0801
	r_a		0.3370	0.0471	-0.0743	-0.0135	0.0220
CLASS	r_g			0.2257	0.0428	-0.1045	-0.0411
	r_f			0.2094	0.0417	-0.0941	-0.0186
	r_a			-0.0780	-0.0122	-0.0624	-0.2225
PHt	r_g				0.3052	-0.4399	0.2670
	r_f				0.2924	-0.3752	0.2190
	r_a				0.0122	-0.0833	0.1657
HD	r_g					-0.1381	0.2323
	r_f					-0.1231	0.1753
	r_a					-0.1035	0.0946
PROT	r_g						0.0592
	r_f						0.0504
	r_a						0.0378

YLD: grain yield, TKW: thousand kernel weight, CLASS: first commercial classification, PHt: plant height, HD: days to heading, PROT: protein content, and LODG: lodging.

** *: Significant at 1 and 5% of probability by T test.

obtained, as the grain commercial classification is a time-consuming process that demands a lot of labor. According to Cruz *et al.* (2004), in some cases, progress can be achieved in a faster way by using indirect selection based on the correlated answer than the direct selection of the desired trait.

Trait YLD was positively correlated to trait PHt in terms of genotypic (0.6017) and phenotypic (0.5677) correlation, showing that the selection of taller genotypes would result in genotypes with higher yield, being important in the selection process. Similar associations, although smaller, were observed by Shoufu *et al.* (1996), Bhutta *et al.* (1991), Gut *et al.* (2004) and Bhutta *et al.* (2005) both for two-rowed and for six-rowed barley, confirming the results found herein. However, the phenotypic correlations showed an opposite sign as the values observed in the study carried out by Rutger *et al.* (1967), that although not identical, showed a low magnitude, according to Ceccarelli *et al.* (1992). Since the correlations found in the literature show different magnitudes, it is essential to emphasize that the correlation for each population in particular should be estimated, as was stated by Unêda-Trevisoli (2000).

Ceccarelli *et al.* (1992) found out that the relative efficacy of indirect selection compared to direct selection might be predicted through the magnitude of the heritability and the genetic correlation coefficient. Therefore, since the association between TKW and CLASS, as well as between YLD and PHt, showed high heritabilities (Table II), one might expect that indirect selection as stated by Vencovsky and Barriga (1992) in these cases will be effective. The highest genotypes and with higher weight of grains might be selected. However, according to Briggs (1978), because of the several positive and negative correlations related to the agronomical characteristics and barley quality, this type of selection in a genetic improvement program becomes a complex problem.

In terms of genetic and phenotypic variation, trait TKW was negatively correlated with yield and height, contrary to the results of Shoufu *et al.* (1996), Bhutta *et al.* (2005) and Kole (2006). However, it was concomitant with the results observed by Gut *et al.* (2004) for the two-rowed barley. This discrepancy observed in the literature is related to the different genotypes used and environments in each study.

In all combinations associated to the trait lodging, no difference in sign was found in relation to the genotypic and environmental correlations,

showing that the environment did not similarly interfere on the variables involved. It can be noted through the non-significant genotypic and phenotypic correlation coefficients between plant height and lodging, that lodging can be avoided by using tall-growing plants with a good architecture. This can be explained by the fact that the exiguity observed by the correlation coefficients, according to Ceccarelli *et al.* (1992), reflects the lack of a linear relationship among the evaluated traits (Cruz *et al.*, 2004). These results are similar to the predictions made by genetic improvement programs concerning the selection of short plants to avoid lodging. Lodging is related to morphological and anatomic features of the traits as well as their physiological aspects. These factors are correlated to environmental factors, indicating that the genotypes evaluated in the present study show a small tendency to lodging.

Conclusions

Highly significant genetic effects on the barley tested in irrigated areas of the savannahs were observed for all the agronomic characteristics evaluated.

Low coefficients of environmental variance for all traits, except for lodging, indicated good experimental precision. On the other side, high values of heritability, coefficients of genetic variation and selection accuracy showed the favorable conditions to the selection of materials for the agronomical traits evaluated.

Promising genetic materials for the evaluated agronomical traits were identified in the present study and might be explored in crossing blocks in improvement programs in order to develop cultivars better adjusted to the irrigated crop systems in the savannah.

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ESTIMACIÓN DE PARÁMETROS GENÉTICOS, CORRELACIONES FENOTÍPICAS, GENOTÍPICAS Y AMBIENTALES EN CEBADA (*Hordeum Vulgare* L.) SEMBRADAS BAJO CONDICIONES DE RIEGO EN LA SABANA BRASILEÑA

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RESUMEN

El objetivo del presente estudio es determinar la heredabilidad de características a través de parámetros fenotípicos, genéticos y ambientales relacionados a los componentes de rendimiento y caracteres morfo-fisiológicos: altura de planta (ALT), días a espigamiento, grado de acamamiento, rendimiento de grano (REND), peso de mil granos (PMG), contenido de proteína y clasificación comercial de granos (CLASS) de una colección élite de 39 genotipos de cebada bajo condiciones de riego, evaluados en la sabana de Brasil Central. El experimento fue llevado a cabo en la estación experimental de Embrapa Cerrados, Distrito Federal, Brasil, y el diseño usado fue de bloques completos al azar con cuatro repeticiones. Se observó variabilidad genética entre los genotipos evaluados. Las correlaciones genotípicas encontradas, en valores abso-

lutos, fueron mayores para todas las características que las correlaciones fenotípicas y ambientales correspondientes. Se encontró una influencia significativa de los factores genéticos en la expresión de las características estudiadas y se puede concluir que la expresión fenotípica es disminuida dependiendo de las condiciones ambientales. Las correlaciones fenotípicas y genotípicas de mayor magnitud ocurrieron entre PMG y CLASS. La característica REND tuvo una correlación genotípica y fenotípica positiva con ALT. La precisión de selección fue clasificada como alta para todas las características. Los altos valores encontrados en la estimación de la heredabilidad amplia indicó la existencia de variabilidad genética, demostrando la posibilidad de obtener ganancias genéticas a través de selección para todas las características.

ESTIMATIVAS DE PARÂMETROS GENÉTICOS, CORRELAÇÕES FENOTÍPICAS, GENOTÍPICAS E AMBIENTAIS EM CEVADA (*Hordeum vulgare* L.) IRRIGADA NO CERRADO

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RESUMO

O objetivo deste trabalho foi estimar parâmetros genéticos, fenotípicos e ambientais relacionadas aos componentes de produção e caracteres agromorfológicos: altura de plantas (ALT), espigamento, grau de acamamento, rendimento de grãos (REND), peso de mil sementes (PMS), teor de proteína e classificação comercial de grãos (CLASS) de uma coleção elite de 39 genótipos de cevada irrigada no bioma Cerrado. O experimento foi conduzido num delineamento de blocos ao acaso com quatro repetições, na Embrapa Cerrados, Distrito Federal, Brasil. Foi observada a presença de variabilidade genética entre os genótipos de cevada testados nas condições irrigadas do Cerrado. As correlações genotípicas foram, para todos os caracteres,

em valores absolutos, superiores às suas correspondentes correlações fenotípicas e ambientais. Houve grande contribuição dos fatores genéticos na expressão dos caracteres e que a expressão fenotípica é diminuída ante as influências do ambiente. As maiores magnitudes de correlações genotípica e fenotípica ocorreram entre PMS e CLASS. O caráter REND correlacionou-se genotípicamente e fenotípicamente e de forma positiva ao caráter ALT. A acurácia seletiva foi alta para todos os caracteres. As elevadas magnitudes das estimativas da herdabilidade ampla indicaram a existência de variabilidade genética apontando a possibilidade de obterem-se ganhos genéticos com a seleção para todos os caracteres.