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Genotype-environment interaction in the production of dry matter of edgeless fodder barley (*Hordeum vulgare* L.)

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ABSTRACT

Objective: To analyze the genotype-environment interaction (GEI) within the dry fodder production of 24 edgeless barley fodder lines (*Hordeum vulgare* L.) or commercial controls of the same and other species across five environments.

Design/Methodology/Approach: A randomized complete block design with three repetitions was used in the five trial environments, with fodder harvested at 105 d after sowing. Data were analyzed as combined random blocks over environments and the GEI was analyzed using the AMMI model.

Results: Significance ($p \leq 0.01$) was detected in the main effects and the GEI. Genotypes G26 (Cerro Prieto), G27 (Gabyan95), G10, G3, G19 and even genotype G24, showed interactions close to zero, so they were considered stable, while the edgeless barley lines: G6, G1 and G2 were qualified as desirable for dry fodder production, according to their superiority over the general mean and their low GEI.

Study Limitations/Implications: Results may vary when evaluating other environments and genotypes.

Findings/Conclusions: There are stable and desirable edgeless fodder barley genotypes that represent an option for fodder production in the study region. The oat control was considered the least productive and the locality of Zaragoza, Coahuila, is considered a potential environment for dry fodder production using edgeless fodder barleys such as those evaluated in this study, in addition to showing adequate discriminatory power.

Keywords: edgeless barleys, dry fodder, genotype-environment interaction, AMMI model.

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INTRODUCTION

Among the cereals with small grain used for fodder production, oats (*Avena sativa* L.) is one of the most used during the winter in Mexico, and in this area the state of Coahuila ranks fifth nationally (SIAP, 2015). Dairy farms established in this state carry out intensive fodder production and require forage options that allow them to produce fodder with the required nutritional quality during critical periods such as winter, when alfalfa (*Medicago sativa* L.) reduces its production and before the early sowing of corn (*Zea mays* L.) for silage.

Due to the conditions and needs of this region mentioned, it has been suggested that barley can represent a good option for fodder production, given its precocity compared to

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wheat, oats and triticale; therefore, in the generation of fodder genotypes of this species, they developed with absence of edges in the spike, precocity and production of dry matter (fodder) superior to oats. In the generation of high-yielding genotypes, it is necessary to quantify the genotype-environment interaction (GEI), in order to: (i) use them as parents in a breeding program, or (ii) recommend their use by producers in a given region (Crossa *et al.*, 1990).

The genotype-environment interaction is defined as the differential relative behavior shown by genotypes when evaluated in different environments, and when it is present in large proportion it hinders the genetic progress of selection (Yang and Baker, 1991; Magari and Kang, 1993), thus highlighting the importance of its determination. Additionally and to highlight the importance of the GEI study, in the opinion of Monsour *et al.* (2018) the identification of stable and high-yielding genotypes is essential for food security.

Various parameters and models have been used over time to measure GEI, with the AMMI model being the most effective in the analysis of multiregional trials as it captures a large proportion of the interaction's sum of squares, accurately separating the main effects from those of the GEI (Gauch, 1992). There are few reports on genotype-environment interaction with the AMMI model in winter cereal fodder production, one of them was carried out in triticale to evaluate stability and fodder production through cuttings (Lozano *et al.*, 2009), and recently, it has been studied in flour wheat through three samplings (Ramírez *et al.*, 2021). Presently, there is no knowledge about a study on the stability of fodder production with edgeless barley. Therefore, this study analyzes the genotype-environment interaction in dry fodder production of 24 edgeless barley lines and commercial controls across five environments, and measures the yield potential and discriminatory power of the environments.

MATERIALS AND METHODS

Twenty-four advanced lines of edgeless barley descendent from the fodder variety Gabyan 95 crossed with the Esperanza variety were evaluated together with commercial controls of the same and different species. The malting variety cv. Cerro Prieto and the forage variety Gabyan 95 were used as controls of the same species and oats cv. Cuauhtémoc, triticale cv. Eronga83, and an experimental line of fodder wheat (AN-266-99) as controls of another species, as shown in Table 1.

The environments were formed by the combination of two localities whose evaluations were carried out in different productive cycles. The locality of San Ignacio, Municipality of San Pedro de las Colonias, Coahuila (25° 45' 32" N and 102° 58' 58" W), at an altitude of 1100 masl, with a mean annual temperature of 18 °C and a mean annual precipitation of 400 mm, where evaluations were carried out during the fall-winter (F-W) 2016-2017 and 2018-2019 cycles.

The locality of Zaragoza, Coahuila (28° 28' 31" N and 100° 55' 10" W) registers 360 masl, with a mean annual temperature of 22 °C and a mean annual precipitation of 300-400 mm (Arriaga *et al.*, 2000), where the evaluations were carried out during the F-W 2016-2017, 2017-2018 and 2018-2019 cycles, identifying the environments (Table 2).

Table 1. Identification of the genotypes evaluated in five environments.

Genotype	Genotype
1.- CANI-1	16.- CANI-103
2.- CANI-9	17.- CANI-104
3.- CANI-10	18.- CANI-108
4.- CANI-11	19.- CANI-126
5.- CANI-12	20.- CANI-128
6.- CANI-15	21.- CANI-129
7.- CANI-63	22.- CANI-130
8.- CANI-69	23.- CANI-131
9.- CANI-70	24.- CANI-133
10.- CANI-77	25.- Oats (cv. Cuahutémoc)
11.- CANI-80	26.- Barley cv.Cerro prieto
12.- CANI-82	27.- Barley cv. Gabyan 95
13.- CANI-85	28.- Wheat (AN-266-99)
14.- CANI-99	29.- Triticale (cv. Eronga-83) (Tcl)
15.- CANI-100	

Land preparation consisted of traditional work used for the establishment of small-grain winter cereals in regions where they are sown under irrigated conditions, consisting of fallowing, harrowing, leveling, or framing, and irrigation layout. Sowing was done by manual seed drilling, with a planting density of 95 kg ha^{-1}, applying a fertilization dose of 120N-80P-00K, incorporating nitrogen in a fractionated manner: half at sowing and the other half in the first auxiliary irrigation; and phosphorus, all during sowing.

The experimental plot size was 6.3 m^2 (6 rows, 3 m long by 0.35 m between rows) and the useful plot was 0.175 m^2. At 105 days after sowing (das), 50 cm of one of the rows with full competence was cut at a height of 5 cm above ground level. The harvested material was dried in a roofed sunroom until a constant weight was obtained. Once the fodder weight was determined, it was transformed to t ha^{-1}. The information from the trials was analyzed as randomized complete blocks combined across environments to detect genotype-environment interaction, and the interaction analysis was performed under the following AMMI model:

Table 2. Localities and evaluation cycles and their identification as environment.

Locality and cycle	Environment
San Ignacio O-I 2016-2017	E1
Zaragoza O-I 2016-2017	E2
Zaragoza O-I 2017-2018	E3
San Ignacio O-I 2018-2019	E4
Zaragoza O-I 2018-2019	E5

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \alpha_{jk} \gamma_{jk} + R_{ij}$$

where: Y_{ij}=Yield of the *i*-th genotype in the *j*-th environment, μ=Overall mean, g_i=Effect of the *i*-th genotype, e_j=Effect of the *j*-th environment, λ_k=Eigenvalue square root of the *k*-th axis of the PCA, α_{ik} γ_{jk}=PCA score for the *k*-th axis of the *i*-th genotype and *j*-th environment respectively, and R_{ij}=Residual of the model.

The principal component analysis (PCA) scores for environments and genotypes are expressed as units of the corresponding eigenvalue times the square root of the eigenvalue (Zobel *et al.*, 1988). The sum of squares of the genotype-environment interaction is subdivided into PCA axes, where the k-axis has g+e−1−2k degrees of freedom, where g and e represent the number of genotypes and environments, respectively. Normally only the first two principal components (PCs) are retained in the model; the remaining ones are sent to the residual. The scores assigned to the genotypes can take positive or negative values with respect to the PCs, with those with values close to zero (lower interaction) considered stable genotypes; higher values indicate a higher interaction with the environments and depending on the sign and the quadrant of the generated graph a broader description of the genotypes and environments is made. Additionally, genotypes were qualified as desirable if they have a yield higher than the general mean of the experiment together with lower interactions with the environments. Analyses were performed using the SAS software (1989).

RESULTS AND DISCUSSION

The analysis of variance showed high significance ($p \leq 0.01$) between environments, genotypes and in the genotype-environment interaction (GEI), which when analyzed using the AMMI model (Table 3), also showed high significance in the first two principal components (PCs) with which 77.79% of the GEI was explained. The first component contained 43.64% of the GEI while the second CP explained 34.15% of this interaction.

Table 3. Results of the analysis using the AMMI model for dry fodder yield of the genotypes evaluated in five environments.

Variation source	DF	SS	HS
Replications (Rep)	2	6.166	3.083^{NS}
Environments (Env)	4	2129.560	532.390**
Genotypes (Gen)	28	907.745	32.419**
Env × Gen	112	779.470	6.960**
PC1	31	340.156	43.639**
PC2	29	266.179	34.149**
Residual	52	173.135	3.329

DF=Degrees of freedom, SS=Sum of squares, HS=Half squares, **=Significant at 0.01 probability, NS=Not significant.

The variance explained with the first two principal components was higher than that reported by Lozano *et al.* (2009), but lower than that reported by Ramírez *et al.* (2021) in three samplings and allows a reliable explanation of the GEI, since according to Crossa (1990) and Gutierrez-García *et al.* (2006) the explanation should be greater than 75%.

In malting barley, studies on GEI in grain production have been conducted in the El Bajío region with an explanation of 72.3% of the GEI with the first two principal components, and it has been considered adequate (Pérez-Ruíz *et al.*, 2015). In other latitudes, Monsour *et al.* (2018) have reported an explanation of 62.6% with the first two components and highlighted the usefulness of the AMMI model in the study of GEI. Other studies have been conducted to analyze promising barley lines using the AMMI method and GGE Biplot (Kendall *et al.*, 2019), but there are no reports on GEI in dry fodder production of this species, which limits the comparative study.

By plotting the genotypes and environments on the plane generated with the first two PCs, an adequate visualization of the interaction shown by the genotypes and the behavior of the test environments was obtained, as shown in Figure 1, where the genotypes that showed the least interaction are located near the crossing of the lines that start from the zero point of both axes, whose intersection represents zero GEI. Thus, genotypes G26 (Cerro Prieto), G27 (Gabyan95), G10, G3, G19 and even genotype G24, showed interactions close to zero, so they were considered stable and could be used as parents in a breeding program or recommended for use by producers in the study region (Crossa *et al.*, 1990), 1990), as has been done in flour wheat (Ramírez *et al.*, 2021), genotypes that after 90 days showed low or no GEI, unlike those studied here.

Genotypes G2, G17, G11 and G20 showed small and positive interactions, while the largest and most positive interactions were shown by genotypes G5, G13, G6 and G1. These positive interactions indicate that genotypes exhibiting them may show slightly higher yields than those determined here in the environments where they are positively associated.

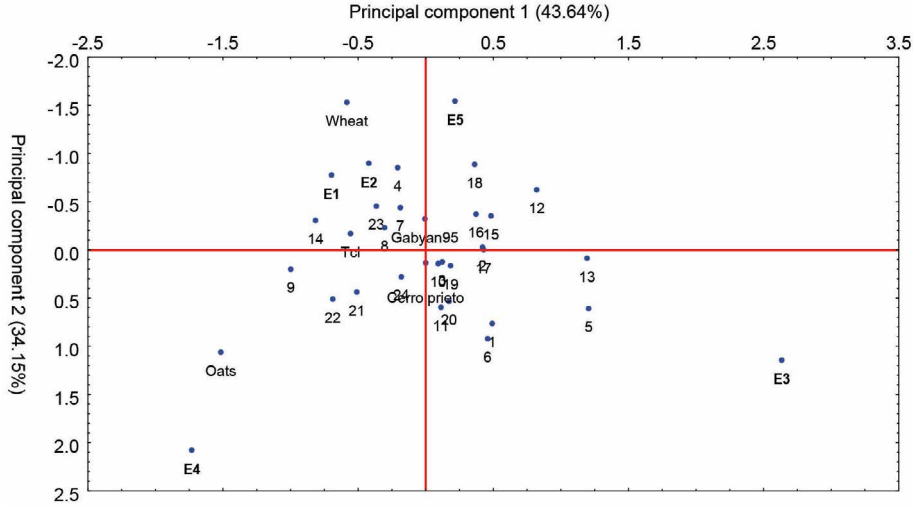

Figure 1. Genotype environment interaction showed by environments (E) and genotypes.

Wheat (G28), barley genotype G14 and Tcl cv. Eronga 83 showed the most negative interactions, together with barley genotypes: G23, G8 and G7, coinciding with that reported by Ramírez *et al.* (2021) for the control Tcl. cv. Eronga 83 with respect to the type of interaction shown. Oats followed by genotypes G9, G22 and G21 showed inconsistency in their interactions that fluctuated between negative interactions detected by PC1 and positive interactions detected by PC2.

The A3 environment (Zaragoza 2017-2018) due to its location in the first quadrant has potential for better yields and is an environment with discriminatory power given the distance to the intersection of the lines that indicate zero GEI; genotypes G5, G13, G6, G1 and G17 were associated to this environment, which will produce more in this environment.

The A1 and A2 environments, on the other hand, exhibited lower potential for increasing yield and lower discriminating power due to the short distance to the intersection of the zero GEI lines. The following genotypes were associated with these environments: wheat (G28), G4, G23, G7, G14, G8 and G29 (Tcl cv. Eronga 83), which will produce better in these environments.

According to PC1, the most negative interactions correspond to the genotypes mentioned above in addition to oats; according to this PC, A4 (San Ignacio 2018-2019) exhibits a high discriminatory power and oats cv. Cuauhtémoc (genotype frequently used in that locality) was strongly associated in this environment, followed by genotypes such as G9, G22, G21 and G24 which could represent an option in fodder production in that locality. Ramírez *et al.* (2021) have reported that this location favored the production of leaf dry matter in wheat and possibly promoted a similar reaction in the barley studied. Negative interactions indicate that genotypes exhibiting them may show yields below those estimated in the study. Environment 5 (Zaragoza F-W 2018-2019) showed good discriminatory power and adequate potential for obtaining higher yields.

A better score of the potential of the genotypes is obtained by elaborating a graph showing the yield achieved by the genotypes and the interaction detected by the first principal component (Figure 2), so that the desirable genotypes (those with yield above the general average and interactions close to zero) can be classified. The line crossing the X axis represents the overall mean of dry fodder estimated at 13.629 t ha^{-1} and the line crossing the Y axis represents zero GEI, in such a way that genotypes such as G6 showed the highest mean dry fodder production and has small and positive interactions, so it can be classified as desirable; genotypes G1 and G2 showed similar behavior although with lower yields, and they are also considered desirable. These genotypes are considered candidates to be registered as varieties and then recommended for exploitation in the study region.

Genotypes such as G11, G19 and G5 showed similar yields to genotypes G23 and G22, with the difference that the latter exhibited small negative interactions while the former showed positive interactions. Those that exhibit positive interactions may perform slightly better than estimated, while those that exhibit negative interactions tend to yield less than estimated or predicted.

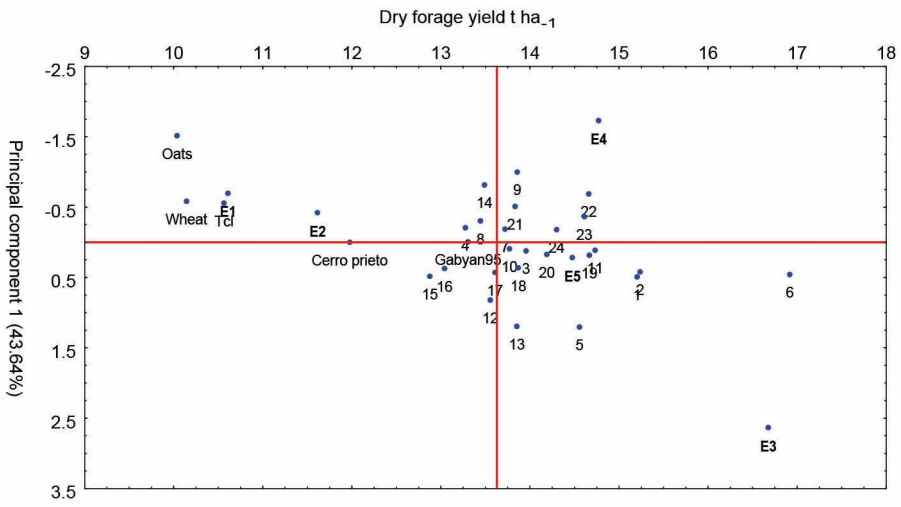

Figure 2. Genotypes and environments (A) based on FST yield and first PC from the AMMI model (GEI) in the first sampling.

Environment 3 (A3; Zaragoza F-W 2017-2018) averaged the highest yield of the environments evaluated, due to which it is considered a favorable environment for fodder production with the barleys evaluated here. Environment 5 (A5; Zaragoza F-W 2018-2019) was located within the same quadrant as A3 although with lower yield, so Zaragoza, Coahuila, could be catalogued as suitable or potential for fodder production using edgeless fodder barley genotypes such as those evaluated in this study. The genotypes that are located within the same quadrant with certain environments tend to be positively associated with them, that is, they produce better in those environments, so they could be specifically recommended for exploitation in the particular environment(s) with which they are associated, as is the case of the genotypes mentioned above.

Oats (genotype 25) presented the lowest yield of the genotypes evaluated, coinciding with that reported by Ramírez *et al.* (2021) when compared with wheat, followed by wheat (genotype 28) and triticale (Tcl, genotype 29), all of them showing negative interactions and associated with the environment 1 (A1) which was the least productive and which can also be exploited in A2. A similar assertion can be made for genotypes G4, G8 and G14 in the same Figure 2.

The separation of controls from different species used in the study (oats cv. Cuauhtémoc, triticale cv. Eronga83, and wheat AN-266-99) on the far left of the graph was mainly due to the precocity of barley as a species, to which the maximum dry matter accumulation has been reported to occur around 106 das (Wilson *et al.*, 2017), a similar time to that of this study and which constitutes a favorable characteristic that is reflected in shorter land occupation time and lower water consumption (Colín *et al.*, 2007). The malting barley cv. Cerro Prieto was intermediate between the fodder barleys and the commercial controls of other species, suggesting differences in the new fodder genotypes when compared to the malting barley. Genotype 27 (Gabyan 95) is parent of the lines evaluated and can be said to impart good stability and production characteristics to its offspring according to the

results found in this study, differing as mentioned from the malting barley cv. Cerro Prieto (genotype 26).

CONCLUSIONS

Genotypes G26 (Cerro Prieto), G27 (Gabyan95), G10, G3, G19 and even genotype G24 were considered stable, since they showed interactions close to zero. The new edgeless barley lines: G6, G1 and G2 were rated as desirable for dry fodder production based on their superiority over the overall mean and their low GEI. The control oats was the least productive of the genotypes evaluated. The locality of Zaragoza, Coahuila, is considered a potential environment for dry fodder production using edgeless fodder barleys such as those evaluated in this study, in addition to showing an adequate power of discrimination.

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