Article

Genotype environment interaction in wheat forage fractions in three samplings

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Abstract

Winter cereals have useful characteristics for forage production and generally have adequate nutritional quality. In the generation of new varieties, it is necessary to quantify the environmental genotype interaction (IGA) to make a more efficient selection. The objectives were to analyze the genotype environmental interaction (IGA) in forage fractions of 22 lines of beardless wheats and three commercial witnesses of another species, through three samplings. A random complete block design was used with three repetitions in four environments, sampling at 75, 90 and 105 days after planting. The production of total dry forage and its fractions was determined, analyzing them using the AMMI model. The results indicated that thirteen wheat lines together with barley had desirable characteristics to produce total dry fodder through sampling carried out according to superiority over the general average. The oat witness was considered the least productive. The portion of stems was the one with the highest contribution to the dry fodder yield, followed by the leaves and spikes. There was a presence of the IGA in the forage fractions, as well as in the total.

Keywords: AMMI model, fodder fractions, dry fodder, stability, wheats without edge.

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Introduction

Winter cereals are a sustainable alternative for livestock production, because of the efficient use of water despite the presence of frosts from climate change, where wheat has a cold tolerance of up to -23 °C (Braun and Soulescu, 2002). They have characteristics that make them useful for fodder, producing high yields and being rich in proteins, vitamins and carbohydrates (Cherney and Marten, 1982; Cash *et al.*, 2004). Globally wheat is the most widely used in human food; being a raw material for the development of a variety of processed foods (FAO, 2005) and used as green food in the animal diet in the form of fodder.

In recent years the use of cereals has expanded, using them in grazing, greening, tedding, chopped and silage (Hughes *et al.*, 1974; Colín *et al.*, 2007) classifying them as a good quality forage resource (Hart *et al.*, 1971; Juskiw *et al.*, 2000), even when its fractions are considered separately (Zamora *et al.*, 2016), there are wheats with production similar to that of oats. Being the Laguna Region the main dairy basin of Mexico, it is one of the areas that in critical times such as winter needs forage options that ensure nutritional quality and allow to continue with production, because of the existence of various options of use and various times of use of fodder.

Although oats are the main winter forage crop in this region and place Coahuila as the fifth largest producer nationwide (SIAP, 2015), wheat is considered a good choice for fodder production. To obtain new high-yield genotypes, plant breeders are looking for new methodologies for evaluating multiple genotypes in a short time (Jackson, 2001). Thus, the environmental genotype interaction (IGA), which is described as the inconsistency of behavior between genotypes from one environment to another and when it occurs in a large proportion decreases the genetic progress of the selection (Yang and Baker, 1991; Magari and Kang, 1993), thus emphasizing their great importance.

Over time, various parameters have been used to measure this interaction, with the AMMI model being the most effective in the analysis of multiregional tests as it captures a large proportion of the sum squares of IGA, precisely separating the main effects of the interaction (Gauch, 1992).

Research on the interaction of environmental genotype with the AMMI model has been carried out for the production of grain in wheat (Rodríguez *et al.*, 2011; Marza *et al.*, 2016) and in sorghum (Williams *et al.*, 2010), as well as in the evaluation of stability and forage production in triticale by cuts (Lozano *et al.*, 2009), but there are currently no work on IGA in wheat forage fractions, only production and nutritional value in fractions of beardless wheat fodder has been reported (Zamora *et al.*, 2016).

Reports of grain yield stability have also been found in wheat genotypes (Hortelano *et al.*, 2013), for grain yield and fodder (Rodríguez *et al.*, 2014) using the Eberhart and Russell model (1966). The objective of this research was to analyze the genotype environmental interaction in forage fractions of 22 lines of beardless flour wheats and three commercial witnesses of another species through three samplings.

Materials and methods

22 lines of wheat without edges plus three commercial witnesses were evaluated: Avena *cv* Cuauhtémoc, Barley *cv* GABYAN 95 and Triticale *cv* Eronga 83 (Table 1), during the autumnwinter (O-I) agricultural cycles, in the towns of Zaragoza, Coahuila, in the cycle (O-I) 2017-2018 (Environment 1) and the O-I cycle 2018-2019 (Environment 2), Navidad, Nuevo León (O-I) 2018-2019 (Environment 3) and San Ignacio, Municipality of San Pedro de las Colonias, Coahuila (O-I) 2018-2019 (Environment 4).

Table 1. Genetic material evaluated.

| Number | Variety | Number | Variety | Number | Variety | Number | Variety |
|--------|-----------|--------|-----------|--------|-----------|--------|---------------------|
| 1 | AN-249-99 | 8 | AN-216-09 | 14 | AN-228-09 | 20 | AN-409-13 |
| 2 | AN-268-99 | 9 | AN-217-09 | 15 | AN-229-09 | 21 | AN-246-13 |
| 3 | AN-263-99 | 10 | AN-218-09 | 16 | AN-264-09 | 22 | AN-310-03 |
| 4 | AN-267-99 | 11 | AN-220-09 | 17 | AN-326-09 | 23 | Oatmeal Cuauhtémoc |
| 5 | AN-244-99 | 12 | AN-221-09 | 18 | AN-7-09 | 24 | Barley Gabyan 95 |
| 6 | AN-236-99 | 13 | AN-222-09 | 19 | AN-241-13 | 25 | Triticale Eronga 83 |
| 7 | AN-209-09 | | | | | | |

The combination of locality and production cycle will be generically referred to as an environment. The information on evaluation locations is cited in Table 2. In each of them, a randomized complete block design with three repetitions was used. The preparation of the land consisted of traditional tasks used for the establishment of winter small grain cereals in the regions where it is sown under irrigation conditions, consisting of fallow, tracking, leveling or square and irrigation stroke.

Table 2. Description of the evaluation locations.

| Locality | Latitude | Longitude | Altitude (m) | Average annual temperature (°C) | Average annual rainfall (mm) | |
|-------------|---------------|----------------|--------------|---------------------------------|------------------------------|--|
| Zaragoza | 28°28' 31" N | 100° 55' 10" W | 360 | 22 | 300 to 400 | |
| San Ignacio | 25° 45' 32" N | 102° 58' 58" W | 1 100 | 18 | 400 | |
| Navidad | 25° 04' N | 100° 56' W | 1 895 | 14 | 400 | |

The planting was carried out manually, with a planting density of 120 kg ha⁻¹, using a fertilization dose of 120-80-00, applying nitrogen in a fractional way: half at sowing and another half at the first aid irrigation of phosphorus all to the planting. In environment 1 was sown on December 18, 2017, in environment 2 on December 6, 2018, environment three was sown on February 6, 2019, as environment 4 was established on November 24, 2018.

The weeds were manually controlled. Three forage samples (at 75, 90 and 105 days after planting) were carried out in all the environments evaluated, in order to estimate the production of dry matter for each. The size of the experimental plot was 6.3 m² (6 rows 3 m long by 0.35 m between rows) and the useful plot was 0.175 m. At each sampling, 50 cm of one of the rows with full competence was cut at a height of 5 cm above the ground surface.

The material harvested at each sampling was manually separated into leaves, stems and spikes, then dried into sundeck until constant weight was obtained to determine dry leaf weight (PSH), stems (PST), and spikes (PSE), with the sum of these three components the total dry fodder (FSTOT) was obtained, being recorded in t ha⁻¹. The information from the test was analyzed as randomized complete blocks in pooled form across environments to detect genotype environment interaction and the analysis of the genotype environment interaction was performed under the following AMMI model: N, $Y_{ij} = \mu + g_i + e_j + \sum = \lambda_k \alpha_{ik} \gamma_{jk} + R_{ij}$, k=1. Where: $Y_{ij}=$ yield of the i-th genotype in the j-th environment, $\mu=$ general mean, $g_i=$ effect of the i-th genotype, $e_j=$ effect of the j-th environment, $\lambda_k=$ square root of the eigenvalue of the k-th axis of the ACP, $\alpha_{ik} \gamma_{jk}=$ ACP score for the k-th axis of the i-th genotype and j-th environment respectively and $R_{ij}=$ residual of the model.

Principal Component Analysis (ACP) scores for environments and genotypes are expressed as units of the eigenvalue corresponding by the square root of the eigenvalue (Zobel $et\ al.$, 1988). The sum of squares of genotype-environment interaction is subdivided into axes of the ACP, 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 (CP) are retained in the model, the rest are sent to the residual.

The scores assigned to the genotypes can take positive or negative values with respect to the CP, with stable genotypes being considered those with near-zero values (less interaction), higher values indicate greater interaction with environments, and depending on the sign and quadrant of the generated graph a broader description of genotypes and environments is made. In addition, genotypes were rated as desirable if they have a yield above the general average of the experiment coupled with lower interactions with environments. The analyses were carried out using the SAS program (1989).

Results and discussion

In the first sampling all forage fractions and total dry fodder (FSTOT) had statistical significance ($p \le 0.01$) in the genotype environment interaction (IGA) (Table 3), according to the model of additive principal effects and multiplicative interaction (AMMI), performed with the routine developed by Vargas and Crossa (2000) which contemplates repetitions as a principal factor.

The analysis showed that the IGA is explained with the first two principal components (CP), where the lowest explanation was in the order of 82% and corresponded to the FSH, this percentage being the lowest obtained; while for FSTOT and FST, more than 85% was explained unlike the FSE which was explained in 100%, only with the first CP, these percentages being higher than those reported by Lozano *et al.* (2009), which allows a reliable explanation of the IGA, as long as it is greater than 75% (Crossa, 1990). Table 3 shows that the first component was highly significant for all variables, as the second component showed significance to ($p \le 0.05$) only in the FSH variable.

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|--|----|--------|----|--------|----|-------|----|-------|----|
| FV | GL | FSTOT | | FST | | FSE | | FSH | |
| Repeats (Rep) | 2 | 5.571 | ** | 1.228 | ** | 0.001 | | 1.585 | ** |
| Environments (Amb) | 3 | 30.285 | ** | 11.569 | ** | 0.045 | ** | 9.846 | ** |
| Genotypes (Gen) | 24 | 1.84 | ** | 0.976 | ** | 0.008 | ** | 0.347 | ** |
| Amb x Gen | 72 | 0.699 | ** | 0.223 | ** | 0.008 | ** | 0.169 | ** |
| CP1 | 26 | 1.219 | ** | 0.413 | ** | 0.024 | ** | 0.221 | ** |
| CP2 | 24 | 0.495 | | 0.134 | | 0 | | 0.181 | * |
| Residual | 22 | 0.306 | | 0.096 | | 0 | | 0.095 | |

Table 3. Average squares and AMMI significance for the first sampling.

FV= source of variation; GL= degrees of freedom; FSTOT= total dry forage; FST= dry forage of stems; FSE= dry forage of spike; FSH= dry forage of leaf.

With the yield data and the principal component 1 of the AMMI analysis, Figure 1 was prepared, which made it possible to qualify as desirable in FSTOT production in the first sampling of genotypes 15 (AN-229-09), 2 (AN-268-99), 19 (AN-241-13) and 7 (AN-209-09), by obtaining yields above the general mean (3.25 t ha⁻¹) and showing small and negative interactions. Genotype 3(AN-263-99) also exceeded the general mean but exhibited positive interactions.

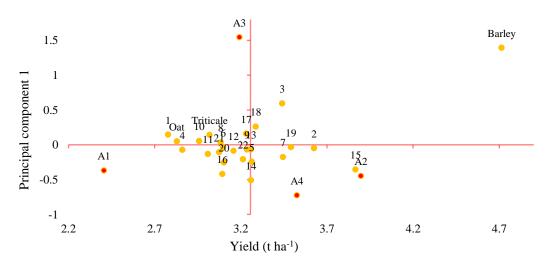


Figure 1. Genotypes and environments (A) based on FSTOT yield and first CP of AMMI (IGA), at first sampling.

It should be noted that 75 days after planting (dds), the most profitable genotype was GABYAN 95 with 4.71 t ha⁻¹, with large and positive interactions; this fact is mainly explained by the precocity presented by barley, being a favorable characteristic that is reflected in a shorter time of occupation of the land (Colín *et al.*, 2007). Oat cv. Cuauhtémoc was the least profitable showing near-zero interactions, being surpassed by wheats and commercial witnesses of triticale and barley, thus confirming the existence of forage wheats with mayor production than oats *cv* Cuauhtémoc at 75 dds. Environment 3 (Navidad O-I 2018-2019) provoked large and positive interactions, possibly because the temperature has accelerated the phenology of the genotypes (Karsai *et al.*, 2008), given

the late planting date in this environment that averaged in the months of the experiment a maximum temperature of 27.8 °C and a minimum of 15.2 °C according to the National Meteorological Service (SMN, 2019), while environments 1 (Zaragoza O-I 2017-2018), 2 (Zaragoza O-I 2018-2019) and 4 (San Ignacio O-I 2018-2019) provoked negative interactions and these three environments had lower average temperatures than environment 3 during the evaluation period.

Genotype 15(AN-229-09) was strongly associated with environment 2 (Zaragoza O-I 2018-2019), this being the most productive. At Navidad O-I 2018-2019 (A3), genotype 3(AN-263-99) and barley *cv* Gabyan 95 were positively associated and in Zaragoza O-I 2017-2018 (A1) being the environment that showed the lowest yield, genotypes 4 (AN-267-99), 11 (AN-220-09), 16 (AN-264-09) and 20 (AN-409-13) were associated. The environment 1 showed the lowest average maximum temperatures of the environments studied, so it was delayed the phenological stage of the cereals evaluated and therefore their biomass. Genotype associations with the above environments indicate that they will produce a good amount of total dry fodder in the environment with which they were associated.

By graphing the IGA explained by the first CP of the AMMI and stem production (Figure 2), GABYAN 95 was found to have obtained the highest stem production, showing large and positive interactions, followed by genotypes 15 (AN-229-09), 2 (AN-268-99), 19 (AN-241-13) and 21 (AN-246-13) which showed yields higher than the general mean (1.41 t ha⁻¹) and small and positive interactions except genotypes 15 (AN-229-09) and 21 (AN-246-13) with negative interactions.

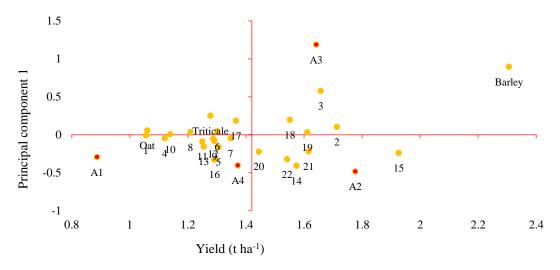


Figure 2. Genotypes and environment (A) based on FST yield and first CP of the AMMI (IGA) in the first sampling.

Genotype 3(AN-263-99) also exceeded the general mean but exhibited large and positive interactions. Oatmeal cv. Cuauhtémoc presented in this variable the lowest yield and zero interactions. Environment 3 (Navidad, O-I 2018-2019) provoked positive interactions and environments 1, 2 and 4 (Zaragoza O-I 2017-2018, O-I 2018-2019 and San Ignacio O-I 2018-2019) negative interactions, just as it happened in the FSTOT variable.

To environment 2 (Zaragoza, O-I 2018-2019) genotypes 15 (AN-229-09), 21 (AN-246-13), 22 (AN-310-03) and 14 (AN-228-09) were associated, this being the most productive environment in stems, and to the environment 3 (Navidad, O-I 2018-2019) genotypes such as 3 (AN-263-99) and Gabyan 95were associated, while environment 1 (Zaragoza O-I 2017-2018), was the least favorable, to which genotypes 1 (AN-249-99), 4 (AN-267-99) and 10 (AN-218-09) were associated.

Genotypes 13 (AN-222-09), 5 (AN-244-99), 9 (AN-2 17-09) and 7 (AN-209-09) were qualified as desirable to produce dry forage of leaves, having a higher production than the general average (1.82 t ha⁻¹) and showing positive interactions close to zero, with the exception of genotype 7(AN-209-09) when presenting large interactions (Figure 3). Barley cv. Gabyan 95 obtained the highest leaf production, presenting large and negative interactions, however, one of the genotypes evaluated for wheat (21) with small and negative interactions was placed as the lowest leaf production.

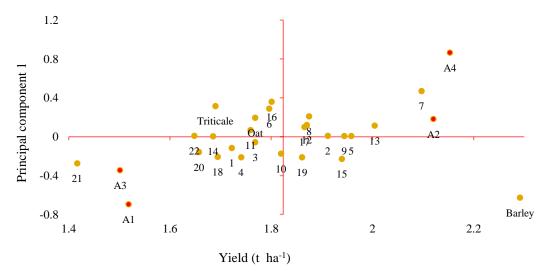


Figure 3. Genotypes and environment (A) based on FSH yield and first CP of the AMMI (IGA) at first sampling.

Oatmeal *cv* Cuauhtémoc presented a favorable yield, but without exceeding the general mean and with near-zero interactions. With positive interactions the environments 2 (Zaragoza O-I 2018-2019) and 4 (San Ignacio O-I 2018-2019) were maintained, this last environment was considered the most suitable for leaf production, to which genotype 7(AN-209-09) was positively associated, environments 1 (Zaragoza O-I 2017-2018) and 3 (Navidad O-I 2018-2019) provoked negative interactions, existing between these very little difference in leaf production, even so, environment 3 was distinguished as the least favorable, where genotype 21(AN-246-13) maintained association. The production of leaves is of some importance, since genotypes when presenting more leaves are considered for hay production (Feyissa *et al.*, 2008).

In analyzing the IGA explained by the first CP of AMMI analysis and spikes production, genotypes 21 (AN-246-13), 18 (AN-7-09), 22 (AN-310-0 3), 19 (AN-241-13) and 3 (AN-263-99) were considered desirable when exceeding the general mean (0.0122 t ha⁻¹) and showing positive interactions close to zero (Figure 4). The barley cv. Gabyan 95 was the genotype with the highest spike production with a yield of 0.115 t ha⁻¹ and large and positive interactions.

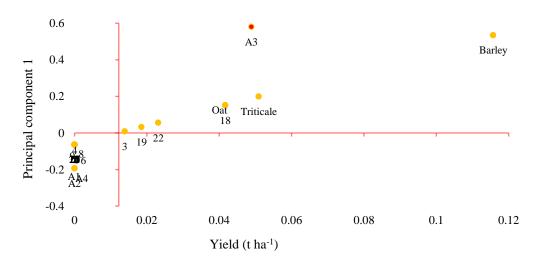


Figure 4. Genotypes and environments (A) based on FSE yield and first CP of the AMMI (IGA) at first sampling.

The witnesses of triticale *cv* Eronga 83 and oatmeal *cv* Cuauhtémoc were also called desirable when exceeding the general mean, exhibiting positive interactions; according to the precocity presented by these witnesses, they showed a phenological stage of spike emergency, but with low fodder yield, coinciding with Torres *et al.* (2019) who reported the 90 dds having found in oats and triticale an emergency stage of spike with low forage yields.

It is only possible to distinguish the environment 2 (Zaragoza O-I 2018-2019) that caused negative interactions and environment 3 (Navidad O-I 2018-2019) positive interactions, this environment being the most production, where the evaluated witnesses maintained positive association. It should be noted that most genotypes did not yet have spikes in this first sampling (Figure 4).

For the second sampling, the variance analysis exhibited differences ($p \le 0.01$) for FSE in the genotype environment interaction, suggesting that in stem and leaf fractions and in total dry fodder genotypes had similar behavior on test environments, which is desirable in production systems and allows their recommendation in test environments and areas of similar characteristics. The AMMI analysis explained 84% of the IGA in the FSE, with the first two components.

Detecting that the first two principal components exhibited high statistical significance ($p \le 0.01$) in the FSE, and significance ($p \le 0.05$) for the first component in the FSH, although the variance analysis did not detect significance in the environmental genotype interaction of dry leaf fodder, suggesting that AMMI analysis of IGA may consider significant small variations in IGA, in a similar way to when the tests of undemanding means declare significance when the variance analysis declared no significance in the variable under study. The second CP was significant ($p \le 0.01$) only in FSE (Table 4).

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|--|----|-----------|--------------|--------------|-------------|--|--|
| FV | GL | FSTOT | FST | FSE | FSH | | |
| Repeats (Rep) | 2 | 1.868 | 0.547 | 0.108 | 0.125 | | |
| Environments (Amb) | 3 | 157.557** | 56.087** | 16.979** | 85.967** | | |
| Genotypes (Gen) | 24 | 5.339** | 2.478^{**} | 0.576^{**} | 1.29** | | |
| Amb x Gen | 72 | 1.155 | 0.471 | 0.165** | 0.266 | | |
| CP1 | 26 | 1.839 | 0.609 | 0.282^{**} | 0.428^{*} | | |
| CP2 | 24 | 0.855 | 0.531 | 0.109^{**} | 0.246 | | |
| Residual | 22 | 0.674 | 0.242 | 0.086 | 0.095 | | |

Table 4. Average squares and AMMI significance for second sampling.

FV= source of variation; GL= degrees of freedom; FSTOT= total dry fodder; FST= dry fodder of stem; FSE= dry fodder of spikes; FSH= dry fodder of leaf.

With the results of dry fodder of spikes and the first principal component of the AMMI analysis, Figure 5 was generated, where genotype 21(AN-246-13) was placed as the most productive and showing itself near the line that marks zero interactions. Wheat genotypes: 22 (AN-310-03), 2 (AN-268-99), 19 (AN-241-13), 20 (AN-409-13), 3 (AN-263-99), 18 (AN-7-09), 15 (AN-229-09), 14 (AN-326-09) and triticale, exceeded the general mean and exhibited negative interactions close to zero, qualifying them as desirable in the production of spikes, behavior due to the positive response they presented to the increase in temperature in the environment 3, confirming what was reported by Karsai *et al.* (2008).

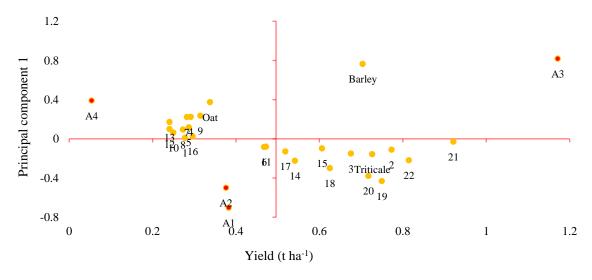


Figure 5. Genotypes and environments (A) based on FSE yield and the first CP of the AMMI (IGA) in the second sampling.

The barley and triticale witnesses showed similar production, but with opposing interactions, difference in behavior due mainly to the precocity of barley that allowed it to glean more quickly. Environments 3 (Navidad O-I 2018-2019) and 4 (San Ignacio O-I 2018-2019) provoked positive interactions and environments 1 (Zaragoza O-I 2017-2018) and 2 (Zaragoza O-I 2018-2019) negative interactions, in this way.

The association maintained by genotypes 13 (AN-222-09), 12 (AN-221-09), 10 (AN-218-09) and oats to environment 4 (San Ignacio O-I 2018-2019) was observed, being this environment the least suitable for spike production and environment 3 (Navidad O-I 2018-2019) was considered the most favorable, since it created higher maximum temperatures than the rest of the environment and where barley cv. Gabyan 95 and Genotype 21(AN-246-13) maintained a positive association (Figure 6), due to their greater precocity that was favored by higher temperatures (Karsai *et al.*, 2008).

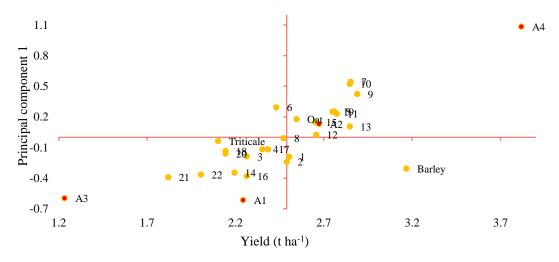


Figure 6. Genotypes and environments (A) based on FSH yield and first CP of the AMMI (IGA) in the second sampling.

It should be noted, that the variance analysis did not exhibit significant differences for leaf production, but the principal component 1 of the AMMI analysis was significant ($p \le 0.05$), managing to identify genotypes 13 (AN-222-09), 11 (AN-220-09) and 19 (AN-241-13) that had positive interactions close to zero, and genotypes 9 (AN-217-09), 10 (AN-218-09) and 7 (AN-209-09) also with positive interactions, but larger, qualifying as desirable by exceeding the general mean (2.49 t ha⁻¹).

Gabyan 95 was the genotype with the highest leaf production with a yield of 3.16 t ha⁻¹, exhibiting negative interactions; just as it happened at 75 dds, the genotype 21(AN-246-13) was placed in last place according to the low leaf production that it presented. Environments 2 (Zaragoza O-I 2018-2019) and 4 (San Ignacio O-I 2018-2019) provoked positive interactions and contrary to environments 1 (Zaragoza O-I 2017-2018) and 3 (Navidad O-I 2018-2019) provoked large and negative interactions. The most productive environment was environment 4 (San Ignacio O-I 2018-2019) to which no genotype maintained obvious association, while at Navidad O-I 2018-2019 (A3), less favorable environment was associated with genotype 21 (AN-246-13).

For the third sampling at 105 dds, the variance analysis exhibited highly significant differences in the environment genotype interaction for the FSE variable and significance at ($p \le 0.05$) for FSH, while for FSTOT and FST there was no significance. As happened in the second sample, FSE continued to manifest IGA and in this FSH sample did so significantly, even if there was no statistical difference in some of the production variables, the AMMI analysis was performed, in which this analysis explained 82% for dry fodder of leaf and 87% for dry fodder of spikes, using the first two CP.

The first principal component showed statistical significance ($p \le 0.01$) for FSE and FSH and significance to ($p \le 0.05$) for FST, while the second component showed no statistical significance for any variable (Table 5).

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| FV | GL | FSTOT | FST | FSE | FSH |
|--------------------|----|--------------|-------------|--------------|----------------|
| Repeats (Rep) | 2 | 0.825 | 0.366 | 0.221 | 0.571 |
| Environments (Amb) | 3 | 445.737** | 224.244** | 26.429** | 120.419^{**} |
| Genotypes (Gen) | 24 | 8.889^{**} | 3.185** | 2.973^{**} | 1.968** |
| Amb x Gen | 72 | 2.16 | 0.989 | 0.403^{**} | 0.55^{*} |
| CP1 | 26 | 3.365 | 1.438^{*} | 0.681^{**} | 0.877^{**} |
| CP2 | 24 | 1.451 | 0.737 | 0.321 | 0.417 |
| Residual | 22 | 1.509 | 0.735 | 0.165 | 0.309 |

FV= source of variation; GL= degrees of freedom; FSTOT= total dry fodder; FST= dry fodder of stem; FSE= dry fodder of spikes; FSH= dry fodder of leaf.

Based on the results obtained from stem production and the first principal component of the AMMI analysis, Figure 7 was elaborated, where the wheat genotypes: 15 (AN-229-09), 20 (AN-409-13) and 14 (AN-228-09), by placing themselves as the most productive wheats and approaching the line that marks zero interactions, followed by genotypes 9 (AN-217-09), 22 (AN-310-03) and 18 (AN-7-09) with positive interactions and wheats 19 (AN-24 1-13), 21 (AN-246-13) and 2 (AN-268-99) with negative interactions, being referred to as desirable when exceeding the general mean (4.7 t ha⁻¹).

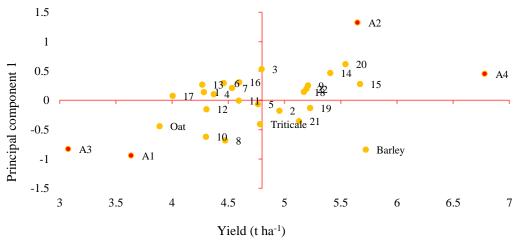


Figure 7. Genotypes and environments (A) based on FST yield and first CO of the AMMI (IGA) in the third sampling.

Gabyan 95 barley showed slightly higher yield than the wheats already mentioned with the only difference being large and negative interactions. According to these results obtained, it coincides with Feyissa *et al.* (2008) reporting that the stems represent more than 50% of the total dry fodder production in all genotypes evaluated. Oatmeal was the least produced genotype of stems, exhibiting small and negative interactions, associated with environment 1 (Zaragoza O-I 2017-2018) along with genotypes 10 (AN-218-09) and 8 (AN-216-09) and environment 2 (Zaragoza O-I 2018-2019) wheats were associated: 15 (AN-229-09), 20 (AN-409-13) and 14 (AN-228-09).

These witnesses mentioned were increasing by almost 100% their stem production through the sampling carried out, presenting the following yields for barley: 2.30, 4.43 and 5.7 t ha⁻¹ and for oats: 1.1, 2.2 and 3.8 t ha⁻¹, for the first, second and third sampling, respectively. On the other hand, environments 2 (Zaragoza O-I 2018-2019) and 4 (San Ignacio 2018-2019) provoked positive interactions and environments 1 (Zaragoza 2017-2018) and 3 (Navidad O-I 2018-2019) provoked negative interactions, reporting to Navidad O-I 2018-2019 as the least productive environment.

Conclusions

Based on the results obtained it is concluded that, in the early stages of development (75 dds) it was manifested IGA in dry fodder and its fractions, while in more advanced stages (90 and 105 dds), only the dry weight of leaves and spikes showed interaction. The absence of IGA in FSTOT and FST in the second and third sampling is a desirable feature, as this suggests that the genotypes have production stability, even though the spikes fraction continued to show interaction in such samples.

The stage where less IGA was presented was at 90 dds, managing to detect that environment 3 (Navidad O-I 2018-2019) promoted greater production of spikes and environment 4 (San Ignacio O-I 2018-2019) favored the production of leaves. Thirteen wheat genotypes were considered desirable for forage production, along with witness GABYAN 95 which was the most productive genotype in all sampling. According to this study, the forage wheats evaluated are an alternative for the production of dry matter in winter and from 90 dds they presented low or no IGA.

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