Article

Genotype-environment interaction of yield in yellow corn hybrids, using AMMI and SREG

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Abstract

It is indispensable for corn (*Zea mays* L.) plant breeding programs to select homogeneous materials, with high yield and with stable agronomic attributes; also, that they have a good adaptability in contrasting environments. The objective of the work was to evaluate the stability and genotype-environment interaction of the yield of 36 hard yellow corn hybrids, evaluated in seven environments of Peru, during 2016-2018, these materials were analyzed using the AMMI (additive main effects and multiplicative interaction) and SREG (site regression) models. The design used in each experiment was a 6×6 lattice with three repetitions, and the response variable was grain yield. A combined analysis of variance was performed, in which statistical differences between them ($p \leq 0.05$) were detected, then the Tukey mean test ($p \leq 0.05$) was applied, finally the AMMI and SREG models were run and the biplot graphs of each statistical model were obtained. Of the interaction between PC1 and PC2, AMMI explained 45.5% and 15.3%, respectively, and SREG with 59.8% and 12.2%, for the same components. The trilinear hybrids Dk-5005 and AG-01 outperformed the double-cross hybrids. The AMMI model detected the existing GE interaction in grain yield, and the SREG accurately grouped the assessment sites into six mega-environments. The three environments of La Molina and that of Huánuco identified the two hybrids (Dk-5005 and AG-01) with the highest grain yield (11.524 and 11.359 t ha^{-1}, respectively).

Keywords: *Zea mays*, biplot graph, double and trilinear hybrids, stability and adaptability.

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Introduction

In Peru, the harvested area of hard yellow corn (*Zea mays* L.) in 2018 was 246 594 ha, of which 80% was produced under rainfed conditions and the remaining 20% (1 265 072 t) with irrigation, with an average yield of 5 100 t ha^{-1} (MINAGRI, 2020). Grain yield is the most important characteristic to consider when conducting corn evaluations in different localities, as environmental effects (E) have the largest percentage of the sum of squares over genotypes (G) and genotype-environment interaction (GE) (Lozano-Ramírez *et al*., 2015; López-Morales *et al*., 2019). The GE interaction is the differential relative behavior shown by genotypes when evaluated in different environments (Vallejo and Estrada, 2002).

Therefore, when plant breeders look for genotypes with higher yields for different localities or environmental conditions, they face challenges such as stability and adaptability (Lozano-Ramírez *et al*., 2015). Stability is the ability of the genotype to behave consistently with high or low levels of yield across environments and adaptability is the ability of the genotype to manifest optimal performance under various environmental conditions (Vargas *et al*., 2016). Eberhart and Russell (1966) pointed out that stability is a genetic characteristic and that genotypes with broad adaptability have a low GE interaction; therefore, it is important to determine stability and adaptability for the selection and recommendation of *Z. mays* genotypes in specific environments (Gómez *et al*., 2018).

In addition to the above, environmental conditions change 'year after year', even in the same localities; therefore, it is advisable to evaluate various genotypes (experimental and commercial varieties). Such evaluations should be carried out in different localities and for several years, which will allow selecting the materials with the greatest stability and adaptability (Camargo-Buitrago *et al*., 2011). The most used models in the last two decades for the study of genotypic stability and adaptability across environments are that of additive main effects and multiplicative interaction (AMMI) and those of regression sites (SREG) (Farias *et al*., 2016).

The AMMI joins the analysis of variance with the analysis of principal components, with the assumption that the main products (G and E) are additive in nature and the GE interaction is multiplicative in nature (Cristiano *et al*., 2018), while the SREG eliminates the individual environmental effect (G + GE) to examine only the effect of the G and the GE interaction. The ability to discriminate, visualize the similarities and differences between test Es and Gs is elementary because it allows defining mega-environments, as well as the magnitude of the interaction within any genotype or locality (Ledesma-Ramírez *et al*., 2012).

Authors such as Dia *et al*. (2016); Yan (2016) have documented that both models (AMMI and SREG) complement each other, allowing a better interpretation through the biplot graphs (Cristiano *et al*., 2018; Fayeun *et al*., 2018). The graphical analysis of AMMI allows obtaining conclusions about the stability, the behavior of the genotype, the genetic difference between genotypes and the environments with an adequate yield, the SREG complements the environmental stratification of AMMI, generating mega-environments and identifying genotypes with an outstanding yield in each group. In both models, the relevant variable is yield, since it is the most affected by the GE interaction (Castillo *et al*., 2012; Lozano-Ramírez *et al*., 2015) because it is a polygenic quantitative characteristic.

For all the above, it is essential to generate knowledge that helps us discard experimental hybrids that do not meet certain characteristics such as yield, homogeneity (plant and ear heights, days to male and female flowering) and with certain agronomic attributes (such as number of rows, length and diameter of ear) and select those materials that are more yielding with stability and adaptability in contrasting environments. Therefore, the objective of this study was to evaluate the stability and adaptability of grain yield in 36 hard yellow corn hybrids adapted to the coastal and Sierra areas of Peru, using the AMMI and SREG models, under the hypothesis that the SREG allows identifying those materials with greater stability and adaptability in terms of grain yield.

Materials and methods

Genetic material

Of the 36 hard yellow corn hybrids evaluated, 29 were of double cross of yellow grain, crystalline texture and cylindrical ear, which originated from the lines of the CIMMYT; likewise, four genotypes: PM-212 (double-cross hybrid) and the experimental hybrids PM-9, PM-12 and PM-13. All the crosses of the 33 materials mentioned above were generated by the Corn Research and Social Projection Program (PIPS, for its acronym in Spanish), of the La Molina National Agrarian University (UNALM, for its acronym in Spanish), with geographical coordinates 12° 04’ 55” S and 76° 56’ 53” W, which is located at 241 masl, where the humid semi-warm climate prevails (SENAMHI, 2020). The three commercial controls evaluated were: DK-5005 (trilinear, of US origin, adapted to the conditions of Peru), AG-01 (trilinear, of Brazilian origin, with a wide adaptation) and XB-8010 (double-cross hybrid, of Brazilian origin, highly productive).

Location of experiments, design and experimental unit

In 2016, experiments were established with all hybrids in the localities of La Molina (LM-2016) and Cañete (CA-2016) in the coastal area, and in Huánuco (HU-2016) and Pillco Marca (PM-2016), belonging to the low sierra region. For the 2017 agricultural cycle, the evaluation was made in the localities of La Molina (LM-2017) and Huánuco (HU-2017) and for 2018 the hybrids were evaluated only in La Molina (LM-2018). The coastal area has a humid semi-warm climate and the low Sierra region a humid temperate climate (SENAMHI, 2020). Edaphoclimatic characteristics and agronomic management are shown in (Table 1).

Table 1. Agronomic management and conditions of the seven evaluation environments (2016-2018).

Environments	Province	Altitude (m)	Date sowing/harvest	Type of soil	Rainfall (mm)[†]	T (°C)	
						Max	Min
La Molina (LM-2016)	Lima	241	16-04/15-11-16	Leptosol	10.8[a]	27.5	15.5
La Molina (LM-2017)	Lima	241	16-04/15-11-17	Leptosol	10.6[a]	26.7	14.3
La Molina (LM-2018)	Lima	241	16-04/18-11-18	Leptosol	10.4[a]	27.1	15.4
Huánuco (HU-2016)	Huánuco	1 894	03-10/15-03-17	Inceptisol	388.5[b]	26.5	8.2
Huánuco (HU-2017)	Huánuco	1 894	07-10/16-03-18	Inceptisol	384.9[b]	26	8.5
Pillco Marca (PM-2016)	Huánuco	1 930	09-10/20-03-17	Inceptisol	374.1[b]	26.7	7.9
Cañete (CA-2016)	Cañete	38	15-06/21-01-17	Fluvisol	11.4[a]	24.5	16.4

[†]= annual average; [a]= sowing with initial irrigation and five supplemental irrigations; [b]= rainfed sowing with initial irrigation; Max.= maximum temperature; Min.= minimum temperature (during the sowing/harvest period).

The design used in all localities and years was a 6×6 lattice with three repetitions, the experimental unit consisted of two furrows six m long and 0.8 m wide. Three seeds per bush were sown at a distance of 40 cm and a thinning was carried out one month after sowing, leaving 64 plants per experimental plot, for a population density of 62 500 plants ha^{-1}.

Fertilization and trial management

In the locality of La Molina (LM-2016, LM-2017 and LM2018) and Cañete (CA-2016), the fertilization formulas 190-160-160 and 210-80-00 (N-P-K, kg ha^{-1}) were used, respectively, applying, at the time of sowing, all phosphorus and 50% of nitrogen and potassium (the latter element only for La Molina) 15 days after sowing (DAS) and the rest at the end of the cultivation work.

In the two localities, a preliminary irrigation and five supplemental irrigations were applied during the cultivation cycle. For Huánuco (HU-2016 and HU-2017) and Pillco Marca (PM-2016), the formula 220-115-82-21S-18Mg was used, applying 110 units of nitrogen and 100% of the other elements at 15 DAS and the nitrogen difference at 40 DAS, these localities were rainfed, with an irrigation at the beginning of sowing. In the second cultural work, for the control of weeds in the seven localities, the herbicides with active ingredient glyphosate and atrazine were applied separately, at doses of 1.5 and 1 kg ha^{-1}, respectively, and for the fall armyworm [*Spodoptera frugiperda* (J. E. Smith)] the insecticide chlorpyrifos was used with a dose of 5 kg ha^{-1}, which were independently diluted in 200 L of water.

Response variable

The grain yield (kg ha^{-1}) was calculated with the formula described by Manrique (1997): $Y= \frac{10\,000}{A} \times 0.971 \times PS \times y$. Where: A= area of the plot; PS= percentage of shelling (grain weight between ear weight by 100); y= yield of the experimental unit in kg adjusted to 14% of moisture. The value 0.971 corresponds to the boundary coefficient which is a constant of the experimental unit.

Statistical analysis

With the grain yield data of the 36 hybrids in the seven environments, an analysis of variance and the Gollob test were performed, using the GLM procedure of SAS® version 9.0 (SAS Institute, 2012), when significant differences between hybrids ($p\leq 0.05$) were detected, the Tukey mean test ($p\leq 0.05$) was applied, in addition, AMMI and SREG models were applied to determine the effects of GE interaction, stability and adaptation (Castillo *et al*., 2012; Cristiano *et al*., 2018), with the same statistical package. Finally, a biplot graph was made for each statistical model to show the GE interaction, both biplots were generated with the first two principal components (PC1 and PC2).

Results and discussion

The analysis of variance showed significant statistical differences ($p\leq 0.001$) in all sources of variation for grain yield: environments (E), repetition∗E, genotypes (G) and genotype-environment (GE) interaction, which explained 70.2, 0.5, 13.3, 16%, respectively, of the total sum of squares

(Table 2). The inequality between corn genotypes and environments shows a wide genetic and environmental condition difference that occur 'year after year', respectively (Tadeo-Robledo *et al*., 2015; López-Morales *et al*., 2019). The significant statistical differences (Table 2) for the mean squares of all sources of variation in the analysis of variance and Gollob test coincide in significance with what was reported in the two models AMMI and SREG by (Fritsche-Neto *et al*., 2010; Lozano-Ramírez *et al*., 2015).

Table 2. Analysis of variance and Gollob test of the AMMI and SREG models for grain yield in 36 hard yellow corn hybrids in seven environments in Peru (2016-2018).

Source	DF	SS	MS	$PC^{1,2}$	$DF^{1,2}$	SS^1	MS^1	$(\%)^1$	SS^2	MS^2	$(\%)^2$
Environments (E)	6	2137.2	356.2^{***}	CP1	40	222.7	5.5^{***}	45.5	535.4	13.3^{***}	59.8
Repetition∗E	2	13.4	6.7^{***}	CP2	38	74.9	1.9^{***}	15.3	109.7	2.8^{***}	12.2
Genotypes (G)	35	406	11.6^{***}	CP3	36	66.4	1.8^{***}	13.5	71.2	1.9^{***}	7.9
GE	210	488.8	2.3^{***}	CP4	34	51.6	1.5^{*}	10.5	61.3	1.8^{***}	6.8
Error	502	462	0.9	CP5	32	41.2	1.2	8.4	44.5	1.3^{*}	4.9

*, ***= significance at $p\leq 0.05$ and $p\leq 0.001$, respectively; GE= genotype-environment interaction; DF= degrees of freedom; SS= sum of squares; MS= mean squares; PC= principal components; (%)= percentage of the SS of the interaction explained by the PC; ^{1}= AMMI model; ^{2}= SREG model.

For the AMMI and SREG models, the first four and five principal components (PC), respectively, were statistically significant ($p\leq 0.001$), which means that there is a statistical difference due to the effect of the GE interaction in multiplicative terms, where the sum of squares of the first five PCs explained 93.5% for AMMI and 91.9% for SREG of the total GE interaction, Table 2, lower results were found by Fritsche-Neto *et al*. (2010); Ndhlela *et al*. (2014) and in each of the models for corn crop, this difference may be due to the fact that they evaluated fewer genotypes and environments with respect to the present study. The first two principal components explained 60.9 and 71.1% of the variation in AMMI and SREG, respectively (Table 2), similar findings were reported by Castillo *et al*. (2012); Lozano-Ramírez *et al*. (2015) in each model (AMMI and SREG), who recorded values of 62.6 and 79% respectively.

Table 3 shows the average yield per hectare of the 36 corn hybrids in each environment. The highest yields were obtained by the commercial trilinear hybrids Dk-5005 (11.524 t ha^{-1}) and AG-01 (11.359 t ha^{-1}); on the contrary, the experimental hybrid 515×714 had the lowest yield with 8.045 t ha^{-1}, this may be because this genotype is one of the 29 double hybrids that are not adapted for the evaluated areas, especially in the Sierra, where it obtained the lowest yields.

The 36 hybrids exceeded the national average yield of hard yellow corn (irrigation and rainfed), which is 5.1 t ha^{-1} (MINAGRI, 2020) and only 17 hybrids exceeded the overall average, which was 9.188 t ha^{-1}, Table 3, among which the three commercial hybrids used as controls, the four commercial double-cross hybrids of the PIPS and 10 experimental double-cross materials stand out. The corn hybrid 580×575 had a grain yield of 10.042 t ha^{-1}, ranking third in the average yield, being surpassed only by the two commercial trilinear hybrids Dk-5005 and AG-01, which surpassed the four PIPS hybrids and the control XB-8010.

The trilinear hybrids 30) Dk-5005 and 31) AG-01 had the best grain yields ($p \leq 0.05$), possibly because they have a high frequency of genes for adaptation with respect to the rest of the double hybrids between environments, which is in accordance with what was reported by Chura and Huanuqueño (2014); López-Morales *et al*. (2019), when evaluating genetically similar corn materials in Peru. Regarding the environments, the LM-2017 locality had the highest average yield with 12.65 t ha^{-1} of grain, followed by LM-2018 with 10.337 t ha^{-1} (the only two environments that exceeded the overall average of 9.188 t ha^{-1}) while HU-2016 had the lowest value with 7.299 t ha^{-1} (Table 3).

The highest grain yields were expressed by the corn hybrids 30) Dk-5005 (11.524 t ha^{-1}), 31) AG-01 (11.359 t ha^{-1}), 27) 580×575 (10.042 t ha^{-1}) and 34) PM-9 (9.989 t ha^{-1}), but this characteristic changes considerably from one environment to another (Table 3), such behavior is due to the effect of the environment on the genotypes. Hybrids 30) Dk-5005 and 31) AG-01 showed the highest yields, which is consistent with what was found by (Chura and Huanuqueño, 2014) for Dk-5005, who reported that this material had the highest yield with 10.982 t ha^{-1} of grain in three localities in La Molina and one in Puerto Bermúdez, Peru.

Table 3. Means of yield in t ha^{-1} of 36 hard yellow corn hybrids, evaluated in seven environments in three provinces of Peru (2016-2018).

Hybrids	Environments							Mean
	LM-2016	LM-2017	LM-2018	HU-2016	HU-2017	PM-2016	CA-2016	
1) 529×508	10.126	14.531	11.207	7.24	7.953	8.113	7.106	9.468bcde
2) 685×684	8.69	11.266	8.588	7.292	8.381	7.644	6.769	8.376efg
3) 575×510	8.649	11.615	9.575	8.75	7.987	8.043	8.115	8.962bcdefg
4) 575×511	7.875	11.469	9.635	6.953	7.943	7.807	8.763	8.635cdefg
5) 515×714	7.85	11.138	8.73	7.344	7.278	7.285	6.693	8.045g
6) 722×714	9.355	12.107	8.822	8.021	8.358	10.008	7.822	9.213bcde
7) 532×531	8.378	11.674	8.793	7.708	7.473	8.051	8.608	8.669cdefg
8) 592×575	8.651	11.833	10.236	8.333	7.679	9.998	7.858	9.227bcde
9) 733×730	8.561	11.964	8.993	8.125	8.322	7.348	5.949	8.466defg
10) 725×723	8.514	12.723	10.275	6.042	8.15	6.891	7.288	8.555cdefg
11) 728×723	8.139	12.469	10.459	6.562	9.377	7.559	7.828	8.913bcdefg
12) 694×691	9.425	12.983	10.439	8.594	9.641	7.761	8.216	9.58bcd
13) 590×575	9.041	12.821	11.018	6.458	8.203	9.198	7.269	9.144bcdefg
14) 726×723	8.165	12.969	9.985	7.813	8.485	9.127	6.833	9.054bcdefg
15) 743×707	8.315	12.486	10.823	7.812	8.947	8.758	7.93	9.296bcde
16) 591×575	9.543	14.494	11.385	7.813	8.768	7.548	7.672	9.603bcd
17) 704×703	7.106	12.702	10.409	6.604	8.181	8.56	8.347	8.844cdefg
18) 513×531	7.79	11.359	9.441	7.188	8.535	8.507	6.78	8.514defg
19) 739×737	8.815	11.452	9.734	5.937	6.366	7.541	6.634	8.069fg
20) 687×684	8.849	13.135	10.7	6.927	8.673	9.695	8.221	9.457bcde
21) 635×578	8.207	11.336	9.343	6.615	6.966	8.778	8.422	8.524defg
22) 589×575	9.319	12.512	11.822	7.657	8.584	7.767	8.024	9.383bcde

Hybrids	Environments							Mean
	LM-2016	LM-2017	LM-2018	HU-2016	HU-2017	PM-2016	CA-2016	
23) 697×691	10.238	13.592	10.624	7.135	8.549	7.638	8.953	9.533bcd
24) 570×714	8.403	11.773	8.524	6.615	8.966	9.143	7.703	8.733cdefg
25) 729×723	8.791	13.836	9.947	6.719	8.298	8.288	7.751	9.09bcdefg
26) 736×730	8.829	12.036	10.533	7.292	8.558	9.203	7.247	9.1bcdefg
27) 580×575	10.7	13.104	14.088	7.083	8.155	9.14	8.024	10.042b
28) 742×737	8.48	11.564	8.807	6.823	8.732	7.891	7.103	8.486defg
29) 717×714	8.354	11.344	9.387	8.448	8.76	9.345	7.311	8.993bcdefg
30) Dk-5005	13.392	15.926	14.125	7.24	12.851	8.943	8.19	11.524a
31) AG-01	11.514	15.476	13.064	8.489	12.221	10.38	8.37	11.359a
32) XB-8010	8.687	10.934	9.365	7.761	9.399	10.328	7.885	9.194bcdef
33) PM-212	10.848	14.188	9.238	7.605	7.564	9.421	8.906	9.681bc
34) PM-9	11.257	13.35	10.796	7.292	9.684	8.958	8.584	9.989b
35) PM-12	10.061	13.526	12.065	6.302	8.61	9.583	6.725	9.553bcd
36) PM-13	9.933	13.741	11.16	6.198	9.874	8.017	7.548	9.496bcde
Mean	9.134c	12.65a	10.337b	7.299f	8.062d	8.557d	7.707e	9.188

From 01 to 29= experimental corns; PM= corn program (PIPS); LM= La Molina; HU= Huánuco; PM= Pillco Marca; CA= Cañete. Means of the genotypes and environments with equal letters do not differ statistically from the Tukey test ($p \leq 0.05$). With honest significant difference of 1.143 t ha^{-1} and 0.386 t ha^{-1} between genotypes and environments, respectively.

AMMI analysis

Figure 1 shows that corn hybrids 26) 736×730, 15) 743×707, 14) 726×723 and 25) 729×723 were the closest to the origin of the axes; that is, they were less influenced by GE (greater stability) (Vargas *et al*., 2016). All of them are experimental hybrids with average yields of 9.1, 9.296, 9.094 and 9.09 t ha^{-1}, respectively, close to the average of the corn hybrids evaluated in this research (9.188 t ha^{-1}).

Corn hybrids 30) Dk-5005, 31) AG-01, 36) PM-13, 27) 580×575, 32) XB-8010 and 21) 635×578 were the genotypes with the least stability (Figure 1), since they were concentrated away from the two-dimensional center. On the other hand, the hybrids 32) XB-8010, 6) 722×714 (9.213 t ha^{-1}) and 29) 717×714 (8.993 t ha^{-1}) showed low adaptability to the seven environments (Figure 1). The LM-2016 environment was the most stable and the other six environments evaluated in the present study are far from the origin (central part of Figure 1), indicating that they contributed the most to the GE interaction.

Authors such as (Vargas *et al*., 2016) indicated that in environments with angles < 90º, genotypes will preserve a similar spatial distribution, which occurred between environments LM-2016, LM-2017 and LM-2018. A similar situation with angles < 90º occurred between the environments HU-2016, PM-2016 and CA-2016. On the other hand, environments with angles greater than 90º do not order genotypes in the same way, as happened with HU-2016 and HU-2017, LM-2016 or LM-2018 and CA-2016 (Figure 1).

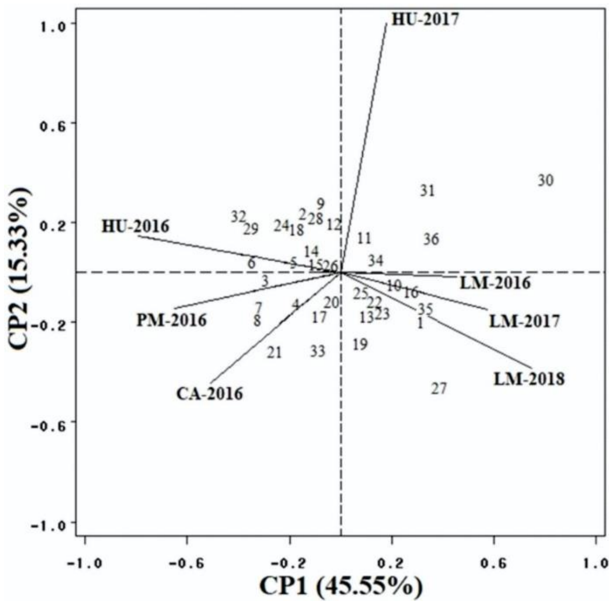

Figure 1. AMMI biplot with the first two principal components (PC1 and PC2) of the average yield of 36 hard yellow corn hybrids in seven environments in Peru.

The environments that are located at an angle of 180º order the corn genotypes in the opposite way, which makes it difficult to select through these environments because they are of contrasting conditions (Yang *et al*., 2009; Kandus *et al*., 2010), as happened in the environments LM-2016, LM-2017 and LM-2018 against HU-2016 (Figure 1), possibly because the first corn materials are from the coast and the other from the Sierra of Peru.

The vectors with the groups of the environments LM-2016, LM-2017 and LM-2018, as well as the environments HU-2016, PM-2016 and CA-2016 are too close to each other, which may be due to the edaphoclimatic similarity (fertilization, soil type, precipitation and temperature with minor differences). Thus, in the first case (the environments of La Molina), it is the same site, but evaluated in a different year (Table 1); that is, the fact that the environments are very close to each other in Figure 1 and in a similar quadrant (similar direction of the vectors) means that they are very similar to the GE. In the second case, the three environments belonged to the same year of evaluation (2016), which could be a determining factor for the proximity between them; results similar to the findings of the present work were found by (Castillo *et al*., 2012; López-Morales *et al*., 2019) under the same conditions.

SREG Analysis

The corn hybrid 30) Dk-5005 was the one with the highest yield ($p \leq 0.05$); while the hybrid 5) 515×714 had the lowest yield. The Dk-5005 hybrid was not only the one with the highest yield but also the one with the greatest adaptability and stability in the seven environments (Figure 2).

Other stable materials were the hybrids: 21) 635×578, 2) 685×684, 7) 532×531, 18) 513×531, 28) 742×737, 26) 736×730 and 12) 694×691, all experimental corns. Also, in environments, the length of the vector indicates the variability in yield explained in each environment and vice versa (Crossa *et al*., 2015).

On the other hand, six mega-environments (region with homogeneous environment for a crop species) were found (Figure 2) and where each mega-environment (between red lines in Figure 2) will locate hybrids with a high yield at the vertices that will form a polygon and all environments that are outside this polygon allow discrimination between hybrids (Yan *et al*., 2011; 2016).

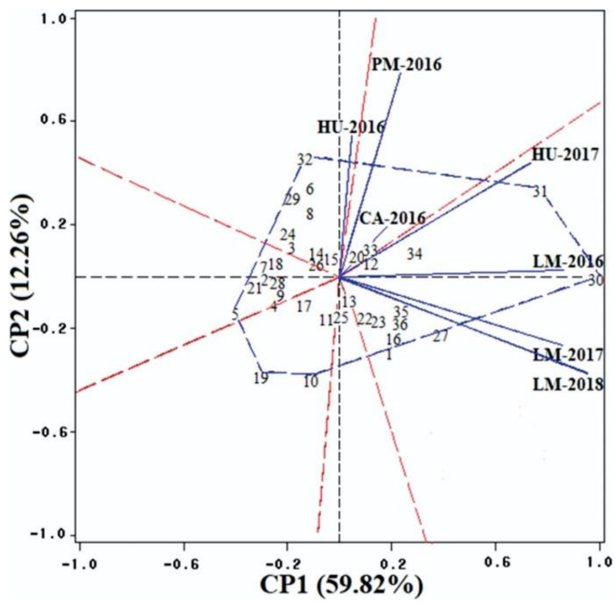

Figure 2. SREG biplot with the first two principal components (PC1 and PC2) of the average yield of 36 hard yellow corn hybrids in seven environments in Peru.

This happened with the mega-environment where the corn hybrid 30) Dk-5005 showed the highest yield between genotypes (11.524 t ha^{-1}) and included the environments LM-2016 (the most stable of the four, but the only one that did not discriminate between genotypes), LM-2017, LM-2018 (the three environments with the best yields according to the Tukey test: 9.134, 12.65 and 10.337 t ha^{-1}, respectively) and HU-2017 (8.062 t ha^{-1}).

Other materials with good response in the same mega-environment, with the highest yields among the materials evaluated, were the corn genotypes 31) AG-01 and 27) 580×575 (experimental corn). Both Dk-5005 and AG-01 are trilinear hybrids with a high frequency of genes due to their genetic constitution of three lines, producing a high adaptive capacity for several areas, as indicated by the results of Chura and Huanuqueño (2014); López-Morales *et al*. (2019) with the materials of three lines in different regions of Peru.

The sites PM-2016 and CA-2016 were located in a mega-environment, but in this one there was no corn hybrid that excelled in yield, even though the PM-2016 environment discriminated between hybrids. Such behavior could be due to the large edaphoclimatic differences between the two environments, especially in the amount of rainfall, Table 1. Between the first and second quadrant of the biplot of Figure 2 is another mega-environment where the only environment was HU-2016, for which the corn hybrid 32) XB-8010 was the ideal.

The other three mega-environments did not include any environment, probably because the seven environments manifested yield averages similar to a group of hybrids. The ideal hybrids in each of these mega-environments were: 5) 515×714, double-cross hybrid with the lowest yield (8.045 t ha^{-1}) and genotypes 19) 739×737 and 10) 725×723, located in the last places of yield (with 8.069 and 8.555 t ha^{-1}, respectively), together in a single mega-environment (Figure 2).

In general, in Figure 2 the hard yellow corn hybrids, located at the right vertices, are those with the highest grain yield (Dk-5005 and AG-01) and are intimately linked to adjacent environments. The localities were grouped into three of the six mega-environments. Hybrids located between quadrants II and III away from the lines of the localities showed poor yield performance, as they were far away from the localities.

The corn hybrids studied in the present work consistently had high positive scores in PC1, which means high production, and decreases in absolute scores of PC2 are indications of high stability. Similarly, environments with low absolute values in PC2 have more representativeness, and high positive evaluations in PC1 indicate greater discriminatory capacity of hybrids in terms of the main genotypic effect (Yan *et al*., 2011; 2016).

Conclusions

The hard yellow corn trilinear hybrids Dk-5005 and AG-01 were the most outstanding for their broad stability and adaptability in the genotype-environment interaction. The AMMI (additive main effects and multiplicative interaction) model is useful for understanding the genotype-environment interaction existing in grain yield and genotype discrimination. The application of SREG (regression sites) was highly effective compared to AMMI, allowing the identification of six mega-environments. The three environments of La Molina (LM-2016, LM-2017, LM-2018) and one of Huánuco (HU-2017) allowed the identification of the corn genotypes with the highest grain yields. The corn hybrid Dk-5005 had high stability and adaptability in four environments with a high average grain yield, being the most appropriate hybrid for grain production in the coastal and low sierra areas of Peru.

Cited literature

Camargo, B. I.; Quiros, M. E. y Gordon, M. R. 2011. Identificación de mega-ambientes para potenciar el uso de genotipos superiores de arroz en Panamá. Pesquisa Agropecuária Brasileira. 46(9):1061-1069. Doi.org/10.1590/S0100-204X2011000900013.

Castillo, D.; Matus, I.; Pozo, A.; Madariaga, R. and Mellado, M. 2012. Adaptability and genotype × environment interaction of spring wheat cultivars in Chile using regression analysis, AMMI, and SREG. Chilean J. Agric. Res. 72(2):167-174. Doi.org/10.4067/S0718-58392012000200001.

Chura, C. J. y Huanuqueño, C. E. H. 2014. Comportamiento de ocho poblaciones de maíz amarillo (*Zea mays* L.) en cruzas con un probador. Anales Científicos. 76(1):78-86. Doi.org/10.21704/ac.v76i1.767.

Crossa, J.; Vargas, M.; Cossani, C. M.; Alvarado, G.; Burgueño, J.; Mathews, K. L. and Reynolds, M. P. 2015. Evaluation and interpretation of interactions. Agron. J. 107(2):736-747. Doi.org/10.2134/agronj2012.0491.

Dia, M.; Wehner, T. C. and Arellano, C. 2016. Analysis of genotype × environment interaction using SAS programming. Agron. J. 108(5):1838-1852. Doi.org/10.2134/agronj2016.02.0085.

Eberhart, S. A. and Russel, W. A. 1966. Stability parameters for comparing varieties. Crop Sci. 6(1):36-40. Doi.org/10.2135/cropsci1966.0011183X000600010011x.

Farias, F. J. C.; Carvalho, P. L.; Silva, F. J. L. and Teodoro, E. P. 2016. Biplot analysis of phenotypic stability in upland cotton genotypes in Mato Grosso. Genet. Mol. Res. 15(2):1-10. Doi.org/10.4238/gmr.15028009.

Fayeun, L. S.; Alake, C. G. and Akinlolu, O. A. 2018. GGE biplot analysis of fluted pumpkin (*Telfairia occidentalis*) landraces evaluated for marketable leaf yield in Southwest Nigeria. J. Saudi Soc. Agric. Sci. 17(4):416-423. Doi.org/10.1016/j.jssas.2016.10.001.

Fritsche, N. R.; Vieira, M. G.; Oliveira, D. R. and Namorato, S. H. 2010. Factor analysis and SREG GGE biplot for the genotype × environment interaction stratification in maize. Ciência Rural. 40(5):1044-1048. Doi.org/10.1590/S0103-84782010000500007.

Gómez, M. Y.; Boicet, F. T.; Tornés, O. N. y Meriño, H. Y. 2018. Interacción genotipo ambiente de cuatro variedades de tomate en la provincia Granma. Rev. Centro Agrícola. 45(2):21-28.

Kandus, M.; Almorza, D.; Boggio R. R. and Salerno, J. C. 2010. Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays* L.). International J. Exp. Bot. 79(1):39-46. Doi:10.32604/phyton.2010.79.039.

Ledesma, R. L.; Solís, M. E.; Suaste, F. M. P.; Rodríguez, C. J. F. y Cruz, G. M. L. 2012. Análisis GGE biplot del rendimiento de trigo (*Triticum* spp.) con riego normal y restringido en el Bajío, México. Agrociencia. 46(2):119-131.

López, M. F.; Chura, C. J. y García, P. G. 2019. Interacción genotipo por ambiente del rendimiento de maíz amarillo en híbridos trilineales, Perú. Rev. Mex. Cienc. Agríc. 10(4):859-872. Doi.org/10.29312/remexca. v10i4.1696.

Lozano, R. Á.; Santacruz, V. A.; San-Vicente, G. F.; Crossa, J.; Burgueño, J. y Molina, G. J. D. 2015. Modelación de la interacción genotipo ambiente en rendimiento de híbridos de maíz blanco en ambientes múltiples. Rev. Fitotec. Mex. 38(4):337-347. Doi.org/10.35196/rfm. 2015.4.337.

Manrique, C. P. A. 1997. El maíz en el Perú. Consejo Nacional de Ciencia y Tecnología. (CONCYTEC). Lima, Perú. 362 p.

MINAGRI. 2020. Ministerio de Agricultura y Riego. Sistema de información de cultivos de maíz amarillo duro. Lima, Perú. http://sissic.minagri.gob.pe/sissic.

Ndhlela, T.; Herselman, L.; Magorokosho, C.; Setimela, P.; Mutimaamba, C. and Labuschagne, M. 2014. Genotype environment interaction of maize grain yield using AMMI biplots. Crop Science. 54(5):1992-1999. Doi.org/10.2135/cropsci2013.07.0448.

Neisse, A. C.; Kirch, L. J. and Hongyu, K. 2018. AMMI and GGE biplot for genotype × environment interaction: a medoid-based hierarchical cluster analysis approach for high-dimensional data. Biometrical Letters. 55(2):97-121. Doi.org/10.2478/bile-2018-0008.

SAS Institute. 2012. User's Guide of SAS. SAS Institute Inc. Cary, North Carolina, USA. 550 p.

SENAMHI. 2020. Servicio Nacional de Meteorología e Hidrología del Perú. Mapa climático nacional. Ministerio del Ambiente. Lima, Perú. https://www.senamhi.gob.pe/?&p=mapa-climatico-del-peru.

Tadeo, R M.; Espinosa, C. A.; Guzmán, M. R.; Turrent, F. A.; Zaragoza, E. J. y Virgen, V. J. 2015. Productividad de híbridos varietales de maíz de grano amarillo para Valles Altos de México. Agron. Mesoam. 26(1):65-72. Doi.org/10.15517/am.v26i1.16921.

Vallejo, C. F. A. y Estrada, S. E. I. 2002. Interacción genotipo-ambiente. *In*: Vallejo, C. F. A. y Estrada, S. E. I. (Ed.). Mejoramiento genético de plantas. Universidad Nacional de Colombia. Palmira, Colombia. 189-202 pp.

Vargas, E. E. A.; Vargas, S. J. E. y Baena, G. D. 2016. Análisis de estabilidad y adaptabilidad de híbridos de maíz de alta calidad proteica en diferentes zonas agroecológicas de Colombia. Acta Agronómica. 65(1):72-79. Doi.org/10.15446/acag.v65n1.43417.

Yan, W.; Pageau, D.; Frégeau, R. J.; Lajeunesse, J.; Goulet, J.; Durand, J. and Marois, D. 2011. Oat mega-environments and test-locations in Quebec. Canadian J. Plant Sci. 91(4):643-649. Doi.org/10.4141/cjps10139.

Yan, W.; Frégeau, R. J.; Pageau, D. and Martin, R. 2016. Genotype-by-environment interaction and trait associations in two genetic populations of oat. Crop Sci. 56(3):1136-1145. Doi.org/10.2135/cropsci2015.11.0678.

Yang, R. C.; Crossa, J.; Cornelius, P. L. and Burgueño, J. 2009. Biplot analysis of genotype environment interaction: proceed with caution. Crop Sci. 49(5):1564-1576. Doi.org/10.2135/cropsci2008.11.0665.