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**ORIGINAL ARTICLE**

## **Performance And Adaptation of Barley Genotypes (*Hordeum vulgare* L.) to Diverse Locations**

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### **ABSTRACT**

A study was conducted, during the 2005-2006 cropping season, with the aim to quantify genotype x location experienced by barley and to determine stable genotypes under diverse Algerian growing conditions. Field experiments were conducted with twelve genotypes at six locations across the country, in a completely randomized block design with three replications in each environment. The combined analysis of variance showed significant genotype x location interaction. The additive main effect and multiplicative interaction analysis revealed that 29.33% of the treatments variability was accounted for by the interaction. The first two interaction principal components absorbed 82.6.5% of the interaction sum squares. The additive main effect and multiplicative interaction analysis identified Fouara and Acsad<sub>176</sub> as genotypes having wide adaptation, above average grain yield, high nominal yield and high yield stability. Bahia exhibited a specific adaptation. Plant traits acting as major sources of interaction were plant height, straw yield, number of days to heading, number of spikes m<sup>-2</sup>, and number of grains per spike. Variation in accumulated rainfall in winter and June, as well as the mean winter temperature were among the environmental co-variables causal of the interaction.

**Key words:** Barley, AMMI analysis, GL interaction, nominal yield, stability.

### **Introduction**

Barley (*Hordeum vulgare* L.) is grown, in Algeria, under rainfed conditions on the high plateaus area where the incidences of unpredictable stresses are high [1]. Improvement of this crop has focused on developing high yielding cultivars to exploit as much of the yield potential as possible. The area under improved cultivars is still minimal, but a clear trend shifting from local landraces to newly released genotypes is observed. To achieve yield improvement, selection of high yielding and adapted

genotypes is conducted at several locations across the country, covering a large spectrum of growing conditions. Such strategy enhances, according to Basford and Cooper [2], stress tolerance and yield potential improvement. Even though, selection in low yielding conditions may favor yield stability and minimizes risk for low inputs agriculture [3]. High yield potential and adaptation, across varied environments, are difficult to estimate accurately, in the presence of the genotype x environment interaction [4]. Large genotype x environment interaction (GE) affects negatively the selection

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efficiency, because some cultivars exhibit high yield in some environments, while other cultivars excel in other environments [5,6]. Several studies have been devoted to GE analysis with the aims to identify high-yielding and stable genotypes with either specific or large adaptation [7]. Several statistical methods have provided tools, among which the joint regression and the AMMI, to analyze and interpret the genotype x environment interaction [8,9,10]. The objective of this study was to assess the performances of a set of barley genotypes (*Hordeum vulgare* L.) grown at different locations in Algeria and to investigate the magnitude and pattern of the GE.

## Materials and methods

### *Experimental Details and Crop Husbandry:*

Twelve barley genotypes, from the Sétif Agricultural Research Station breeding program, were evaluated across six locations in Algeria, during the 2005-06 cropping season. The locations were, from the east to the west, Khroub (KHR, 713 masl), Sersour (SER, 920 masl), Sétif (SET, 1023 masl), Algiers (ALG, 34 masl), Sidi Bel Abbes (SBA, 483 masl) and Saida (SAI, 1013 masl). Even though these six test locations do not encompass the entire range of potentially desirable selection environments, they have been historically used for variety testing and are intended to represent the major barley-growing regions in Algeria. At each location, a randomized complete block design with three replications was used. Plot dimensions were 1.2 m wide and 10 m long, with 0.20 m row spacing. Sowing was done during the second half of November, at a seeding rate of 250 viable seeds per m<sup>2</sup>. Before sowing, trials were fertilized with 100 kg ha<sup>-1</sup> of triple super phosphate (46% P<sub>2</sub>O<sub>5</sub>), and 100 kg ha<sup>-1</sup> of urea (35% N) were broadcasted at the onset of the jointing growth stage (GS 31, [11]). Weeds were controlled chemically with GranStar [*Methyl Tribenuron*], at 12 g ha<sup>-1</sup> rate.

### *Measurements and Data Analysis:*

Several traits were measured, but only grain yield is analyzed and discussed herein. Trials were harvested at maturity with a combine to determine plot grain yield. An analysis of variance was performed for each location separately as a randomized complete block design. A combined analysis of variance was performed from the mean data of each location, considering location effects as random and the genotype effects as fixed. For the AMMI and the joint regression analyses, the cross site analysis subroutine procedure of the Cropstat 7.2.3 software package [12] was performed on the

matrix of the genotype x location grain yield residuals. Genotypic stability was approached through the regression coefficient [8], the deviation from regression (S<sup>2</sup>di) [13], and the AMMI stability value (ASV) [14]. The ASV was calculated as follow:  $ASV = \{[(SS_{IPCA1}/SS_{IPCA2})(GIPCA_1)]^2 + (GIPCA_2)^2\}^{0.5}$ , where  $SS_{IPCA1} / SS_{IPCA2}$  is the weight given to the IPCA1 value by dividing the IPCA<sub>1</sub> sum of squares (SS) by the IPCA<sub>2</sub> SS,  $GIPCA_{1score}$  is the IPCA<sub>1</sub> score for the specific genotype, and  $GIPCA_{2score}$  is the IPCA2 score for the same genotype. The nominal grain yield of each genotype was estimated as the genotypic main effect plus the product of genotype and location IPCA<sub>1</sub> scores. Nominal yield was plotted against location IPCA<sub>1</sub> scores, to identify the environments shearing the same highest yielding cultivars. To provide biologically meaningful interpretation of the GEI, simple correlations between genotypic IPCA<sub>1</sub> scores from AMMI and genotypic co-variables were determined. Similarly, environmental co-variables for locations were explored to identify important climatic factors correlated with environmental IPCA<sub>1</sub> scores. Phenotypic correlation coefficients and Spearman rank correlation coefficients were calculated with Openstat software package [15].

## Results and discussion

### *Magnitude and Pattern of Genotype X Location Interaction:*

The analysis of variance of grain yield, of individual location, indicated a significant genotype effect, suggesting differential yielding ability among the tested cultivars (Table 1). The mean yield of the 12 genotypes ranged from 1.11 t ha<sup>-1</sup>, exhibited by the cultivar Jaidor at Saida (SAI) location, to 6.48 t ha<sup>-1</sup>, yield achieved by the genotype Bahia at Algiers (ALG) site. Acsad<sub>176</sub>, Rahma, Rihane and Fouara ranked among the top yielding genotypes in at least 3 out of six locations. Begonia, Bahia, Saida and Tichedrett were also among the top yielding entries in at least one location (Table 2). Tests of significance from the combined analysis of variance are valid, only, if error terms, from the different environments, are homogeneous [16]. F<sub>max</sub> indicated that error variances were not homogeneous. This was mostly due to KHR and ALG locations that showed high location mean yield associated with high error variance (Table 1). The combined analysis of variance was then, done with the log-transformed data. This analysis indicated a highly significant genotype x location interaction (GL). The location was the most important source of variation (62.94%), while GL sum square explained 29.33% of the total sum squares, accounted for by location, genotype and GL interaction (Table 3).

**Table 1:** Mean square of single location grain yield analysis of variance.

Source of Variation	Locations						
	DF	KHR	SER	SET	ALG	SBA	SAI
Genotype	11	2.991**	0.218**	2.380**	5.619**	0.296**	0.321**
Block	02	0.275	0.118	0.162	0.267	0.011	0.025
Error	22	0.512	0.060	0.113	0.315	0.037	0.0300
CV (%)		16.8	11.7	8.7	16.4	6.5	13.2

\*\* = significant effect at the 0.01 probability level

**Table 2:** Genotypic grain yield means (t ha<sup>-1</sup>), coefficient of regression (b), deviation mean square from regression (S<sup>2</sup>di) and intercept (a, t ha<sup>-1</sup>) of the 12 barley genotypes evaluated at 6 locations

Genotype	SBA	KHR	SER	SAI	ALG	SET	X <sub>G<sub>geno</sub></sub>	b	s <sup>2</sup> di	a
Acsad176	3.39 <sup>a</sup>	4.19	2.52 <sup>a</sup>	1.80 <sup>a</sup>	4.13	4.10	3.36	0.885 <sup>b</sup>	0.16 <sup>ns</sup>	0.72
Bahia	2.78	2.85	1.75	1.19	6.48 <sup>a</sup>	4.75	3.30	1.084 <sup>b</sup>	3.03 <sup>**</sup>	0.07
Barberousse	2.80	3.37	1.95	1.28	4.00	3.60	2.84	0.877 <sup>b</sup>	0.37 <sup>ns</sup>	0.23
Begonia	2.89	4.86 <sup>a</sup>	2.02	1.12	1.90	3.47	2.71	0.922 <sup>b</sup>	0.99 <sup>**</sup>	-0.04
Fouara	3.20 <sup>a</sup>	5.56 <sup>a</sup>	2.08	1.17	4.60	5.63 <sup>a</sup>	3.71	1.700 <sup>c</sup>	0.20 <sup>ns</sup>	-1.36
Jaidor	2.62	3.24	1.80	1.11	3.06	2.99	2.47	0.737 <sup>b</sup>	0.09 <sup>ns</sup>	0.27
Plaisant	2.85	3.54	2.08	1.36	2.54	2.81	2.53	0.645 <sup>b</sup>	0.11 <sup>ns</sup>	0.61
Rahma	3.22 <sup>a</sup>	4.08	2.52 <sup>a</sup>	1.76 <sup>a</sup>	1.92	2.68	2.70	0.570 <sup>a</sup>	0.75 <sup>**</sup>	1.00
Rihane	3.09 <sup>a</sup>	4.45 <sup>a</sup>	2.16 <sup>a</sup>	1.37	3.80	4.25	3.19	1.081 <sup>b</sup>	0.12 <sup>ns</sup>	-0.03
Saida	3.04	5.38 <sup>a</sup>	2.06	1.12	2.95	4.50	3.18	1.387 <sup>b</sup>	0.22 <sup>ns</sup>	-0.95
Tichedrett	2.98	5.13 <sup>a</sup>	2.07	1.15	2.24	3.87	2.91	1.143 <sup>b</sup>	0.57 <sup>*</sup>	-0.50
Tina	2.95	4.34	2.06	1.26	2.98	3.70	2.88	0.966 <sup>b</sup>	0.31 <sup>ns</sup>	0.00
X <sub>Loc</sub>	2.99	4.25	2.09	1.31	3.38	3.86	2.99	--	--	--
LSD <sub>5%</sub>	0.32	1.21	0.41	0.29	1.12	0.57	----	--	--	--

a = Top yielding genotypes at each location , a= slope non significantly different from zero; b= slope non significantly different from 1; c = slope significantly greater than 1; ns, \*,\*\* = variance component non significant and significant at 5% and 1% level, respectively

**Table 3:** Joint regression and AMMI analysis of variance for barley grain yield.

Source of variation	DF	SS	MS
Treatments	71	351.13	4.95**
Location (L)	05	221.02	44.20**
Block (location)	12	01.72	0.14ns
Genotype (G)	11	27.10	2.46ns
G x L	55	103.01	1.87**
Regression	11	20.07	1.82ns
Deviation from regression	44	82.94	1.88**
IPCA <sub>1</sub>	15	62.11	4.14**
IPCA <sub>2</sub>	13	22.56	1.73**
Residual	27	18.34	0.68**
Pooled error	132	26.37	0.20
Total	215	379.23	1.76

ns, \*\* = effects non significant and significant at 5% and 1% level, respectively. MS<sub>Treat</sub>, MS<sub>BlockL</sub>, MS<sub>GxL</sub>, MS<sub>Dev</sub> from regression, were tested against the pooled error term, MS<sub>Loc</sub> was tested against the block within location term; and MS<sub>Genotype</sub> was tested against the GL term.

The results of regression analysis indicated that the linear component of the GL interaction accounted for only 19.48% of the GL sum squares, and was not significant. The mean square due to deviation from regression was significant and accounted for the remaining 80.52% of the GL sum squares (Table 3). This indicated the relative inefficiency of the regression analysis to discriminate between pattern and noise of the GL interaction sum squares, as mentioned by Zobel *et al.*, [10]. The results of the *t*-test of slope values indicated that Fouara had a slope significantly greater than unity, while Rahma showed a slope non-significantly different from zero. The remaining genotypes presented a slope non-significantly different from unity (Table 2). The S<sup>2</sup><sub>di</sub> indicated that Bahia, Begonia, Rahma and Tichedrett were unstable. Acsad<sub>176</sub>, Barberousse, Fouara, Jaidor, Plaisant, Rihane, Saida, and Tina showed a greater phenotypic stability (Table 2). Fouara, with a slope

greater than unity and a non-significant S<sup>2</sup><sub>di</sub>, was stable and responsive to environmental changes. This genotype is to be recommended to high yielding locations (Table 2). Acsad<sub>176</sub>, Rihane and Saida had above average grain yield, a slope equal to unity and a non-significant S<sup>2</sup><sub>di</sub>. They exhibited a general adaptability to all locations. Bahia had above average grain yield but a significant S<sup>2</sup><sub>di</sub>, showing low stability and specific adaptation. The remaining genotypes had below average grain yield (Table 2). The first two IPCA axes of the AMMi<sub>2</sub> model explained 82.19% of the GL sum of squares, which is 4.2 times more than that explained by the linear regression model (Table 3).

The first IPCA captures 60.29% and the second IPCA axis explained 21.90% of the interaction sum squares. This suggested that AMMI model fits well the data, compared to the joint regression analysis. The AMMI<sub>1</sub>-biplot shows the overall average grain

yield achieved by a genotype, and how this was achieved, as far as the locations are concerned. Averaged across locations, Fouara was the top yielding, mainly because of its good yield at the highest yielding sites SET, KHR and ALG. Jaidor was the lowest grain yielding cultivar, as it behaved poorly at these high yielding locations (Figure 1). Based on the relationship between the genotype  $IPCA_1$  ( $GIPCA_1$ ) scores and yield means, Bahia, Begonia and Rahma expressed large interaction (Figure 1). The AMMI<sub>2</sub>-biplot indicated that SET and SBA sites were less discriminating, because of their low LIPCA scores, while ALG, SER, SAI and KHR exerted strong interaction, due to their large LIPCA scores (Figure 2). Bahia showed specific adaptation to ALG location, Begonia was more specifically adapted to KHR location, while Rahma was specifically adapted to SAI location. No genotype showed specific adaptation to SER location. The remaining genotypes are grouped near the origin of the first two  $IPCA$  axes. They exhibited a general adaptation to all locations. Among these entries, Fouara and Acsad<sub>176</sub> had above average grain yield (Figure 2, Table 2).

#### Nominal Grain Yield and Yield Stability:

The nominal grain yield helps to apprehend the general adaptability of each cultivar and to identify genotypes that yielded best at specific location  $IPCA_1$  scores (Figure 3). Fouara showed a higher nominal yield, ranging from 3.66 to 3.83 t ha<sup>-1</sup>, over the entire set of locations tested.

This variety had a large adaptation, compared to Bahia, which exhibited a higher nominal grain yield, ranging from 3.17 to 3.62 t ha<sup>-1</sup>, at locations with an  $IPCA_1$  score less than -0.1015. Bahia showed a specific adaptation to SET and ALG, which were within this  $IPCA_1$  score range. The third cultivar showing a consistent higher nominal yield over the entire range of locations tested was Acsad<sub>176</sub>. This genotype had a nominal yield that ranged, across the test locations, from 3.34 to 3.41 (Figure 3). Fouara could be recommended to all the locations, based on its large adaptability. To reduce from the risk of adopting only one cultivar, the second genotype to be recommended is Bahia for the sub region represented by SET and ALG, and Acsad<sub>176</sub> to the sub region represented by SER, KHR, SAI and SBA.

Grain yield stability is an important characteristic of any cultivar, particularly in environments subjected to severe abiotic stress factors, such as those encountered under arid and semi arid conditions of Algeria. The AMMI stability value (ASV) is of use when the two first  $IPCA$  scores contributed differently to the genotype x location interaction sum squares. This parameter estimates cultivar stability, based on the AMMI model [14]. Smaller ASV values

are indicative of high stability. Tina, Bahia, Rihane and Begonia had low ASV values; they are stable. Fouara, Acsad<sub>176</sub>, Saida and Rahma are unstable genotypes. Tichedrett, Barberousse, Plaisant and Jaidor had intermediate stability (Figure 4). Stability based on the ASV values disagreed with stability based on the coefficient of regression, nominal yield variance, and  $S^2_{di}$ . ASV showed no significant Spearman's rank correlation coefficients with either of these statistics. The rank correlation coefficient values were 0.056<sup>ns</sup>, -0.250<sup>ns</sup>, -0.046<sup>ns</sup>, and -0.280<sup>ns</sup> with grain yield main effect, nominal yield variance, slope, and  $S^2_{di}$ , respectively. These weak relationships suggested that ASV stable genotypes were not necessarily high yielding across the tested locations, nor responsive to favorable growing conditions (Figure 4).

#### Causes of GL Interaction:

In the search for an understanding of the causes of genotype x environment interaction, correlation coefficients between the genotypic and environmental scores derived from the AMMI analysis and genotypic and environmental covariates were calculated. Most of the correlation coefficients between the  $GIPCA_1$  scores and the genotypic grain yield means per location were non-significant. Except one, which was of negative sign, indicated that at this location (ALG), high yielding genotypes had large negative  $GIPCA_1$  scores (Table 4). The correlation coefficients between  $GIPCA_1$  scores and the genotypic covariates varied among locations. The number of spikes m<sup>2</sup>, plant height, number of days to heading and straw yield showed significant correlations with  $GIPCA_1$  scores. This indicated that variation in the mean values of these traits was a major source of interaction among the tested entries. The number of spikes m<sup>2</sup> and to lesser extent the number of grains per spike were the determinant of grain yield, as they exhibited significant correlations with grain yield (Table 4). The LIPCA1 scores showed significant correlation with the amount of rainfall accumulated during the winter (October-February), June month and during the crop cycle (October –June), and with winter mean monthly temperature (Table 5). Variation among locations for these environmental variables caused differential genotypic responses, causing expression of the interaction. Similar results were reported by Vargas *et al.* [17], Yan and Hunt [4], Samonte *et al.* [18] and Rane *et al.* [19].

The stability of cultivar performances across varied locations and broad adaptation are, generally, the main goals of most testing programs. The GL interaction, often, confound the genetic differences that affect yield among genotypes [2,4,10,16,17]. In this study partitioning and interpretation of the GL

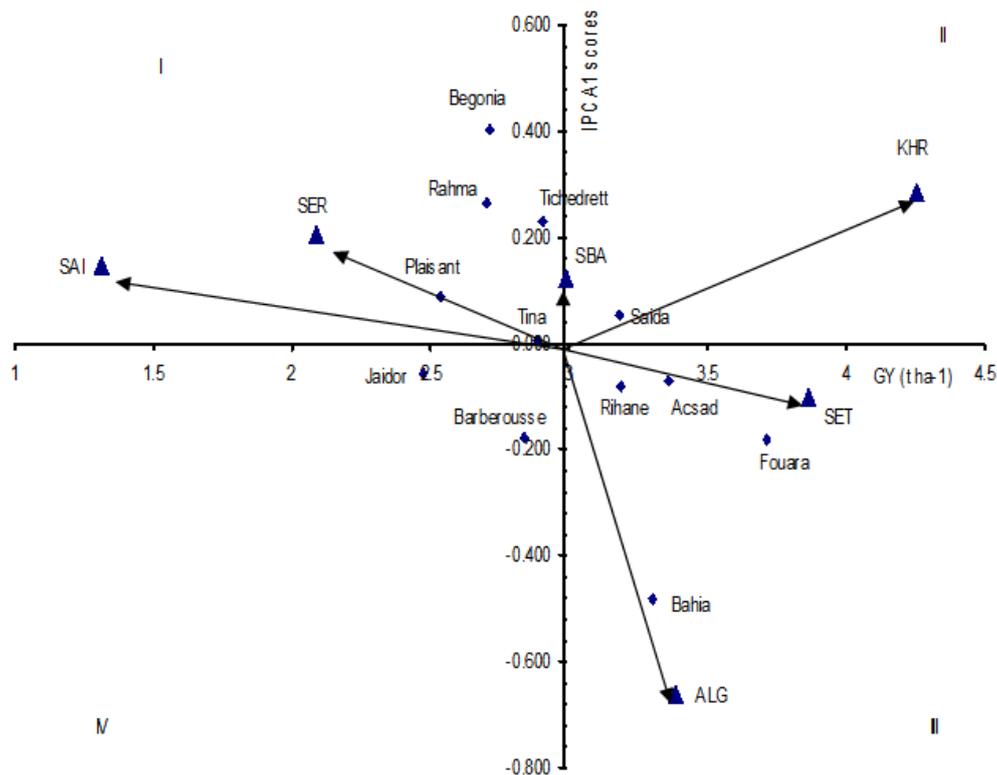
**Table 4:** Correlation coefficients between GIPCA<sub>1</sub> scores, grain yield and agronomic traits measured at each location.

Traits	Locations					
	SBA	KHR	SER	SAI	ALG	SET
	-----GIPCA <sub>1</sub> -----					
GY	0.166	0.462	0.418	0.101	-0.954*	-0.554
SN	0.103	0.576*	-0.235	-0.005	-0.586*	0.677*
GS	0.008	0.049	0.407	.317	0.320	-0.540
TKW	-0.038	-0.451	0.330	0.381	-0.214	-0.681*
PHT	0.139	-0.556*	0.229	-0.625*	0.256	0.147
STRW	-0.661*	0.136	0.587*	-0.025	-0.356	-0.025
DHE	-0.439	-0.417	-0.239	0.574*	-0.402	0.679*
	-----Grain yield-----					
SN	0.564*	0.484	-0.185	0.605*	0.756*	0.656*
GS	0.053	0.660*	0.560*	0.562*	0.235	-0.053
TKW	-0.572*	-0.484	0.631*	0.035	-0.103	0.211
PHT	-0.622*	-0.344	0.418	0.388	-0.323	0.031
STRW	-0.300	-0.203	0.235	-0.122	-0.243	-0.421
DHE	-0.100	-0.011	-0.427	-0.347	-0.352	-0.350

\* Correlation coefficient significant at the 5% level; GY = grain yield (t ha<sup>-1</sup>); SN = number of spikes per m<sup>2</sup>; GS = number of grains per spike; TKW = 1000-kernel weight (g); PHT = plant height (cm); STRW = straw yield (t ha<sup>-1</sup>); DHE= number of calendar days from January 1<sup>st</sup> to the date when 50% of spikes per m<sup>2</sup> fully emerged from the flag leaf.

**Table 5:** Correlation coefficients between LIPCA1 scores and environmental co-variables

Traits	LIPCA1	GY
LIPCA1 scores	1.000	-0.217
Grain yield (t ha <sup>-1</sup> )	-0.217	1.000
Winter rainfall (mm)	-0.879*	-0.220
Spring rainfall (mm)	-0.771	0.194
Cycle rainfall (mm)	-0.865*	-0.034
March rainfall (mm)	-0.709	0.229
April rainfall (mm)	-0.778	-0.227
May rainfall (mm)	0.010	0.315
June rainfall (mm)	-0.901*	-0.014
Number of frosty days	0.285	-0.131
Altitude (m)	0.710	-0.313
Winter mean temperature (°C)	-0.842*	0.318
Spring mean temperature (°C)	-0.647	0.600



**Fig. 1:** AMMI<sub>1</sub>-biplot for grain yield (t ha<sup>-1</sup>) of the 12 barley genotypes evaluated at 6 diverse Algerian locations.

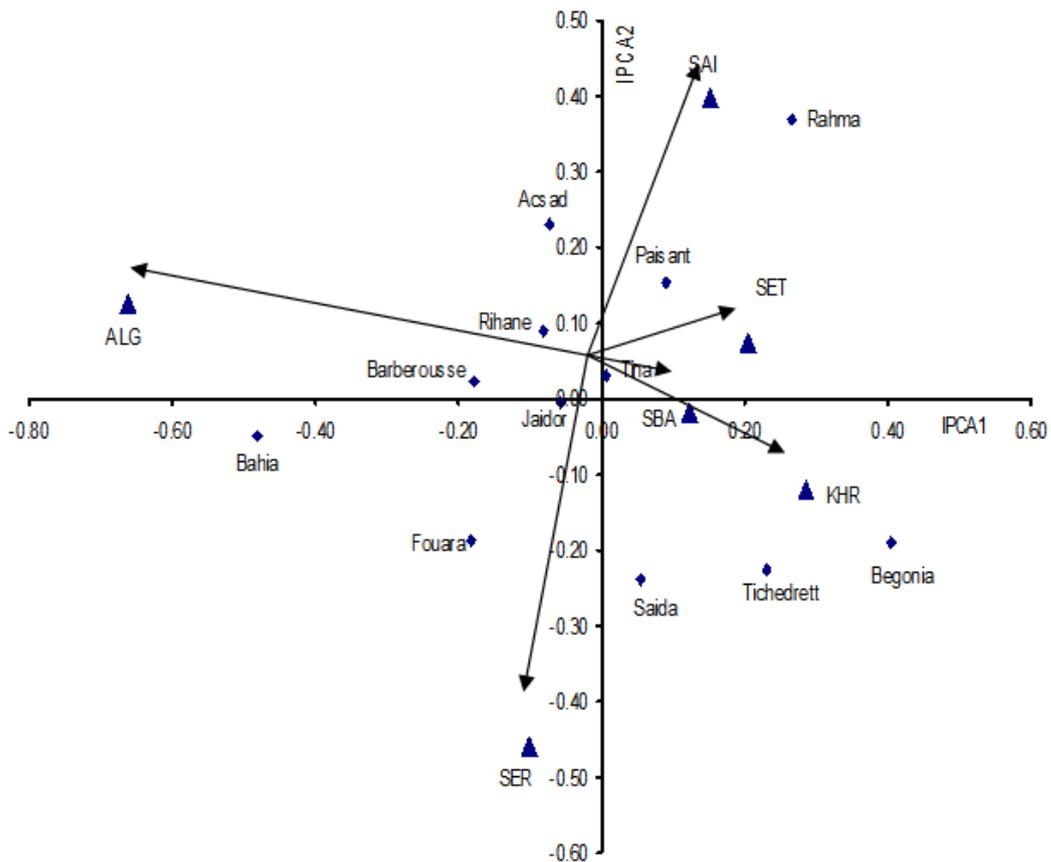


Fig. 2: AMMI<sub>2</sub>-biplot for grain yield of 12 barley genotypes evaluated at 6 diverse Algerian locations.

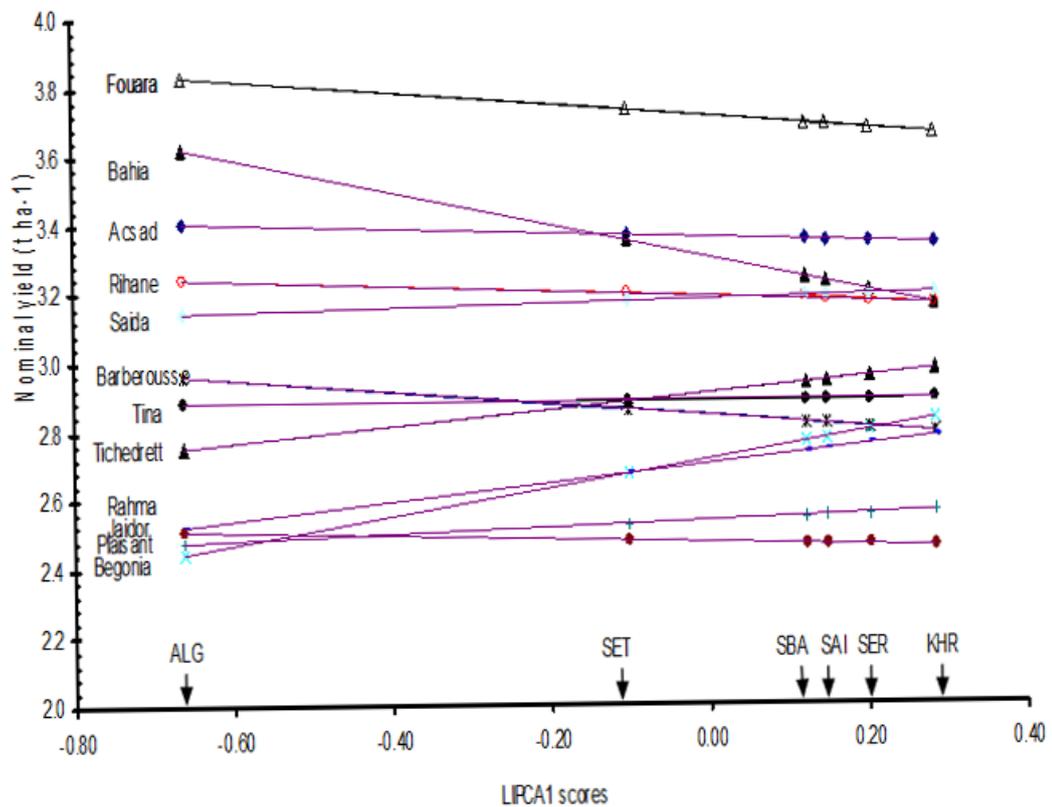
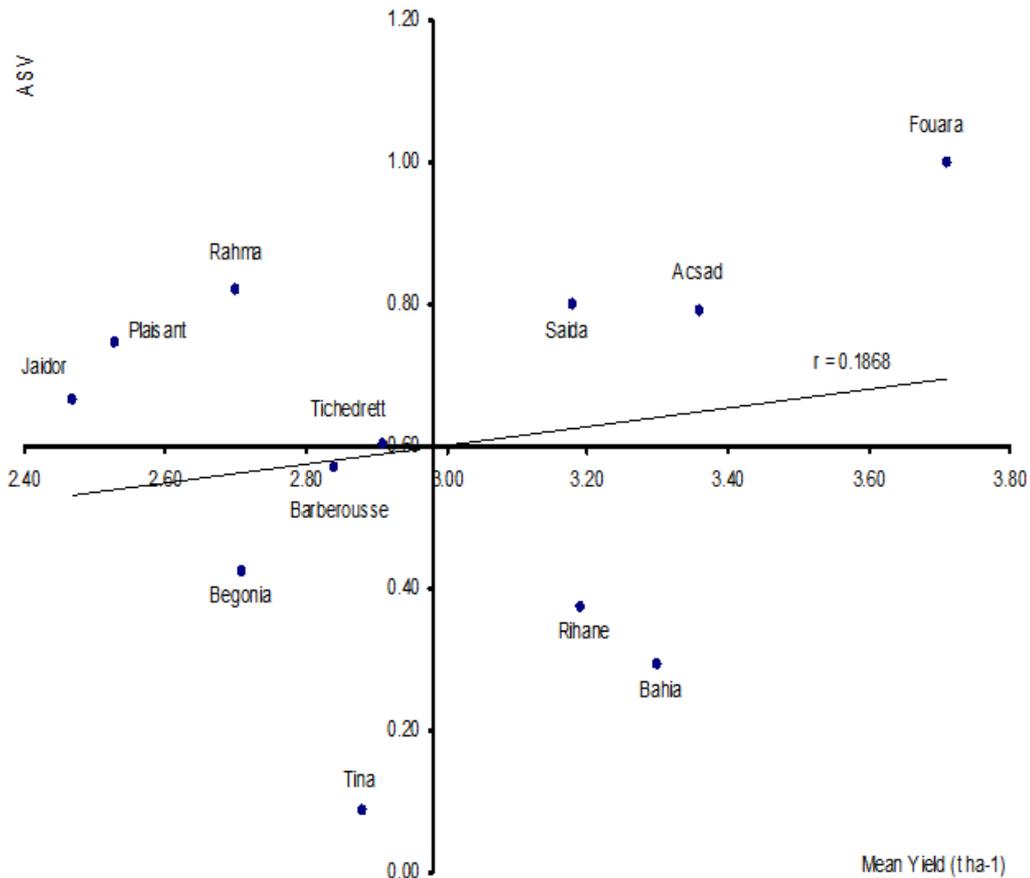


Fig. 3: Variation of the nominal grain yields of 12 barley genotypes across location IPCA<sub>1</sub> scores.



**Fig. 4:** Relationship between ASV and mean grain yield of the 12 barley genotypes evaluated at 6 diverse Algerian locations.

interaction was based on linear regression techniques [8] and multivariate analysis [10]. The regression method showed deficiencies for determining GL interaction patterns and explained a small part of the interaction. This finding corroborated results of similar studies [2,9,10,16,17]. Comparatively, AMMI analysis was more efficient in analysing GL interaction pattern. Some inconsistency was observed in this study, between the different parameters measuring genotypic stability. Some genotypes were stable according to one parameter and unstable when using another parameter. For instance, Fouara was stable according to the  $S^2_{di}$  and unstable (responsive) according to the slope. Bahia was stable according to the slope value and instable according to the  $S^2_{di}$ . Five genotypes showed above average grain yield main effect, and seemed of interest to selection.. Among these, Fouara had a slope significantly greater than unity, a high ASV value, and the best nominal yield. Acsad<sub>176</sub> had a slope equal to one, low  $S^2_{di}$  value, intermediate ASV and nominal yield. Bahia had a slope equal to one, high  $S^2_{di}$  value, a variable nominal yield, and a low ASV value.

Based on nominal yield, Fouara and Acsad<sub>176</sub> showed large adaptation to the entire set of locations

tested, but Bahia had a specific adaptation. The genotypic traits sources of interaction were the number of productive tillers, the number of grains per spike, plant height, 1000-kernel weight, straw yield and the number of days to heading. Winter mean temperature, rainfall accumulated during the crop cycle, and during the winter and June months were the major causes of the yield interaction. These results suggested discarding genotypes with extreme levels of plant height, straw yield and cycle length. With respect to location factors, as variation in accumulated rainfall and average temperature are unpredictable, no single location can be recommended for effective cultivar evaluation. It seems that there is no easier way other than to test over a wide range of locations and years, and select for both average yield and stability.

*Conclusions:*

The linear regression method was inefficient for determining GL interaction patterns. AMMI analysis was more efficient and explained a large part of the interaction pattern. Stability and adaptability of genotypes were estimated though AMMI biplots.

Estimates of genotype nominal grain yield at different environments aided in the identification of the genotype that yielded the highest at specific location IPCA1 ranges. Genotypes Fouara and Acsad<sub>176</sub> showed wide adaptation, above average grain yield, high nominal yield and yield stability based on  $S^2_{di}$  and ASV, respectively. Bahia showed a specific adaptation. Plant traits acting as major source of GL interaction were plant height, straw yield, number of days to heading, number of spikes  $m^{-2}$ , and number of grains per spike. Variation in accumulated rainfall in winter and June, as well as the mean winter temperature were among the environmental variables causing the GL interaction. Selection should avoid extremes values for the genotypic traits related to the interaction and conducted over a wide range of locations and years to identify stable and above average yielding genotypes.

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