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ANALYSIS OF THE GENOTYPE X LOCATION INTERACTION AND GRAIN YIELD STABILITY OF DURUM WHEAT (*TRITICUM DURUM* DESF.) GENOTYPES TESTED ACROSS DIVERSE ALGERIAN LOCATIONS

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Abstract – This investigation was carried out to determine the adaptability patterns of a set of 30 durum wheat (Triticum durum Desf.) genotypes evaluated across four Algerians locations. The results indicated that yield varied widely within and between locations, and was significantly affected by location, genotype and genotype x location interaction, which accounted for 91.78, 2.06 and 6.24% of the treatment variation. Compared to the joint regression which explained only 10.13%, the AMMI analysis explained 92.65% of the sum square of the interaction and indicated that all locations exhibited high interaction and could be grouped into two recommendation domains: Khroub, Sétif and Tiaret vs Oued Smar. Bichena/Ariza2//Solga8 expressed high yield main effect, high stability, good reliability and large adaptability to all locations, while Gcn/4/D68.1.93A//Ruff /Fg/3/Mtl5 showed specific adaptation to Oued Smar location. These results indicated that breeders had the choice to select Bichena/Ariza2//Solga8 due to its large adaptation and above average grain yield against the alternative to recommend this genotype to the sub region represented by Khroub, Sétif and Tiaret locations and to select Gcn/4/D68.1.93A//Ruff /Fg/3/Mtl5 specifically for Oued Smar location. The strategy associating general adaptation to a large sub region with specific adaptation resulted in 7.16% yield gain.

Keywords: *Triticum durum* Desf., AMMI model, interaction, nominal yield, reliability.

I. INTRODUCTION

Durum wheat grain yield, in Algeria, is limited by abiotic stress with a strong effect of rainfall amount and distribution pattern [1]. High grain yield variations, ranging from 1.8 to 3.6 t ha^{-1} from the same site in successive cropping years, were reported by Bahlouli *et al*., (2005) [2]. Low yields were due to the combined effect of winter low temperatures, spring frost hazards, terminal high temperatures and water shortage. Under such variable growth conditions, genotypes x environment interactions exit and are large enough to hinder selection progress. The genotype x environment interaction is a major problem because it complicates the interpretation of yield trials and makes predictions and recommendations difficult. It is a particular problem where genotypes are tested and selected in one environment and targeted to other environments [3],[4],[5]. Differential yield responses of genotypes can be caused by differences in phenology, growth habit, vernalization and/or photoperiodic responses and in the differential genotypic ability to respond to the growth conditions represented by temperature, water and nutrient [6]. Annicchiarico and Perenzin (1994) [7] showed that earliness by cold stress and plant height by drought were sources of genotype x environment interaction in wheat. Ebdon and Gauch (2002) [8] reported that AMMI environmental scores

were correlated with precipitation, mean daily maximum and minimum temperatures, altitude, latitude, N fertilization, and clay content. Samonte *et al.,* (2005) [9] reported that among 29 environmental variables tested for their correlation with environmental principal component interaction scores, mean minimum heat index showed a significantly correlation, suggesting that environments with higher scores were source of significant interaction; Epinat-Le Signor, 2001 [10], found that earliness of flowering, water balance, and mean temperature to be contributors to the observed interaction for maize yield.

In breeding programs, significant genotype x environment interaction should be taken into consideration because it can be properly exploited to advantage through various approaches. Its magnitude, relative to the magnitude of genotype and environment effects on the measured trait, needs to be estimated. To exploit positive genotype x environment interaction, joint regression and additive main effects and multiplicative interaction (AMMI) models are helpful analytical tools ([11]; [12]; [13]; [14]; [15]). In the AMMI model the effects are first accounted for by an analysis of variance, and after that the interaction is handled through a principal component analysis to extract a new set of co-ordinate axis which explains, in more detail, the interaction pattern ([13]; [16]; [8], [17]).

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These methods help to understand the magnitude and the predictability of the interaction which is needed to exploit the genotype x environment effects through appropriate selection strategies aimed at exploiting wide and specific genotype adaptation patterns ([18]; [5]). The results of such analyses can be used to group environments into sub regions on the basis of similarity of cultivar performance ([19]; [5]). Stability is defined as the genotype ability to perform consistently across a wide range of environments. It is a desirable characteristic, whose estimation becomes important, when selecting genotypes for wide adaptation. Lin *et al.,* (1986) [20] described various concepts of stability and statistics used to determine whether a genotype is stable or unstable. Since high yielding genotypes are, usually, unstable; methods that integrate performance and stability have been suggested [21]. The Shukla's variance helps to select for both yield and stability [22]. Reliability allows combining performance and stability too [16]. It is a measure of the genotype merit and a reliable genotype is characterized by consistently above average yield across environments. The objectives of this study were to apply the joint regression and AMMI analyses to determine the magnitude of the genotype x location interaction effects on grain yield and to identify stable durum wheat (*Triticum durum* Desf.) varieties within a set of 30 genotypes evaluated across 4 diverse Algerian locations. The information generated should be useful to fine-tune the testing program by targeting appropriate cultivars to different locations and by identifying redundant locations to use efficiently the limited resources.

II. MATERIAL AND METHODS

Field experiments and methodology

A field trial was carried out during the 2005-06 cropping season at four locations (Table.1), namely Khroub (KR), Setif (ST), Oued Smar (OS) and Tiaret (TR). The experiment was conducted under rainfed conditions. Thirty durum wheat genotypes were tested, including Algerian commercial varieties and advanced lines from the national and CIMMYT-ICARDA durum wheat breeding programs (Table 2). These genotypes were sown in a randomised complete block design with four replications. Sowing was done in November by an experimental drill (12 m^{-2} plots, consisting of six rows with 20 cm left between two successive rows at a seeding rate of 300 seeds m^{-2}.

Nutrient deficiencies were prevented with fertilization at sowing, by an application of 100 kg ha^{-1} of super phosphate 46% and 100 kg ha^{-1} of urea 35% at jointing. Weeds were controlled chemically with GranStar (*Methyl Triberunon*) at 12 g ha^{-1} rate. Data of grain yield were determined by mechanical harvesting all 6 rows per plot. Rainfall, temperature and altitude for the four locations are given in Table 2.

Statistical analysis

The combined analysis of variance was performed according to the following model: $Y_{ijk} = \mu + G_i + L_j + (G \times L)_{ij} + e_{ijk}$ Where Y_{ijk} is the yield of the ith genotype in the jth location and k^{th} block, μ is the grand mean, G_i is the main effect of the ith genotype, l_j is the main effect of the jth location, $(G \times L)_{ij}$ is the interaction term of the ith genotype in the jth location, and e_{ijk} is the error term. To describe the genotype x location interaction of grain yield and to identify stable genotypes for this trait, joint regression and Additive main effects and multiplicative interaction (AMMI) analyses were performed on the $(G \times L)_{ij}$ term. The joint regression analysis was performed according to Finlay and Wilkinson (1963) [13] where the $(G \times L)_{ij}$ effect was partitioned into components $b_i L_j$ and d_{ij}, which accounted for the linear regression of the ith genotype on the jth location yield index and the deviation from regression, respectively. The slope value (b) was determined for each genotype, as well as the genotype contribution to the G X L interaction and deviation from regression. A regression coefficient equal to 1.0 indicated an average stability, and in association with high yield, the entry possesses general adaptability. Regression coefficient values increasing above 1.0 describe genotypes with increasing sensitivity to environmental change, and having below average stability. Regression coefficients decreasing below 1.0 provide a measure of greater resistance to environmental change, this is an indication of above average stability since the greatest stability according to Kang and Magari, (1995) [23] is b = 0. The $(G \times L)_{ij}$ effect was also partitioned according to the AMMI model proposed by Gauch, (1992) [24] as:

$$(G \times L)_{ij} = \sum \iota_n u_{ni} v_{nj} + r_{ij}$$ where $\sum$ is the sum of the n =1, 2… n PC axes included in the model, ι_n is the eigenvalue of the nth PC axis, u_{ni} is the scaled eigenvector of the ith genotype for the nth axis, v_{nj} is the scaled eigenvector of the jth location for the nth axis, and r_{ij} is the residual of the G x L interaction. The reliability index (I) was determined according to the procedure outlined by Annichiarico (2002) - [17], on the basis of the distribution of grain yield means observed across the tested locations. The lowest yield expected at a specified probability of negative events is calculated by: $I_i = Y_{i.} - Z_p\sigma$ Where $Y_{i.}$ is the genotype main effect, σ is the square root of the across locations variance and Zp is the percentile from the standard normal distribution for which the cumulative distribution function reaches the value p, taken here to be equal to 1.645, assuming a low input subsistence agriculture. Calculations were performed by IRRISTAT 5.0 software (2005) [25] using the cross site analysis procedure, which gives outputs of AMMI and joint regression models including analysis of variance, regression coefficients, as well as genotypes and environments means and Biplots graphics[17].3

III. RESULTS AND DISCUSSION

Grain yield performances and magnitude of yield G x L interaction

Single site grain yield analysis of variance indicated significant genotype effect suggesting inherent variability to be exploited. The grain yield mean ranged from 0.72 to 6.55 t ha^{-1}, yield expressed by genotype 8 (Rascon/Sla3/3/Plata1/Snm//Plata9) at Tiaret (TR) location and the genotype 3 (Bichena/Ariza2//Solga8) at Khroub (KR) location, respectively. The site mean yield ranged from 1.00 to 5.55 t ha^{-1}, recorded at locations TR and KR, respectively (Table 3). Each location has its specific top yielding entries which is suggestive of the presence of genotype x location interaction. Genotypes 3 (Bichena/Ariza2//Solga8), 5 (Waha), 12 (Gcn/4/D68.1.93A//Ruff/ Fg/3/Mtl5), and 30 (Mbb/Ofonto//Radiosso/Waha) were among the top yielding

entries in at least two locations (Table 3). Identification of the dominant cultivar that yielded best at a specific growing environment is useful to breeders and growers. Assuming that the results will be repeatable, a grain yield improvement of 4.68-3.64= 1.04 t ha^{-1}, over the 4 locations, could be achieve in the case where only the top yielding genotype (genotype 3 for KR and ST, genotype 12 for OS and genotype 30 for TR) was retained per site (Table 3). The combined analysis of variance, over locations, confirmed the presence of a significant genotype x location interaction for grain yield with a highly significant location effect (Table 4). These results indicated that, under Algerian growing conditions, durum wheat yield was significantly affected by location and genotype x location interaction. The location effect explained 91.78% of the treatments sum squares, while the genotype and the genotype x location interaction explained only 2.06 and 6.24% of the genotype + location + genotype x location (G + L + G x L) variation in grain yield, respectively (Table 4). Even though several authors ([13], [26]; [8]) made the criticism that the regression technique confuses interaction and main effects, partitioning and interpretation of the G x L interaction based on this technique were intended in this study. The linear component, tested against the deviation from regression, was non significant, suggesting the homogeneity of the regression coefficients, while the deviation from regression was highly significant, retaining a sizeable part (89.86%) of the G x L interaction sum squares unexplained (Table 4).

Regression analysis

The results of the t-test of the individual regression coefficient indicated that genotypes 8 (Rascon/Sla3/3/Plata1/Snm//Plata9) and 27 (Boussallem/Ofonto//Waha) had a slope significantly greater than unity while the slopes of the remaining entries were not significantly different from unity (Table 5). Genotypes 7, 8, 12, 13 and 22 contributed significantly to the G x L interaction; while genotypes 6, 7, 12, 13, 22, and 30 had a significant deviation from regression mean square. Genotypes 1, 4, 7, 9, 12, 13, and 21 had positive intercept equal or greater than 0.3 t ha^{-1}, under harsh growth conditions (Table 5). The linear representation of the most interacting genotypes showed that the interaction is best exploited when genotype 3 (Bichena/Ariza2//Solga8) is recommended to the sub region represented by the locations KR and ST and genotype 12 (Gcn/4/D68.1.93A//Ruff/Fg/3/Mtl5) is recommended to the sub region represented by the location OS and TR (Figure 1). Grain yield improvement of 0.56 t ha^{-1}, over the whole region covered by the 4 locations, could be achieve in the case where only these two genotypes (genotype 3 for KR and ST and genotype 12 for OS and TR) were adopted (Table 5, Figure 1).

AMMI analysis

The AMMI analysis results revealed the significance of the two first IPCA which were used to determine the distance from the origin of the AMMI$_2$ biplot as a measure of stability. Both axes accounted for 92.65% (76.01% for the IPCA$_1$ and 16.64% for the IPCA$_2$) of the sum square of the interaction. The residual of the AMM$_2$ model was not significant and of small magnitude (Table 4). Compared to the non significant 10.13% of the G x L interaction explained by the regression

model, these results demonstrated the efficiency of the AMMI analysis, extracting a large part of the G x L interaction (Table 4). According to Gauch (1992) [24] AMMI analysis is effective because it captures a large portion of the genotype x environments sum of squares, separating main and interaction effects, offering different kinds of opportunities, and allowing meaningful interpretation of the data. The AMMI$_1$ biplot, representing graphically the main and IPCA$_1$ effects of both genotypes and locations on grain yield, exhibited 98.52% of the treatment sum squares (SS), with 91.78, 2.06, and 4.67% due to location, genotype and IPCA1 sum squares, respectively (Figure 2, Table 4). The IPCA1 sum square, which explained 76.01% of the GxL SS, was higher than the genotype SS, stressing the importance of taking GXL interaction into consideration when estimating cultivar yield at different locations or when targeting entries onto specific locations. According to Gauch and Zobel (1996) [27] it a common scenario in yield trials, to observe a G x E larger than the genotype main effect.

The IPCA scores of a genotype in the AMMI$_1$ analysis could be used as an indicator of the stability of the given genotype over the locations tested. The greater the IPCA scores, either negative or positive, the more specifically adapted a genotype is to a given location or group of locations. An IPCA score approaching zero is indicative of low interaction or high stability [13]. Genotypes 3, 8, 27 and 24 had low IPCA$_1$ scores; they contributed less to the G x L interaction. They could be regarded as entries with large adaptability to all locations. However they differed in main yield effect (Figure 2). Genotypes 3 and 12 as well as genotypes 7, 13, 15, 28 had similar main effect but differed in their contribution to the interaction. Genotypes 12, 15, 2, 4, 5, 20, 23, 17 and 28 differed in both main effect and interaction, with genotype 12 having a high yield main effect and genotype 28 a low yield main effect (Figure 2). Due to their large IPCA$_1$ scores, all locations exhibited high interaction. KH and ST, grouped in the lower quadrant, showed a high main effect and sheared the same winning genotypes. They represented a similar recommendation domain (Figure 2). OS location was opposed to KH and ST sites; it discriminated differently between the tested genotypes compared to the other locations. OS had an intermediate yield main effect while TR showed the lowest yield main effect (Figure 2). A rough linear relationship between interaction scores and main effects for genotypes appeared in the AMM1 biplot, indicating that genotypes characterized by extreme main effects (entries 7, 12, 13 vs 22, 30, and 16) had opposite interaction scores. The former had large positive interaction scores while the second had negative scores, consequently, they are adapted to different environments. Analyzing together the IPCA$_1$ scores and yield main effect, genotypes 1, 2, 3, 4, 6, 7, 8, 9, 10, 12, 13, 15, and 21 had positive IPCA$_1$ scores similarly to OS location; they showed adaptability to this location. In contrast genotypes 5, 11, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28; 29 and 30 showed adaptability to KH, ST and TR locations which exhibited negative IPCA$_1$ scores (Figure 2).

Durum breeders are targeting high-yielding and across locations stable genotypes. In this context genotype 3 (Bichena/Ariza2//Solga8) cumulated high yield main effect

and high stability. This genotype exhibited large adaptability to all locations, while entries 12 (Gcn/4/D68.1.93A//Ruff /Fg/3/Mtl5), 13 (D68.1.93A//Ruff/Fg/3/Mtl5/4/Lahn) and 7 (Sula/Rbce2/3/Hui//Cit71/CII/4/Ryps) showed specific adaptation to OS location (Figure 2). No high yielding genotypes were specifically adapted to KH, ST or TR, compared to the widely adapted genotype 3 (Bichena/Ariza2//Solga8) (Figure 2). These results indicated that breeders had the choice to select genotype 3 due to its large adaptation and above average grain yield against the alternative to recommend this genotype to the sub region represented by KH, ST and TR locations and to select genotype 12 specifically for OS location. The expected yield improvement was estimated, according to Zobel *et al.,* (1988) [13], from the genotype main effect + location main effect-overall mean + genotype $IPCA_1$x location IPCA1 scores of the given genotype and location. The adoption of genotype 3 over all locations will give a yield improvement estimated to be equal to 4.33-3.64= 0.69 t ha^{-1}, while the yield advantage offered by the alternative will be equal to 4.64-3.64=1.0 t ha^{-1}. The strategy associating general adaptation to a large sub region represented by KH, ST and TR with specific adaptation to OS brought induced a yield gain of 4.64-4.33/4.33= 7.16%, based on the information brought by the $AMMI_1$ biplot (Figure 2).

The study of the $AMMI_2$ biplot, generated using genotypic and environmental scores of the first two AMMI components, revealed that OS and TR locations had opposite $IPCA_1$ scores, and KH and ST had opposite $IPCA_2$ scores. OS, KH and ST exerted strong interactive forces than TR location, due to the relative size of their IPCA scores. Genotypes 3, 8, 11, 14, 19, 21, 24 and 27, posed near the origin, contributed little to the G x L interaction; while genotypes 12, 13, 6, 30, 16, and 22 contributed heavily to the interaction (Figure 3). KH and TR showed similar pattern of interaction while ST and OS had different pattern of interaction, since they are posed in different quadrant of the biplot (Figure 3). Genotype 7 showed specific adaptation to OS location. Genotype 30 has specific adaptation to KH, genotype 16 to TR location and genotype 22 to ST location (Figure 3). Based on the information brought by the $AMMI_2$ biplot, the exploitation of the G x L interaction through the adoption of genotypes specifically adapted to each location will generate a yield improvement estimated to be equal to 4.25-3.64= 0.61 t ha^{-1}.

Targeting durum genotypes based on nominal yield

The determination of genotype nominal yield, based on the AMMI model equation without the environmental deviation across the locations IPCA$_1$ scores (LIPCA1), was sought to visualize adaptability pattern and to identify top yielding genotypes at specific LIPCA$_1$ ranges. Figure 4 indicated that genotype 3 (Bichena/Ariza2//Solga8) had the highest nominal grain yield at LIPCA$_1$ < -0.700. ST location was within this LIPCA$_1$ score range. Based on nominal yield, genotype 3 is specifically adapted to ST location. Genotype 12 (Gcn/4/D68.1.93A//Ruff/Fg/3/Mtl5) exhibited the highest nominal grain yield at locations with LIPCA$_1$ scores greater than -0.700. TR, KH and OS locations were found within this LIPCA$_1$ score range. Genotype 12 should be recommendation to these three locations where it is expected to give high yield

(Figure 4). The variation of the nominal yield across locations could be used as an indication of the stability of genotype nominal yield. Genotype 3 has a static stability since its nominal yield ranged from 4.43 at ST to 4.41 at OS location (Figure 4). Nominal yield of genotype 12 varied from 4.10 to 5.70 t ha^{-1} across the 4 test-location. In comparison, genotype 7 which was top yielding at OS location showed low stability since its nominal yield range from 2.97 to 5.66 t ha^{-1} (Figure 4). Because of their high and stable nominal yields across locations genotypes 3 and 12 were identified as the best genotypes among the thirty entries tested and recommended to ST and to TR, KH and OS locations, respectively. These genotypes could be used as check cultivars for general and specific adaptation and for stability of new promises entries to be tested, as recommended by Samonte *et al.,* 2005 [9].

Reliability

Assuming that the technological level of agriculture in Algeria is of subsistence type, the top reliable entry was genotype 12, with a reliability value of 0.772 t ha^{-1}. This entry was recommended, based on its nominal yield, to the sub region represented by OS, KH and TR locations. The genotype 3, recommended to ST region, ranked 13th (Table 5). The reliability values were significantly correlated with grain yield main effect (r_s = Spearman correlation coefficient = 0.581**), as well as with the genotype IPCA$_1$ scores (r_s= 0.858**). However grain yield main effect was not significantly correlated with the genotype slope (rs= 0.058^{ns}), indicating that recommendation based on the GIPCA1 were in agreement, to some extend, with those based on the reliability index, as both parameters integrated yield potential and stability measures. In this study, partitioning and interpretation of the G x L interaction based on linear regression techniques showed deficiency for determining interaction patterns, which explained the low relationship between yield main effect and the slope.

Stability of cultivar performance for high grain yield across varied environments and broad adaptation are the goals of most breeding programs. Interactions between cultivar and environment often confound the genetic differences that affect yield among cultivars, leading to the evaluation of genotypes across a large number of sites to estimate yield potential and to analyse and understand the interaction pattern, with a possibility to group locations into homogeneous recommendation domains sharing the same winner genotypes [5], [14]. Several methods have been proposed to analyze the interaction [13], [20], [14], [28]. The methods based on the graphical display of the data, such as the joint regression and the AMMI, helped to understand and grasp much of the interaction pattern [13], [14], [29], [8]. In this study the results indicated that under Algerian growing conditions, durum wheat yield was significantly affected by location, genotype and genotype x location interaction which accounted for 91.78, 2.06 and 6.24% of the treatment variation. The joint regression analysis explained only a small fraction of the interaction, compared to the AMMI analysis which accounted for 92.65% of the sum square of the interaction. All locations exhibited high interaction and could be grouped into two recommendation domains: KH, ST and TR vs OS sites. The genotype Bichena/Ariza2//Solga8

expressed high yield main effect, high stability, intermediate reliability and large adaptability to all locations, while Gcn/4/D68.1.93A//Ruff /Fg/3/Mtl5 showed specific adaptation to OS location. The strategy associating general adaptation to a large sub region represented by KH, ST and TR with specific adaptation to OS resulted in a yield gain estimated to be 7.16%.

IV. CONCLUSIONS

This paper demonstrated the usefulness of AMMI model analysis in the interpretation of durum wheat yield data from a multi location experiment. The AMMI model analysis provided estimates of the magnitude and significance of the effect of the genotype x location interaction. Stability and adaptability of genotypes were estimated and aided in the identification of the genotype that yielded the highest at specific location or group of locations. These results lead to the identification of the appropriate check cultivar for all locations and for specific location though the AMMI analysis which proved more efficient than the joint regression analysis. To validate the results reported here and to better understand the genotype x location interaction pattern, future researches targeting the repeatability of the interaction and the main causes of the interaction are suggested.

Acknowledgements

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Table 2. Code and pedigree of the 30 entries tested at 4 locations under Algerian growing conditions during the 2005-2006 cropping season

Code	Pedigree	Code	Pedigree
1	Minimus/Rascon19	16	Inter9/Poho1
2	MCK2/Aco89	17	Kucuk
3	Bichena/Ariza2//Solga8	18	Aaz77.2/Porron11//Busca3
4	Silver26/Toska26	19	Altar84
5	Waha*	20	Boussallem*
6	Minimus7//Auk/Oste/3/Shah26	21	D68.1.93A.1A//Ruff/Fg/3/Mtl5/4/Lhan
7	Sula/Rbce2/3/Hui//Cit71/CII/4/Ryps27	22	Aram5/Cali//Rascon37/3/Plat8
8	Rascon/Sla3/3/Plata1/Snm//Plata9	23	Fl05
9	SnturkMi83-84.375/Nigris5//Tantlo1	24	Fl02
10	Hoggar*	25	Cirta*
11	Snr3/Nigris4//Porto5	26	Ting7/2*green3
12	Gcn/4/D68.1.93A//Ruff/Fg/3/Mtl5	27	Boussallem/Ofonto//Waha*
13	D68.1.93A//Ruff/Fg/3/Mtl5/4/Lahn	28	Ofonto/Waha//MBB*
14	Plata/Snm//Plata9/3/Green	29	Tr32225/Gediz//Ofonto*
15	Gta/Dur*	30	Mbb/Ofonto//Radiosso/Waha*

* = Algerian cultivars and advanced breeding lines

Table 1. Location name, code, latitude, longitude, altitude, annual rainfall and mean temperature

Location	code	Latitude	Longitude	Altitude (m)	rain* (mm)	Temperature (°C)** Winter	Spring
Khroub	KR	36°25' N	6°6'E	713	480	6.8	15.3
Setif	ST	36°12'N,	5°24'E	1023	417	6.2	14.0
Oued Smar	OS	36°70' N	3°16'E	34	650	8.7	17.2
Tiaret	TR	36°23'N	1°19'E	1080	405	6.8	15.4

* annual rainfall, ** mean of the December-February and March-April periods, respectively, for the 2005/06 season.

Table 3. Mean squares of single location analyze of variance for grain yield, trial coefficient of variation, site grain yield mean, least significant difference and top grain yielding durum wheat genotypes per location

Source of Variation	df	KR	Locations OS	ST	TR
Genotype	29	1.30*	3.26**	0.74**	0.69**
Block	2	0.59	1.29	1.19	0.44
Error	22	0.42	0.25	0.10	0.23
CV (%)	--	11.8	16.4	6.4	15.4
GY(t ha^{-1})	--	5.55	3.06	4.93	1.00
Lsd$_{5\%}$	--	0.91	0.71	0.44	0.21
Top[a]	--	3	12	3	30
yielding	--	6	7	5	24
genotypes	--	30	13	12	20
	--	27		22	5

*, ** = significant effect at the 0.05 and 0.01 probability level, respectively; [a] = genotypes with grain yield mean in the range of grain yield max − Lsd$_{5\%}$

Table 4. Joint regression and AMMI analysis of variance for durum wheat grain yield

Source of variation	df	SS	MS	F-value	F-test
Treatments	119	1651.46	13.88	74.41	**
Location (L)	03	1515.78	505.26	315.95	**
Block (location)	12	19.19	1.60	8.57	**
Genotype (G)	29	34.05	1.17	1.01	ns
G x L	87	101.63	1.17	6.26	**
Regression	29	10.30	0.36	0.23	ns
Deviation from regression	58	91.33	1.57	8.44	**
$IPCA_1$	31	77.25	2.49	9.01	**
$IPCA_2$	29	16.91	0.58	2.11	**
Residual	27	7.47	0.28	1.48	ns
Pooled error	348	64.9	0.19	----	---
Total	479	1735.55	----	-----	---

Ns,*,**= effects non significant and significant at the 5 and 1% probability level, respectively.

Table 5. Mean grain yield (GY, t ha^{-1}), coefficient of regression (b), contribution to the genotype x location interaction mean square (MS_{GxL}), mean square deviation from regression ($MS_{DEV.}$), intercept (a, t ha^{-1}) and reliability (I) of the 30 durum wheat genotypes evaluated at 4 locations

Genotype	GY	b	MS_{GxL}	MS_{DEV}	a	$I^{¤}$
1	3.50	0.871	0.32^{ns}	0.38^{ns}	0.33	0.445
2	3.69	0.983	0.12^{ns}	0.19^{ns}	0.11	0.321
3	4.32	1.183	0.16^{ns}	0.03^{ns}	0.01	0.320
4	3.72	0.932	0.09^{ns}	0.11^{ns}	0.33	0.540
5	3.73	1.016	0.07^{ns}	0.11^{ns}	0.03	0.270
6	3.70	0.984	0.64^{**}	0.96^{**}	0.12	0.127
7	3.86	0.842	1.48^{**}	2.06^{**}	0.80	0.425
8	3.74	1.131*	0.08^{ns}	0.01^{ns}	-0.38	0.000
9	3.64	0.884	0.29^{ns}	0.35^{ns}	0.42	0.549
10	3.73	0.955	0.13^{ns}	0.18^{ns}	0.25	0.457
11	3.78	1.015	0.01^{ns}	0.02^{ns}	0.09	0.350
12	4.37	0.972	0.81^{**}	1.21^{**}	0.83	0.772
13	3.90	0.936	0.80^{**}	1.17^{**}	0.49	0.416
14	3.65	1.075	0.08^{ns}	0.08^{ns}	-0.26	0.000
15	3.86	0.986	0.10^{ns}	0.15^{ns}	0.27	0.489
16	3.45	1.008	0.44^{ns}	0.65^{*}	-0.22	0.000
17	3.14	0.979	0.23^{ns}	0.34^{ns}	-0.42	0.000
18	3.64	0.985	0.13^{ns}	0.20^{ns}	0.05	0.264
19	3.56	1.068	0.04^{ns}	0.03^{ns}	-0.33	0.000
20	3.50	0.941	0.09^{ns}	0.11^{ns}	0.07	0.293
21	3.51	0.875	0.10^{ns}	0.06^{ns}	0.33	0.538
22	3.36	1.097	0.59^{**}	0.83^{**}	-0.63	0.000
23	3.39	0.981	0.10^{ns}	0.15^{ns}	-0.18	0.038
24	3.64	0.956	0.02^{ns}	0.02^{ns}	0.16	0.408
25	3.60	1.087	0.17^{ns}	0.21^{ns}	-0.36	0.000
26	3.24	0.968	0.24^{ns}	0.35^{ns}	-0.28	0.000
27	3.80	1.120*	0.06^{ns}	0.00^{ns}	-0.28	0.017
28	3.18	0.981	0.35^{ns}	0.53^{ns}	-0.39	0.000
29	3.53	1.132	0.26^{ns}	0.28^{ns}	-0.59	0.000
30	3.52	1.056	0.45^{ns}	0.66^{*}	-0.32	0.000

* slope significantly greater than 1; ns, *,** = variance component non significant and significant at 5% and 1% level, respectively; $^{¤}$ = negative I values were set at zero.
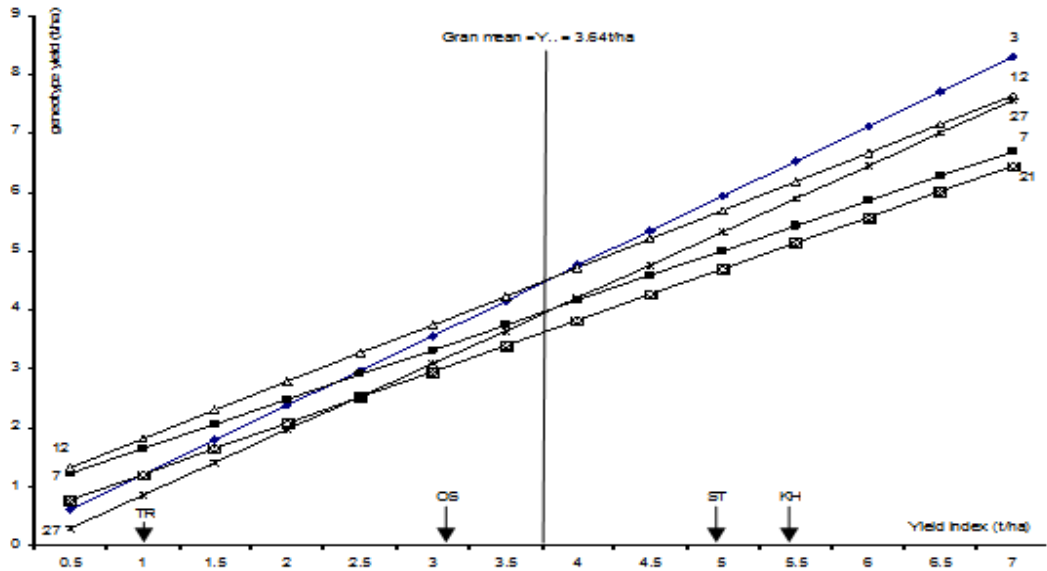
Figure 1. Variation of grain yield of the most interacting durum wheat genotypes according to the location yield index.
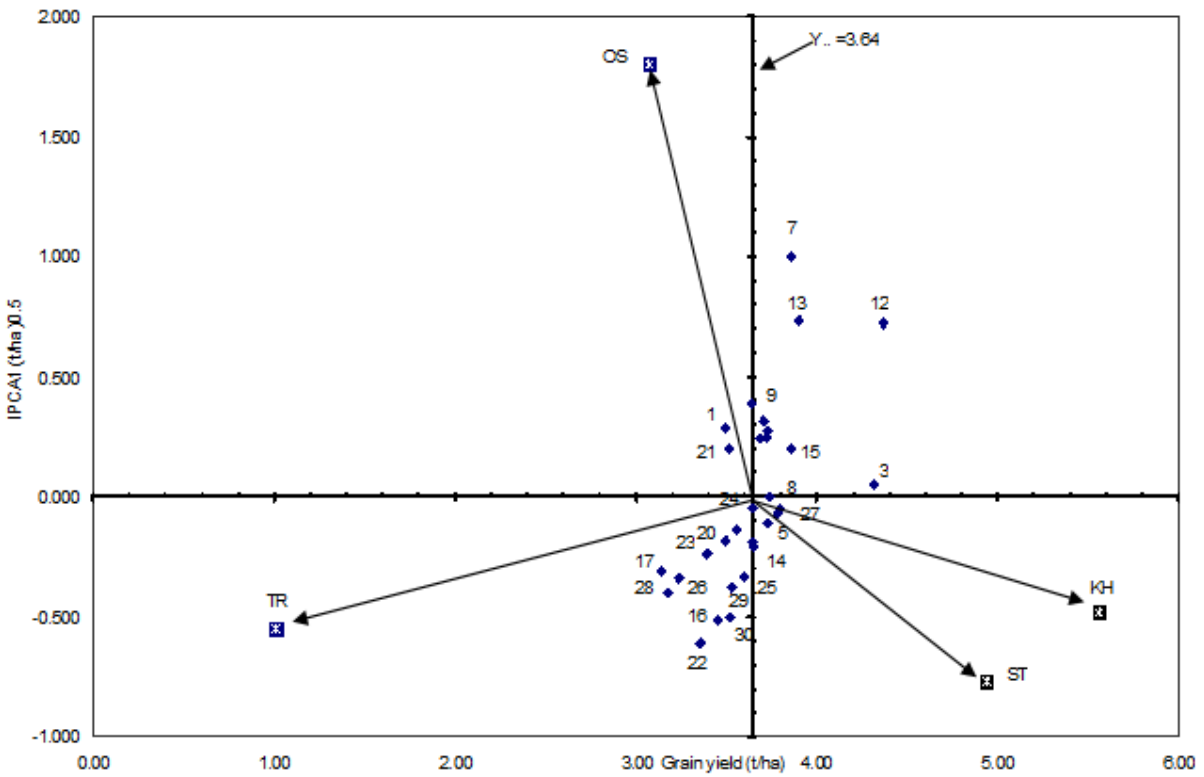

Fig. 2. AMMI₁ biplot of the main and IPCA₁ effects of genotypes and locations on durum wheat yield.
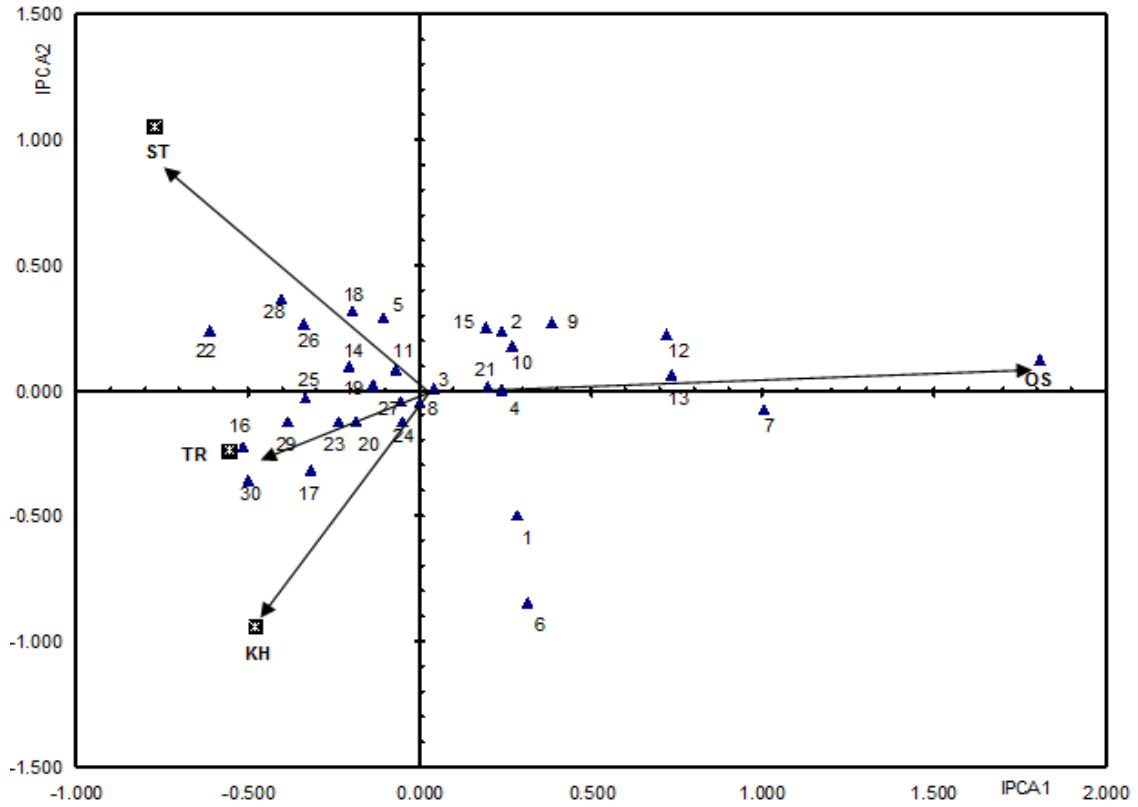
Figure 3. AMMI$_2$ biplot showing G x L interaction of 30 durum wheat genotypes evaluated at 4 locations.
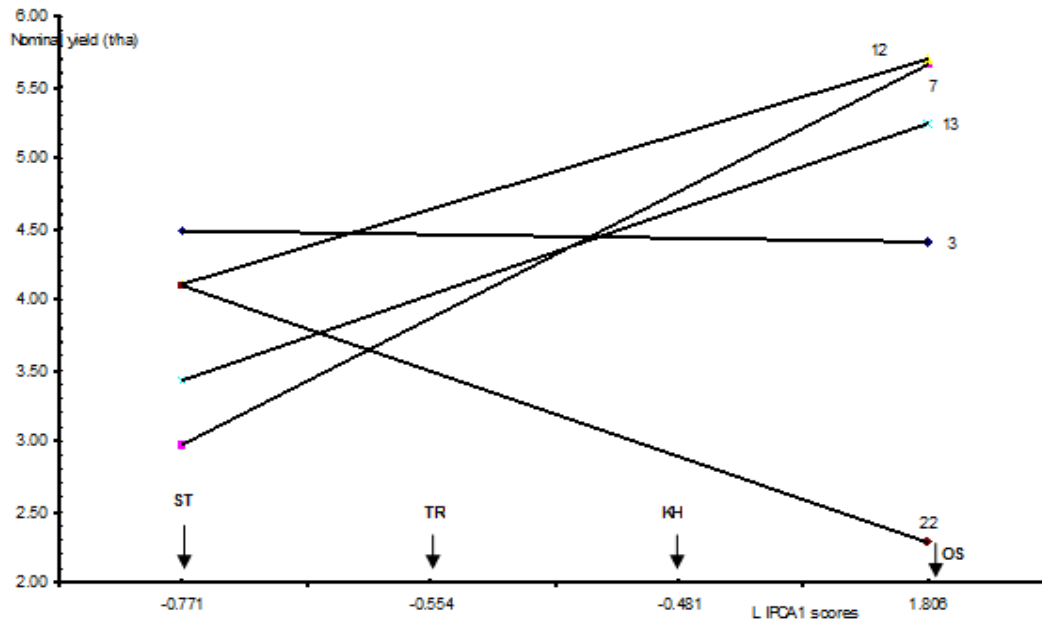

Figure 4. Nominal yield of the top yielding durum wheat genotypes as a function of the LIPCA$_1$ scores of 4 locations