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Adaptability of Durum Wheat Genotypes (*Triticum turgidum* L. Var *durum*) to Contrasted Locations

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ABSTRACT

This investigation was carried out to determine the adaptability patterns of a set of 23 durum wheat (*Triticum durum* Desf.) genotypes evaluated at four contrasted locations during two cropping seasons. The results indicated that yield varied widely and was significantly affected by year, location, year x location, genotype x location and genotype x location x year interactions, which accounted for 0.8, 63.1, 21.0, 5.8, and 3.40% of the treatment sum square, respectively. The joint regression and the AMMI analyses explained 30.08% and 83.35% of the sum square of the interaction, respectively. The results indicated that tested locations exhibited high interaction and could be grouped into two recommendation domains: Khroub vs Tiaret, Setif and Guelma. Genotypes Azeghar-1/3/Mrf-2/Bcr/Gro-1ICD00-0904-H-9AP-AP-1AP-TR, Miki-3ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR and Azeghar-1/Blm//Mrf-2ICD00-0818-C-18AP-AP-9AP-TR exhibited high yield main effect, and large adaptability to all locations, while Mrf1/Stj2/Berch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP showed specific adaptation to Khroub location and Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP expressed a specific adaptation to Tiaret, Setif and Guelma subregion. Based on nominal yield, selection for specific adaptation achieved 7.87% grain yield gain compared to selection for wide adaptation.

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INTRODUCTION

In dry areas, rainfed durum wheat yield is limited by biotic and abiotic stresses. Grain yield reductions were caused, mainly, by the combined effect of winter low temperatures, spring frost hazards, terminal high temperatures and water shortage (Annichiarico *et al.*, 2006; Chenaffet *et al.*, 2006). Grain yield variations, ranging from as low as 1.8 to 3.6 t ha⁻¹, at the same site in successive cropping seasons, were reported by Bahloul *et al.*, (2005) and Nouaret *et al.*, (2012), for durum wheat and by Kadiet *et al.*, (2010), and Mezianiet *et al.*, (2011) for barley. Under such variable growth conditions, genotype x environments interaction is large enough to hinder selection progress, making prediction and genotype recommendation difficult. This is a particular problem where genotypes are tested and selected in one environment and targeted to other environments (Farshadfar and Sutka, 2003; Annichiarico *et al.*, 2006; Kadiet *et al.*, 2010). Differential yield responses of genotypes can be caused by differences in phenology, growth habit, vernalization and/or photoperiodic responses (Oosteroom *et al.*, 1993). In breeding programs, significant genotype x environment interaction can be ignored or properly exploited to advantage through various approaches (Annichiarico *et al.*, 2011). In this context the joint regression and the additive main effects and multiplicative interaction (AMMI) models are helpful analytical tools (Finlay and Wilkinson, 1963; Zobelet *et al.*, 1988; Fan *et al.*, 2007; Annichiarico *et al.*, 2011). These methods help understanding the magnitude of the interaction to be able to exploit its effects through appropriate selection strategies (Annichiarico *et al.*, 2006). The environments can be grouped into sub-regions on the basis of similarity of genotype performances (Annichiarico *et al.*, 2006). The objectives of this study were to evaluate the magnitude of the genotype x location interaction effects on grain yield and to identify stable durum wheat (*Triticum durum* Desf.) genotypes within a set of 23 genotypes evaluated across four diverse locations during two cropping seasons.

MATERIAL AND METHODS

Trials management:

A set of field trials was carried out during the 2008-09 and 2009-2010 cropping seasons at four locations, namely Guelma, Khroub, Sétif and Tiaret, in Algeria. Guelma and Khroub belong to the sub-region B, and the other two sites belong to the sub-region A according to the site classification reported by Annichiarico *et al.*

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al., (2006). Sub-region B is low elevation zone with a milder climate, in contrast to the high elevation and cold prone A sub-region. The experiments were conducted under rainfed conditions. Twenty three durum wheat genotypes were tested, including commercial varieties and advanced breeding lines from the national and Cimmyt- Icarda breeding programs (Table 1).

Table 1: Number, pedigree and acronym of the 23 entries tested at 4 locations during the 2008-09 and 2009-10 cropping seasons.

Entry #	Pedigree	Acronym
1	Hoggar check	Vit
2	MBB check	Mbb
3	Boussellem check	Bss
4	Ter-2/3/HFN94-8/Mrb5/Zna-1 ICD00-1090-T-2AP-AP-2AP-TR	Thm
5	Mgn13/Aghrass2 ICD99-0015-C-9AP-AP-21AP-AP	Mga
6	Adnan-1 ICD00-0866-C-0AP-5AP-AP-8AP-AP	Adn
7	Ter-1/Mrf1/Stj2	Tms
8	Aghrass-1/HFN94N-8/Mrb5/Zna-1 ICD00-1085-T-2AP-AP-2AP-TR	Amz
9	Aghrass-1/3/Mrf1/Mrb16/Ru ICD00-0834-C-32AP-AP-6AP-TR	Amr
10	Amedakul-1 ICD96-0242-T-2AP-0AP-1AP-AP	Amd
11	Bigost-1 ICD96-0887-C-2AP-0AP-5AP-0AP	Big
12	Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP	Msb
13	Aghrass-1/HFN94N-8/Mrb5/Zna-1 ICD00-1085-T-10AP-AP-10AP-AP	Amz2
14	Stj2/Dra-2/Bcr/3/Ter-3	Sdb
15	Beltagy-2 ICD97-0396-T-1AP-AP-5AP-0AP-16AP-AP	Bel
16	Icasyr-1 ICD95-0169-C-0AP-3AP-0AP-5AP-0AP	Ica
17	Azeghar-2/Ch1/F1 13 ICD98-0493-W-AP-2AP-0AP-11AP-AP	Acf
18	Azeghar-1/Blm/Mrf-2 ICD00-0818-C-18AP-AP-9AP-TR	Abm
19	Miki-3 ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR	Miki
20	Azeghar-1/3/Mrf-2/Bcr/Gro-1 ICD00-0904-H-9AP-AP-1AP-TR	Amg
21	Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP	Tsb
22	Ammar-2 ICD94-0918-C-12AP-0AP-6AP-0AP-3AP-0AP	Amm
23	Aghrass-1/3/HFN94N-8/Mrb5/Zna-1 ICD00-1065-T-4AP-AP	Amz3

These genotypes were sown in a randomised complete block design with four replications. Sowing was done in November with an experimental drill, in 1.2 m wide x 05 m long plots, at a seeding rate of 300 seeds m⁻². Nutrient deficiency was prevented with fertilization at sowing, by an application of 80 kg ha⁻¹ of mono ammonium phosphate (52% P₂O₅ and 12% N), followed, at jointing, by an application of 75 kg ha⁻¹ of sulfazote (26% N and 35% SO₃). Weeds were controlled chemically with GranStar [*Methyl Tribenuron*] at 15 g ha⁻¹ rate. Data of grain yield were determined by mechanical harvesting all 6 rows per plot. Sites characteristics are given in Table 2.

Statistical analysis:

An analysis of variance was conducted in each environment (location per year) to test significant differences among genotypes. The homogeneity of error variances was tested according to F max prior to perform the combined analysis of variance, with the following model: $Y_{ijk} = m + G_i + L_j + Y_k + Br(Y_k L_j) + (G \times L)_{ij} + (G \times Y)_{ik} + (L \times Y)_{jk} + (G \times L \times Y)_{ijk} + e_{ijk}$, where Y_{ijk} is the grain yield of the i th genotype, in the j th location, in the k th year, in the r th replication. m is the grand mean yield. G , L , Y are the main effects; and $G \times L$, $G \times Y$, $L \times Y$, $G \times L \times Y$ are the two and three-way interaction effects of the genotypes, locations and years, respectively. Blocks are nested into years and locations (Annichiarico *et al.*, 2006). In this model, the genotype and location factors were regarded as fixed effects while years and blocks were regarded as random effects. Locations and years main effects were tested against the blocks within years and locations ($Br(Y_k L_j)$). Genotype main effect was tested against the genotypes x locations interaction ($G \times L$). The $G \times L$ interaction was tested

against the G x Y interaction, and the G x Y and L x Y were tested against the G x L x Y interaction. The three-way interaction was tested against the pooled error (Annichiarico, 2002).

Table 2: Test locations name, cropping seasons, acronym, latitude, longitude, altitude (m), annual rainfall (mm).

Site	saïson	Acronym	latitude	Longitude	Altitude	Rain (mm)
Guelma	2008-09	G09	36°45'	7°47'	272	655.6
Guelma	2009-10	G10				400.0
Khroub	2008-09	K09	36°26' N	6°66'E	713	427.4
Khroub	2009-10	K10				357.0
Setif	2008-09	S09	36°12'N,	5°24'E	1023	287.4
Setif	2009-10	S10				314.2
Tiaret	2008_09	T09	36°5' N	1°6'E	1003	435.4
Tiaret	2009-10	T10				422.0

To describe the genotype x location interaction for grain yield, joint regression and additive main effects and multiplicative interaction (AMMI) analyses were performed on the (G x L)_{ij} terms. The joint regression analysis was performed according to Finlay and Wilkinson (1963) where the (G x L)_{ij} effect was partitioned into components b_{ij} and d_{ij}, which accounted for the linear regression of the *i*th genotype on the *j*th 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 the deviation from regression. The (G x L)_{ij} effect was also partitioned according to the AMMI model proposed by (Gauch, 1992) according to the following model: (G x L)_{ij} = Σ u_n v_{nj} + r_{ij}, where Σ is the sum of the n = 1, 2... n PC axes included in the model, u_n is the eigenvalue of the *n*th PC axis, v_{nj} is the scaled eigenvector of the *i*th genotype for the *n*th axis, v_{nj} is the scaled eigenvector of the *j*th location for the *n*th axis, and r_{ij} is the residual of the G x L interaction. Nominal yield was deduced as the sum of the estimated entry mean yield and the product of the entry by the site scaled scores on IPCA1 and plotted against the IPCA1 scores of the environments (Zobel *et al.*, 1988). Analyses were performed with Cropstat 7.3 software (Cropstat, 2009) using the balanced analysis of variance and cross-site analysis subroutines (Annichiarico, 2002).

RESULTS AND DISCUSSION

Grain yield performances and magnitude of genotype x environment interaction:

Single site grain yield analysis of variance indicated significant genotype effect suggesting inherent variability to be exploited through selection (Table 3). Site mean grain yield ranged from 1.76 to 6.72 t ha⁻¹, recorded at Tiaret (T09) and Khroub (K09) sites, respectively, during the 2008-09 cropping season (Table 3). Each environment had its specific top yielding entries, which is suggestive of the presence of genotype X location interaction. Genotypes Miki-3 ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR (entry # 19, table 1), Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (entry # 21) and Azeghar-1/3/Mrf-2/Bcr/Gro-1 ICD00-0904-H-9AP-AP-1AP-TR (entry # 20) appeared among the top yielding entries at five, and four environments, respectively (Table 3).

Table 3: Mean squares of single site analysis of variance for grain yield, site grain yield mean and top grain yielding durum wheat genotypes per site.

Source	Blocks	Entries	Residual	CV%	Site meanyield	Top yield entries(a)
DF	3	22	66			
K09	0.04	4.03**	0.16	5.90	6.72	5,7, 11, 12,16
S09	0.72	0.38**	0.06	6.90	3.49	6, 9, 19, 20, 21
G09	0.22	1.39**	0.12	6.60	5.21	2, 12, 20, 21
T09	0.16	0.21**	0.07	15.30	1.76	9, 11, 17, 19
K10	0.16	2.94**	0.11	5.70	5.94	19
S10	0.56	1.37**	0.11	8.70	3.84	19, 20, 21
T10	0.16	1.20**	0.09	8.40	3.50	18, 19, 21
G10	0.15	0.55**	0.05	8.60	2.69	15, 20

*, ** = 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 - 1 Lsd5%

The combined analysis of variance showed significant year and site effects, and a non-significant genotype effect. Two and three-way interactions were highly significant. Site and site x year interaction had strong effect on grain yield variation, explaining 63.1% and 21.0% of the total sum squares, respectively;

followed by the G x S interaction with 5.8% (Table 4). This indicates the predominant importance of the environmental factors, characterizing locations (S) and cropping seasons (Y), in determining durum wheat yield in Algeria.

Regression and AMMI analyses of the genotype x location interaction:

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 (69.02%) of the G x L interaction sum squares unexplained (Table 4).

Table 4: Joint regression and AMMI analyses of variance of grain yield.

Source of variation	DF	SS	MS	F-test	%SS
Treatments	183	2085.33	11.39	**	
Years (Y)	1	16.45	16.45	**	
Sites (S)	3	1352.9	450.96	**	
Bocks/S x Y	24	4.58	0.19	ns	
Y x S	3	449.86	149.95	**	
Genotypes (G)	22	46.4	2.1	ns	
Y x G	22	23.44	1.06	ns	
S x G	66	123.94	1.71	*	
Regression	22	37.28	1.69	ns	30.08%
Deviation from regression	44	86.65	1.97	**	
IPCA1	24	103.3	4.30	**	83.35%
Residual	42	20.64	0.49	ns	
Y x S x G	66	72.31	11.23	**	
Pooled error	540	152.66	0.28		
Total	735	2242.58	2.91		

This result corroborated the criticism made by several authors that the regression technique confuses interaction and main effects (Zobel *et al.*, 1988; Ebdon and Gauch, 2002). The results of the t-test of the regression coefficients indicated that Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (entry # 21, table 1) had a slope of 0.547, significantly smaller than unity while the slopes of the remaining entries were not significantly different from unity (data not shown). The AMMI results indicated the significance of the first IPCA which accounted for 83.35% of the sum squares of the G x L interaction and a non-significant residual (Table 4). Compared to the non-significant portion of the G x L interaction showed by the regression model, these results suggested the relative efficiency of the AMMI analysis, in extracting a sizeable part of the G x L interaction (Table 4). The AMMI1 biplot explained 67.0% of the treatment sum squares (SS), with 60.33, 2.07, and 4.61% due to location, genotype and IPCA1 SS, respectively (Figure 1, Table 4). The IPCA SS was higher than the G SS, stressing the importance of taking G x L interaction into consideration when targeting genotypes into specific locations. Nsarellah *et al.*, (2011) reported that the IPCA1 of the AMMI was highly significant, and explained 60.44% of G x L interaction sum of squares. While the regression analysis extracted only 37.7% of the G x L interaction sum of squares. According to Zobel *et al.*, (1988), The IPCA scores are indicators of genotype adaptability and stability over the tested locations. Hoggar (entry #1, table 1), Ter-2/3/HFN94-8/Mrb5/Zna-1 ICD00-1090-T-2AP-AP-2AP-TR (entry # 4), Adnan-1 ICD00-0866-C-0AP-5AP-AP-8AP-AP (entry # 6), Aghrass-1/HFN94N-8/Mrb5/Zna-1 ICD00-1085-T-2AP-AP-2AP-TR (entry # 8), Azeghar-1/Blm/Mrf-2 ICD00-0818-C-18AP-AP-9AP-TR (entry # 18) et Miki-3 ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR (entry # 19) and Azeghar-1/3/Mrf-2/Bcr/Gro-1 ICD00-0904-H-9AP-AP-1AP-TR (entry # 20), having low score values, ranging from 0.0967 to -0.0929, contributed less to the G x L interaction. They are stable and adapted to the tested locations (Figure 1). Among these entries, Miki-3 ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR (entry # 19), Azeghar-1/3/Mrf-2/Bcr/Gro-1 ICD00-0904-H-9AP-AP-1AP-TR (entry # 20) and Azeghar-1/Blm/Mrf-2 ICD00-0818-C-18AP-AP-9AP-TR (entry # 18) exhibited high grain yield main effects, with 4.45, 4.37 and 4.35 t ha⁻¹, respectively. Thus, these entries are selected on the basis of their stability, adaptability and high grain yield performance. Among the remaining entries, genotypes Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP (entry # 12) and Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (entry # 21) differed in both main effect (4.53 vs 4.30 t ha⁻¹) and contribution to the G x L interaction (score values -0.4457 vs 0.6551) (Figure 1). Both genotypes are instable; Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP is specifically adapted to Khroub location while Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP is specifically adapted to the remaining three sites (Figure 1). Because of their large IPCA1 scores, Tiaret and Khroub locations exhibited high interaction. Khroub located in the lower quadrant, showed a high main effect while Tiaret had a lower grain yield main effect; Setif and Guelma sites being intermediate (Figure 1). These results indicated that breeders had the choice to select Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP (entry # 12) to the subregion represented by Khroub location and Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (entry # 21) to the subregion represented by Guelma, Setif and Tiaret against the alternative to select Miki-3 ICD94-0994-C-10AP-0AP-2AP-0AP-9AP-0TR (entry #

19) for the entire zone due to its large adaptation and above average grain yield. The expected yield was estimated, according to Zobel *et al.*, (1988), as the genotype main effect + location main effect overall mean + genotype IPCA1 x location IPCA1 scores. Selection for specific adaptation achieved a yield gain of 7.87% over the selection for large adaptation (4.80 vs 4.45 t ha⁻¹).

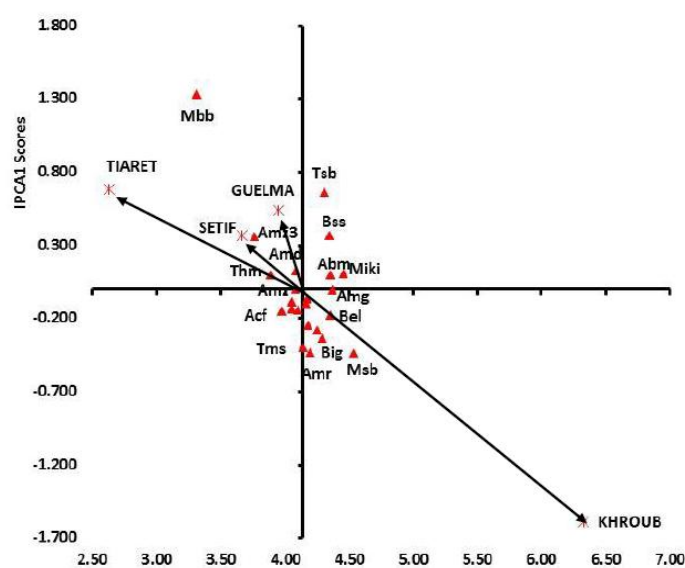


Fig. 1: AMMI1 biplot of the main and IPCA1 effects of genotypes and locations of grain yield.

Genotype selection based on nominal yield:

The adaptability pattern of the top yielding genotypes over locations, based on the nominal yield is shown in figure 2. This pattern confirmed the results derived from the AMMI analysis. That is Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP (Msb) exhibited a specific adaptation to Khroub location where it expressed its highest nominal grain yield; While Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (Tsb) achieved its highest nominal yield at Tiaret location to which it is specifically adapted. Three genotypes, Azeghar-1/3/Mrf-2/Bcr/Gro-1 ICD00-0904-H-9AP-AP-1AP-TR (Amg), Miki-3/ICD94-0994-C-10AP-0AP-9 2AP-0AP-9AP-0TR (Mik) and Azeghar-1/Blm//Mrf-2 ICD00-0818-C-18AP-AP-9AP-TR (Abm) showed a large adaptability to the four locations representing both subregions (Figure 2). These genotypes exhibited a static stability since their nominal yields ranged from 4.20 to 4.45 t ha⁻¹. While the variation of the nominal yield of Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP (Msb) and Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (Tsb) varied from 4.20 to 5.20 t ha⁻¹, and from 3.30 to 4.70 t ha⁻¹, respectively. These genotypes could be used as check cultivars for general and specific adaptation and for stability of new promising entries to be tested, as suggested by (Samonte *et al.*, 2005).

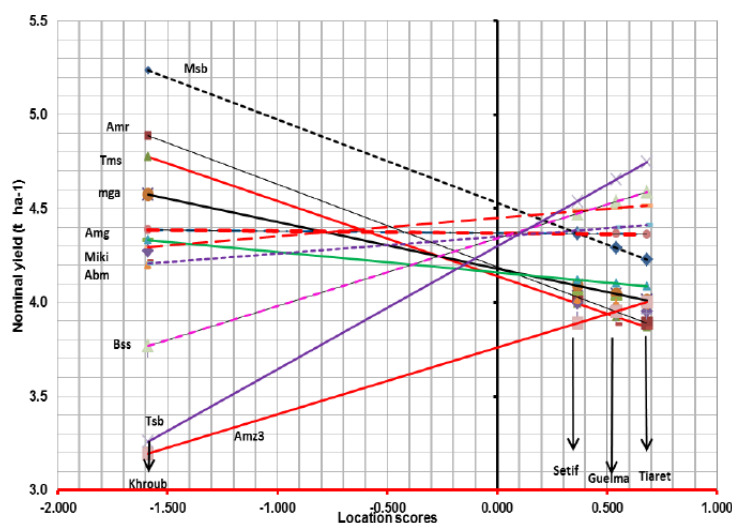


Fig. 2: Nominal yield of the top yielding durum wheat genotypes as a function of the LIPCA1 scores.

In drought-prone environments, progress in grain yield improvement may be achieved through the identification of specifically adapted genotypes to the targeted geographical area, rather than altering the environment (Ceccarelli, 1996). Based on modeled genotype grain yields, the results of the present investigation indicated the possibility to select for large as well as specific adaptation, this later strategy being more efficiency in terms of grain yield gain. These results corroborated those reported by Annicchiarico *et al.*, (2002) who observed a yield gain varying from 10 to 12% by selecting specifically adapted cultivars. Similar results were reported by Nouaret *et al.*, (2012) who found that the additivemodel as well as the joint regression proved to be inefficient in the interpretation of the results compared to the AMMI analysis of variance which explained 90.8% of the sum of squares of the interaction.

Conclusion:

The results of this study indicated that under the prevailing growing conditions, durum wheat yield was significantly affected by location, genotype and genotype x location interaction. The joint regression analysis explained only a small fraction of the interaction, compared to the AMMI analysis which accounted for 83.35% of the sum square of the interaction. Two locations exhibited high interaction and could be grouped into two recommendation domains: Khroub vs Tiaret, Setif and Guelma sub-regions. The genotype Mrf1/Stj2/Bcrch1 ICD99-0027-C-0AP-14AP-AP-9AP-AP (Msb) expressed high yield main effect and specific adaptability to Khroub location, while Ter-1/3/Stj3/Bcr/Lks-4 ICD99-1036-T-0AP-7AP-AP-3AP-AP (Tsb) showed specific adaptation to sub-region represented by Tiaret, Setif and Guelma locations. Selection for specific adaptation to each sub-region against selection for general adaptation to both sub-regions resulted in a yield gain estimated to be 7.87%. Selection based on nominal yield confirmed the results deduced from the analysis of AMMI1 biplot.

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