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Identification of stable lentil genotypes through genotype by environment interactions on yield potential in Morocco

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Abstract

Genotype by environment (G×E) interaction study becomes essential for selecting high and stable yielding genotypes. Altogether 64 lentil genotypes representing improved varieties, landraces and advanced lines were evaluated under 6 environments for green cover, phenological characters, grain yield and 1000 seed weight. Variance analysis revealed highly significant effects of genotype, environment and genotype by environment interaction for all studied traits. The environment had the greatest effect with 75.7% of the total sum of squares. AMMI-GGE biplot identified 3 mega-environments where Z32 advanced lines were performed in the first one (E1, E4 and E5); Z33 was the best in the second mega-environment (E2 and E3), of which E2 (SAD18) was characterized as discriminating and representative environment for selecting adaptable genotypes. While VR4 and LR4 were the winning genotypes in the third mega-environment represented by E6. According to 7 stability methods, Z33, Z32, Z31, Z13 and G03 lines were the most stable and resilient in all environments. In addition, five landraces (PA6, LR4, LR10, LR6 and PA1) showed a high yielding potential that could be used as a source of genotype candidates to develop novel resilient varieties of lentils. Varieties VR9 was recommended for both favorable and unfavorable environments, VR6 for unfavorable and VR3 for favorable environment. Otherwise, genotypes were grouped into 3 clusters with 90% of similarity. The third one gathered the highest yielding genotypes (Z33 and Z32), which were the most stable that could be promoted for developing resilient varieties for climatic changing environments.

Keywords

Lentil, grain yield, G×E interaction, AMMI-GGE, biplot analysis

Introduction

Lentil (*Lens culinaris* Medik.) is a self-pollinating diploid species (2n = 2x= 14) (1) and one of the most ancient food legume crops grown in the world (2). It is cropped in a total of 5 million hectares of land worldwide, with 3 % in the African region (3). The total lentil cultivated area in Morocco is estimated around 40560 ha, with annual production and yield of 9044 t and 0.22 t/ha respectively (3). Lentil production is low and unstable, depending mainly on climatic conditions during the growing season, such as drought and heat and on biotic constraints such as diseases, pests and plant parasites.

Lentil crop offers various environmental and ecological benefits thanks to the symbiotic relationship with the rhizobium allowing the biological fixation of atmospheric nitrogen (4). Furthermore, lentil grains represent a rich source of proteins (20.6–31.4%) (5), representing approximately twice that of most of the common cereals such as wheat, oats, barley and rice; and similar content as in meat (6). In addition, lentils' grains contain essential minerals such as iron (7.1 mg/100 gm) and zinc (3.55 mg/100 gm) (7). Indeed, the high nutritive value of lentil grains is used in enriching wheat flour as an adopting strategy to combat malnutrition, particularly in developing countries (8). Thus, lentil grains might play a great role in ensuring the nutritional security of low-income people, mainly in the climate change context (9, 10).

Since the yield potential of varieties/genotypes depends on the genotype performance and the environment characteristic; the reaction of genotypes to the environmental conditions is not always the same (11). For that, the study of genotype by environment (G×E) interaction leads to determining the genotype performance and stability according to some concepts such as mega environment, specific adaptation and stability. Having knowledge of this interaction and the stability in lentil genotype is necessary for an effective selection of performed genotypes (12, 13).

Various methodologies have been proposed for investigating G×E interactions; the Additive Main Effects and Multiplicative Interaction (AMMI) multivariate analysis model may lead to predicting adaptation and stability of advanced genotypes. AMMI simultaneously uses ANOVA to analyze the main effects (additive part) and Principal Component Analysis (PCA) to analyze the non-additive residual left over by the ANOVA (14). In addition, the GGE-biplot is an effective tool widely applied as a graphical demonstrating analysis for G×E interaction patterns based on both yield and stability and evaluation of test environments from a discrimination aspect. G×E interaction studies on lentil yield stability using the GGE biplot method have been reported in Iran (15) and in India (16).

Table 1. Site location, climatic and soil traits of the tested experimental sites.

Site name	Entry	Growing season	Env	Coordinates/ Altitude	Soil type	Humidity (%)!	Rainfall (mm)**	Temperature (°C)*		
								Mean	Min	Max
Marchouch	MCH18	2017–2018	E1	33°60'N, 6°71W 395 m	Clay loam	84.6	464.2	13.1	-1.66	32.0
	MCH20	2019–2020	E4			77.4	232.4	15.3	0.44	39.6
Sidi El Aydi	SAD18	2017–2018	E2	33°10'N, 7°645W 239 m	Clay loam	78.3	313.8	13.8	-1.82	33.7
	SAD20	2019–2020	E5			75.4	173.8	16.3	1.62	40.8
Douyet	LDY18	2017–2018	E3	34°02N, 5°07W 416 m	Clay limestone	68.1	191.0	14.1	4.00	35.0
	LDY20	2019–2020	E6			64.5	382.8	17.4	6.00	41.0

! mean humidity during the growing season , ** sum of daily rainfall during the growing season, * temperature (mean = mean of daily mean temperature during the growing season), (min = minimum daily temperature during the growing season), (max = maximum daily temperature during the growing season), Env = Environment

This study aims (i) to identify performed genotypes that have a high and stable yield in the tested environments to be selected as resilient varieties, (ii) to select landraces characterized with high yielding performance to be used as genetic resources and (iii) to recommend performed varieties in specific environments using AMMI and GGE biplot model.

Materials and Methods

Plant materials

The experimental material for the present study comprised 64 lentil genotypes, including (i) 9 Moroccan released varieties, (ii) 17 lentil landraces collected from the main produced lentil regions in Morocco and (iii) 38 advanced lines originated from national and international lentil breeding program (Supplementary Table).

Growing environmental conditions

Field experiments were conducted during 2 growing seasons, 2017/2018 and 2019/2020, at 3 Moroccan experimental locations of the National Institute of Agricultural Research (INRA). The test sites were Marchouch (MCH), Sidi El Aydi (SAD) and Douyet (LDY), representing contrasted agro-climate traits and covering the main lentil growing areas in Morocco (Table 1). The agro-climatic factors variation in each environment is shown in Fig. 1. The germplasm was evaluated in 6 environments defined as year-location combinations (Table 1).

Field experiments

The 64 lentil genotypes were laid out using a randomized split-plot design with three replications. The plot size was 1.5 m^2; each plot had two rows of 2.5 m in length spaced 0.3 m and 0.9 m between plots. The sowing rate was 30 kg/ha. Soils were fertilized at sowing using 28 kg/ha of nitrogen (N), 56 kg/ha of phosphorus (P) and 28 kg/ha of potassium (K). Sowing was carried out manually on a prepared seedbed in December.

Data recording

Three plants of each genotype were selected from each replication. Studied characters were green cover (GC %) using Canopeo application and measured 30 days after

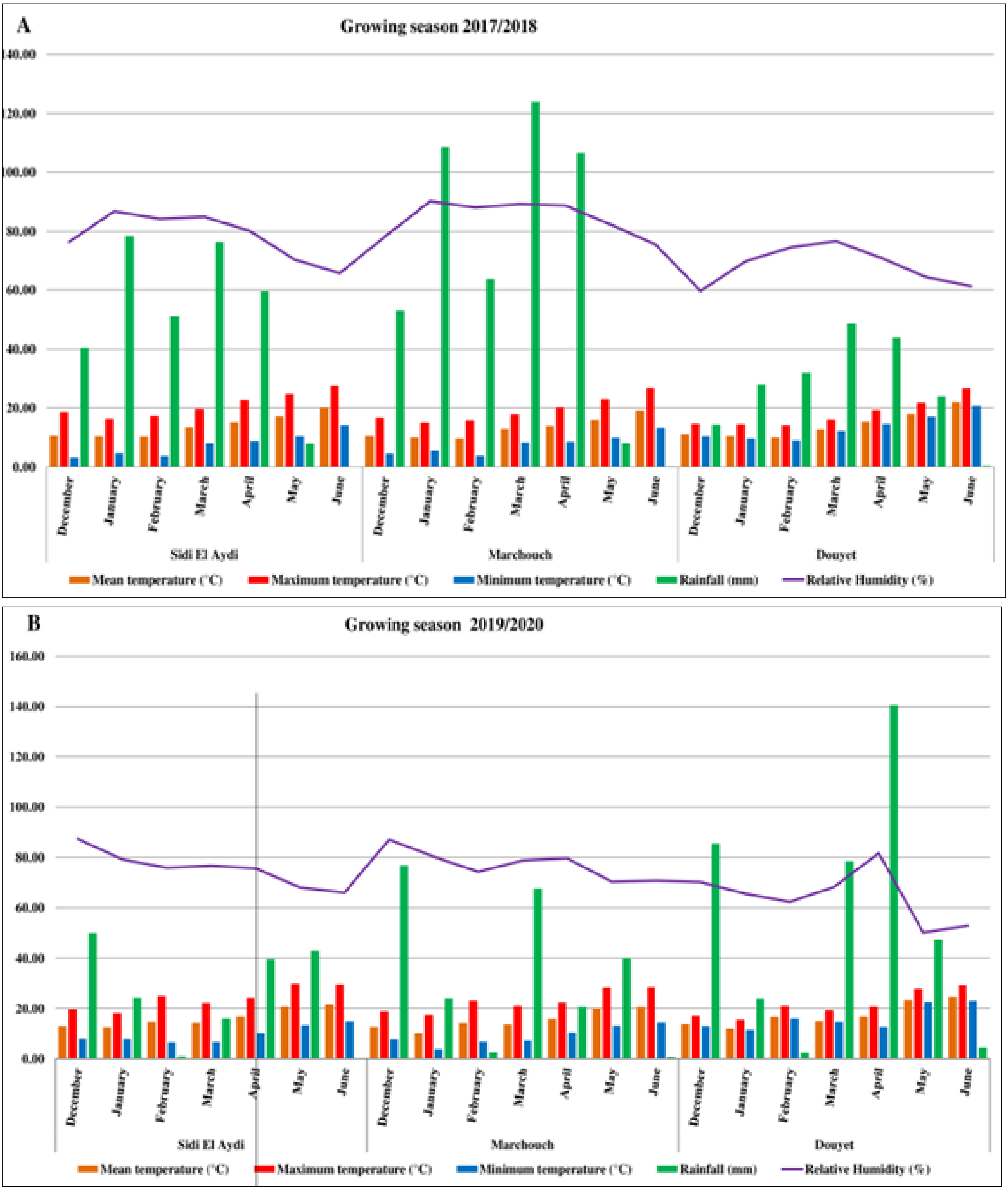

Fig. 1. Agro climatic factors variation in each environment **(A)** during 2017/2018 growing season and **(B)** during 2019/2020 growing season.

sowing; phenological parameters as earliness (DF) (number of days to 10% flowering), number of days to green seeds (GrS) and number of days to 90% of pods maturity (MAT). At seed maturity, plots were harvested by hand, and total seed yield (kg/ha) (YD) and 1000 seed weight (gm) (TSW) were measured.

Statistical analysis

Analysis of variance (ANOVA) was computed for all traits using GLM (General Linear Model). The least significant difference (LSD) was used to compare treatment means. Duncan's Multiple Range Test was applied to compare differences between the mean values. Correlation coefficients (Pearson's) were calculated to study the strength relationships between the 6 studied traits. The statistical software SAS ver.9.1 was used for this purpose.

Based on studied traits, genotypes were displayed to identify relatively homogeneous groups using hierarchical cluster analysis (Ward's squared Euclidean distance method) via SPSS.

On the other hand, genotype by environment interaction was described for seed yield determining the most stable and high-yielding genotypes in multi-environment trials. To explore this interaction, the Additive Main effects and Multiplicative Interaction model (AMMI) (17) and Genotype and Genotype by Environment model (GGE) (18) were used via the SAS package (ver.9.1).

The stability and adaptability analysis for seed yield was used according to seven univariate stability methods. The deviations from linear regression *(S2di)* (19) and regression coefficient *(bi);* the superiority index *(Pi)* (20); the two stability concepts *(Si1)* and *(Si2)* (21, 22)*;* the coefficients of determination *(R2)* (23) and the regression coefficient *PJ* (24) were computed. The association with these univariate stability methods and high mean yield indicate the general adaptability of genotypes under all environments.

Results and Discussion

Genotype, environment and GE interaction effects

Based on the analysis of variance, highly significant effects of genotype, environment and genotype by environment interaction (GE) were observed for all studied traits (Table 2). Several researchers reported significant genotype by environment interaction in the lentil (15, 16, 25, 26).

Table 2. Variance analysis of main agronomic traits.

Variable	Green cover (%)	Earliness	Green Seed	Seed Maturity	Yield (kg/ha)	Thousand seed weight (gm)
Sum of squares						
Genotype (G)	303.5***	73.11***	81.5***	81.3***	45.87***	241.3***
Environment (E)	6393.1***	25722.0***	22757.1***	23374.1***	6376.9***	10623.0***
GE	223.1***	62.8***	60.8***	61.3***	23.4***	39.4***
F-value	3.24***	10.6***	10.0***	9.90***	22.1***	17.0***
Mean ± *SE*	57.0±*0.39*	93.4±*0.37*	129.4±*0.35*	150.4±*0.36*	861.4±*0.19*	34.8±*0.26*
G mean range	45.6–65.5	88.6–97.5	124.7–133.8	145.6–154.6	625.7–1430.6	29.1–48.9
E mean range	48.1–62.0	71.8–104.9	108.8–140.8	128.8–160.8	431.9–1994.8	26.3–44.1
LSD	1.98	1.23	1.19	1.22	0.45	0.70

*** highly significant at 0.001 probability level, SE= standard error

The mean yield (861.4 kg/ha) (Table 2) ranged between the global mean genotypes from 625.7 (VR1) variety to 1430.6 kg/ha (Z33) advanced line (SupplementaryTable) and between environments from 431.9 (E5) to 1994.8 kg/ha (E2) (Table 3). Yield performance of tested genotypes was highest in the E2 environment [where rainfall (313.8 mm) and temperature (13.7 ° C) were considered favorable compared to the other agro -climate traits of tested environments], however, it was lowest in the E5 environment, [where climatic parameters were unfavorable (rainfall 173.8 mm and temperature 1.62–40.8 °C)] (Table 1). The decrease in genotype yield performance in E5 might be a result of the decrease in thousand seed weight (26.3 gm) compared to the grand mean of 34.8 gm (Table 3). Indeed, yield variation across environments is due to climatic variation conditions among environments confirmed by green cover and earliness. Green cover varied from 48 % (E3) to 62 % (E4) (Table 3) among environments and from 46 % (Z04) to 66 % (Z28) among genotypes (Supplementary Table). While genotype earliness varied from 72 days in E5 to 101 days in E2 (Table 3). The decrease in the vegetative growth period in E5 might be related to drought stress leading genotypes to earlier flowering.

Grain yield was positively and significantly correlated to green cover (r=0.098***), earliness (r=0.394***), green seed (0.262***) and seed maturity (r=0.268***) (Table 4). The positive correlation between phenological parameters and seed yield was in agreement with several studies (27, 28). As well, thousand seed weight and earliness correlations were in good line with the earlier study (29).

AMMI analysis

AMMI analysis showed that lentil seed yield was highly and significantly affected by the environment (E), genotypes (G) and by the interaction of G×E (Table 5). The greatest effect was attributed to the environment with about 75.7% of the total sum of squares. This result revealed the environment's diversity and a differential yield performance among the lentil genotypes. The high environmental effect on lentil genotypes is reported in several studies (16, 25, 30, 31). The greatest magnitude of GE interaction (17.5%) than the G effect (6.8%) can suggest the existence of genotypic differences across environments. The high magnitude of GE interaction than the G result is in agreement with several studies (30, 32-34).

The interaction of genotype with the environment was clearly demonstrated by the Principal Components (PC) of the AMMI model (Table 5). The first two PC [PC1 (40.1 %) and PC2 (29.0 %)] cumulate 69% of total variation suggesting a best predictive model for AMMI analysis as reported by (15,16). Furthermore, tested environments were diverse in terms of climatic conditions, justifying AMMI analysis to predict yield and yield stability of tested genotypes.

Table 3. Mean of studied traits per environments.

Environments	Green cover (%)	Earliness	Green Seed	Seed Maturity	Yield (kg/ ha)	Thousand seed weight (gm)
E1	61.9^{a}	105.0^{a}	140.8^{a}	160.8^{a}	855.3^{b}	36.5^{c}
E2	57.2^{b}	100.8^{b}	132.2^{b}	152.6^{cd}	1994.8^{a}	31.3^{d}
E3	48.1^{d}	95.1^{d}	133.1^{b}	152.1^{d}	559.9^{d}	28.2^{e}
E4	62.0^{a}	91.5^{e}	128.5^{c}	154.5^{b}	768.3^{c}	44.1^{c}
E5	50.9^{c}	71.8^{f}	108.8^{d}	128.8^{e}	431.9^{e}	26.3^{f}
E6	60.9^{a}	96.3^{c}	133.3^{b}	153.3^{bc}	558.1^{d}	42.5^{b}
Mean	57.0	93.4	129.4	150.4	861.4	34.8

values are mean of sixty-four studied genotypes according to each trait under each environment. significant means are separated at 5% level of probability according to Duncan's multiple range test.

Table 4. Coefficient of correlation among studied traits of lentil genotypes.

	Green cover	Earliness	Green Seed	Seed Maturity	Yield	Thousandseed weight
Green cover	1.000					
Earliness	0.184***	1.000				
Green Seed	0.171***	0.975***	1.000			
Seed Maturity	0.209***	0.947***	0.971***	1.000		
Yield	0.098***	0.394***	0.262***	0.268***	1.000	
Thousand seed weight	0.278***	0.260***	0.275***	0.365***	0.053^{ns}	1.000

*** highly significant at 0.001 probability level

Table 5. AMMI analysis model based on mean seed yield.

Source of variation	Df	SS	MS	Explained %	TSS explained %
Genotype (G)	63	2882.6	45.8***	6.80	82.5
Environment (E)	5	31884.6	6376.9***	75.7	75.7
GE	315	7363.8	23.4***	17.5	100.0
PC1	67	2954.9	44.1***	40.1	40.1
PC2	65	2137.7	32.9***	29.0	69.2
PC3	63	1070.9	16.9***	14.5	83.7
PC4	61	795.8	13.0***	10.8	94.5
Residuals	768	3837.9	4.99		

*** highly significant at 0.001 probability level, Df = degree freedom. SS = sum of squares. MS = mean squares

Visualization of the mega-environments and environments classification

The GGE biplot polygon of which-won-where (Fig. 2), taking into consideration the genotype main effect and the G×E interaction, was formed by the winning genotypes (Z33, Z32, LR4, VR4, VR1, LR5, LR8 and VR7) connected each other with straight lines. The specific adaptation and the mega-environment differentiation can be graphically given to show which genotypes performed best in which environment (35-37).

The biplot was divided into many sectors, of which three included both environments and genotypes (Fig. 2). The first one gathered E1 (MCH18), E4 (MCH20) and E5 (SAD20), representing the first mega-environment with Z32 advanced line as the most productive and includes Z17, Z20 and Z23 lines which represent a large adaptation. The second mega-environment grouped E2 (SAD18) and E3 (LDY18) with Z33 advanced line as the most productive and five advanced lines of G03, Z11, Z27, Z30, Z31 and Z33; and two improved varieties of VR6 and VR9 having a large adaptation. While the third sector, including the E6 (LDY20) mega-environment, included 13 genotypes with VR4 variety and LR4 landraces as the winning genotypes in it (Fig. 2).

The environments can be classified on the bases of their discriminating ability and suitability of representation. The environment's discriminating ability was visualized by a remarkable length of the environment vectors within the concentric circles (Fig. 3). Results revealed that E1 (MCH18), E4 (MCH20), E2 (SAD18) and E6 (LDY20) were the most discriminating between genotypes. Average

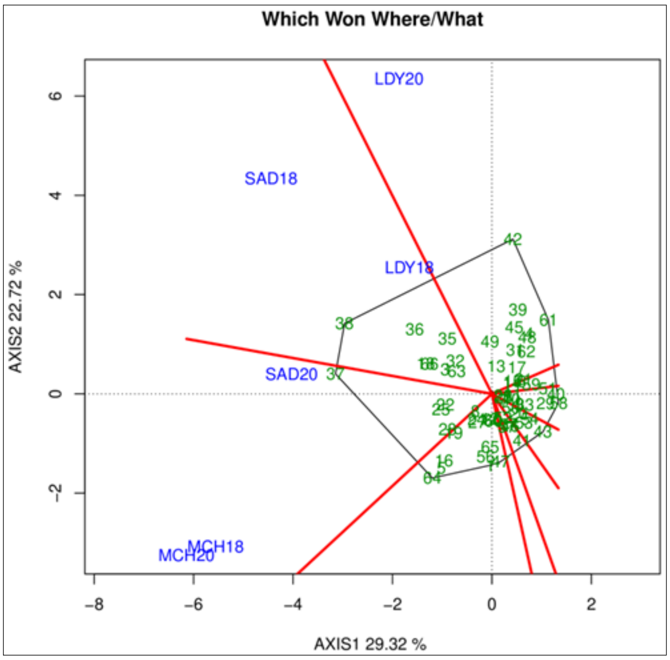

Fig. 2. GGE biplot identification of winning genotypes and their related mega-environments. Where MCH18 = E1, SAD18 = E2, LDY18 = E3, MCH20 = E4, SAD20 = E5 and LDY20 = E6; Each number correspond to a genotype in Table 1.

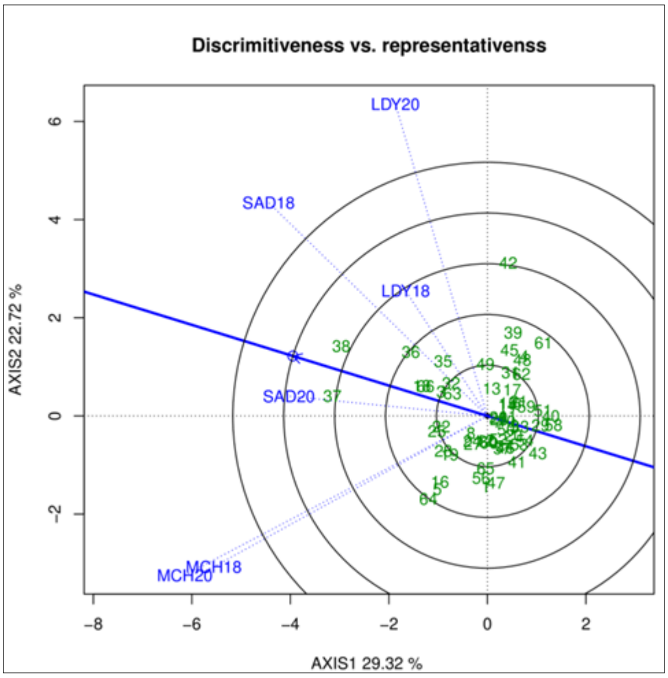

Fig. 3. GGE biplot of discriminating ability vs representativeness of testing environments. Where MCH18 = E1, SAD18 = E2, LDY18 = E3, MCH20 = E4, SAD20 = E5 and LDY20 = E6; Each number correspond to a genotype in Table 1.

Tester Coordinate (ATC) is the line passing through the average environment and the biplot origin. An environment showing a smaller angle with the ATC is more representative than others tested environments (38). Thus, E5 (SAD20) was the most representative, followed by E3 (LDY18) and E2 (SAD18). In addition, angles formed between E1 (MCH18) and E4 (MCH20); between E2 (SAD18) and E3 (LDY18); and between E3 (LDY18) and E6 (LDY20) are smaller, suggesting a positive correlation as reported by (39). Whereas the angles formed between vectors of E6 (LDY20) and E1 (MCH18) and between E6 (LDY20) and E4 (MCH20) was obtuse, revealing a negative correlation (Fig. 3).

Otherwise, E5 (SAD20) and E2 (SAD18) were closer to the concentric center that could be considered ideal environments for selecting performed genotypes (Fig. 4).

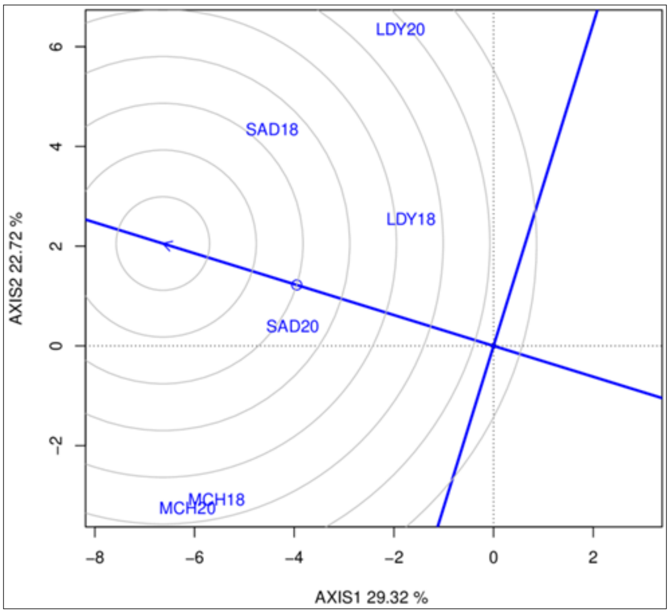

Fig. 4. GGE biplot based on environment focused for comparing environments with ideal environment. Where MCH18 = E1, SAD18 = E2, LDY18 = E3, MCH20 = E4, SAD20 = E5 and LDY20 = E6.

Hence, it has been concluded that the environment characterized by both discriminating ability and representativeness was E2 (SAD18) (Fig. 3), otherwise, this environment was identified as the most ideal (Fig. 4).

Yield and yield stability

According to Fig. 5, 11 advanced lines (Z33, Z32, Z31, Z30, Z27, G03, Z17, Z20, Z14, Z23, Z13 and Z03) and VR9 variety formed a smaller length at the time of the projection onto the average tester coordinate (ATC) line. These genotypes could be considered the most stable. Moreover, Z33 and Z32 advanced lines were closer to the center of concentric circles expressing the higher mean yield. These advanced lines are interesting for developing novel varieties and they could be considered ideal genotypes (40).

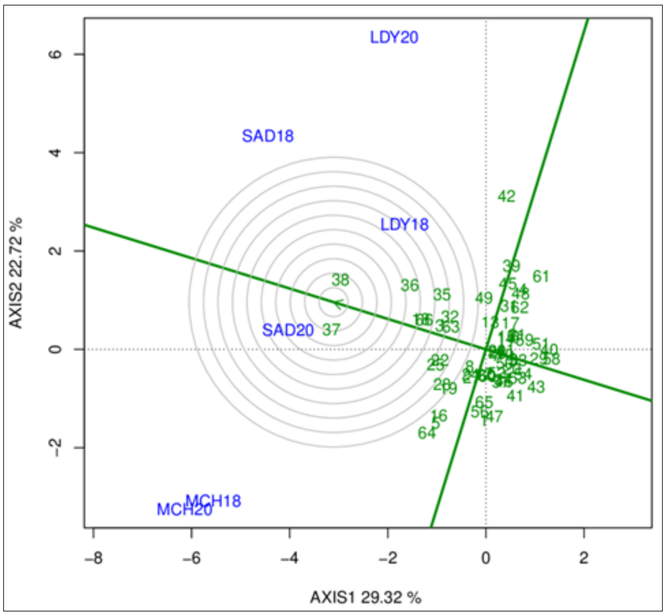

Fig. 5. GGE biplot of ideal genotype and comparison of the genotypes with the ideal genotype. Where MCH18 = E1, SAD18 = E2, LDY18 = E3, MCH20 = E4, SAD20 = E5 and LDY20 = E6; Each number correspond to a genotype in Table 1.

To confirm the selection of these stable and high-yielding genotypes with wider adaptability over environments, the stability parameters given in Supplementary Table can allow an important identification.

The lower values of the deviations from linear regression (*S2di*) were recorded for 14 advanced lines, 5 landraces and 2 varieties (VR1, VR2). As well, *S2di* values tend to be zero for Z27, Z03 and Z19 advanced lines revealing their yield stability which agreed with their high yielding (Supplementary Table).

Whereas small *Pi* values were recorded for Z32, Z33, Z13, Z17 and Z31 advanced lines indicating a less distance between these genotypes and the genotype with maximum performance in all environments. These genotypes are stable in accordance with an earlier study (41). Based on regression coefficient (*bi*), twelve advanced lines, 5 landraces and 3 varieties showed a specific adaptation to favorable environments (from *bi* > 1). Eight advanced lines of them (Z33, Z32, Z31, Z13, Z17, Z30, Z27 and G03) showed high yielding and were stable, according to Fig. 5. While, eighteen advanced lines, 8 landraces and 2 varieties showed a specific adaptation to unfavorable environments (0<*bi* <1). Four advanced lines of them (G05, Z20, Z11, Z22) showed high yielding (Supplementary Table). Based on the positive regression coefficient (*PJ)*, 13 advanced lines, 5 landraces and 3 varieties are stables. High regression coefficient (*PJ)* was recorded for 9 advanced lines (Z23, G03, Z32, Z17, Z33, Z30, Z27, Z13 and Z31), considering the performance and the stability in favorable environments supporting *Pi* and *bi* results. The coefficients of determination (R^2) values ranged from 0.33 to 0.98, explaining various genotype responses across tested environments. Higher (R^2) values were recorded for Z27, Z31, Z30, Z03, Z33, Z13 and G02 advanced lines, showing their high seed yield and their yield stability in tested environments that support the predictions of previous parameters (Supplementary Table 1).

Considering site and year as predictable and unpredictable components; seventeen genotypes were considered stable according to the stability concept of *Si1* of which five advanced lines (Z32, Z33, Z13, Z17 and Z31) were the most performed as revealed by previous parameters (Supplementary Table). As well as for *Si2* stability concept that revealed the high stability of Z32 and Z33 in addition to their high yield potential. Thus, considering previous parameters, genotypes Z33 and Z32 might be considered as the most performed and stable genotypes in testing environments.

The stable genotypes showing a large adaptation and high yielding were provided chiefly from the advanced lines, which means that our proposed advanced genotypes compared to the Moroccan varieties and landraces can be an efficient source for developing novel varieties.

Genotypes distribution

Cluster analysis grouped genotypes into three clusters with 90% similarity (Fig. 6). The first cluster (I) grouped 23 genotypes, the second grouped 34 genotypes and the third one (III) grouped 7 genotypes. Genotypes in cluster I was characterized by higher yield (855.3 kg/ha) and higher seed size (34.5 gm), compared to genotype characteristics in cluster II with 806.1 kg/ha and 34.2 gm respectively (Table 6).

While genotypes (6 advanced lines and 1 variety) in cluster III were characterized by earliness and showed the highest mean yield (1155.5 kg/ha) and the heaviest seed weight (35.5 gm) (Table 6). Among genotypes of this cluster, 2 advanced lines Z32 and Z33, formed a sub-cluster. These genotypes were previously considered the most stable with high yield and might be considered the ideal genotypes for developing novel performed varieties.

Genotypes classification based on yield performance

According to Fig. 7, all genotypes have the highest mean grain yield under E2 and E1; and the lowest under E5; this result may be associated with favorable climatic characteristics of E1 and E2 and unfavorable climatic characteristics of E5 as previously demonstrated.

Generally, in our study, the advanced lines showed the highest mean yield under all environments except in 3 environments, where mean varieties in E1 (923.4 kg/ha), E3 (592.5 kg/ha) and E6 (588.8 kg/ha) were nearly the highest (Fig. 7).

In line with the mean of each environment, several genotypes have exceeded these means. Based on Fig. 6 and Supplementary Table and considering each type of genotype, 16 and 14 advanced lines were highest than the E2 mean (1994.8 kg/ha) and E1 mean (855.3 kg/ha) respectively. Seven advanced genotypes of them (Z33, Z32, Z13, Z17, Z30, Z27 and G03) under these favorable environments were previously considered the most performing genotypes in yield and yield stability. E3 and E4 means have been overtaken by 13 and 20 advanced lines; and (Z33, Z32, Z31 and G03) and (Z33, Z32, Z31, Z13, Z17 and G03) were the most performing genotypes in it respectively. As well as Z33, Z32, Z31, Z30 and Z13 from the 16 advanced genotypes, which exceeded from E6 mean (558.1 kg/ha), was one of the same stable genotypes as previously mentioned. Even though E5 was an unfavorable environment, 25 advanced lines were superior from the environment mean (431.9 kg/ha) and Z22, Z33, Z32, Z31, Z30, Z27and G03 were the most performed of them.

From the environment mean grain yield, the highest landraces genotype of each environment was recorded by LR8, LR10, PA1 and PA6 in E1; by LR2, LR4, LR6, PA1 and PA3 in E2; by LR1, LR2, LR3, LR7, LR9 and LR10 in E3; by LR3, LR7, LR8, PA3 and PA7 in E4; and by LR1, LR4, LR6, LR9, LR10 and PA10 in E6. However, 9 landraces were performed from the mean landraces grain yield under E5 (Supplementary Table) of which LR1 was the highest one (Fig. 7). Among all tested landraces, 5 genotypes (PA6, LR4, LR10, LR6 and PA1) were founded performed in several environments due to their high yielding and can be proposed as a genetic source for Moroccan gene bank. There were no landraces above the environment mean yield in E5 (Fig. 7).

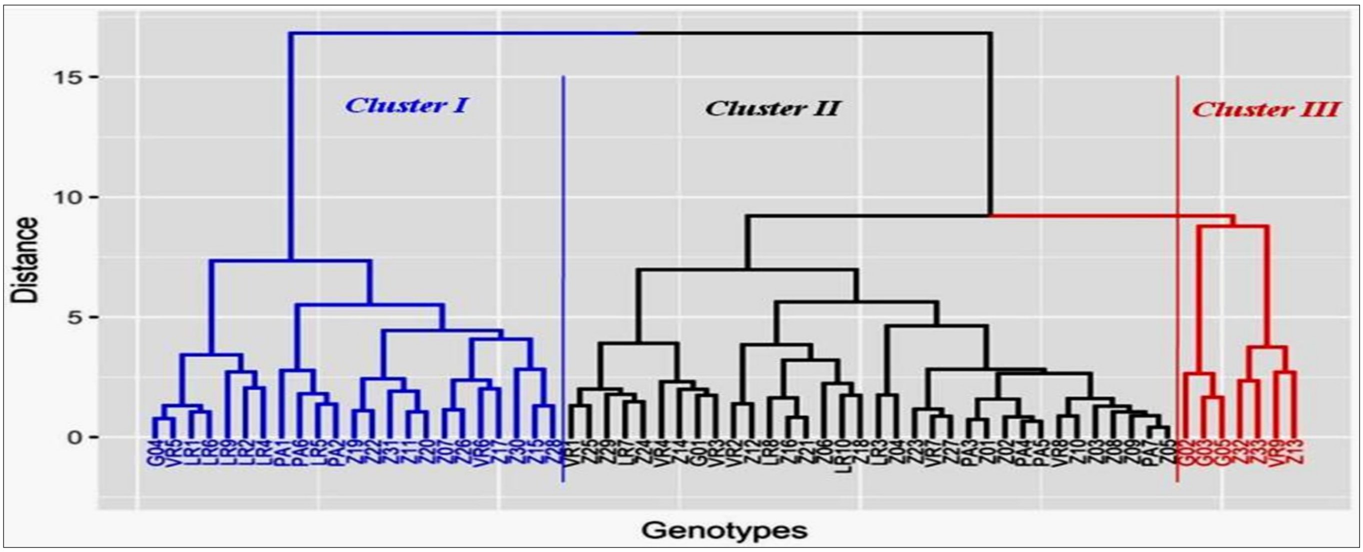

Fig. 6. Dendrogram showing the distance among 64 lentil genotypes.

Table 6. Summary of cluster analysis showed the 64 lentil genotypes.

		Genotypes type	Traits Mean				
			Earliness	Green Seed	Seed Maturity	Yield (kg/ ha)	Thousand seed weight (gm)
Cluster I	23 genotypes	12 Advanced lines	91.2	117.9	148.0	904.3	33.8
		9 Landraces	91.3	127.0	147.9	787.8	35.4
		2 Varieties	92.0	127.5	148.0	884.0	34.6
		Mean	*91.3*	*122.7*	*148.0*	*855.3*	*34.5*
Cluster II	34 genotypes	20 Advanced lines	94.6	130.9	151.9	808.5	34.0
		8 Landraces	94.9	130.9	151.8	791.9	33.0
		6 Varieties	94.3	130.5	151.5	817.8	36.4
		Mean	*94.6*	*130.8*	*151.8*	*806.1*	*34.2*
Cluster III	7 genotypes	6 Advanced lines	94.0	130.0	151.0	1078.0	31.0
		0 Landraces	-	-	-	-	-
		1 Varieties	90.3	131.0	151.8	1155.5	40.0
		Mean	*90.3*	*131.0*	*151.8*	*1155.5*	*40.0*

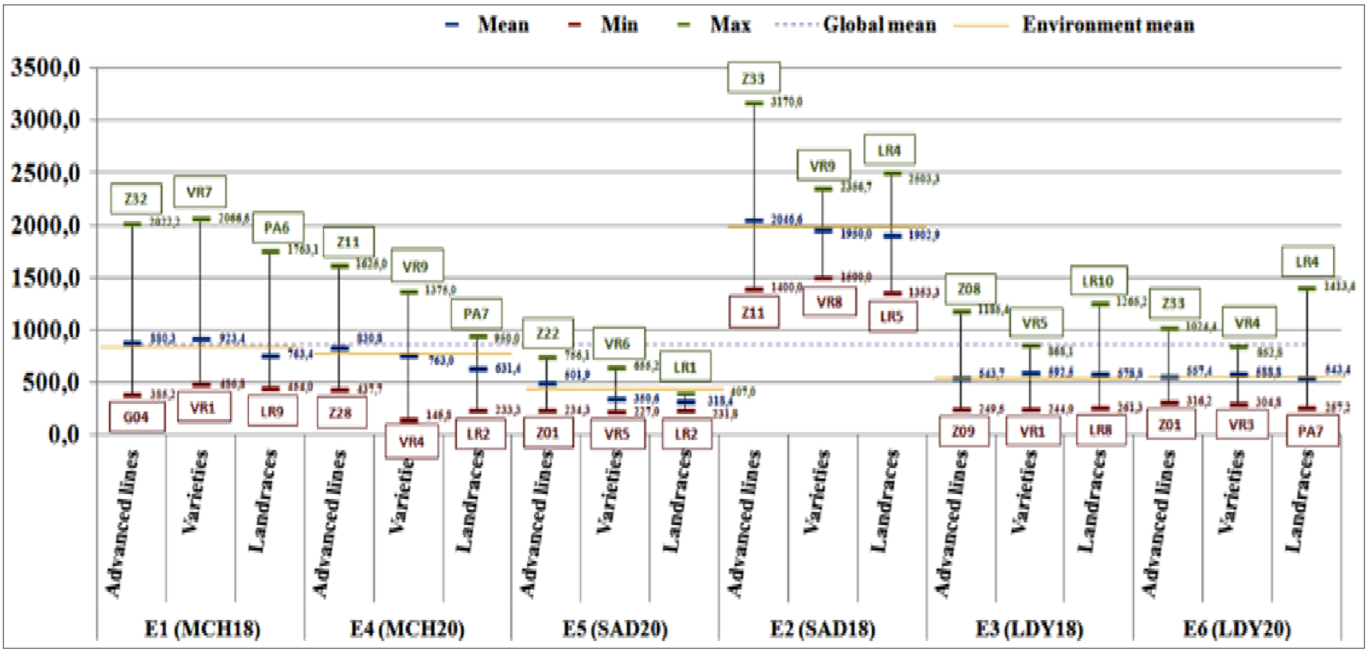

Fig. 7. Mean yield identification of advanced lines, landraces and varieties genotypes under the tested environments.

Of the 9 studied varieties, 5 varieties (VR9, VR5, VR3, VR7 and VR8) have exceeded the favorable mean environments (E1 and E2). Otherwise, two varieties (VR6 and VR9) showed a specific adaptation to the mean of the unfavorable environment E5, of which VR6 (655.2 kg/ha) recorded the maximum mean yield (Fig. 7). VR2, VR3, VR4, VR5 and VR9; and VR6, VR7, VR8 and VR9 have a superior mean yield than respectively E3 (191.0 mm, 14.1 °C) and E4 (232.4 mm, 15.3 °C) mean yield (Table 1) (Fig. 7). Under E6 (382.8 mm, 17.4 °C) (Table 1) the mean yield of 4 varieties (VR2, VR4, VR6 and VR9) was recorded to be higher than the environment mean yield, of which VR4 was the maximum mean yield (Fig. 7).

Nevertheless, VR9 showed a high mean yield under all the environments except in E1 and was considered the most stable variety in the previous analysis and can be one of the varieties recommended under favorable and unfavorable environmental conditions; VR3 can be recommended for the favorable environment and VR6 for the unfavorable. However, VR1 showed the minimum mean yield under E1 and E3 (Fig. 7).

Conclusion

Our results strengthen that the GGE biplot and AMMI analysis were powerful tools to identify Z32 and Z33 advanced lentil lines as high yielding and stable under tested environments. They were identified as performed genotypes to develop novel resilient varieties. Environments of E2 and E3; E5, E1 and E4; and E6 have been selected respectively as mega-environments. Of which E2 (SAD18) environment might be a discriminate and representative environment. However, 5 advanced lentil lines (Z33, Z32, Z31, Z13 and G03) were performed in almost environments. Otherwise, 5 landraces (PA6, LR4, LR10, LR6 and PA1) showed high yielding potential. These local germplasm may be used as sources of favorable traits in the breeding program to develop new varieties of lentils and can be served as a genetic resource to improve the Moroccan gene bank of lentil genotypes. Among the 9 studied varieties, VR3 can be recommended for the favorable environmental conditions and VR6 for the unfavorable. Moreover, VR9 showed high mean yield stability under almost environments and was recommended for favorable and unfavorable environmental conditions. The accuracy of G×E estimates could be improved using biotechnologies tools to identify regions of the genome that are responsible for G×E.

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Authors contributions

Author AB collected the primary data and drafted the manuscript. FG performed the statistical analysis. MT and AS reviewed the manuscript. NB reviewed the manuscript and supervised the findings of this work. All authors read and approved the final manuscript

Compliance with ethical standards

Conflict of interest: The authors declare that this research is conducted with no conflict of interest.

Ethical issues: None.

Supplementary data

Supplementary Table 1. Detailed list of 64 studied genotypes and their mean seed yield and yield stability parameters.

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