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RESEARCH ARTICLE

Targeting resilient lentil genotypes with an adding value of nutritional quality by using AMMI and GGE biplots analysis

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Abstract

The current study aims to assess the impact of different genotypes, environmental conditions, and their interactions (G×E) on lentil yield and nutritive traits in various agro-ecological locations across Morocco. To achieve this, two analysis methods, Analysis of Main Additive Effects and Multiplicative Interaction (AMMI), and Genotype and Genotype by Environment (GGE) were used. The study involved evaluating sixty-four lentil genotypes in six diverse environments during the 2017–2018 and 2019–2020 seasons. Results from the analysis of variance revealed that environmental variation significantly influenced grain yield (75.7%), zinc (48.4%), and magnesium (73.3%). In contrast, genotype by environment interaction (G×E) played a more substantial role in determining protein (45.7%), iron (53.2%), and manganese (49.6%) content. The first two components explained 69.2%, 78.3%, 90.5%, 79.3%, 71.4%, and 74.3% of the variation in grain yield, protein content, iron, zinc, manganese, and magnesium, respectively. The GGE biplot analysis identified specific environments (E3 and E5) as representative and discriminative for yield, zinc, and manganese. Similarly, E3 and E4 were discriminative for iron and protein and magnesium, respectively. Seventeen lentil genotypes exhibited high performance, combining yield and nutritional quality. Notably, genotypes LN34 and VR28 performed well in the Marchouch 2019-2020 environment, while genotype LN54 excelled in the Douyet and Sidi el Aydi environments during 2019-2020. Furthermore, three advanced lines (LN34, LN58 and LN64) expressed stability in yield and most nutrient traits, outperforming released lentil varieties. These promising lines hold potential for developing novel, resilient lentil varieties with both high yield and nutritive quality.

Keywords

Yield performance; stability; nutritive quality; lentil; Morocco

Introduction

Lentil (*Lens culinaris* Medik. subsp. *culinaris*), originated from the near East and Central Asia, is one of the earliest domesticated crops in the world (1). Nowadays, it is grown worldwide mainly in Canada, India, Australia, Turkey, and Ethiopia (2). Morocco is the second-largest producer of lentil in Africa after Ethiopia, with an annual average production of 37,095 tons and an area of 40,207 ha (3). Lentil crop is the third rainfed food legumes crop produced in Morocco, after faba bean and chickpea (4).

Otherwise, lentil is cultivated in cereal-based systems and contribute to the environmental sustainability thanks to its ability to fix atmospheric nitrogen through its symbiotic association with *Rhizobium leguminosarum* (5). In addition, the high nutritive value of lentil grains contributes to human diet by providing proteins, essential amino acids, fiber and minerals with healthy benefic particularly for low -income people (6,7). FAOSTAT investigation revealed an increase in hunger worldwide during the last three years (2019–2021) (8). Indeed, 700 million people worldwide are undernourished, with 36.6% from Africa, of which 0.8% are from Morocco, representing 2.1 million people. Additionally, micronutrient malnutrition affects more than 2 billion people worldwide, with at least half of them in poor countries (9). Proteins and micronutrients are the most common dietary deficiencies that negatively impact health, social, and economic well-being. Thus, increasing lentil grains consumption would provide consumers with proteins and essential nutrients, mainly iron and zinc. Consequently, this might ensure the food security with beneficial health impact.

Otherwise, the lentil crop is generally exposed to several environmental constraints, such as drought and heat, which significantly decrease the yield potential (10). Therefore, many researchers are interested in understanding the impact of the interaction between the environment and genotype on yield and nutritional quality. Previous studies have reported high effects of genotype by environment interaction on yield, protein and minerals content in lentils (11), cowpea (12), wheat (13, 14), and maize (15). The Analysis of Main Additive Effects and Multiplicative Interaction (AMMI) method, along with the Genotype and Genotype by Environment Interaction (GGE) approach, has been effectively applied to analyze data from multi-location experiments (16). These methods estimate Genotype and Genotype by Environment effects, enabling the efficient identification of mega-environments and appropriate attribution of genotypes to specific or mega-environments. The partition of Genotype by Environment interaction (G×E) remains an accurate indicator to identify genotypes with broad or specific adaptation (17–20).

In this context, the current study aims to evaluate the interaction of sixty-four lentil genotypes in six contrasting environments concerning seed yield, proteins, and mineral components using AMMI analysis and GGE biplot to identify potential genotypes to be used as candidates for releasing resilient varieties combining high productivity and high nutritive value.

Materials and Methods

Plan material

The genetic material used in this study consisted of sixty-four lentil genotypes, which included nine Moroccan released varieties (VR), seventeen landraces (LR) originating from the main lentil cropped regions in Morocco, and thirty-eight advanced breeding lines (LN) (Table S1).

Field experimentation

The study was conducted in three climatically contrasting INRA's experimental locations, covering the main lentil growing areas in Morocco (i) Marchouch (MCH) located in Zaer region (33°60'N, 6°71'W); (ii) Sidi El Aydi (SAD) located in the Chaouia-Ouardigha region (33°10'N, 7°64'W); and (iii) Douyet (DYT) located in the Saïs region (34°02'N, 5°07'W). These experiment were carried out during two growing seasons, 2017–2018 and 2019–2020. A total of six environments were defined as year-location combinations (Table 1).

Trials were set up in December, and the sowing rate was 30kg/ha. Sowing was done manually on a prepared seedbed. Soils were fertilized at sowing with 28 kg/ha of nitrogen (N), 56 kg/ha of phosphorus (P), and 28 kg/ha of potassium (K). Each experiment was laid out in a randomized split-plot design with three replicates. Individual plots were composed of two rows, each 2.5 m long, spaced 0.3 m apart. The area of each plot was 1.5 m^2, and the inter-plot spacing was 0.9 m. Climatic parameters varied among the growing years and between locations (Table 1).

Yield and nutritional quality traits assessment

At seed maturity, plots were harvested by hand, and the total seed yield ($kgha^{-1}$) was measured at each location. Seeds from each genotype were then analyzed for crude protein and mineral concentration determinations. Nitrogen concentration in grains samples was determined using Kjeldahl procedure (21). Seed samples from each genotype was weighted and digested with sulfuric acid for one hour with three replicates. The solution was then alkalized by adding sodium hydroxide (NaOH), and distillated with chloric acid. Protein concentration in grains was estimated by multiplying nitrogen values by the 6.25 coefficient. Mineral concentrations were estimated using inductively coupled plasma-optical emission spectroscopy (ICP-OES) (iCAP-7000 Duo, Thermo Fisher Scientific).

Table 1. Temperature and rainfall variation in the six studied environments.

Environment	Experimental sites	Soil type	Growing season	Rainfall* (mm)	Temperature** (°C)		
					Mean	Min	Max
E1	**Douyet**	Clay and limestone	***2017–2018***	191.0	14.5	4.00	28.0
E2			***2019–2020***	382.8	17.7	6.00	35.0
E3	**Marchouch**	Vertisol	***2017–2018***	464.2	12.0	6.75	18.0
E4			***2019–2020***	232.4	14.4	8.14	21.8
E5	**Sidi El Aydi**	Clay loam	***2017–2018***	313.8	13.7	2.00	31.0
E6			***2019–2020***	173.8	17.4	6.00	39.0

*Rainfall during the growing season, **Average temperature during the growing seasons

Statistical analysis

Combined analysis of variance (ANOVA) of grain yield, grain protein, and mineral data from the six environments was carried out using the Statistical Analysis System (SAS version 9.1). Least significant differences were used to compare means ($P \leq 0.05$). Analysis of Main Additive Effects and Multiplicative Interaction model (AMMI), and the Genotype plus Genotype by Environment (GGE) biplot methodology were employed to assess G×E interaction. These approaches incorporate several factors such as environment and genotype, which have multiplicative effects (22–26). They allow for visual assessment of significant issues related to genotype evaluation and test-environment evaluation (16).(16).

The AMMI model is as follows (Eqn. 1):

$$Yij = \mu + gi + ej + \sum_{n=1}^{N} \lambda n\, \gamma in\, \sigma jn + \rho ij$$

(Eqn. 1)

Where:

Yij: Mean yield of the ith genotype in the jth environment;

μ : Grand mean;

gi : Genotype deviations from the grand mean;

ej : Environment deviations from the grand mean;

n : Number of principal components retained in the model;

λn: Eigenvalue of the PC analysis axis n;

γin: Genotype eigenvectors for axis n;

σjn: Environment eigenvectors for axis n;

ρij : Error.

Stability parameters such as the deviations from linear regression *(S^2di)* (27) and the regression coefficient *(bi),* were analyzed to identify genotype stability for yield and nutritional quality traits. Hierarchical analysis based on Euclidean distance (Cluster) was performed to group genotypes with similar traits using the ward method in R software.

Results

Variance analysis

The analysis of variance for AMMI of yield and nutritional traits of sixty-four lentil genotypes over six environments revealed highly significant effects ($p<0.001$) for environment (E), genotype (G), and the G×E interaction (Table 2). The environment effect was highly significant for yield, zinc, and magnesium, explaining 75.4%, 48.1% and 73.0% of variations, respectively (Table 2). The mean values of grain yield (880.0kgha^{-1}), zinc (3.90mg/100g), and magnesium (112.5mg/100g) varied from 430.0 (E6) to 2100.0kgha^{-1} (E5), from 3.46 (E3) to 4.92mg/100g (E1), and from 94.6 (E6) to 125.0mg/100g (E1), respectively. The highest grain yield and high minerals concentrations were recorded at E5 (313.8 mm and 13.7°C), and E1 (382.8mm and 14.5°C), respectively, qualified as favorable environments (Table 1). Meanwhile, the lowest yield and magnesium values were obtained in E6 (173.8mm and 17.4°C), where drought occurred from February (1mm) to March (16mm) coinciding with the flowering period. This variation in yield and quality parameters could be related to the environmental climatic conditions, particularly rainfall and temperature. Genotype by environment interaction effects were significant for crude protein, iron, and manganese representing 45.3%, 52.5%, and 49.6% of variation, respectively (Table 2). Mean protein content

Table 1. Temperature and rainfall variation in the six studied environments.

		Yield			Protein			Iron			Zinc			Manganese			Magnesium		
Source of variation	**DF**	**MS**	**TSSD**	**TSSDC**	**MS**	**TSSD**	**TSSDC**	**MS**	**TSSD**	**TSSDC**	**MS**	**TSSD**	**TSSDC**	**MS**	**TSSD**	**TSSDC**	**MS**	**TSSD**	**TSSDC**
Environment (E)	5	6376,9***	75,7	75,7	159,5***	34,3	34,3	86,4***	26,4	26,4	34,6***	48,4	48,4	4,48***	19,0	19,0	17935,8***	73,3	73,3
Genotype (G)	63	45,8***	6,80	82,5	7,41***	20,0	54,3	5,29***	20,4	46,8	1,19***	21,0	69,4	0,59***	31,4	50,4	150,1***	7,73	81,1
G×E	315	23,4***	17,5	100,0	3,38***	45,7	100,0	2,76***	53,2	100,0	0,35***	30,6	100,0	0,19***	49,6	100,0	73,5***	18,9	100,0
PC1	67	44,1***	40,1	40,1	8,68***	54,6	54,6	10,5***	80,7	80,7	0,93***	57,3	57,3	0,49***	56,3	56,3	146,5***	42,4	42,4
PC2	65	32,9***	29,0	69,2	3,87***	23,6	78,3	1,32***	9,88	90,5	0,37***	22,0	79,3	0,14***	15,1	71,4	113,3***	31,9	74,3
Residuals	384	4,99			0,34			0,21			0,09			0,01			12,33		

MS: Mean Square, **TSSD:** Total Sum of Square Deviation (%) and **TSSDC:** Total Sum of Square Deviation Cumulated (%)

Table 3. Mean performance and descriptive statistics of sixty-four lentil genotypes evaluated under the six environments.

		Yield (kgha^{-1})	Protein (%)	Iron (mg/100g)	Zinc (mg/100g)	Magnesium (mg/100g)	Manganese (mg/100g)
Environments							
E1	*Mean*±Sd.E	560.0±0.02	24.3±0.11	7.88±0.20	4.92±0.08	125.0±0.52	2.08±0.04
	Range	210.0–1140.0	22.1–27.0	4.37–12.2	3.00–7.00	106.4–134.1	1.10–2.80
E2	*Mean*±Sd.E	570.0±0.21	23.5±0.16	5.96±0.05	3.71±0.03	104.30±0.66	1.95±0.02
	Range	260.0–2020.0	20.1–27.2	4.50–7.00	3.10–5.50	93.3–134.3	1.40–2.40
E3	*Mean*±Sd.E	860.0±0.036	22.67±0.11	6.53±0.08	3.46±0.03	116.5±0.81	1.53±0.03
	Range	360.0–2100.0	20.4–25.8	4.40–8.40	2.80–4.60	90.6–134.6	0.90–2.20
E4	*Mean*±Sd.E	770.0±0.03	23.2±0.13	5.74±0.05	3.80±0.05	110.3±0.72	1.97±0.02
	Range	150.0–1630.0	19.0–28.0	4.30–6.80	2.90–5.60	90.1–133.4	1.20–2.60
E5	*Mean*±Sd.E	2050.0±0.04	21.0±0.09	5.85±0.16	3.85±0.05	124.2±0.59	1.93±0.04
	Range	830.0–3370.0	19.0–23.1	3.80–10.5	2.90–5.40	105.1–135.0	0.80–2.80
E6	*Mean*±Sd.E	430.0±0.01	23.2±0.16	5.87±0.04	3.63±0.03	94.6±0.24	1.87±0.03
	Range	200.0–790.0	19.0–28.0	4.50–6.80	2.90–4.50	90.1–101.4	1.00–2.50
	Mean	880.0±1.63	23.0±0.29	6.31±0.16	3.90±1.97	112.48±11.0	1.89±0.01
	Range	430.0–2050.0	21.0–24.3	5.74–7.88	3.46–4.92	94.6–125.0	1.53–2.08
	LSD	0.31***	0.13***	0.10***	0.07***	0.82***	0.02***
	CV %	72,3	7,79	23,7	18,3	11,4	21,2

Sd.E: Standard Error

(23.0% DM), iron concentration (6.31mg/100g), and manganese concentration (1.89mg/100g) varied from 21.0 (E5) to 24.3% DM (E1); from 5.74 (E4) to 7.88mg/100g (E1), and from 1.53 (E3) to 2.08mg/100g (E1), respectively (Table 3). The lowest iron value was recorded in E4, characterized by drought during pod filling period (April 20.6 mm). Protein and manganese showed low levels in E5 and E3, respectively, considered as favorable environments.

The AMMI model showed that the first two PC explained 69.1% to 90.5% of the total variation in the studied traits (Table 2), implying a better prediction of GE interaction effect (28–30).

Identification of the mega-environments and environments

The partitioning of G×E interaction through GGE biplot analysis showed that the first and second principal components (PC1 and PC2) explained a total variation of 50.1%, 71.25%, 64.52%, 78.33%, 65.8%, and 65.5% for yield, protein, iron, zinc, manganese, and magnesium, respectively (Fig. A-F). The 'Which-won-where' biplot allowed the grouping of performed genotypes into several mega-environments (Fig. 1). The yield biplot grouped the six environments into two mega-environments (E4, E3, and E6) and (E5, E2, and E1) (Fig 1.A). The protein and manganese biplots grouped the three favorable environments into one mega-environment (E5, E1, and E3)

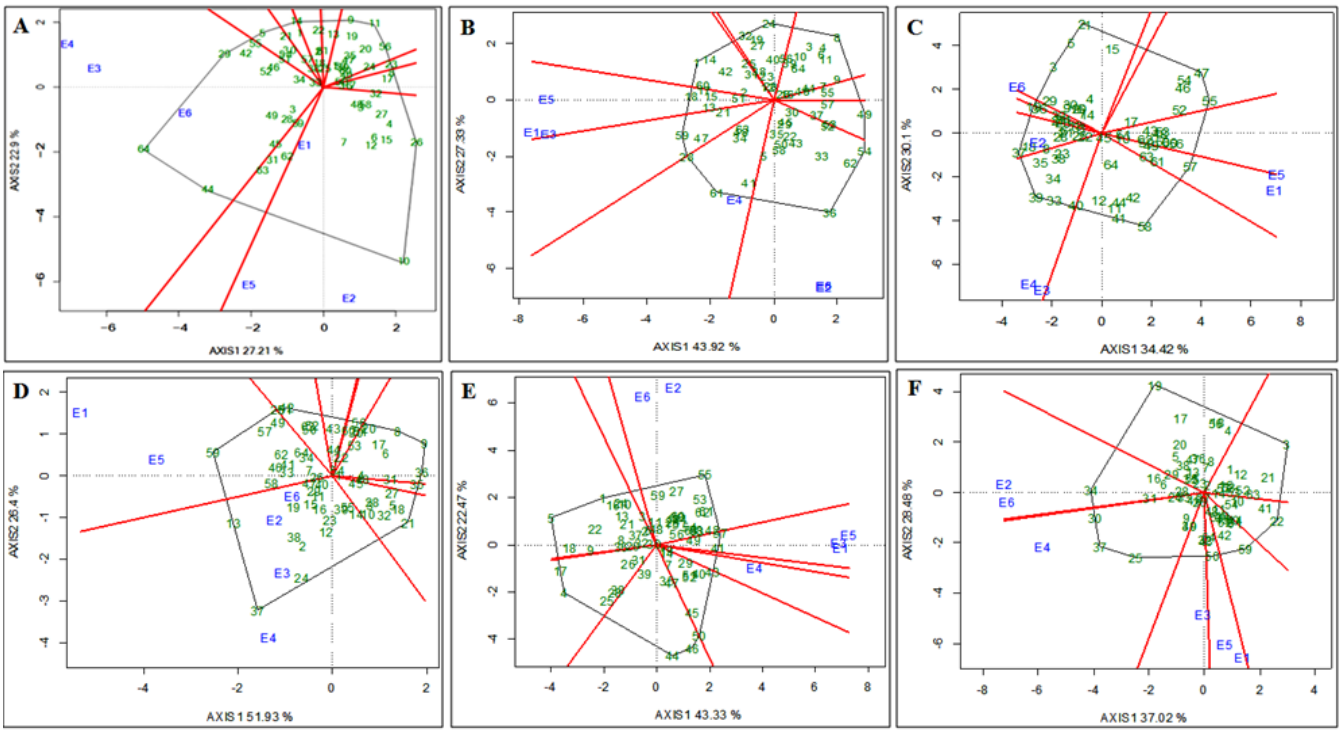

Figure 1. "Which won where" GGE biplot identification of winning genotypes and their related mega-environments for seed lentil (A) Yield, (B) Protein, (C) Iron, (D) Zinc, (E) Manganese and (F) magnesium of 64 genotypes under 6 environments. The ID numbers represents genotypes from Table S1. E1 = (Douyet 2017-2018), E2 = (Douyet 2019–2020), E3 = (Marchouch 2017–2018), E4 = (Marchouch 2019–2020), E5 = (Sidi el Aydi 2017–2018) and E6 = (Sidi el Aydi 2019–2020).

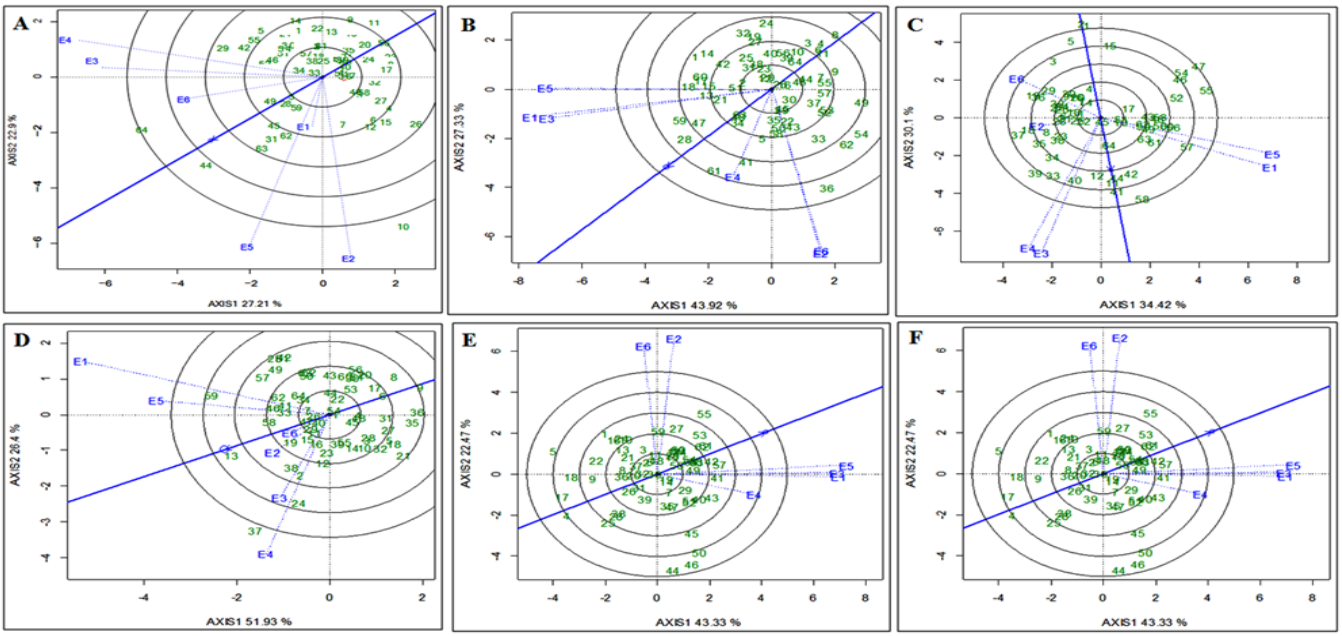

Figure 2. GGE biplot "Descriminitiveness vs. Representativeness" pattern of genotype comparison with ideal genotype showing G + G × E interaction effect of 64 genotypes under 6 environments for seed lentil (A) Yield, (B) Protein, (C) Iron, (D) Zinc, (E) Manganese, and (F) Magnesium. The ID numbers represents genotypes from Table S1. E1 = (Douyet 2017–2018), E2 (Douyet 2019–2020), E3 = (Marchouch 2017–2018), E4 = (Marchouch 2019–2020), E5 = (Sidi el Aydi 2017–2018) and E6 = (Sidi el Aydi 2019–2020).

and the unfavorable environment into two mega-environments (E6 and E2) and (E4) (Fig. 1.B) (Fig. 1.E). The favorable environments (E1 and E5) formed one mega-environment in the iron (Fig. 1.C), zinc (Fig. 1.D), and magnesium (Fig. 1.F) biplots. However, the four remaining environments were partitioned into three mega-environments (E3, E4), (E6), and (E2) for iron, one mega-environment (E6, E2, E3, and E4) for zinc, and into three mega-environments (E6 and E2), (E4), and (E3) for magnesium (Fig. 1).Long environment vectors identified discriminating environment; E4, E2 and E5 for yield (Fig 2.A); E1 and E3 for protein content (Fig 2.B); E3, E4 for iron (Fig 2.C); E1 and E4 for zinc (Fig 2.D); E5 and E3 for manganese (Fig 2.E); and E2 and E6 for magnesium (Fig 2.F). Shorter angles formed between environment vectors and the AEC (average environment coordinate) indicated the representativeness environments, which are suitable for selecting potential genotypes. E3 and E5 were identified for yield, zinc, and manganese content; E4 for protein and magnesium; and E3 for iron.

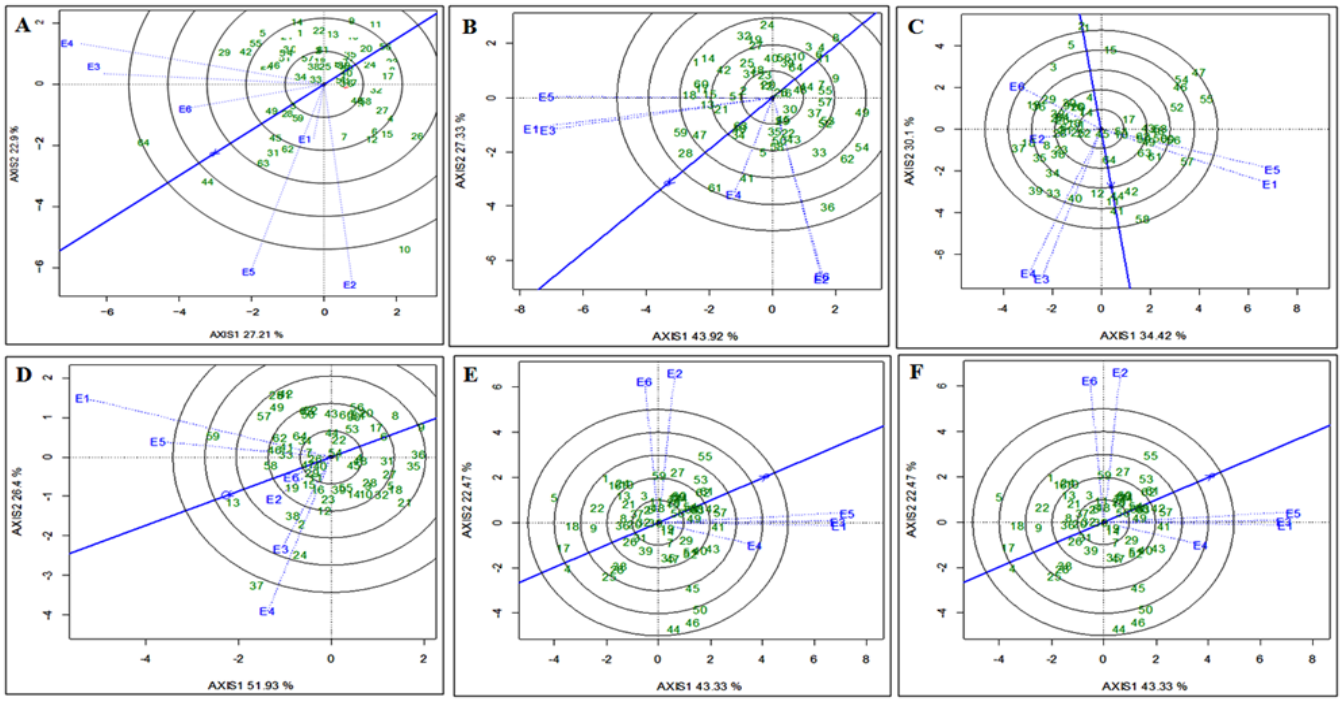

Figure 3. "Mean vs. stability" pattern of GGE biplot illustration interaction effect of 64 genotypes under six environments for seed lentil (A) Yield, (B) Protein, (C) Iron, (D) Zinc, (E) Manganese and (F) Magnesium of 64 genotypes and 6 environments. The ID numbers represents genotypes from Table 1. E1 = (Douyet 2017–2018), E2 (Douyet 2019–2020), E3 = (Marchouch 2017–2018), E4 = (Marchouch 2019–2020), E5 = (Sidi el Aydi 2017–2018) and E6 = (Sidi el Aydi 2019–2020).

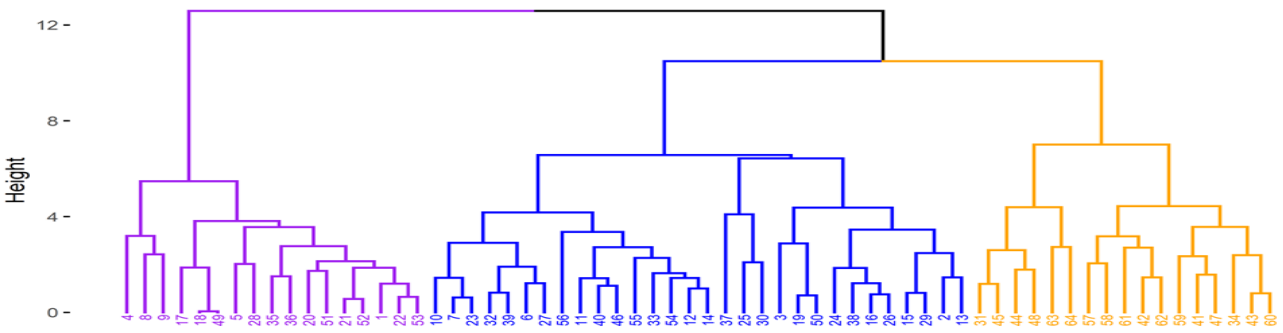

Figure 4. Dendrogram showing hierarchical classification of 64 lentil genotypes based on Ward's method.

Genotype stability

GGE analysis

Fig. 3 showed that 35%, 44%, 48%, 45%, 42% and 39% of genotypes were positioned above the origin of the ranking plot, representing potential for yield, protein, iron, zinc, magnesium, and manganese, respectively. Some of them were assumed as stable based on their small projection on the average environment coordinate (AEC) (31). Greater stability on yield was revealed for seven advanced lines (LN44, LN45, LN49, LN59, LN3, LN34 and LN33) and the released variety (VR28) (Fig. 3.A) under the first mega-environment (E4, E3 and E6) (Fig. 1.A). VR28, LN34, and LN45 performed well in E4, and in (E2 and E6) environments, respectively, with an added value of proteins (Fig. 2.B). A positive correlation between yield and protein (r = 0.390***) was revealed (Table 4). However, eleven stable genotype, including LN58, LN41, LR11, LN44, LN42, LN12 and LN64, showed high iron concentration (Fig. 3C). Particularly, LN64 positioned near the origin of iron GGE biplot, indicates its stability under almost all environments (Fig. 1.C). Additionally, fourteen genotypes representing four advanced lines (LN58, LN46, LN33, and LN11) (Fig. 2.D) and two landraces (LR13, LR19) were stable in zinc content under (E1 and E5) and (E6, E2, E3, and E4) mega-environments, respectively. Positive correlations were revealed between zinc and iron (r = 0.462), zinc and magnesium (r = 0.341***), and zinc and manganese (r = 0.346***) (Table 4). The obtained results revealed the performance and stability of LN58 advanced line for these nutritional traits.

Stability parameters

The regression coefficient (bi) parameter ranged from 0.50 to 1.70 for yield, from 0.21 to 2.10 for protein; from -0.36 to 2.43 for iron; from 0.05 to 2.06 for zinc; from -0.09 to 2.53 for manganese and from 0.18 to 1.50 for magnesium (Table S1).

Based on seed yield, no significant deviation from regression (S^2di=0) was recorded for three genotypes; LN58 (1009.0 kgha^{-1}) showed specific adaptability to the favorable environment (bi>1); while LN34 (870.0kgha^{-1}) and LR10 (922.0kgha^{-1}) were widely adapted to the unfavorable environment (bi<1). The most highly performed genotypes in mean yield among the sixty-four studied genotypes were the advanced lines LN64 (1431.0kgha^{-1}), LN44 (1163.0kgha^{-1}) and LN62 (1160.0kgha^{-1}), which were widely adapted to the favorable environments. While, the variety VR9 (1078.0kgha^{-1}) was stable, having specific adaptability to most environmental conditions (bi=1) (Table S1).

Protein content analysis recorded four genotypes; LR8 (21.4% DM), VR26 (22.8% DM) and LR11 (21.9% DM) exhibiting high mean, low mean performance of regression value (bi<1), and no significant deviation from regression (S^2di =0) indicating high stability and wider adaptability across unfavorable environments. Otherwise, genotype LR16 (22.8% DM) exhibited the same stability but under favorable environments (bi>1).

Genotype LN64 (6.93mg/100g) and LN31 (6.10mg/100g) exhibited the highest iron mean value and

Table 4. Coefficient of correlation among grain yield and nutritional traits.

	Yield	Protein	Iron	Zinc	Manganese	Magnesium
Yield	1					
Protein	0.3901	1				
	<0.001					
Iron	0.2280	0.1238	1			
	<0.001	<0.001				
Zinc	0.3154	0.2337	0.4621	1		
	<0.001	<0.001	<0.001			
Manganese	0.0712	0.0264	0.4686	0.3464	1	
	0.0485	0.4658	<0.001	<0.001		
Magnesium	0.0462	-0.1564	0.2817	0.3409	0.0978	1
	0.2006	<0.001	<0.001	<0.001	0.0067	

indicated wide adaptation for favorable (bi>1) and unfavorable (bi<1) environments, respectively. Zinc mean (4.08 mg/100g) was recorded by the stable advanced line LN64 (adapted to the favorable environment) and the stable variety VR29 (adapted to the most environment conditions), as well as three landraces (LR14, LR16) and (LR7) were well adapted to the unfavorable and favorable environments, respectively. Genotypes LN34 and LN33, having high manganese concentration (2.06mg/100g), were stable and adaptable to unfavorable environments. Among the five stable genotypes in magnesium, one advanced line LN39 (115.68mg/100g) showed the highest mean performance and special adaptation to favorable environments, while the four other genotypes registered lower mean manganese seed concentration but a specific adaptation under the unfavorable environments.

Cluster analysis

Cluster analysis grouped genotypes into three clusters based on yield, proteins iron, zinc, magnesium, and manganese (Fig. 4). Seventeen genotypes were placed in each of cluster I and cluster III, while thirty genotypes were assigned to cluster II (Fig. 4). Genotypes in cluster I were characterized by low and unstable performance in all studied traits. On the other hand, genotypes in cluster II (VR29, LR14, LR16, LR7, LR19, LN46, LN33, LN40, LR11, VR26, and LR7) exhibited stable and high performance for zinc concentration (4.01 mg/100g). Furthermore, the results demonstrated that genotypes in cluster III showed the best performance, particularly in mean yield (985.1 kgha-1), mean proteins (23.5 %DM), mean iron (6.97 mg/100g), mean zinc (3.99 mg/100g), mean magnesium (113.8 mg/100g), and mean manganese (2.05 mg/100g). These findings align with the AMMI-GGE biplots analysis and stability parameters, especially for LN34, LN58, LN64, LN44, LN45, LN42, LN41, and LN48 advanced lines.

Discussion

The highly significant differences recorded for genotype, environment, as well as their interaction effects, indicate that the genotypes used in our study exhibit variable performance from one environment to another, depending on the genotype. Similar observations of significant genotype and genotype-by-environment interaction effects have been reported in the lentil gene pool for yield, grain protein, and micronutrient content (11, 32–36). This wide variation within genotypes has also been reported for numerous other crops, including wheat (37), sorghum (38), pearl millet (39), chickpea (40), and maize (41). Likewise, G×E effects on productivity and nutritional traits is critical for breeders (42,43), they can either select genotypes for a specific environment or extensively adjusted genotypes across several environments (44).

Due to the significant environmental impact in this study, drought stress during the flowering period in Sidi El Aydi (E6) and pod filling in Marchouch (E4) decreased grain production, magnesium, and iron by 51.0%, 15.9% and 7.30%, respectively. These percentages explain the significant impact of climatic constraints on yield and/or on the nutritional quality of lentil germplasm. These findings are consistent with prior research in lentil (29,45–47), durum wheat (48), bean (20), faba bean (49). and cowpea (50).

Some nutritional characteristics (protein, zinc, and manganese) showed low values under Marchouch (E3) and Sidi El Aydi (E5), which were characterized as favorable. This may be related to the influence of G×E effects on these nutritional traits, affecting their uptake by roots, translocation through shoots, and assimilation in grains (51). Additionally the positive correlation between zinc and manganese might have contributed to their simultaneous decrease under the favorable environment E3.

According to Dehghani and Kaya studies (52, 53), grouping environment into a mega-environment is related to the high correlation between them based on the short angle between their vectors (Fig. 2). Several mega-environments were identified for each studied trait. However, over the six studied environments, an overall examination of stability characteristics revealed that no single genotype was ideally stable for all the studied traits. Similarily, results obtained from GGE and AMMI analysis, along with the stability parameters, consistently identified stable genotypes for each trait or group of traits under high-input, low-input, or most environment conditions (54). Advanced lines LN34 and LN58 were selected under unfavorable and favorable environments, respectively, for potential yield, protein content, zinc, iron, and manganese. Based on the yield GGE biplot, LN34 and LN58 were very close to the origin of the plot, indicating high stability under both mega-environments. This suggests that they respond similarly in almost all environmental conditions. Furthermore, genotype LN64 was the most productive one among all the studied genotypes and was stable in iron and zinc under favorable environments. This result aligns with a previous study where LN64 was selected as the most high-performing genotype in terms of productivity (55). Considering the cluster analysis, these selected genotypes were grouped in cluster III in which 27% of the lentil genotypes exhibited the most outstanding performance for all studied traits. This cluster includes the advanced lines and one variety (VR31). The specificity of this variety is that it performs well in almost all the studied traits, which is in line with the criteria of cluster III. This cluster includes the advanced lines and one variety (VR31). The specificity of this variety is that it performs well in almost all the studied traits, which is in line with the criteria of cluster III. Additionally, it is positioned in the sector between the two mega-environments and is close to the GGE biplot origin of yield, confirming its stability and performance under almost all environmental conditions. Moreover, it was highly adapted and stable in iron under unfavorable environments. This variety (named Zaâria) was previously selected based on its stability and adaptability in terms of yield performance under almost all environmental conditions (45). Thus, genotype by environment interactions highlights the stability and adaptability of these proposed genotypes, indicating the usefulness of biplots application in genotype selection (56).

Conclusion

The lentil genotypes investigated in this study exhibited wide variability for yield and nutritional traits, which can be tapped by including them in breeding programs for productivity and nutrient enhancement. These genotypes showed wide adaptation under six environments. Based upon representativeness and discriminativeness, E3 was selected for iron, E4 for iron and magnesium, and E3 and E5 for zinc, manganese, and yield content, which were considered as ideal environments. Stability analysis using GGE-AMMI and stability parameters revealed that three advanced lines (LN34, LN58, and LN64) could be used as genetic resources in lentil breeding programs for developing the mapping populations. Furthermore, these lines might be considered novel and resilient candidates for release. By hybridizing these selected genotypes with indigenous lines, the genetic base can be broadened while simultaneously breeding for high nutrient content. Therefore, it is essential to develop high-yielding nutrient-rich varieties with increased tolerance to heat and drought stress for the sustainable production of lentils.

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Authors' contributions

Author AB collected the primary data and drafted the manuscript. FG performed the statistical analysis. YR contributed to the laboratory work. 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.

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