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GGE BIPLOT BASED ASSESSMENT OF YIELD STABILITY AND ADAPTABILITY IN LENTIL (*LENS CULINARIS* MEDIK.)

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ABSTRACT

The present study evaluated 46 lentil genotypes across three consecutive rabi seasons (2022–2025) to assess yield performance and stability using genotype main effect plus genotype-by-environment interaction (GGE) biplot analysis. The experiment was conducted in an augmented block design with three standard checks under uniform agronomic management. Significant effects of genotype, environment, and their interaction were observed for plant height (PH), number of secondary branches / plant (SBR), number of pods / plant (NPP), total biomass (TB), grain yield / plant (GYP), and chlorophyll content (CHL), indicating substantial genetic variation and differential response across seasons. The first two principal components jointly explained 92.83% of the total G + GE variation. E1 was identified as the most representative and discriminating environment. The "which-won-where" biplot identified P13143 and P13107 as the best performing genotypes in environments E1 and E3, respectively. The average environment coordination (AEC) biplot further identified P13112, P13130, PL97, and P13135 as high-yielding and stable genotypes with broad adaptability. Overall, the study demonstrated the utility of GGE biplot analysis in identifying both widely and specifically adapted lentil genotypes, providing valuable insights for the development of stable, high-yielding cultivars suitable for variable environmental conditions.

***Keywords* :** lentil, GGE biplot, genotype × environment interaction, stability, grain yield.

Introduction

Lentil (*Lens culinaris* Medik.) is one of the most important cool-season pulse crops, valued for its high protein content, ability to fix atmospheric nitrogen, and vital role in sustainable cropping systems. Originally domesticated in the Fertile Crescent alongside wheat and barley, it has now become the world's fifth most important legume, only after common bean, pea, chickpea, and cowpea (Naik *et al*., 2024). Lentil grains are highly nutritious, containing 60–67% carbohydrates, 20–36% protein, and < 4 % fat (Bhatty, 1988). They are also an excellent source of essential minerals like magnesium, zinc, iron, and potassium. Thanks to their high lysine content, lentils, when consumed with cereals, offer a complete amino acid profile beneficial for human health. Furthermore, compared to rice and wheat, lentils have superior mineral and vitamin profile which makes them a popular choice for healthy diets (Johnson *et al*., 2020). Beyond their nutritional importance, lentils contribute significantly to soil fertility and ecosystem sustainability through biological nitrogen fixation and carbon sequestration, thereby enhancing the productivity and sustainability of cereal-based cropping systems.

Globally, lentil cultivation covered approximately 5.5 million hectares in 2022, producing about 6.8 million tonnes with an average productivity of 1218 kg ha^{-1} (Dimech *et al*., 2024). Australia, India, Canada, Nepal, China, Turkey, and the United States are the major contributors. Canada leads the global production, accounting for over 34% of the total (FAOSTAT, 2024). India, meanwhile, holds the largest share in terms of cultivated area and ranks second in overall production. Within India, it is the second most important rabi pulse crop after chickpea, with the Ministry of Agriculture & Farmers Welfare's third advanced estimate for 2023-24 reporting a production of 1.7 million tonnes from 1.9 million hectares (Parihar *et al*., 2025). However, productivity in India remains relatively low and highly variable across regions and years due to its sensitivity to environmental fluctuations, such as temperature, rainfall, and soil fertility variations (Kumar *et al*., 2023).

Developing genotypes with high yield potential and stable performance across diverse environments is the primary objective of any lentil breeding program. However, the presence of genotype × environment interaction complicates this selection process, as it often leads to changes in relative performance of genotypes across environments. Consequently, a thorough understanding and quantification of GEI are essential for identifying genotypes that offer consistent performance with either specific or broad adaptation. Conventional stability analyses, such as regression-based methods or variance components approaches, provide useful information but are often limited in visual interpretation and in capturing both genotype main effects and GEI simultaneously (Abebe *et al*., 2024; Yadav *et al*., 2024). Whereas multivariate statistical methods, such as AMMI and GGE biplot analyses, have emerged as powerful tools to address these limitations by providing a more comprehensive understanding of GEI (Hashim *et al*., 2021; Joshi & Vandemark, 2025).

The genotype main effect plus genotype-by-environment interaction (GGE) biplot method proposed by Yan *et al*. (2000) has emerged as a powerful multivariate tool for analysing multi-environment trial (MET) data. This approach effectively partitions the yield variation into genotype main effects and GEI effects, allowing visual assessment of genotype performance, stability, and mega-environment delineation. It facilitates identification of high-yielding and stable genotypes, as well as environments that discriminate effectively among genotypes. Its application in various crops, including cereals, oilseeds, and pulses, has demonstrated its utility in breeding programs aiming for yield stability and adaptation analysis (Pobkhunthod *et al*., 2022; Greveniotis *et al*., 2023; Kumar *et al*., 2024). However, in lentil, yield stability studies based on GGE biplot analysis is still limited compared to other crops. Considering the crop's expansion into new agro-ecological niches and the increasing need for climate-resilient cultivars, understanding the behaviour of promising genotypes across seasons and environments is essential. Multi-season evaluation provides a robust basis for assessing genotypic adaptability and stability under varying environmental conditions. With this background, the present study was undertaken to evaluate the yield performance and stability of 46 lentil genotypes across three consecutive cropping seasons using GGE biplot analysis. The specific objectives were: (i) to assess the magnitude of genotype, environment, and GEI effects on seed yield and (ii) to identify stable and high-yielding genotypes across environments.

Materials and Methods

Study Site and Experimental Materials

The experiment was conducted over three consecutive rabi seasons, specifically 2022–2023, 2023–2024, and 2024–2025, at the research farm of the Division of Genetics, Indian Agricultural Research Institute, New Delhi. This experimental site is located at an elevation of 228.61 m above mean sea level, at 28.38° N latitude and 77.10° E longitude (Tripathi *et al*., 2022). It has a subtropical, semi-arid climate characterized by very hot summers, cold winters, and low annual rainfall. The plant material comprised 46 advanced lentil breeding lines, of which 33 originated from ICARDA. Detailed information regarding these genotypes is presented in Table 1.

Table 1 : Details of 46 genotypes used in the study.

Sl. No.	Genotype	Sl. No.	Genotype
1	P13119	24	P13108
2	IG69568	25	MC6
3	P14105	26	PL97
4	P3235	27	P13135
5	P3234	28	P3236
6	P8112	29	P15213
7	PL639	30	P13138
8	NDL1	31	P13112
9	LL1122	32	P13143
10	L4649	33	P15115
11	ILWL118	34	P13142
12	P117	35	P13130
13	10-3-1-26	36	P15104
14	P13133	37	L11-223

15	P13145	38	P13115
16	P15111	39	P15121
17	P14903	40	P8110
18	P13122	41	P13157
19	P16205	42	P13109
20	P8103	43	P13128
21	P13123	44	L11-292
22	P14109	45	P15207
23	P13107	46	P13131

Experimental Design and Data Collection

The experiment was laid out in an augmented block design consisting of three blocks, each accommodating 15 test genotypes along with three standard check varieties (L4717, L4727, and L4729) replicated in every block. Each genotype was sown in a single row of 5 m length with a row-to-row spacing of 25 cm. Standard agronomic practices recommended for lentil cultivation were followed (Sarkar *et al.*, 2025). Observations were recorded on five randomly selected plants from each genotype for six morphological and yield-related traits: plant height (PH, cm), number of secondary branches per plant (SBR), number of pods per plant (NPP), total biomass (TB, g), grain yield per plant (GYP, g), and chlorophyll content (CHL). The harvest index (HI) was subsequently computed as the ratio of grain yield to total biomass, providing an estimate of the efficiency of biomass partitioning towards grain production.

Statistical Data Analysis

The data on grain yield and related yield-contributing traits of lentil lines evaluated across three environments were analysed using combined analysis of variance (ANOVA) to assess the effects of genotype, environment, and their interaction. All statistical analyses were carried out in R Studio version 4.3.2 utilizing the Metan package version 1.19.0 (Olivoto and Lucio, 2020). The genotype × environment interaction (GEI) effects were further studied using the GGE biplot approach. The GGE biplot model (Yan *et al.*, 2007), which is based on singular value decomposition (SVD) of principal components, can be presented as:

$$Y_{ij} - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

where Y_{ij} represents the performance of the i^{th} genotype in the j^{th} environment, μ is the overall mean, and β_j denotes the main effect of environment j. The term λ_k represents the singular value of the k^{th} principal component (PC), while α_{ik} and γ_{jk} are the eigenvector scores of the i^{th} genotype and j^{th} environment for the k^{th} PC, respectively. The residual error linked with i^{th} genotype in j^{th} environment is represented by ϵ_{ij} .

Results and Discussion

Analysis of Variance (ANOVA)

The combined analysis of variance (ANOVA) for the studied traits in lentils across three seasons revealed highly significant differences ($p < 0.001$) among seasons, genotypes, and their interactions (Table 2). A significant effect of season was observed for all the studied traits, including plant height (PH), number of pods per plant (NPP), number of secondary branches per plant (SBR), total biomass (TB), grain yield per plant (GYP), harvest index (HI), and chlorophyll content (CHL). The high seasonal variation suggests that climatic fluctuations such as temperature, rainfall, and photoperiod during different years had a considerable impact on lentil growth and productivity. Similar environmental effects on lentil yield and related traits have been reported by Nath *et al*. (2014) and Yohane *et al*. (2021), emphasizing the importance of multi-season testing for reliable genotype assessment.

Table 2 : Combined analysis of variance (ANOVA) table demonstrating the presence of significant variation among 46 lentil genotypes for the studied traits

Source of Variation	Df	Mean sum of squares						
		PH	**NPP**	**SBR**	**TB**	**GYP**	**HI**	**CHL**
Season	2	4.312^{**}	10744^{***}	453.7^{***}	89417^{***}	3708^{***}	16197^{***}	1.127^{***}
Genotype	48	20.435^{***}	419^{***}	6.6^{***}	857^{***}	39^{***}	94^{***}	0.296^{***}
Genotype × season	96	6.639^{***}	219^{***}	3.5^{***}	526^{***}	29^{***}	74^{***}	0.221^{***}
Residuals	12	0.42	1.00	0	1.00	0	0	0.002

^{ns} $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$, ***$p \leq 0.001$.

The genotypic mean squares were also highly significant for all traits, indicating the existence of substantial genetic variability among the 46 lentil lines. Therefore, these traits can be effectively improved through selection. Furthermore, the genotype × season (G×S) interaction was highly significant, indicating differential performance of genotypes across seasons. Substantial crossover interactions were present and the ranking of genotypes changed depending on the seasonal conditions. Consequently, simple selection based on the overall mean performance across seasons is inadequate and necessitates the adoption of multivariate statistical methods, such as the GGE biplot for better interpretation.

The residual mean squares were low for all traits, confirming the precision of the experiment and the reliability of the observed differences. Overall, the ANOVA results clearly indicate that both genetic and environmental factors significantly contributed to trait variability in lentil, and that the high G×S interaction necessitates the use of multivariate stability analyses such as the GGE biplot, to identify high-yielding and stable genotypes across diverse growing conditions.

Mean Performance

Based on mean performance across three seasons, significant genetic variation was recorded among the 46 lentil genotypes for the studied traits (Table 3). The average plant height was 30.37 cm, ranging from 21.44 cm (P3235) to 35.89 cm (P15121). Genotypes LL1122, P13130, and P13142 were among the tallest, each exceeding 33 cm in height. The number of pods per plant also varied widely, with a mean of 42.19 pods /plants. Genotypes LL1122, P3234, and NDL1 produced the highest amount of pods/plant. Secondary branches per plant showed a range from 4.05 to 10.98, with an average of 8.15. NDL1, P13119, and P13122 were the genotypes with the highest number of secondary branches. Total biomass displayed significant variation, with values spanning from 30.52 g to 97.56 g, and a population mean of 38.19 g. Genotypes P13143, P13130, and P15121 displayed the highest biomass. Grain yield per plant ranged from 4.88 g to 18.37 g, with a mean of 11.21 g. High-yielding genotypes included P13143, MC6, P8112, P3234, and P13131, all exceeding 15 g /plant, highlighting their promise for yield enhancement. The harvest index (HI) varied between 16.94 % and 36.68 %, with an average of 27.33%. Chlorophyll content also ranged from 1.04 to 2.47, averaging 1.56 across genotypes. Genotypes P3234, LL1122, and PL639 exhibited the highest chlorophyll levels, suggesting better photosynthetic efficiency. Overall, the results revealed wide genetic variation among the evaluated genotypes, with P13143, P3234, LL1122, and P15121 showing consistently superior performance across multiple yield and physiological traits. These genotypes can serve as promising candidates for selection and breeding aimed at enhancing yield potential and stability in lentil.

While the mean performance analysis provided insights into the overall productivity and trait expression of individual genotypes, it did not fully account for environmental influences on genotype behaviour across seasons. Therefore, a GGE biplot analysis was then carried out to study the pattern of genotype × environment interaction and to identify genotypes that combine high yield with stable performance under variable conditions.

Table 3 : The top 5 best performing genotypes and the best check for each trait identified based on mean performance across three consecutive seasons.

Trait	Top five genotypes	Check variety
Plant height (cm)	P15121 (35.89), LL1122 (34.39), P13130 (33.45), P13142 (33.44), PL639 (33.11)	L4717 (30.67)
Number of secondary branches	NDL1 (10.98), P13119 (9.72), P13122 (9.71), PL639 (9.53), P13145 (9.49)	L4727 (8.33)
Number of pods per plant	LL1122 (67.89), P3234 (67.11), NDL1 (65.56), P14903 (63.11), P15121 (55.33)	L4717 (61.17)
Total biomass (g)	P13143 (61.20), P13130 (58.35), P15121 (52.64), P3234 (52.35), P13135 (49.76)	L4717 (45.49)
Grain yield per plant (g)	P13143 (18.37), MC6 (17.13), P8112 (16.96), P3234 (16.11), P13131 (15.25)	L4717 (11.62)
Harvest index (%)	IG69568 (36.68), P8112 (36.23), P13123 (35.98), P13131 (34.05), P13107 (33.81)	L4729 (29.53)
Chlorophyll content	P3234 (2.47), LL1122 (2.18), PL639 (2.00), NDL1 (1.99), P117 (1.96)	L4717 (1.37)

Values of the traits for genotypes are provided in parentheses.

Stability analysis

The GGE biplot based on the first two principal components (PC1 = 64.76 %, PC2 = 28.07 %) accounted for 92.83 % of the total variation caused by genotype and G × E interaction (Fig. 1A). Therefore, it is adequate to explain the majority of the variation present in the dataset. Here, the arrangement of genotypes and environments on the biplot reflects both their performance and interaction patterns. Genotypes located away from the origin showed a stronger and more specific response to certain environments, whereas those positioned closer to the centre demonstrated consistent and stable performance across diverse environments. The discriminating ability of genotypes and the representativeness of environments are two key attributes presented in the discriminativeness vs representativeness biplot (Fig. 1B). These characteristics are crucial for assessing environments based on how effectively they differentiate genotypes and thus aid in selecting superior lines. Environments represented by longer vectors possess greater discriminating power, meaning they can better distinguish among genotypes, while shorter vectors indicate limited differentiation ability. Representativeness, on the other hand, is determined by the angle between an environment's vector and the average environment coordinate (AEC) axis smaller angles suggest greater similarity and representativeness of the overall test environments. Therefore, an ideal testing environment is one that combines both strong discriminating power and high representativeness, allowing for precise and reliable identification of superior genotypes. In this study, E1 followed by E3 had the longest vectors and thus they were the most discriminating environments. Conversely, E2 had the shortest vector and was the least discriminating environment. Furthermore, E1, having the smallest angle with the AEC axis, was identified as the most representative environment.

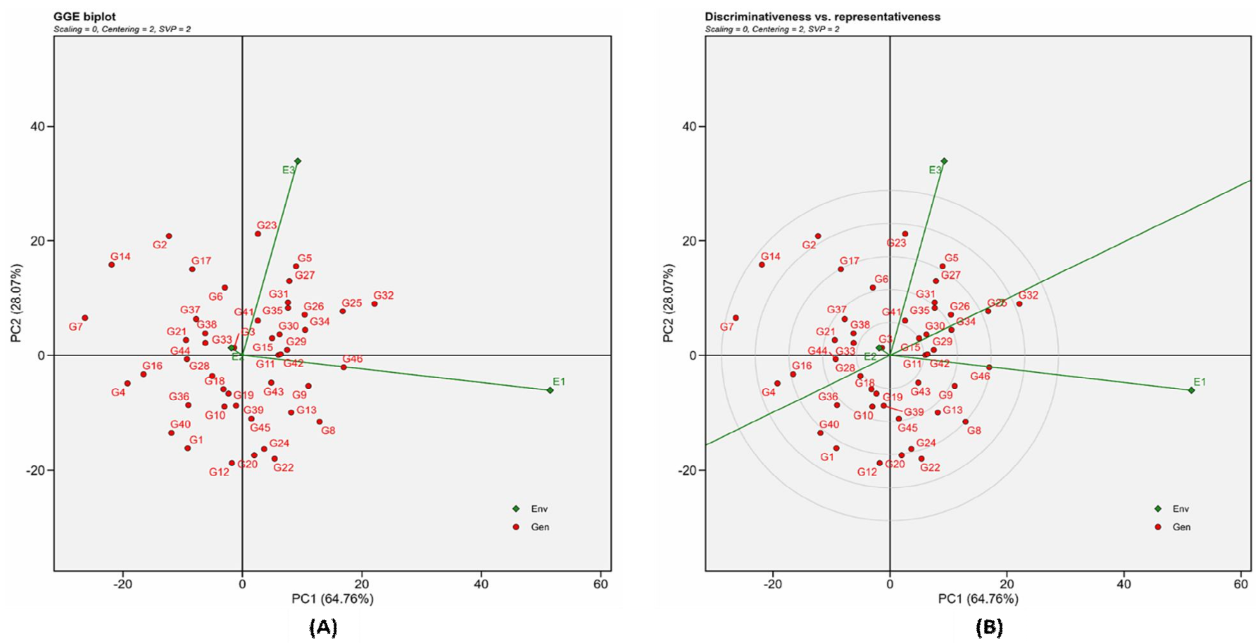

Fig. 1 : GGE biplot analysis (A) basic biplot; (B) discriminativeness vs representativeness biplot.

An ideal environment can be simply described as one that represents the average of all test environments while efficiently discriminating among the evaluated genotypes. In Fig. 2A, the ideal environment is represented by a small circle positioned along the average environment axis (AEA). Environments closer to this point are considered more suitable (better discriminating ability and representativeness), whereas those away from it have less discriminating ability. Based on this, the environments could be ranked as E1 > E3 > E2 in the present study. Similar ranking approaches were adopted by Reddy *et al*. (2022) in pearl millet and Das *et al*. (2025) in chickpea, where the most effective testing locations were identified based on discriminating ability and representativeness. Such information is crucial in multi-environment trials, as the selection of non-redundant representative testing environments will significantly improve breeding efficiency. Furthermore, another unique feature of GGE biplot is its ability to compare all genotypes against an "ideal genotype," which serves as a benchmark representing the highest performance. In Fig. 2B, concentric circles are drawn around the ideal genotype keeping it at the centre which allowed a clear assessment of how close or distant each genotype is from the ideal. Genotypes positioned nearer to it are considered more desirable, as they are expected to display superior performance. In the present study, genotypes 25 (MC6), 5 (P3234), 32 (P13143), 27 (P13135), and 26 (PL97) were located closest to the ideal genotype point and thus were identified as the most desirable. Whereas, genotypes 7 (PL639), 14 (P13133), 4 (P3235), and 16 (P15111) were positioned far away from the centre, indicating their lower yield potential.

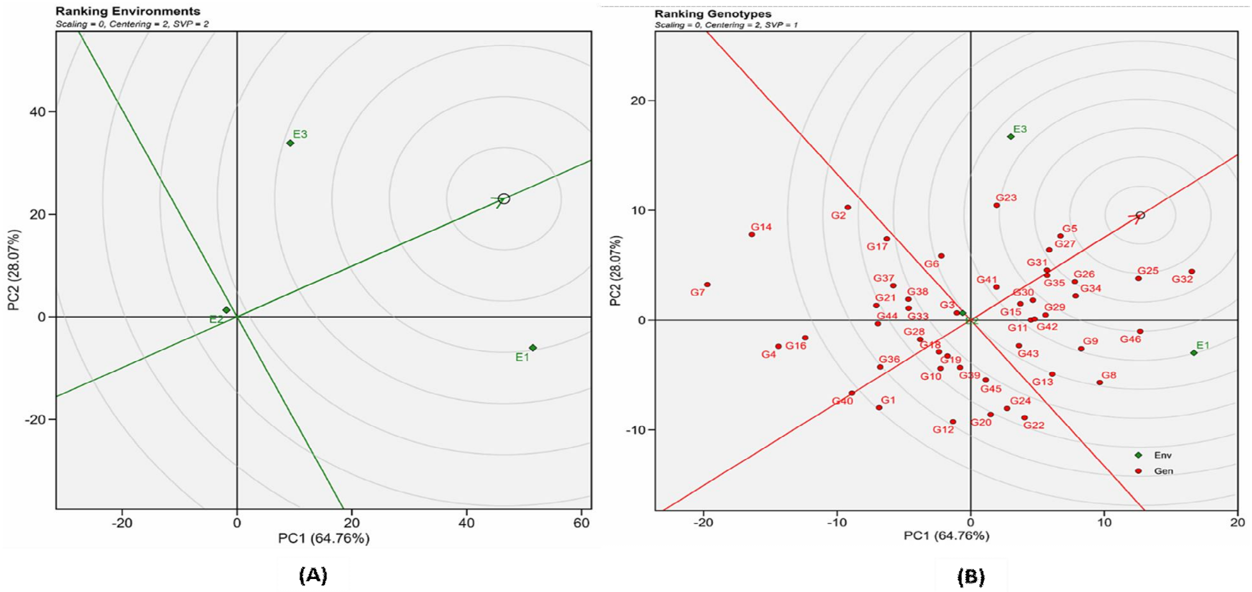

Fig. 2 : GGE biplot showing the (A) ranking of environments and (B) ranking of genotypes.

To visualize and interpret the interaction pattern between genotypes and environments for grain yield, the ‘‘which-won-where’’ biplot was used (Fig. 3A). In this biplot, the genotypes positioned at the vertices of the polygon: genotypes 2, 7, 14, 4, 40, 1, 12, 22, 8, 32, and 23 were those with the most distances from biplot origin in their respective directions. Thus, they were the best or worst performing lines in one or more environments and showed specific adaptation. As presented in Fig. 3A, Genotype 32 (P13143) was the best performing genotype in environment E1, indicating its specific adaptation and high yield potential under those climatic conditions. Similarly, Genotype 23 (P13107) was the winner in environment E3. E2 was positioned close to the biplot origin and did not have a clear winner, suggesting that most genotypes performed similarly in E2 with no single genotype showing a distinct advantage over others. The Average Environment Coordination (AEC) method (Fig. 3B) was further used to integrate both grain yield and stability performance of the genotypes, enabling identification of the highest yielding as well as stable genotypes. Here AEC abscissa, a single arrowed line passing through the biplot origin, represented the mean performance of genotypes. The direction of the arrow indicated higher yield. Genotypes located away from the origin and towards positive side of AEC abscissa exhibited higher yield, whereas those towards negative side represented lower-yielding genotypes. The AEC ordinate, drawn perpendicular to the abscissa, represented stability. A longer projection from this axis indicated lower stability.

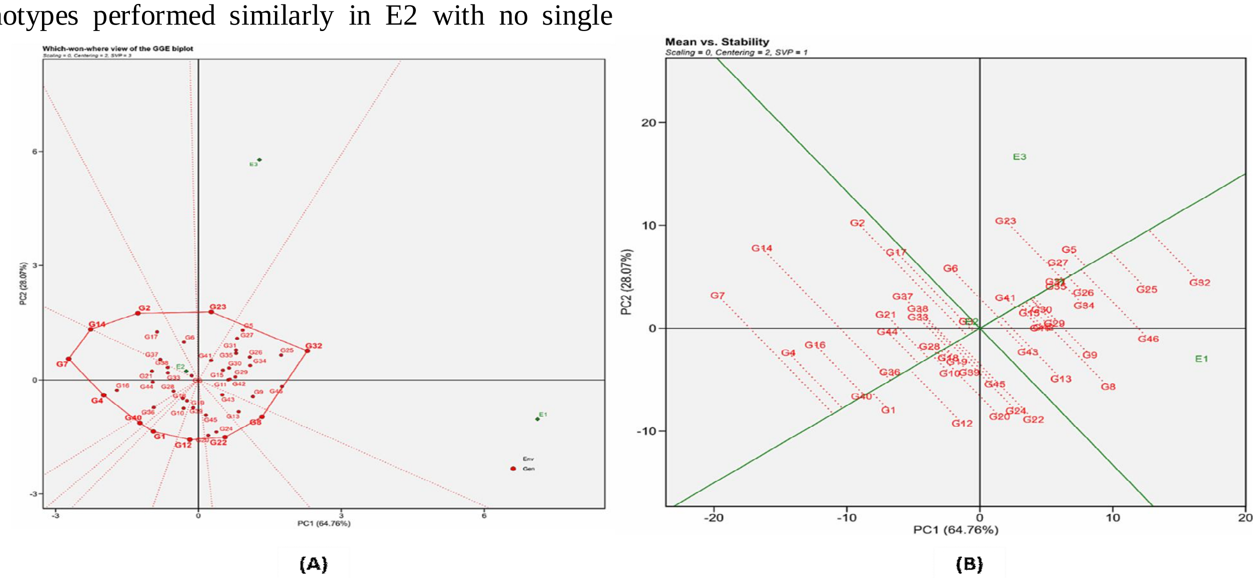

Fig. 3 : (A) Which-won-where view of the GGE biplot; (B) Mean vs Stability biplot.

As presented in Fig. 3B, Genotype 32 (P13143) recorded the highest mean yield, followed by Genotype 25 (MC6). However, both showed relatively larger projections from the AEC axis, indicating lower stability across environments. Thus, they were considered specifically adapted to particular environmental conditions. In contrast, Genotypes 31 (P13112) and 35 (P13130) exhibited high stability with moderate yield, suggesting their consistent performance. Similarly, Genotypes 5 (P3234), 26 (PL97), and 27 (P13135) combined good yield potential with moderate stability. Therefore, they were considered as widely adapted genotypes. On the other hand, Genotypes 40 (P8110) and 36 (P15104), though highly stable, produced lower yields. They might be suitable for cultivation in stress-prone or less favourable environments. Such patterns are consistent with reports in other crops like in wheat and chickpea where GGE biplot based stability analysis led to the identification of three and six high yielding as well as stable genotypes, respectively (Saeidnia *et al*., 2023; Amiri *et al*., 2025). Similarly, Karimizadeh *et al*. (2013) evaluated 18 diverse lentil genotypes across 4 locations that revealed the existence of three mega-environments and ultimately identified a genotype that showed high performance and stability across all test locations. The genotypes identified in present study will serve as valuable genetic resources in future breeding programs for improving both yield as well as stability of existing cultivars.

Conclusion

The present study demonstrated the effectiveness of GGE biplot analysis in dissecting the genotype × environment interaction and identifying high-yielding and stable lentil genotypes across multiple seasons. The combined analysis of variance revealed significant variation among genotypes and environments and thus confirmed the influence of both genetic potential and environmental factors on yield performance. The first two principal components (PC1 and PC2) together explained over 90% of the total G + GE variation, indicating the robustness of the GGE model in capturing most of the variation. Biplot analysis revealed that P13143 and MC6 were the genotypes with the highest yield but low stability, indicating their specific adaptation. Conversely, P13112, P13130, PL97, and P13135 combined moderate yield with high stability. The identified stable and high-performing genotypes will serve as promising parental lines in future breeding efforts to develop stable and high-yielding lentil cultivars suitable for variable environmental conditions.

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Competing interests

Authors have declared that no competing interests exist.

Authors' contributions

Conceptualization (MSA, PSY); Methodology (MSA, RS, P); Formal analysis and investigation (RS, P, BR); Writing - original draft preparation (RS, P); Writing - review and editing (BR, JR); Supervision (MSA, PSY).

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