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MULTI-ENVIRONMENT EVALUATION OF *BRASSICA JUNCEA* L. GENOTYPES FOR STABILITY AND PERFORMANCE IN SEED YIELD AND OIL CONTENT USING GGE BIPLOT

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SUMMARY

Brassica juncea L. is one of the major oilseed crops in Pakistan and globally, with productivity sensitive to environmental variation. Forty-five *B. juncea* genotypes, evaluated across four locations over two years in Khyber Pakhtunkhwa, Pakistan, used a randomized complete block design with two replications. Significant ($p \leq 0.01$) genotype and genotype × environment interaction (GEI) differences for seed yield and oil content led to genotype plus genotype × environment (GGE) biplot analysis to identify high-performing and stable genotypes across test environments. The GGE biplot view for mean vs. stability identified AUP-618, AUP-619, and AUP-623 for seed yield and AUP-625, AUP-626, and AUP-653 for oil content as high-yielding and stable genotypes. The polygon view revealed two mega-environments per trait, indicating crossover GEI. For seed yield, Peshawar and Mardan (2017-18) formed one possible mega-environment with AUP-600 and AUP-619 as winning genotypes, while Kohat (2016–17) and Bannu (2017–18) constituted the second with AUP-645. For oil content, Peshawar and Bannu comprised one potential mega-environment with AUP-645, whereas Mardan created the second with AUP-632. Furthermore, Mardan (2016–17) for seed yield and Peshawar (2017–18) for oil content emerged as the tentative ideal environments. GGE biplot analysis effectively identified high-yielding and relatively stable *B. juncea* genotypes for diverse Khyber Pakhtunkhwa environments.

Keywords: *B. juncea*, genotype-by-environment interaction (GEI), stability analysis, GGE biplot, seed yield, oil content

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Key findings: The *B. juncea* genotypes AUP-618, AUP-619, and AUP-623 for seed yield and AUP-625, AUP-626, and AUP-653 for oil content succeeded in their identification as high-yielding and relatively stable genotypes. Two possible mega-environments, detected for both traits, indicated crossover GEI, with Mardan (2016–17) and Peshawar (2017–18) identified as the ideal environments for seed yield and oil content, respectively.

INTRODUCTION

The genus *Brassica* (Brassicaceae) includes several economically important species, with genetic relationships described by the U-Triangle model of Nagaharu (1935)—the allotetraploid *Brassica juncea* (AABB, 2n = 36) originated from natural hybridization between *B. rapa* (AA, 2n = 20) and *B. nigra* (BB, 2n = 16). *B. juncea* (Indian mustard) is a widely cultivated crop in South Asia because of its broad adaptability, rapid development, and its tolerance to heat, drought, major diseases, and insect pests. Its seeds contain 44%–46% high-quality oil, while the residual meal has 38%–40% protein with a balanced amino acid profile, making it valuable for both human consumption and livestock feed (Abdulameer *et al*., 2021; Rathnakumar and Sujatha, 2022).

Global rapeseed-mustard production in 2024 gave estimates between 86.0 and 92.3 million tons, with an average yield of about 2070 kg ha^{-1} (USDA, 2024). In Pakistan, the crop produced 0.796 million tons of seed with a yield of 1335.57 kg ha^{-1} (MNFSR, 2023). In Khyber Pakhtunkhwa province, mustard cultivation remained limited to 133,700 hectares, yielding only 561 kg ha^{-1}. Pakistan imported 2.681 million tons of edible oil in 2023, costing USD 3.56 billion, while domestic production was only 0.496 million tons (MNFSR, 2023). These figures highlight the urgent need to develop high-yielding, oil-rich cultivars well-adapted to local agro-climatic conditions to reduce import dependence.

The success of any crop improvement program largely depends on the magnitude of genetic variability and its interaction with environmental factors (Begna and Teressa, 2024). Seed yield and oil content are traits of considerable economic importance, having significant influences from genotype, environment, and their interaction (Bascuñán-Godoy *et al*., 2023). The presence of genotype-by-environment interaction (GEI) complicates the selection process, as genotypes often exhibit variable performance across different locations and years. Therefore, understanding GEI is crucial for identifying genotypes with either broad adaptability or specific suitability to particular environments (Zewdu *et al*., 2020; Ahakpaz *et al*., 2021).

The combined analysis of variance (ANOVA) has become commonly used to quantify GEI effects; however, it provides limited insight into the stability of genotypic performance across environments (Pour-Aboughadareh *et al*., 2022). Addressing this limitation enabled various statistical approaches to be developed for the assessment of GEI. Among these, several parametric and non-parametric techniques have been options to evaluate GEI, including genotype plus genotype × environment interaction (GGE) biplot analysis (Mullualem *et al*., 2024).

The GGE biplot model is a widely used multivariate tool for analyzing GEI because it removes environmental main effects and emphasizes genotype and GEI components (Dang *et al*., 2024). It facilitates the identification and ranking of high-yielding and stable genotypes, reveals crossover interactions and mega-environments, and assists in selecting test environments with high discriminating ability and representativeness (Rashid *et al*., 2025).

This study evaluated GEI for seed yield and oil content in *B. juncea* using GGE biplot analysis to identify stable, high-performing genotypes and mega-environments for breeding applications.

Table 1. *Brassica juncea* L. genotypes used in the study collected across Pakistan.

Line	Genotype	Line	Genotype	Line	Genotype
1	AUP-600	16	AUP-623	31	AUP-653
2	AUP-601	17	AUP-624	32	AUP-654
3	AUP-602	18	AUP-625	33	AUP-655
4	AUP-604	19	AUP-626	34	AUP-656
5	AUP-605	20	AUP-627	35	AUP-657
6	AUP-606	21	AUP-628	36	AUP-658
7	AUP-609	22	AUP-630	37	AUP-659
8	AUP-610	23	AUP-632	38	AUP-663
9	AUP-611	24	AUP-633	39	AUP-1800
10	AUP-614	25	AUP-634	40	AUP-2727
11	AUP-615	26	AUP-641	41	UCD-635
12	AUP-616	27	AUP-642	42	UCD-636
13	AUP-617	28	AUP-645	43	UCD-638
14	AUP-618	29	AUP-649	44	UCD-10/8 (check)
15	AUP-619	30	AUP-652	45	NIFA-Raya (check)

UCD = University of California Davis, United States of America

MATERIALS AND METHODS

Plant material

The evaluation of *Brassica juncea* genotypes totaled 45 in this study, including two check cultivars: UCD-10/8 (University of California, Davis, USA) and NIFA-Raya (Nuclear Institute for Food and Agriculture, Peshawar, Pakistan) (Table 1). Of these, 40 collected accessions came from diverse agroecological regions of Pakistan, with five exotic lines from the University of California, Davis, USA. All genotypes were advanced through two generations of selection and seed multiplication to ensure genetic uniformity before field evaluation.

Experimental sites and design

Field experiments, conducted across two cropping seasons (2016–17 and 2017–18), occurred at four locations in Khyber Pakhtunkhwa, Pakistan. These were the University of Agriculture, Peshawar; Amir Muhammad Khan Campus, Mardan; Barani Agricultural Research Station, Kohat; and Agricultural Research Station, Serai Naurang (Bannu). The selected sites cover a range of agroecological conditions characteristic of subtropical semi-arid to sub-humid environments where mustard cultivation dominates. Peshawar (34.008° N, 71.580° E; 331 m) represents a warm semi-arid plain with relatively mild winters (Table 2). Mardan (34.200° N, 72.033° E; 311 m) lies in a sub-humid zone with slightly higher precipitation. Kohat (33.583° N, 71.433° E; 489 m) sits in a dry, moderately elevated valley with greater diurnal temperature variation, while Bannu (32.985° N, 70.604° E; 376 m) represents a warmer low-elevation environment typical of southern plains (Khan and Hasan, 2019).

Sowing commenced in the third week of October at all locations in both years, using a randomized complete block design with two replications. Planting genotypes occurred in five-row plots (5 m long), with a row spacing of 75 cm and a plant-to-plant spacing of 30 cm. Fields reached plowing and planking to a fine tilth, with seeds dibbled at 1–2 cm depth, irrigation applied at critical growth stages, and weeds removed manually and mechanically.

Oil content determination

Determining the seed oil content (%) happened at the Crop Breeding Section, Biochemical Laboratory, NIFA, Peshawar, Pakistan. Clean, well-dried seeds from each genotype underwent analysis using near-infrared reflectance spectroscopy. Each sample, scanned three times, had the mean value used for statistical analysis.

Table 2. Description of experimental locations.

Test site	Latitude (N)	Longitude (E)	Altitude (m)
Peshawar	34.008°	71.580°	331
Mardan	34.200°	72.033°	311
Kohat	33.583°	71.433°	489
Bannu	32.985°	70.604°	376

Statistical analysis

Data on seed yield and oil content across environments sustained an ANOVA, following the procedure described by Steel *et al*. (1997). The statistical model included the effects of genotype, location, year, and their interactions. Performing ANOVA used the SAS software (SAS, 2004). When detecting significant differences, separating treatment means utilized the least significant difference (LSD) test at the 5% probability level.

Stability analysis

Assigning numbers to 45 *Brassica juncea* genotypes listed in Table 1 began from Line 1 to Line 45 for the graphical analyses. Each location × year combination, considered a separate environment, received designation as E1 (Peshawar 2016–17), E2 (Peshawar 2017–18), E3 (Mardan 2016–17), E4 (Mardan 2017–18), E5 (Kohat 2016–17), E6 (Kohat 2017–18), E7 (Bannu 2016–17), and E8 (Bannu 2017–18). Following the detection of significant GEI, GGE biplot analysis for seed yield and oil content proceeded across these environments.

Genotype plus genotype × environment interaction biplot analysis

Performing the GGE biplot analysis for seed yield and oil content used the GEA-R version 4.1 (Pacheco-Gil *et al*., 2015). The model's basis is on singular value decomposition, implemented as described by Yan and Tinker (2006):

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

In the model, Y_{ij} denotes the mean performance of the i^{th} genotype in the j^{th} environment, μ is the grand mean, and β_j represents the main effect of the j^{th} environment. The parameters λ_1 and λ_2 are the singular values associated with the first and second principal components (PC1 and PC2), respectively. The scores ξ_{i1} and ξ_{i2} are the eigenvectors of the i^{th} genotype for PC1 and PC2, whereas η_{j1} and η_{j2} are the corresponding eigenvectors of the j^{th} environment. The residual term ε_{ij} represents the unexplained variation for the i^{th} genotype in the j^{th} environment.

RESULTS

Analysis of variance

The pooled ANOVA detected highly significant ($P \leq 0.01$) differences among genotypes (G), locations (L), years (Y), and all interaction terms (L × Y, G × L, G × Y, G × L × Y) for both seed yield and oil content (Table 3). Islam *et al*. (2024) reported significant effects of genotype, environment, and genotype × environment interaction for seed yield and oil content in five *Brassica* genotypes evaluated across five environments, corroborating the results of the presented study. The two-year average across test locations, seed yield ranged from 1922 kg ha^{-1} (AUP-614) at Kohat to 4318 kg ha^{-1} (AUP-619) at Peshawar (Table 4). Based on overall means, the genotype AUP-641 recorded the highest seed yield (4141 kg ha^{-1}), followed by AUP-619, whereas check cultivars exhibited comparatively lower yields. Among locations, Peshawar (3134 kg ha^{-1}) and Mardan (2998 kg ha^{-1}) produced higher seed yields than Kohat (2922 kg ha^{-1}) and Bannu (2873 kg ha^{-1}). For oil content, the two-year

Table 3. Mean squares of *Brassica juncea* genotypes for seed yield and oil evaluated across four locations and two years.

Source of variation	d.f.	Seed yield	Oil
Location (L)	3	2319325**	547.31**
Year (Y)	1	8206980**	666.82**
L×Y	3	3338250**	26.46**
Rep w/n (L×Y)	8	49749	34.5
Genotype (G)	44	4472284**	13.13**
G×L	132	51485**	2.00**
G×Y	44	121004**	0.98**
G×L×Y	132	107999**	1.02**
Error	288	13471	0.8
CV (%)		5.62	2.03

** = significant at 1% level of probability.

Table 4. Mean performance of *Brassica juncea* genotypes evaluated across four locations and two years.

Location	Values	Seed yield (kg ha^{-1})	Oil content (%)
Peshawar	Minimum	2460 (AUP-630)	42.6 (UCD-636)
	Maximum	4318 (AUP-619)	47.6 (AUP-1800)
	Checks' mean	2163	45.7
	Mean	3134	45.7
Mardan	Minimum	2262 (AUP-627)	42.9 (AUP-633)
	Maximum	4297 (AUP-641)	48.4 (AUP-626)
	Checks' mean	2245	45.5
	Mean	2998	45.7
Kohat	Minimum	1922 (AUP-614)	40.6 (AUP-606)
	Maximum	4087 (AUP-641)	46.3 (AUP-1800)
	Checks' mean	2095	42.3
	Mean	2922	42.8
Bannu	Minimum	1976 (AUP-616)	40.1 (UCD-636)
	Maximum	3994 (AUP-619)	44.9 (AUP-628)
	Checks' mean	2056	43.5
	Mean	2873	42.6
Across all test environments	Minimum	2365 (AUP-605)	42.0 (UCD-636)
	Maximum	4141 (AUP-641)	46.3 (AUP-1800)
	Checks' mean	2140	44.2
	Mean	2982	44.2

mean across locations varied from 40.1% (UCD-636) at Bannu to 48.4% (AUP-626) at Mardan (Table 4). The genotype AUP-1800 recorded the topmost overall mean oil content (46.3%) across locations compared with check cultivars. Environmental means indicated relatively higher oil content at Peshawar and Mardan, both averaging 45.7%. Sharma and Kumar (2023) evaluated morpho-physiological traits of *B. juncea* genotypes and reported seed yield ranging from 2005 to 2583 kg ha^{-1}, while Bassegio and Zanotto (2020) recorded oil content values of 37.7%–44.3% in eight *B. juncea* genotypes.

Genotype-by-environment interactions

Seed yield

The GGE biplot for seed yield showed the first two PCs (PC1 = 28.95% and PC2 = 21.88%) together explained 50.83% of the total GEI variation (Figure 1a). Genotypes AUP-645 (Line 28), AUP-604 (Line 4), AUP-655 (Line 33), and

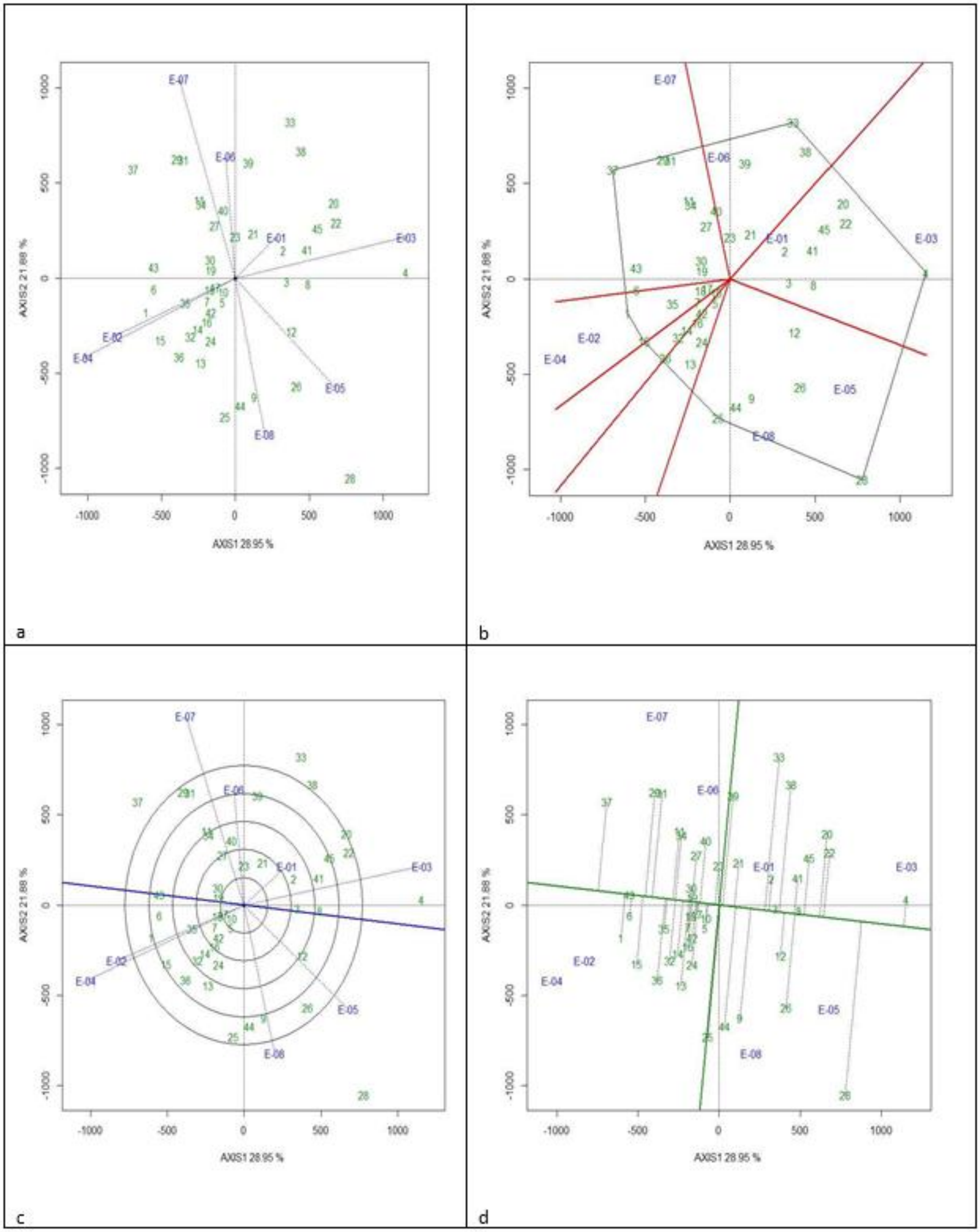

Figure 1. GGE biplot analysis for seed yield of 45 *Brassica juncea* genotypes evaluated across four locations over two years: (a) GGE biplot overview, (b) site-specific performance, (c) discrimination vs. representativeness of environments, and (d) mean vs. stability.

AUP-659 (Line 37) displayed positions farther from the biplot origin for the studied trait, whereas AUP-605 (Line 5), AUP-614 (Line 10), and AUP-624 (Line 17) showed locations closer to the origin. Sincik *et al*. (2021) also reported that the first two PCs explained more than 50% of the total variation for seed yield in GGE biplot analysis of 15 *Brassica* genotypes evaluated across eight different environments.

Among environments, E-07 (Bannu 2016–17) had the longest vector for seed yield, followed by E-04 (Mardan 2017–18), E-03 (Mardan 2016–17), and E-08 (Bannu 2017–18) (Figure 1a). Environments E-01 (Peshawar 2016–17) and E-06 (Kohat 2017–18) showed relatively shorter vectors. Specific GEIs were evident, including AUP-600 (Line 1) with E-02 (Peshawar 2017–18), AUP-611 (Line 9) with E-08 (Bannu 2017–18), and AUP-616 (Line 12) with E-05 (Kohat 2016–17). Smaller intervector angles were notable between E-02 and E-04 and between E-06 and E-07.

Site-specific performance of genotypes

The 'which-won-where' biplot divided the test environments into five sectors containing environments and identified two possible mega-environments for seed yield (Figure 1b). The first mega-environment comprised E-02 (Peshawar 2017–18) and E-04 (Mardan 2017–18), with AUP-600 (Line 1) and AUP-619 (Line 15) as the vertex genotypes. The second mega-environment included E-05 (Kohat 2016–17) and E-08 (Bannu 2017–18), with AUP-645 (Line 28) identified as the winning genotype. Environment E-01 (Peshawar 2016–17) gave a position near the biplot origin and has no association with a specific winning genotype.

Discriminating ability and representativeness of test environments

The discriminating vs. representativeness biplot for seed yield showed that environment E-01 (Peshawar 2016–17) had a short vector and a relatively large angle with the average environment axis (AEA), whereas E-03 (Mardan 2016–17) exhibited a longer vector with a smaller angle with the AEA (Figure 1c). Environments E-02 (Peshawar 2017–18) and E-04 (Mardan 2017–18) had long vectors and comparatively large angles to the AEA. Environment E-07 (Bannu 2016–17) displayed the longest vector and a large angle with the AEA. Environments E-05 (Kohat 2016–17), E-06 (Kohat 2017–18), and E-08 (Bannu 2017–18) showed moderately long vectors accompanied by relatively large angles to the AEA.

Means vs. stability of genotypes

The average-environment coordination (AEC)-based biplot for seed yield indicated that genotypes AUP-655 (Line 33), AUP-663 (Line 38), and AUP-1800 (Line 39) provided a positioning on the negative side of the AEC abscissa, with longer projections onto the ordinate (Figure 1d). In contrast, genotypes AUP-618 (Line 14), AUP-619 (Line 15), and AUP-623 (Line 16) locations were on the positive side of the AEC, with shorter projections. Check cultivars UCD-10/8 (Line 44) and NIFA-Raya (Line 45) showed farther positioning from the origin and the AEC.

Oil content

For oil content, PC1 and PC2 explained 26.95% and 23.50% of the total GEI variation, respectively (Figure 2a). Genotypes AUP-641 (Line 26), AUP-645 (Line 28), AUP-630 (Line 22), and AUP-632 (Line 23) entailed positions away from the biplot origin, while AUP-657 (Line 35), AUP-652 (Line 30), and AUP-642 (Line 27) had locations close to it. These results corroborate the findings of Kakaei *et al*. (2024), who reported that the first two PCs explained more than 50% of the total GEI variation for oil content in 14 *Brassica* genotypes evaluated across four environments.

Environment E-05 (Kohat 2016–17) showed the longest vector for the studied trait, followed by E-02 (Peshawar 2017–18), E-04 (Mardan 2017–18), and E-03 (Mardan 2016–17) (Figure 2a). Environments E-07 (Bannu 2016–17) and E-08 (Bannu 2017–18) had comparatively shorter vectors. Positive GEIs emerged for genotypes AUP-605 (Line 5) and AUP-645 (Line 28) with E-01 (Peshawar 2016–

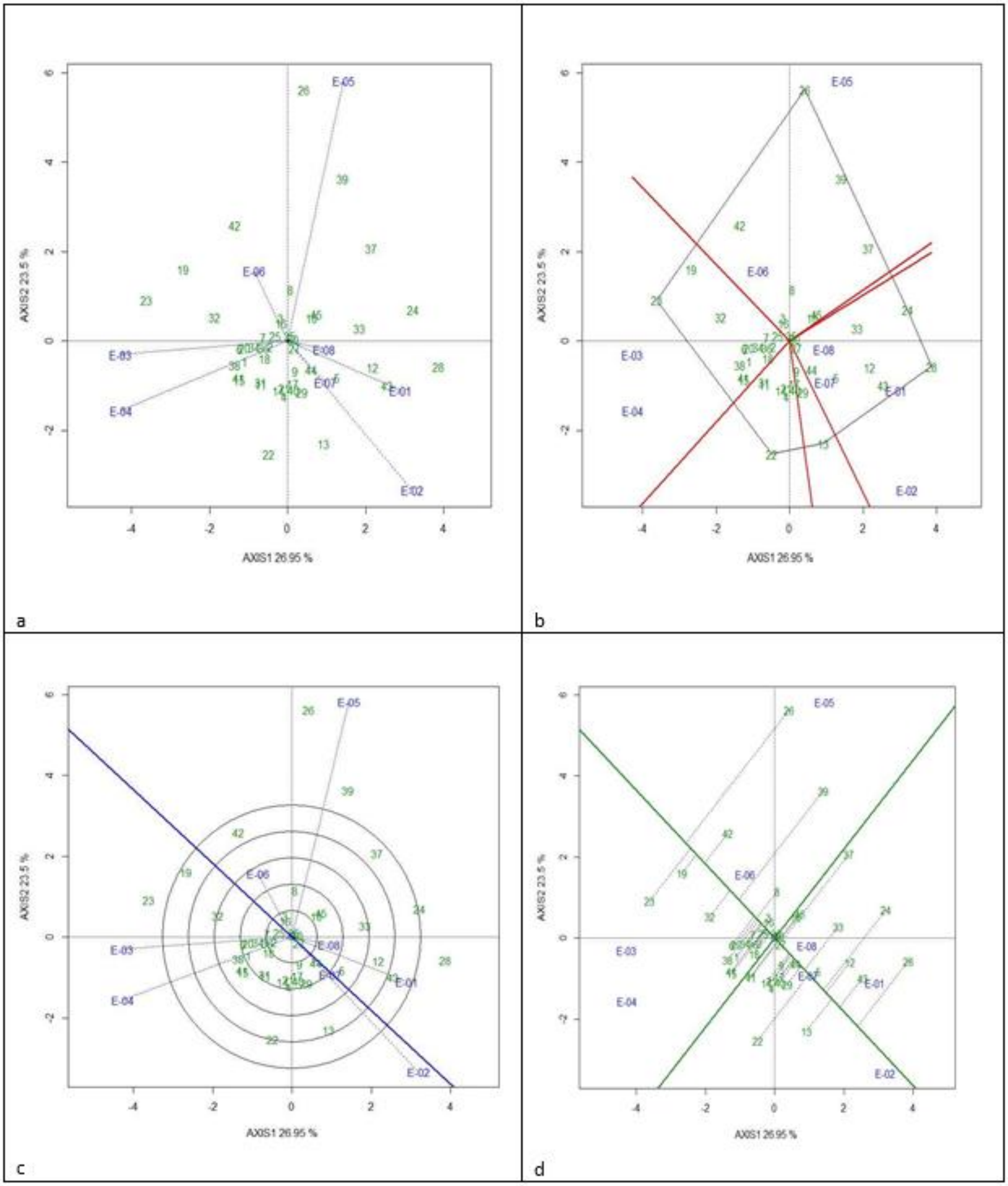

Figure 2. GGE biplot analysis for oil content of 45 *Brassica juncea* genotypes evaluated across four locations over two years: (a) GGE biplot overview, (b) site-specific performance, (c) discrimination vs. representativeness of environments, and (d) mean vs. stability.

17), AUP-617 (Line 13) with E-02, AUP-641 (Line 26) and AUP-1800 (Line 39) with E-05, AUP-654 (Line 32) with E-03, and AUP-663 (Line 38) with E-04.

Site-specific performance of genotypes

The polygon view divided genotypes into six sectors for oil content, three of which contained test environments (Figure 2b). The identification of two potential mega-environments was successful for the studied trait. The first mega-environment included E-01 (Peshawar 2016–17), E-02 (Peshawar 2017–18), E-07 (Bannu 2016–17), and E-08 (Bannu 2017–18), with AUP-645 (Line 28) as the vertex genotype. The second mega-environment comprised E-03 (Mardan 2016–17) and E-04 (Mardan 2017–18), with AUP-632 (Line 23) as the winning genotype.

Discriminating ability and representativeness of test environments

For oil content, the discriminative power vs. representativeness graph identified that environment E-05 (Kohat 2016–17) had a longer vector and larger angle with the AEA (Figure 2c). Environment E-02 (Peshawar 2017–18) revealed characteristics of the longest vector and a smaller angle with the AEA. Environments E-01 (Peshawar 2016–17), E-06 (Kohat 2017–18), E-07 (Bannu 2016–17), and E-08 (Bannu 2017–18) showed shorter vectors with smaller angles relative to the AEA. Environments E-03 (Mardan 2016–17) and E-04 (Mardan 2017–18) exhibited moderately long vectors with comparatively large angles to the AEA.

Means vs. stability of genotypes

The AEC-based biplot for oil content showed that UCD-636 (Line 42), UCD-638 (Line 43), and AUP-633 (Line 24) indicated positions on the negative side of the AEC with longer projections (Figure 2d). Genotypes AUP-626 (Line 19), AUP-653 (Line 31), and AUP-625 (Line 18) exhibited locations on the positive side of the AEC, with shorter projections. Check cultivars had positions near the origin with limited projections onto the ordinate.

DISCUSSION

The study identifies several *Brassica juncea* genotypes that combine high mean performance with stability across multiple environments while simultaneously indicating that GEI influences both seed yield and oil content. The results highlight broadly and specifically adapted genotypes for seed yield and oil content.

Significant differences among genotypes, environments, and their interaction for both traits indicate considerable genetic variability in the evaluated genotypes. The GEI reflects differential genotype responses across locations and years, suggesting essential multi-environment testing for accurate genotype evaluation. Changes in genotype ranking across environments further indicate the influence of environmental differences. The observed variability likely reflects the diverse genetic origins of the tested material, developed under contrasting agroclimatic conditions. These findings are consistent with earlier reports on *B. juncea* documenting significant genotypic and GEI effects for seed yield and oil content (Qasemi *et al*., 2022; Islam *et al*., 2024; Kakaei *et al*., 2024).

The wide ranges observed for seed yield and oil content indicate significant scope for selecting superior genotypes, combining productivity and oil content (Bassegio and Zanotto, 2020; Sharma and Kumar, 2023). Genotypes AUP-641 and AUP-619 for seed yield and AUP-626 and AUP-1800 for oil content exhibited superior mean performance and, therefore, represent promising genetic resources for breeding programs. The consistently superior performance of genotypes recorded at Peshawar and Mardan suggests favorable agroclimatic conditions, supporting their suitability as effective test environments for *B. juncea* evaluation.

The proportion of GEI variation explained by PC1 and PC2 for both traits (~50%) was lower than that reported by Sincik *et al*. (2021) and Kakaei *et al*. (2024), who found >70% cumulative variance. Such differences likely reflect the broader environmental range and larger genotype set evaluated in this study. A higher genotype count in multi-environment trials usually generates more complex GEI structures, reducing the variance captured by the first two PCs (Pour-Aboughadareh *et al*., 2022). This emphasizes the need for extensive multi-environment testing before selecting stable genotypes.

The contrasting positions of genotypes for seed yield and oil content relative to the biplot origin support earlier findings that proximity to the origin indicates greater stability (Sincik *et al*., 2021). Environments with longer vectors exerted stronger discrimination, while shorter vectors reflected greater stability, a pattern consistent with reports by Shojaei *et al*. (2023). Correlated environments identified for both traits, characterized by small intervector angles, agree with principles reported by Motahhari *et al*. (2020), indicating that genotype performance is predictable across similar sites.

The 'which-won-where' pattern revealed distinct possible mega-environments for both traits, with vertex genotypes indicating crossover GEI and differential genotype adaptation. Such patterns are valuable for identifying both broadly and specifically adapted genotypes and have been emphasized as a key strength of GGE biplot methodology (Barpete *et al*., 2025).

Discriminating vs. representativeness analysis clarified the relative suitability of test environments for genotype evaluation. Environments with long vectors and small angles with the AEA appeared most effective for selecting broadly adapted genotypes, whereas those with large angles are more informative for detecting specific adaptation (Demelash, 2024). In this study, Mardan (2016–17) for seed yield and Peshawar (2017–18) for oil content emerged as favorable test environments. Although an ideal test environment rarely exists, its conceptual definition provides a standard for assessing and optimizing multi-environment trial sites (Al-Ghumaiz *et al*., 2025).

The mean vs. stability GGE biplot analysis using AEC enables simultaneous assessment of genotype performance and stability. In the biplot, the AEC abscissa represents the genotype main effect across environments, whereas the ordinate perpendicular to the AEC reflects genotype instability within the total GEI. Genotypes with shorter projections onto the AEC ordinate are considerably more stable, while those with longer projections exhibit greater sensitivity to environmental variation. Similarly, genotypes AUP-618, AUP-619, and AUP-623 for seed yield and AUP-625, AUP-626, and AUP-653 for oil content were notable as having superior mean performance across environments, consistent with the interpretation of Wondaferew *et al*. (2024).

Although the first two GGE axes explained approximately 50% of the GEI variation for the studied traits, the remaining principal components may contain biologically relevant patterns that this study did not examine. Future research should focus on validating the most promising genotypes—AUP-618, AUP-619, AUP-623, AUP-625, AUP-626, and AUP-653—through multi-year, on-farm trials by integrating GGE, AMMI, stability indices, and mixed-model BLUP analyses, complemented by molecular marker-based genomic selection. Overall, this study provides a comprehensive assessment of GEI in *B. juncea* genotypes and identifies candidate genotypes with strong potential for both broad and specific adaptation.

CONCLUSIONS

Significant GEI for seed yield and oil content succeeded in using GGE biplot analysis, identifying AUP-618, AUP-619, and AUP-623 for seed yield and AUP-625, AUP-626, and AUP-653 for oil content as relatively stable, high-performing genotypes; simultaneously, AUP-600, AUP-619, AUP-645, and AUP-632 showed specific adaptation in their respective possible mega-environments. Mardan (2016–7) for seed yield and Peshawar (2017–18) for oil content tended to be the most productive test environments. Overall, the study demonstrates the importance of GGE biplot methodology for mustard improvement under variable environments, identifying promising candidates for variety development and release as cultivars in Khyber Pakhtunkhwa, Pakistan.

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