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Application of AMMI and GGE biplot to analyse the stability and G X E interaction of buckwheat genotypes in Prayagraj

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Abstract

Buckwheat (*Fagopyrum* sp.) is a nutritionally rich and climate-resilient crop; however, its genetic potential for consistent performance under variable environmental conditions is still underexploited. To address this gap, the present study assessed genotype-by-environment (G×E) interaction effects on seed yield across 15 buckwheat genotypes evaluated in three distinct environments using AMMI and GGE biplot models. Combined ANOVA revealed significant contributions of genotype (G), environment (E), and their interaction (G×E) to yield variability, indicating strong differential responses among genotypes. AMMI analysis identified G5, G15, and G14 as the highest-yielding genotypes, while G8, G10, G9, and G7 exhibited remarkable stability across environments. The GGE biplot, which accounted for 95.9% of total variation through the first two principal components, provided clear insights into genotype performance and interaction patterns. The "which-won-where" analysis delineated three mega-environments, with G5 dominating in E1, G13 in E2, and G15 in E3. Among the test sites, E3 emerged as the most discriminating and representative environment for genotype evaluation. Considering mean performance, genotypes G15, G5, and G14 were superior yielders, while G14, G8, and G7 demonstrated broad adaptability and high stability. Overall, G15 was identified as the ideal genotype for favourable conditions, whereas G14 combined high yield with wide environmental adaptability. These results offer valuable genetic resources and insights for developing resilient buckwheat varieties suited to diverse and challenging agro-climatic conditions.

1. INTRODUCTION

Rapid population growth and changing dietary demands have intensified global concerns regarding food and nutritional security (Usman et al., 2022). Diversification of cropping systems through the inclusion of nutrient-dense and climate-resilient crops is therefore imperative. In this context, pseudocereals have gained increasing attention due to their superior nutritional composition, adaptability to marginal environments, and potential contribution to sustainable agriculture. Among pseudocereals, buckwheat (*Fagopyrum spp*.) represents a strategically important crop. The two major cultivated species *Fagopyrum esculentum* and *Fagopyrum tataricum* are valued for their high-quality protein, balanced amino acid profile, dietary fiber, minerals, and bioactive compounds such as flavonoids. Beyond its nutritional attributes, buckwheat contributes significantly to agroecosystem sustainability. It functions effectively as a short-duration crop, enhances biodiversity, suppresses weeds through rapid canopy development, improves soil health as a cover crop, and supports ecological restoration in low-input systems. Furthermore, the gluten-free nature and established health-promoting properties of buckwheat have strengthened its recognition as a functional food. Moreover, buckwheat is considered a resilient alternative to wheat under extreme drought conditions (Martínez-Goñi et al., 2023), making it valuable for climate-smart agriculture.

Plant breeders continually work to enhance crop yield, quality, and resilience in the face of increasing biotic and abiotic stresses (Irfan Ullah et al., 2021; Alambo et al., 2022; Jędzura et al., 2022). Evaluating genotypes for consistent performance across diverse environments is essential for strengthening global food security. Modern breeding programs therefore prioritize developing competitive, stable, and high-yielding genotypes suited to a wide range of environmental conditions (Pour-Aboughadareh et al., 2022; Souza et al., 2023; Khare et al., 2024). However, genotype adaptability and stability are strongly influenced by genotype-by-environment (G×E) interaction (Biswas et al., 2014; Goa et al., 2022; Azon et al., 2023; Kondombo et al., 2024). Large G×E interactions weaken the direct association between phenotypic expression and genetic potential, complicating the selection of superior genotypes. Understanding the nature and magnitude of G×E interaction is therefore crucial for efficient evaluation and selection. Bilbro and Ray (1976) emphasized that incorporating adaptation and stability parameters alongside yield greatly improves the characterization of advanced breeding lines. Typically, the decision to release a genotype is based on its comparative performance against standard cultivars across multiple seasons. Through systematic screening and selection, breeders can accelerate genetic progress by identifying genotypes exhibiting broad adaptability and high stability before their release as cultivars (Atlin et al., 2017; Snowdon et al., 2020). Consequently, studies on stability and adaptation remain indispensable for determining whether genotypes are suitable for cultivation across wide or specifically targeted environments.

Several statistical methods are available for analysing genotype stability and adaptation, among which AMMI and GGE biplot models are the most widely used in multi-environment trials. The AMMI model captures both additive main effects and multiplicative interaction effects (Baraki et al., 2020; Krishnamurthy et al., 2021; Pramanik et al., 2024), while GGE biplot analysis visualizes genotype performance and genotype-by-environment interaction patterns (Saeidnia et al., 2023; Hossain et al., 2023; Yan et al., 2000). These tools effectively interpret complex multi-environment data and are especially useful in plant breeding programs (Yan, 2021). By simplifying interaction patterns, AMMI and GGE biplots help identify superior genotypes with high stability, broad adaptability, or specific environmental suitability (Yan et al., 2007). Since farmers require cultivars that consistently deliver high yield and desirable agronomic traits, identifying such stable and productive genotypes remains a key challenge for breeders. The ongoing scarcity of widely adaptable, high-yielding cultivars across diverse agro-ecological zones underscores the need for robust stability analyses.

Despite the agricultural importance of the agroclimatic region of Prayagraj, buckwheat cultivation is constrained by environmental variability and the limited availability of high-performing genotypes. Evaluating genotype performance under region-specific conditions is essential to enhance yield stability and local food security. Therefore, this study aimed to identify buckwheat genotypes exhibiting stable performance across diverse environments within the Prayagraj region, as well as those showing superior performance under specific environmental conditions.

2. MATERIALS AND METHODS

2.1. Experimental Materials and Experimental Design

For this study, 15 buckwheat genotypes were obtained from the Germplasm Evaluation Division, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India. The genotypes comprised *Fagopyrum esculentum* and *Fagopyrum tataricum* accessions, as listed in Table 1, along with their respective accession/genotype numbers. The experiment was conducted during three consecutive Rabi seasons, i.e., 2020–21 (E1), 2021–22 (E2), and 2022–23 (E3). The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications in each of the three environments (Vadala

et al., 2025). Each experimental plot had an area of 3.75 m², comprising three rows of 5 m length, with a spacing of 25 cm between rows and 10 cm between plants within a row (Raghav et al., 2025).

Table 1
Buckwheat genotypes used in the study and their source information

S. No.	Genotype/Accession No.	Species	Source
1	IC-46160	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
2	IC-59921	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
3	IC-16552	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
4	IC-356112	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
5	IC-47929	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
6	IC-341674	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
7	IC-32779	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
8	IC-447576	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
9	EC-216635	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
10	EC-332723	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
11	SHIMLA-B-1	*Fagopyrum tataricum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
12	VL-7	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
13	PRB-1	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
14	CGBW 20 – 1	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India
15	CGBW 20 – 2	*Fagopyrum esculentum*	Germplasm Evaluation Division, ICAR-NBPGR, New Delhi, India

2.2. Data Collection

For response variable i.e., seed yield per plant (g), average of five randomly selected plants from each experimental unit (plot) were used. The five representative plants per plot were randomly selected from the central row excluding the border rows (Destaw et al., 2024).

2.3. Analysis of variance (ANOVA)

Data was subjected to combined analysis of variance (ANOVA) (Fisher, 1935) across environments to estimate the existence variations among the treatments, years and year × treatments. Bartlett's tests of homogeneity of variances were used to determine the homogeneity of the error variances of the individual location experiments.

2.4. AMMI Analysis

AMMI model significantly enhances the precision of selection in breeding programme and facilitates the visualization of adaptive responses across multi-environmental conditions. AMMI analysis was performed using the following model Hu (2014).

$$Y_{ij} = \mu + G_i + E_j + \sum_{K=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

(Y_{ij}) is the response of genotype *i* in environment *j*; (\mu) is the grand mean; (G i) and (E j) are genotype and environment effects; (\lambda k) is the eigenvalue of axis *k*; (\alpha_{ik}) and (\gamma_{jk}) are genotype and environment PCA scores; (n) is the number of components retained; and (\varepsilon_{ij}) is the error term.

2.5. GGE Biplot Analysis

Based on the singular value decomposition of the first two principal components, the model for a GGE biplot is:

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

(Y_{ij}) is the response of genotype *i* in environment *j*; (\mu) is the grand mean; (\beta_j) is the environmental main effect; (\lambda_k) is the eigenvalue of axis *k* (with (\lambda_1) and (\lambda_2) as singular values of PC1 and PC2); (\xi_{i1}) and (\xi_{i2}) are genotype scores for PC1 and PC2; (\eta_{j1}) and (\eta_{j2}) are environment eigenvectors for PC1 and PC2; and (\var epsilon_{ij}) is the error term (Yan and Hunt, 2002; Yan et al., 2002).

3. RESULTS

3.1. AMMI biplot analysis

The Additive Main Effects and Multiplicative Interaction (AMMI) analysis was conducted to investigate the genotype-by-environment (G × E) interaction and determine the stability of 15 genotypes (G1-G15) across three different environments (E1, E2, E3) for seed yield (SY). The results are visualized in the AMMI1

biplot (Yield vs. PC1) and the AMMI biplot (PC1 vs. PC2).

3.2. AMMI 1 Biplot: Mean Performance and Stability

The differences between genotypes in terms of direction and magnitude along the X-axis (yield) and Y-axis (IPCA 1 score) are significant in the AMMI 1 biplot. The displacement along the X-axis indicates differences in main (additive) effects, while the displacement along the Y-axis indicates differences in interaction effect. The first two principal components (PC1 = 79.6%, PC2 = 20.4%) together explain ~ 100% of the G×E interaction, making this plot highly informative. Genotypes located near the origin—such as G7, G10, G9, G8, and G1—show minimal interaction and therefore exhibit the highest stability across environments. The environment vectors indicate that E3 is the most discriminating and informative testing environment, while E1 and E2 show contrasting interaction patterns. Genotype performance aligns with environment direction: G5 performs best in E1, G13 in E2, and G15 in E3 (Fig. 1).

3.3. AMMI 2 Biplot: Specific Genotype-Environment interactions

In this plot (Fig. 2), genotypes such as G5, G15, and G14, which lie far to the right with moderate or high PC1 scores, show high yield potential but stronger interaction. Genotypes near the origin i.e., G7, G8, G9, G10 are broadly adapted to all tested environments. G11 shows a strong positive interaction with Environment E1. G6 is specifically adapted to Environment E2. G15 shows a strong positive association with Environment E3. G5, the highest-yielding genotype overall, is far from the origin. Genotypes such as G6 with large negative PC1 scores indicate specific adaptation to environments with negative interaction patterns. Environments E1 and E3 have strong positive interactions, while E2 shows strong negative.

3.4. GGE biplot analysis

3.5. Which-won-where:

The What-Won-Where GGE biplot (Fig. 3,4) identified three sectors, each with a different winning genotype (Mullualem et al., 2024). The polygon connecting genotypes farthest from the origin (G6, G13, G14, G5, G10, G11) highlights those most responsive to environmental variation. Environment E2 falls into the sector where G6 is vertex. Similarly, E1 and E3 cluster in a sector where G5 and G15 dominate. Genotypes positioned near the origin such as G1, G2, G3, G4, G7, G8, G12 show consistent but moderate performance,

3.6. Comparison of the environments:

In this biplot (Fig. 5), E1 and E3 have longer vectors. Conversely, E2 shows a moderate vector length. The angle between environment vectors reflects their correlation: the smaller angle between E1 and E3 suggests a strong positive relationship, A wider angle between E2 with E1 and E3 indicates weaker correlations. However, In the biplot, the vectors for environments E1, E2, and E3 all form acute angles (less than 90°) with each other. Genotypes positioned closer to an environmental vector perform better in that particular environment. Here, G15 and G5 align closely with E1, while G13 and G14 show better association with E3. Genotypes near the origin (e.g., G1–G4, G7, G8) exhibit average performance with stable but less responsive behavior.

3.7. Discriminating ability and representativeness of test environments

The discriminating ability of each test environment is indicated by the length of its vector from the biplot origin, where longer vectors reflect stronger power to distinguish among genotypes (Memon et al., 2023). In this GGE biplot (Fig. 6), E3 shows the longest vector, making it the most effective environment for identifying genotypic variation. In contrast, E1 and E2 have much shorter vectors. The representativeness of an environment is determined by the angle between its vector and the Average Environment Axis (AEA). In this biplot, all three environments form small, acute angles with the AEA. Among them, E3 shows the smallest angle, making it the most representative and ideal environment for selection.

3.8. Mean vs Stability

In (Fig. 7), G14, G8, G7, G3, G1 and G10 are the most stable as they are positioned very close to the AEA line whereas, G5, G11, and G6 are the least stable, indicated by their large distance from the AEA line and based on their projection on the abscissa towards the ordinate. Genotypes were partitioned into two groups based on their ordinate values, namely those that produced yields above and below the average. G15, G5, G14 and G13 exhibited means that were significantly higher than the average means. In contrast, G10 and G9 exhibit values that are comparatively lower than the mean. Genotypes located further to the right along the AEA have higher mean yields. The arrow's direction indicates the order of varieties in ascending rank based on their performance for higher trait values, as indicated on the AEA abscissa. The order of the genotype is as follows: G15 > G5 > G14 > G13 > G6 > G8 > G12 > G7 > G2 > G11 > G4 > G3> G1 > G9 > G10.

4. DISCUSSION

Buckwheat is an ancient and globally cultivated crop valued for its nutritional richness and cultural significance **(**Rayeen, 2025**).** It forms the basis of iconic foods such as Japanese soba noodles, Eastern European kasha, French galettes, and Italian pizzoccheri, while in India, *kuttu ka atta* holds traditional importance during religious fasting. Its successful integration into diverse cuisines highlights its long history of cultivation across varied climatic regions. However, the commercial expansion of buckwheat is hindered by its low and highly unstable seed yield, a major agronomic limitation reported across studies **(**Jacquemart et al., 2012; Naik et al., 2024). This instability largely stems from Genotype-by-Environment Interaction (GEI), where genotypes respond differently across environments, causing frequent shifts in yield rankings and complicating the selection of superior cultivars **(**Begna, 2020**).** While GEI has been extensively characterized in major cereals such as wheat, rice, and maize, buckwheat remains an under-researched orphan crop, lacking robust multi-environment trial (MET) datasets. This knowledge gap restricts breeding efforts, as understanding adaptation patterns is essential for developing stable, high-yielding varieties.

4.1. AMMI biplot analysis

The Additive Main Effects and Multiplicative Interaction (AMMI) model is a powerful statistical tool that combines analysis of variance for the main effects of genotype and environment with principal component analysis for the interaction effects. Hu (2014**)** showed that ranking of genotype stability models were AMMI, ANOVA, Shukla's stability variance model, finlay-Wilkinson model and Eberhart-Russell model but in this study ranking of best fit models are Finlay-Wilkinson model, AMMI model, Eberhart-Russell model and Shukla's stability variance model. He showed that AMMI model was the best fit model for identifying stable genotype. The analysis of AMMI biplot for yield and yield attributing traits across the fifteen genotypes and environments provides valuable findings into the yield performance and stability of various genotypes. In this study, the AMMI analysis was instrumental in visualizing the complex GEI for seed yield. The AMMI1 biplot, which plots the main effect (mean seed yield) against the IPCA1 scores (the largest component of the GEI), provided a clear and simultaneous assessment of genotype performance and stability. In this biplot, the mean seed yield of genotypes and environments is plotted on the x-axis (abscissa), while the scores of the first interaction principal component axis (IPCA1) are plotted on the y-axis (ordinate). The displacement of genotypes along the x-axis reflects their average yield potential, while their displacement along the y-axis indicates their level of interaction with the environments, a proxy for stability.

The AMMI1 biplot uses the horizontal axis to represent mean seed yield and the vertical axis (IPCA1) to indicate stability. Genotypes G5, G15, and G14 had the highest mean yields, while G10 was the lowest. Stability was reflected by IPCA1 values close to zero; thus, G8, G10, G9, and G7 were the most stable across environments. Genotypes with large positive or negative IPCA1 scores, such as G5, G15, G6, and G11, were unstable and showed specific adaptation to particular environments. This helps breeders identify genotypes combining desirable yield and stability. The AMMI2 biplot (IPCA1 vs. IPCA2) provided further insight into specific genotype–environment interactions. Genotypes appearing in the same quadrant as an environment and far from the origin showed strong positive interaction and specific adaptation. G11 was best suited to environment E1, G6 to E2, and G15 to E3. Genotypes near the origin—G7, G8, G9, and G10—showed broad adaptability, aligning with the observations of Krishnamurthy et al. (2021), who reported that genotypes close to zero IPCA scores are the most stable. Genotypes positioned farther away, including G5, G11, and G15, display stronger interactions and tend to perform well only in specific environments, a pattern similarly noted by Yan et al. (2007) **and** Pramanik et al. (2024**).** Anandan et al. (2009) used AMMI analysis in rice and found that high-yielding but interaction-sensitive genotypes tend to lie far from the origin, similar to G5 and G15 in the present biplot. Although G5 was the highest yielder, its high interaction scores indicated instability and environment-dependent performance. In contrast, G14 combined high yield with low interaction effects, making it a promising and widely adapted genotype. Overall, the AMMI analysis supports targeted and efficient genotype selection.

4.2. GGE biplot analysis

The GGE biplot is a powerful tool for analysing multi-environment trial data, integrating both genotype (G) performance and genotype-by-environment interaction (GE). A key feature is the polygon, or "which-won-where," view that identifies winning genotypes in specific environments, highlights crossover interactions, and defines mega-environments **(**Mullualem et al., 2024). The What-Won-Where GGE biplot identifies the best-performing genotypes across environments by forming a polygon that connects genotypes farthest from the origin, representing those most responsive to environmental variation. In this study, the biplot divided the environments into three distinct sectors, each with a different winning genotype. Vertex genotypes such as G6, G13, G14, G5, G10, and G11 were positioned at the extremes, indicating high environmental responsiveness. These findings are consistent with previous studies, where Yan and Rajcan (2002) and Yan and Tinker (2006) demonstrated that polygon views effectively reveal mega-environments and winning genotypes for targeted breeding. The biplot is constructed using IPCA1 and IPCA2, the first two principal components derived through singular value decomposition of environment-centred yield data. These components effectively summarise genotype performance patterns and interaction effects, making the GGE biplot widely applicable in crop improvement research **(**Yan et al., 2001; Erdemci, 2018**).** The first two principal components of the GGE model for this dataset explained a cumulative 95.9% (PC1 = 76.9%, PC2 = 19.0%) of the total G + GE variation.

The GGE biplot analysis provided a highly accurate and reliable representation of the genotype–environment data, clearly revealing a strong crossover interaction. Mega-Environment 1 consisted solely of E2, where G13 was the winning genotype. Mega-Environment 2 contained only E3, dominated by G15, while Mega-Environment 3 included only E1, where G5 performed best. This pattern indicates that the test environments are not interchangeable and represent different agroecological zones. Although G10 and G6 appeared as vertex genotypes, no environment fell within their sectors, meaning their high responsiveness was consistently associated with inferior yield. Such genotypes are unsuitable for cultivation or use as parents, as they consistently underperform across environments. The GGE biplot also enabled evaluation of the environments based on discriminating ability and representativeness. The red vectors represent the test environments, where the length of each vector indicates the environment's discriminating ability (longer = better at distinguishing genotypes), and the angle between vectors shows their similarity (smaller angle = more correlated). The red diamond marks the average environment, while the blue point marks the ideal environment, surrounded by concentric circles that depict increasing "ideality." The vectors (E1, E2, E3) originate from the biplot origin, and their lengths indicate discriminating power. The environmental vector view of GGE biplot, the line adjoining testing location or environment to the midpoint of biplot are considered as environment lines or vectors **(**Shojaei et al., 2022). The length of an environment vector indicates its power to differentiate genotypes. E3, with the longest vector, was identified as the most discriminating environment, whereas E1 and E2 offered weaker differentiation. These interpretations are consistent with earlier findings where the environment view effectively identified the most informative testing sites **(**Yan & Tinker, 2006**).** Similar patterns were reported in rice by Anandan et al. (2009) and in maize by Fan et al. (2007), where environments with longer vectors were identified as key locations for genotype differentiation. Representativeness, determined by the angle with the Average Environment Axis, was also highest for E3, which had the smallest angle. Thus, E3 emerged as the ideal test environment, combining both high discrimination and strong representativeness, making it the most efficient location for future selection and germplasm evaluation. The GGE biplot genotype view was used to evaluate the tested genotypes based on their mean performance and stability relative to a defined "ideal genotype". The average environment coordination (AEC) approach is fundamental for identifying genotypes that combine high yield potential with consistent performance across environments graphically **(**Jocković et al., 2019). The single arrowhead line passing through the biplot's origin and line points towards higher mean values is known as the AEC abscissa. There is an additional line that passes through the origin of biplot and also perpendicular to AEC is termed as AEC ordinate. Closer the genotype to AEC abscissa, the

more consistent or stable across various test environments (Kona et al., 2024). This GGE biplot shows the genotype-focused view for seed yield (SY), illustrating how genotypes perform and how stable they are across environments using the first two principal components (PC1 = 76.9%, PC2 = 19%). The dashed blue line represents the average environment axis (AEA), which is the main indicator of mean performance: genotypes positioned further to the right along this axis have higher average yield, while those to the left perform below average. The concentric circles around the blue diamond indicate the ideal genotype, meaning high performance and high stability; therefore, genotypes closest to this point (e.g., those near the centre of the circles) are both productive and consistent. Distance from the AEA indicates instability, so genotypes placed far from the axis show stronger genotype-by-environment interaction and less predictable performance. The genotype-focused biplot ranked genotypes on mean yield and stability. Yield ranking (highest to lowest) was: G15 > G5 > G14 > G13 > G6 > G8 > G12 > G7 > G2 > G11 > G4 > G3 > G1 > G9 > G10. Stability was highest in G14, G8, G7, G3, G1, and G10, while G5, G11, and G6 were least stable. The close agreement between AMMI and GGE outcomes reinforces the reliability of these conclusions. The above results for AMMI and GGE biplot analysis for yield and its component traits for buckwheat and other crops are in conformity with the findings of earlier workers viz., **Dehgalni et al. (2006)**, Rodriguez et al. (2007), **Jalata (2011)**, Mohammadi et al. (2013), Kumar et al. (2016).

The AMMI and GGE biplot analyses clearly demonstrated strong genotype, environment, and G×E interaction effects influencing buckwheat seed yield. AMMI results showed that while genotypes G5, G15, and G14 produced the highest yields, they also exhibited strong interaction effects, indicating instability and environment-specific performance. In contrast, G7, G8, G9, and G10 were the most stable, showing minimal interaction and broad adaptability. The GGE "which-won-where" analysis revealed distinct mega-environments: G13 performed best in E2, G15 in E3, and G5 in E1, confirming the presence of strong crossover interactions. Environment evaluation identified E3 as the most discriminating and most representative site for selecting superior genotypes. The genotype-focused GGE view ranked G15, G5, G14, and G13 as top-yielding genotypes, whereas G14, G8, G7, and G3 were among the most stable. The close agreement between AMMI and GGE results strengthens confidence in identifying suitable genotypes and environments for buckwheat improvement.

5. Conclusion

The study demonstrated that buckwheat seed yield is strongly influenced by genotype, environment, and their interaction (G×E), highlighting the need for multi-environment evaluation in breeding programs. AMMI and GGE biplot analyses provided a robust and complementary understanding of genotype performance and stability across three contrasting environments. AMMI identified G5, G15, and G14 as the highest-yielding genotypes, while G8, G10, G9, and G7 exhibited the greatest stability. The GGE biplot confirmed strong crossover interactions and defined three distinct mega-environments, with G5, G13, and G15 emerging as the respective winners. Among the test sites, E3 was the most discriminating and representative environment, making it the most effective location for future selection and evaluation. These insights allow targeted genotype recommendations based on breeding goals. For maximizing yield under favourable conditions, G15 is the most suitable genotype, particularly for E3. For broad adaptability, G14 is the strongest candidate, as it uniquely combines high yield with stability. Additionally, highly stable genotypes such as G8 and G7, though moderate yielders, provide valuable resilience traits for developing stress-tolerant cultivars. Overall, this study provides a strong foundation for strategic buckwheat improvement by enabling the selection of widely adapted or specifically tailored genotypes to enhance productivity and sustainability.

Declarations

1. **FUNDING**

The authors received no financial support for the research, authorship, or publication of this article.

2. **ETHICS AND CONSENT TO PARTICIPATE**

The plant genetic resources used in this study were obtained from the ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India. No wild plant material was collected by the authors for this study. The use of the *Fagopyrum* germplasm was conducted in accordance with applicable institutional and national guidelines and regulations governing the use of plant genetic resources.

3. **PERMISSION TO COLLECT PLANT MATERIAL**

The buckwheat germplasm used in this study was obtained from the Germplasm Evaluation Division, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India. The germplasm was received for research use, and the research based on these accessions was undertaken with the permission of the National Genebank, ICAR-NBPGR.

4. **DATA AVAILABILITY STATEMENT**

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

5. **CONFLICT OF INTEREST**

The authors declare no conflict of interest.

6. **COMPLIANCE WITH ETHICAL STANDARDS**

This study was conducted in accordance with institutional and ethical guidelines. The research did not involve human participants or animals. All experimental procedures were performed following standard laboratory and biosafety protocols.

Author Contribution

Rajkaran Tripathi conceptualized the study, conducted the experiments, performed data interpretation, and prepared the original manuscript draft. Nidhi Pandey contributed to experimentation, data collection, literature review, manuscript preparation, and editing. Dixit Tagra and Mohd Harun contributed to statistical analysis and interpretation of experimental data. Devanshi, Harsh Yadav and Sandeep Nalla provided the two-year experimental dataset used for stability analysis. J.C. Rana and G.P. Singh provided the necessary genotypes and supported germplasm-related resources essential for the study. Praveen Kumar Singh, Kuldeep Tripathi, and Satish Kumar Yadav contributed to the conceptualization, planning, and overall research strategy. Vaidurya Pratap Sahi, as the Master's supervisor, provided guidance, supervision, and critical inputs throughout the research process. All authors reviewed and approved the final manuscript.

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Figures

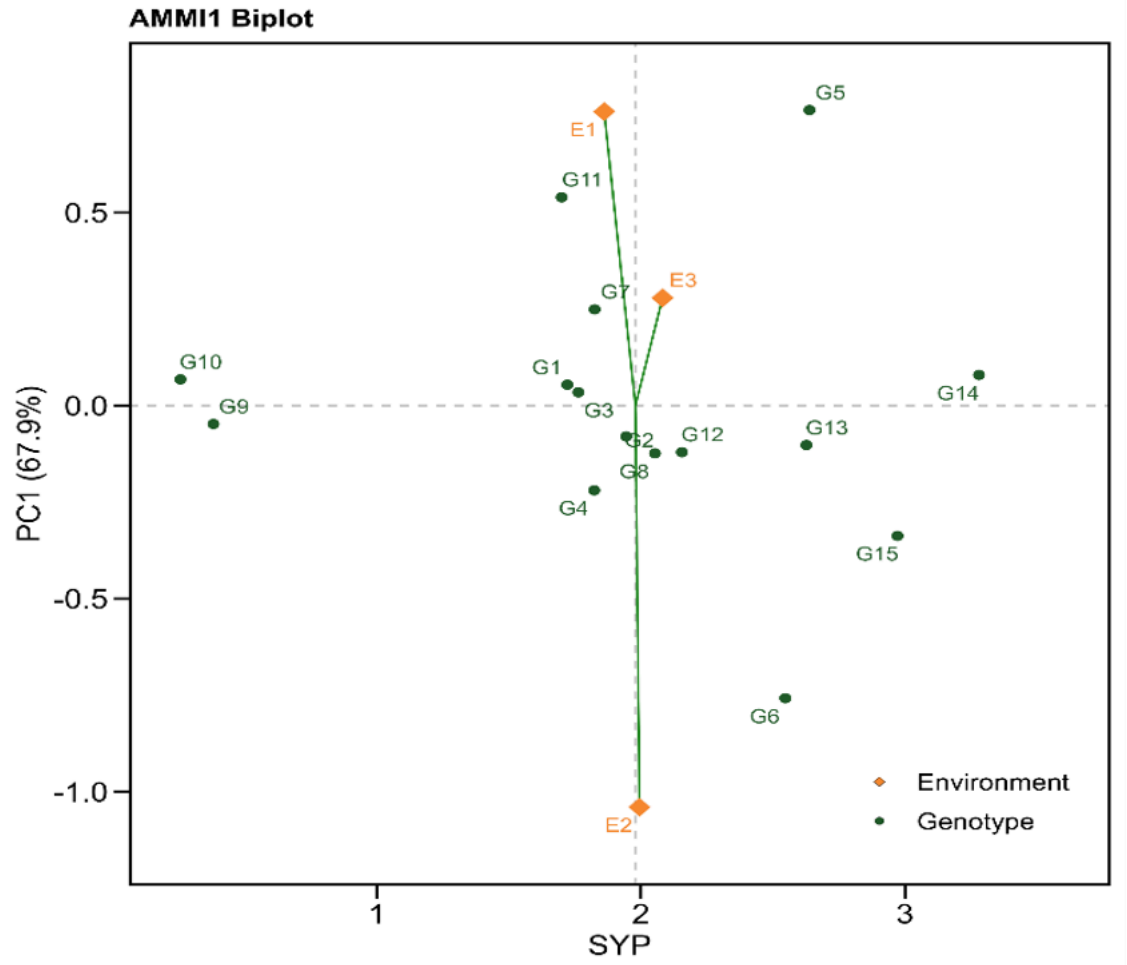


Figure 1

AMMI 1 biplot for seed yield per plant (g)

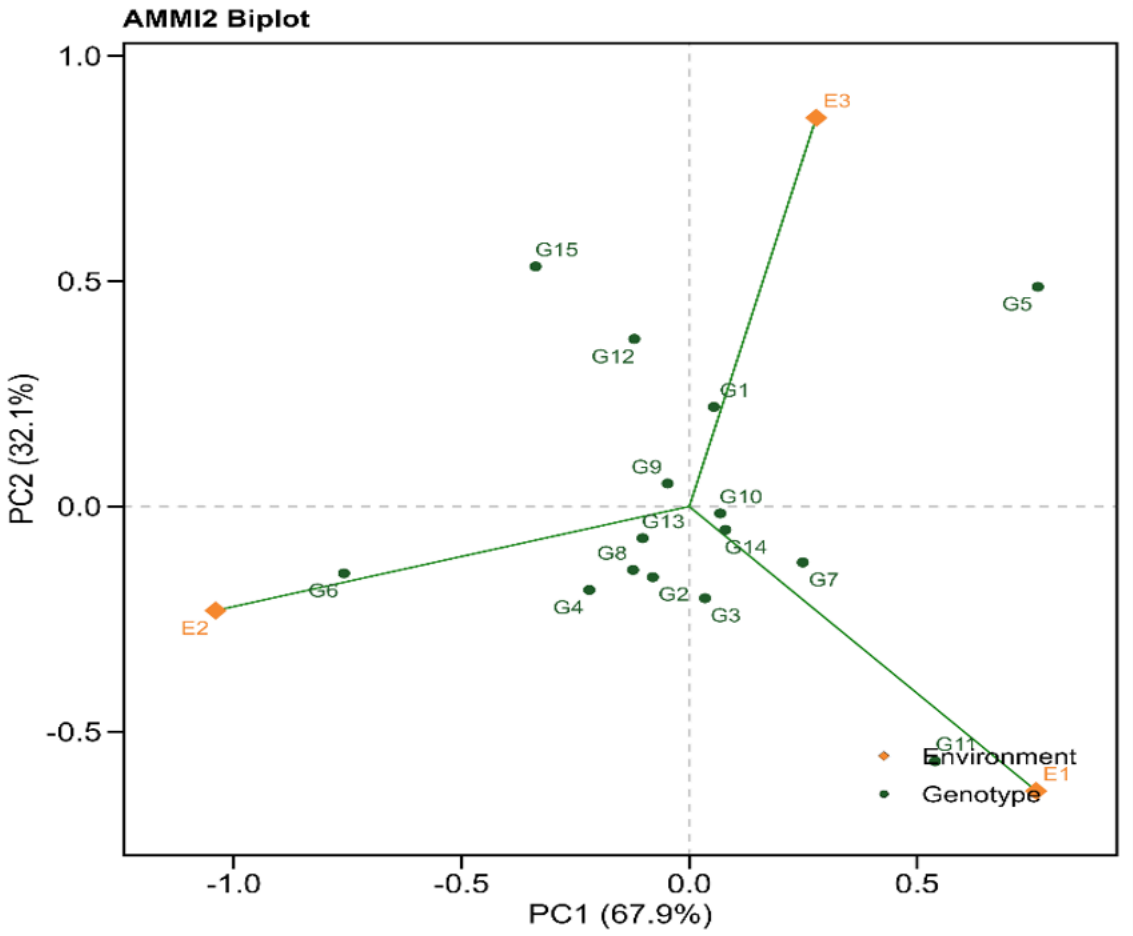


Figure 2

AMMI 2 biplot: specific genotype environment interaction for seed yield per plant (g)

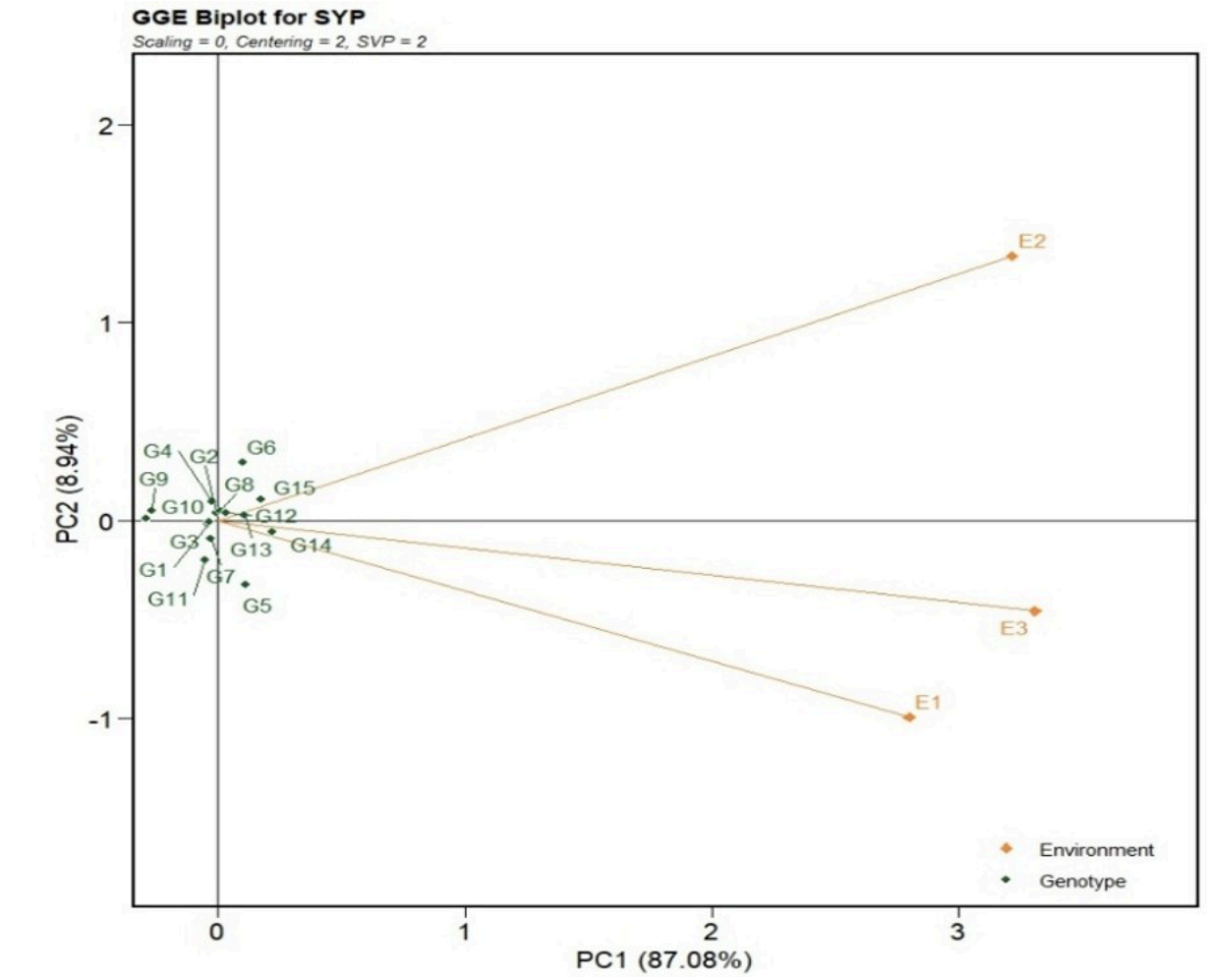


Figure 3

Genotype by Genotype-Environment interaction biplot for seed yield per plant (g)

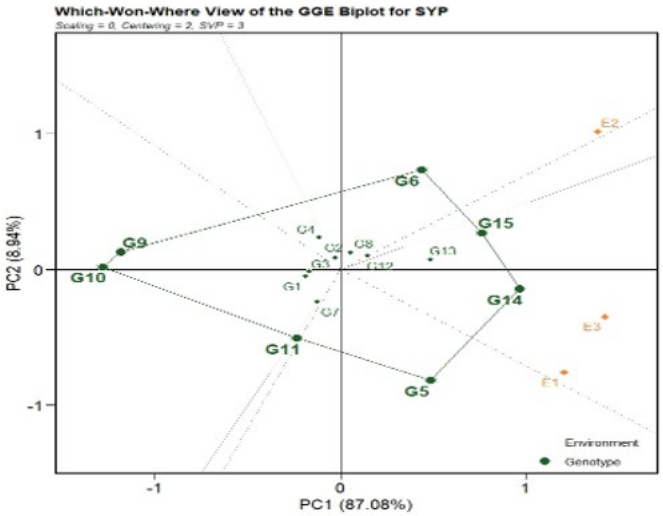


Figure 4

Which-won-where view of the GGE Biplot for Seed yield per plant (g)

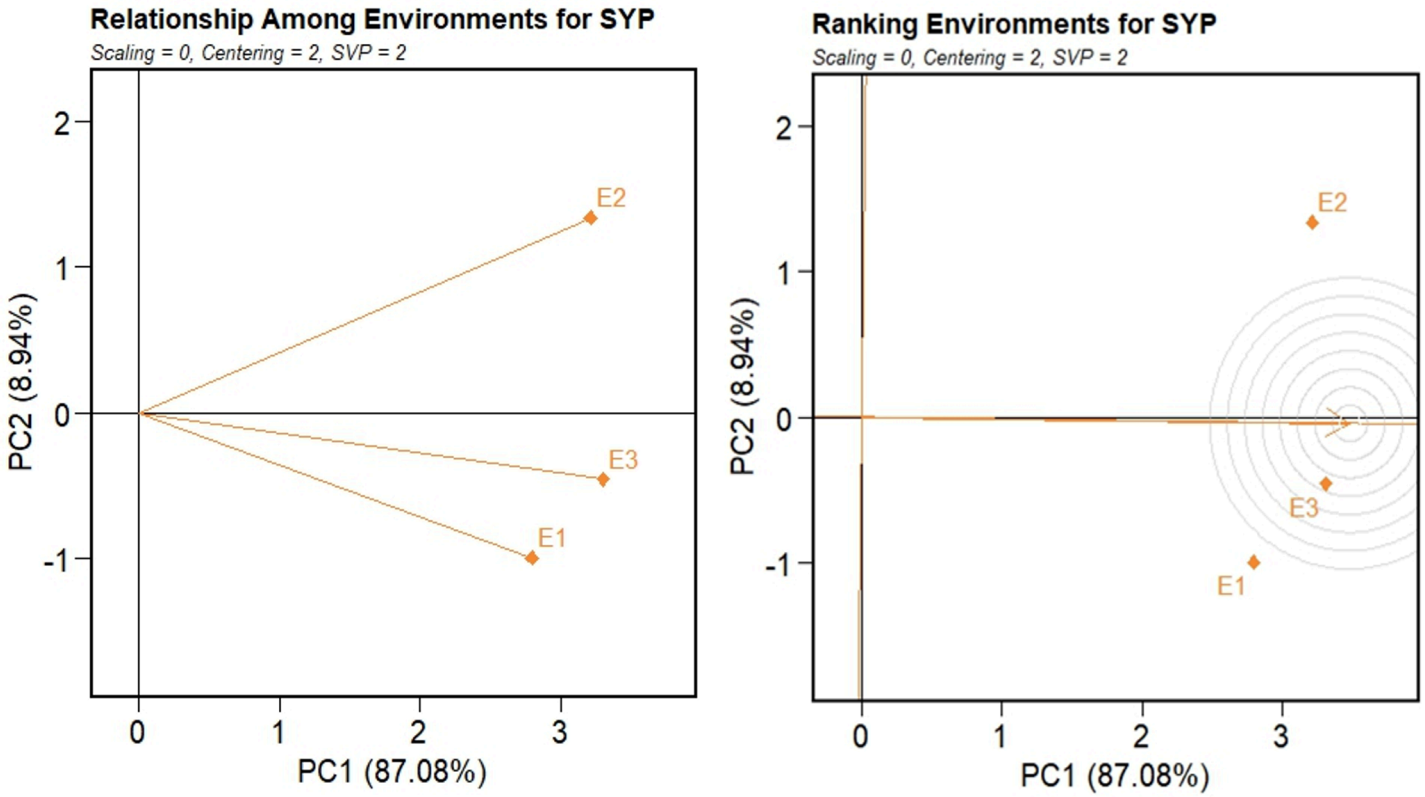


Figure 5

Relationship and Ranking environment for seed yield per plant (g)

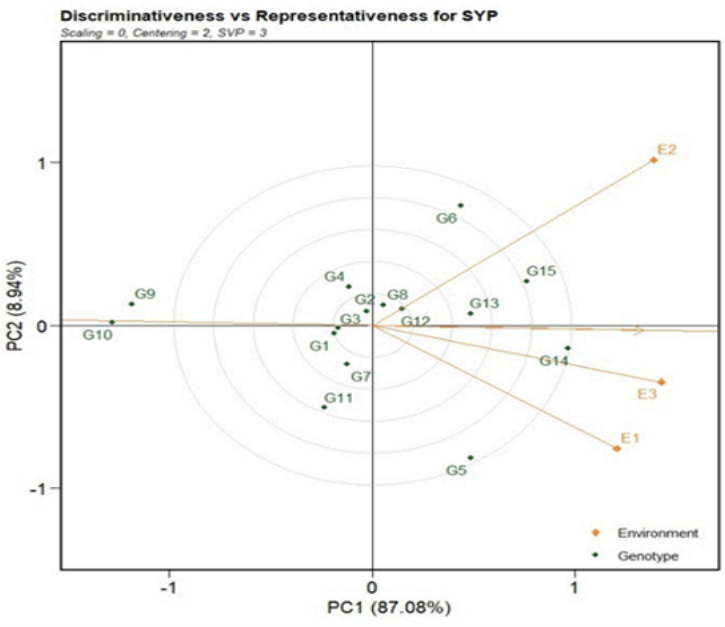


Figure 6

Discriminativeness vs Representativeness for seed yield per plant (g)

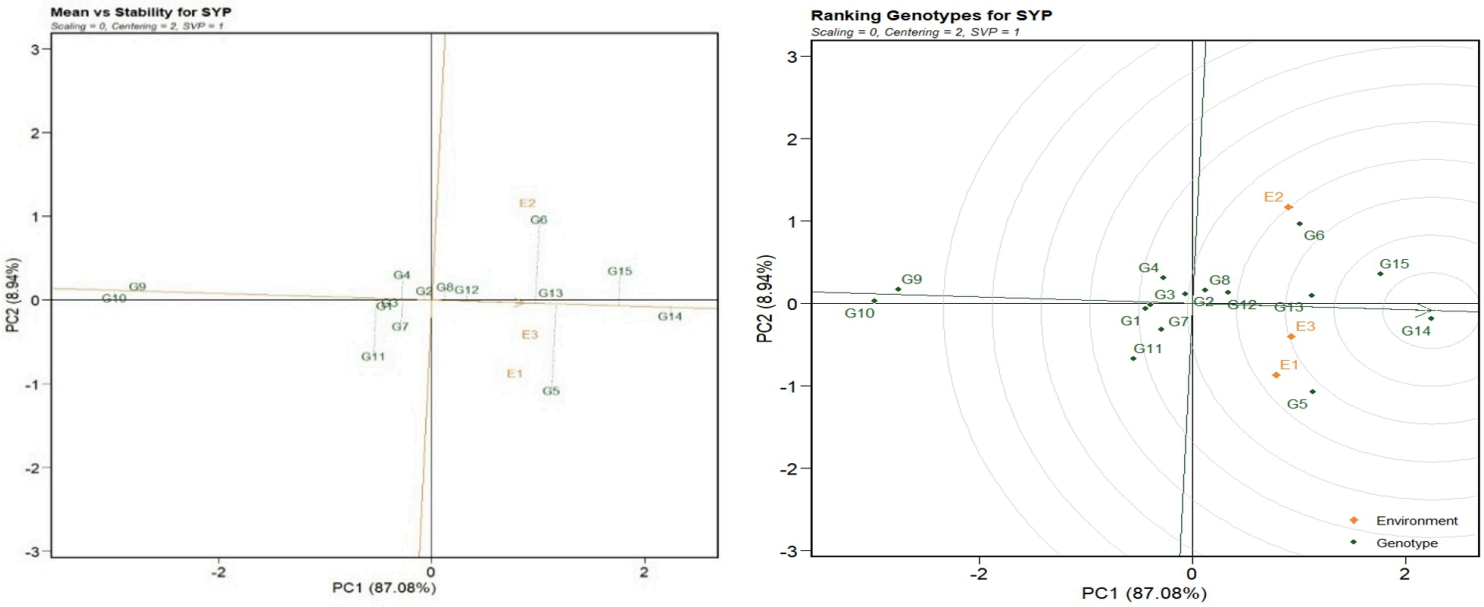


Figure 7

Mean vs Stability and Ranking genotypes for seed yield per plant (g)