Biological Forum
an International Journal **17(5): 163-167(2025)**
ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Deciphering Yield Stability and Genotype × Environment Interaction in Okra (*Abelmoschus esculentus* L. Moench) under Multi-season Evaluation

Sandeep N.*, Dushyantha Kumar B.M. and Vishal Reddy
Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, 577201 (Karnataka), India.

(Corresponding author: Sandeep N.)*

(Received: 05 March 2025; Revised: 10 April 2025; Accepted: 08 May 2025; Published online: 29 May 2025)
(Published by Research Trend)

DOI: https://doi.org/10.65041/BiologicalForum.2025.17.5.25

ABSTRACT: Genotype × environment interaction (GEI) poses a major challenge in identifying stable and high-yielding okra genotypes across diverse seasons. The present study evaluated the yield stability of 24 okra genotypes, including released varieties and advanced breeding lines, across three environments (Rabi 2020, Kharif 2020 and Kharif 2021) using a randomized complete block design with two replications. Fruit yield per plant data were subjected to pooled ANOVA, Eberhart and Russell regression model and Additive Main Effects and Multiplicative Interaction (AMMI) analysis. Pooled ANOVA revealed highly significant effects of genotypes, environments and GEI, indicating differential genotype responses across seasons. AMMI analysis showed that the first two interaction principal components (IPCA1 and IPCA2) accounted for 79.5% and 20.5% of GEI variation, respectively, cumulatively explaining 100% of the interaction. Based on mean performance, regression coefficient ($b_1 \approx 1$) and non-significant deviation from regression (s^2di), genotypes such as Arka Anamika, Parbhani Kranti, UAHS-11, UAHS-3 and Varsha Upahar were identified as widely adapted and stable. Genotypes UAHS-17, UAHS-18 and UAHS-19 exhibited higher b_1 values (>1) with superior mean yield, indicating specific adaptation to favorable environments, particularly Kharif 2021. AMMI biplots further corroborated these findings by positioning stable genotypes near the origin, while season-specific adaptation was reflected by larger IPCA scores. The combined use of Eberhart-Russell and AMMI models provided complementary insights, facilitating reliable identification of stable and high-yielding okra genotypes for diverse agro-ecologies.

Keywords: Okra, genotype × environment interaction, stability analysis, Eberhart–Russell, AMMI, yield adaptability.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is one of the most important vegetable crops cultivated extensively in tropical and subtropical regions, particularly in India, owing to its adaptability, short duration, nutritional richness, and year-round market demand (Elkhalifa *et al.*, 2021). The crop serves as a vital source of dietary fiber, vitamins, minerals and bioactive compounds, while also providing substantial income to small and marginal farmers. Despite its economic and nutritional importance, okra productivity remains highly unstable across seasons and locations, primarily due to pronounced environmental variability and differential genotype responses (Singh and Nigam 2023).

Yield expression in okra is a complex quantitative trait governed by multiple genetic factors and strongly influenced by environmental conditions such as temperature, rainfall distribution, humidity, soil fertility, and photoperiod. Seasonal fluctuations, particularly between Rabi and Kharif seasons, often lead to inconsistent genotype performance (Haq *et al.*, 2023; Venkatesh *et al.*, 2023). A genotype exhibiting superior yield in one environment may perform poorly in another, thereby complicating varietal selection and recommendation. This phenomenon, known as genotype × environment interaction (GEI), poses a major challenge to plant breeders aiming to develop widely adapted and stable cultivars (Mullualem *et al.*, 2024).

Multi-environment trials (METs) are therefore indispensable in crop improvement programs to evaluate genotype performance across diverse environments. However, simple mean-based comparisons are inadequate in the presence of significant GEI. To address this limitation, several statistical models have been developed to quantify and interpret GEI and to identify stable genotypes (Smith *et al.*, 2021). Among these, the regression-based model proposed by Eberhart and Russell (1966) has been extensively used due to its simplicity and biological interpretability. According to this model, an ideal genotype should exhibit high mean yield, a regression coefficient (b_1) close to unity indicating average responsiveness and minimal deviation from regression (s^2di), reflecting stability.

Although the Eberhart–Russell model effectively captures linear responses of genotypes to environmental indices, it may fail to explain complex, non-linear interaction patterns that commonly occur in MET data. To overcome this limitation, multivariate approaches such as the Additive Main Effects and Multiplicative Interaction (AMMI) model have been developed. The AMMI model combines analysis of variance (ANOVA) for additive main effects of genotypes and environments with principal component analysis (PCA) for the multiplicative GEI component (Rodrigues *et al.,* 2016). This dual approach enhances the precision of interaction interpretation and facilitates graphical visualization through biplots.

AMMI biplots, particularly AMMI1 (mean yield vs IPCA1) and AMMI2 (IPCA1 vs IPCA2), are powerful tools for identifying stable genotypes, discriminating environments, and detecting specific adaptation patterns (Hossain *et al.,* 2023). Genotypes positioned near the origin are considered stable, whereas those with large IPCA scores exhibit specific adaptation to particular environments. Similarly, environments with longer vectors are more discriminating, while those close to the origin are more representative (Rani *et al*., 2023).

In okra, stability studies employing either regression-based or AMMI models have been reported; however, comprehensive studies integrating both approaches using the same dataset across contrasting seasons remain limited. Such integration is particularly important for strengthening varietal recommendations and enhancing selection efficiency. Therefore, the present investigation was undertaken with the following objectives: (i) to assess the magnitude and nature of GEI for fruit yield per plant in okra across three contrasting seasons, (ii) to identify stable and widely adapted genotypes using Eberhart–Russell stability parameters, and (iii) to elucidate genotype adaptation patterns through AMMI analysis and biplot interpretation. The findings are expected to provide robust insights for okra breeding programs and varietal deployment strategies under variable agro-climatic conditions.

MATERIALS AND METHODS

Experimental material and design. A total of 24 genotypes, including advanced breeding lines obtained from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, Karnataka, India, were evaluated in this stud). The experiments were conducted at the Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India, during Kharif 2020, Rabi 2020-21 and Kharif 2022. The experimental site is located at 13°55′N latitude, 75°34′E longitude, with an elevation of 640 meters. The station receives an average annual rainfall of 900 mm and has red sandy loam soil. The experiment was laid out in a randomized complete block design (RCBD) with two replications. Seeds of each genotype were sown in 5 m long rows at a spacing of 60 × 45 cm. Fruit yield per plant (FYPP) was recorded for all genotypes to assess yield performance and stability.

Statistical Analysis

Pooled Analysis of Variance (ANOVA). A pooled analysis of variance (ANOVA) across environments was conducted to assess the significance of genotypes (G), environments (E), and their interactions (G × E). Replications were considered nested within environments. This analysis allowed the identification of genotypic differences, environmental effects, and the contribution of genotype × environment interaction to variation in fruit yield per plant (FYPP).

Eberhart and Russell Stability Analysis. Genotypic stability was evaluated following the method of Eberhart and Russell (1966). Stability parameters estimated included mean yield (b_0), regression coefficient (b_1), and deviation from regression (s^2di). Genotypes with high mean yield, regression coefficient (b_1) close to 1, and non-significant deviation from regression (s^2di) were considered widely adapted and stable across environments.

AMMI Analysis. The Additive Main Effects and Multiplicative Interaction (AMMI) model was employed to further dissect the G × E interaction. The interaction was partitioned into interaction principal component axes (IPCA). Graphical representations were generated using the AMMI1 biplot, plotting genotype mean against IPCA1 scores, and the AMMI2 biplot, plotting IPCA1 against IPCA2 scores to visualize patterns of interaction between genotypes and environments. All statistical analyses, including pooled ANOVA, Eberhart and Russell stability parameters, and AMMI analysis, were performed using metan R package were employed for ANOVA, stability analysis, and generation of biplots (Olivoto and Dal'Col Lúcio 2016).

RESULTS AND DISCUSSION

Pooled Analysis of Variance. The pooled analysis of variance across three environments revealed highly significant ($p < 0.01$) effects of environments, genotypes, and genotype × environment interaction (GEI) for fruit yield per plant (Table 1). The significant environmental effect indicated substantial seasonal variability, reflecting differences in climatic conditions between Rabi 2020, Kharif 2020 and Kharif 2021. The highly significant genotypic effect demonstrated the presence of ample genetic variability among the evaluated okra genotypes, providing scope for effective selection.

Table 1: Pooled analysis of variance for fruit yield per plant in okra across three environments.

Source of Variation	df	Sum of Squares	Mean Square	Pr (>F)
Genotypes (GEN)	23	123,761.94	5,380.95**	1.81×10^{-13}
ENV + (GEN × ENV)	48	32,361.95	674.21**	0.001
ENV	1	16,276.47	16,276.47**	0.0026
GEN × ENV	23	12,493.31	543.19**	0.0013
Total	71	156,123.89	2,198.93**	

** indicates significance at $p < 0.01$

The significance of GEI clearly indicated differential responses of genotypes across environments, justifying the application of stability models (Sood *et al.,* 2020). Partitioning of GEI into linear and non-linear components further revealed that the linear component (GEN × ENV linear) was significant, suggesting predictable genotype responses to environmental changes.

AMMI analysis of variance

AMMI analysis partitioned the GEI sum of squares into interaction principal component axes (IPCAs) (Table 2). The first interaction principal component axis (IPCA1) accounted for 79.5% of the total GEI variation, while IPCA2 explained the remaining 20.5%, cumulatively accounting for 100% of the interaction variance. The dominance of IPCA1 suggested that most of the GEI was systematic and could be effectively captured using the AMMI1 biplot.

The relatively lower and non-significant contribution of IPCA2 indicated that higher-order components contributed minimally to interaction patterns. Therefore, interpretation based on the first two IPCAs was considered adequate for identifying stable and specifically adapted genotypes (Hossain *et al.*, 2023).

Table 2: AMMI analysis of variance showing partitioning of genotype × environment interaction into IPCA1 and IPCA2 with percentage contribution and cumulative variance.

Source	Df	Sum of Squares	Mean Square	F value	Proportion (%)
ENV	2	16,276.47	8,138.23	38.07**	–
REP(ENV)	3	641.28	213.76	1.89	–
GEN	23	123,761.94	5,380.95	47.48**	–
GEN × ENV	46	16,085.49	349.68	3.09**	–
PC1	24	12,792.81	533.03	4.70**	79.5
PC2	22	3,292.67	149.67	1.32	20.5
Residuals	69	7,819.53	113.33	–	–
Total	189	180,670.20	955.93	–	–

** indicates significance at $p < 0.01$.).

AMMI1 Biplot Interpretation

The AMMI1 biplot (Fig. 1), which plots mean fruit yield per plant against IPCA1 scores, provided a simultaneous assessment of genotype performance and stability. Genotypes such as Arka Anamika, Parbhani Kranti, UAHS-11, UAHS-3, and Varsha Upahar were located close to the origin with above-average mean yield, indicating wide adaptation and high stability across environments. These genotypes exhibited minimal interaction effects and consistent performance across seasons (Taherian *et al.*, 2024).

In contrast, genotypes UAHS-17, UAHS-18, and UAHS-19 recorded higher mean yields but were positioned farther from the origin, reflecting greater sensitivity to environmental changes. These genotypes showed specific adaptation to favorable environments, particularly Kharif 2021, which was characterized by positive IPCA1 scores. Rabi 2020 exhibited a strong negative IPCA1 score, indicating that genotypes located in the opposite direction were better adapted to this environment (Panda *et al.*, 2023).

AMMI2 Biplot Interpretation

The AMMI2 biplot (Fig. 1), depicting IPCA1 versus IPCA2 scores, further elucidated interaction patterns. Genotypes clustered near the origin were least sensitive to environmental fluctuations, confirming their stability. Environments with longer vectors, particularly Kharif 2021, were more discriminating and contributed strongly to GEI, whereas Kharif 2020 was relatively neutral and closer to the origin (Birhanu *et al.*, 2023).

The angular relationship between genotype and environment vectors indicated the nature of their interaction. Acute angles suggested positive interactions, while obtuse angles indicated negative associations. This graphical representation enabled clear identification of genotypes with specific adaptation to individual seasons.

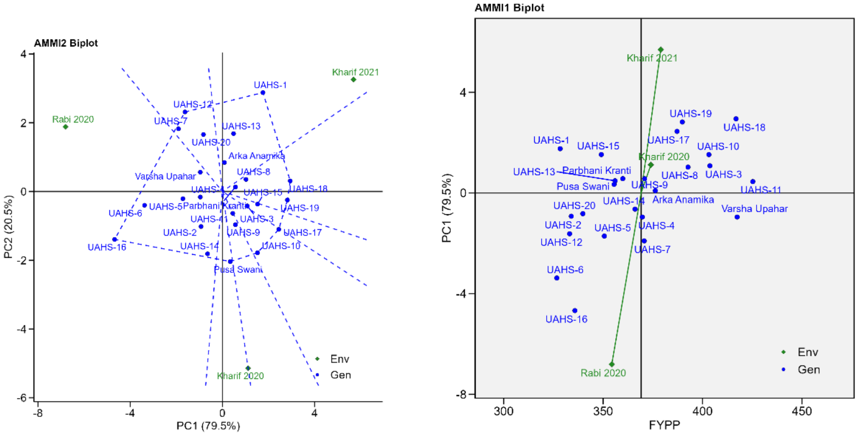

Fig. 1. Combined AMMI biplots of okra genotypes and environments: AMMI1 biplot depicting mean fruit yield per plant versus IPCA1 scores, and AMMI2 biplot showing genotype × environment interaction patterns based on IPCA1 and IPCA2 scores.

Eberhart and Russell Stability Analysis. Eberhart and Russell stability parameters further substantiated the AMMI results (**Table 3**). Genotypes Arka Anamika, Parbhani Kranti, UAHS-11, UAHS-3, and Varsha Upahar exhibited regression coefficients (b_1) close to unity along with non-significant deviations from regression (s^2di), indicating average responsiveness and wide adaptability.

Genotypes UAHS-10, UAHS-17, UAHS-18, and UAHS-19 recorded b_1 values significantly greater than unity coupled with high mean yields, suggesting high responsiveness to improving environments and suitability for favorable conditions. Conversely, genotypes UAHS-16 and UAHS-6 exhibited b_1 values less than unity with significant deviations, indicating adaptation to poor or stress-prone environments but lower overall stability (Patel *et al.*, 2023).

Comparative Interpretation of Stability Models. The integration of AMMI and Eberhart-Russell models provided complementary and consistent insights. Genotypes identified as stable by regression analysis were also positioned near the origin in AMMI biplots, validating their wide adaptability. High-yielding but environment-sensitive genotypes were distinctly separated in both approaches, enabling targeted recommendation for specific seasons. Overall, the combined analytical framework enhanced confidence in genotype classification and facilitated robust decision-making for varietal advancement and release in okra.

Table 3: Eberhart and Russell stability parameters for fruit yield per plant in okra genotypes.

Sr. No.	GEN	Mean yield (b_0)	Regression coefficient (b_1)	Deviation from regression (s^2di)	F(s^2di=0)
1.	UAHS-1	328.39	1.66	377.41	7.66
2.	UAHS-10	403.19	1.84	20.00	1.35
3.	UAHS-11	425.26	1.25	-45.99	0.19
4.	UAHS-12	333.16	0.08	85.67	2.51
5.	UAHS-13	356.02	1.13	71.64	2.26
6.	UAHS-14	366.04	0.80	96.85	2.71
7.	UAHS-15	349.08	1.75	-56.65	0.00
8.	UAHS-16	335.81	-1.15	204.53	4.61
9.	UAHS-17	387.18	2.24	-47.56	0.16
10.	UAHS-18	416.83	2.39	-13.09	0.77
11.	UAHS-19	389.81	2.36	-48.15	0.15
12.	UAHS-2	334.01	0.62	5.08	1.09
13.	UAHS-20	339.80	0.50	25.86	1.46
14.	UAHS-3	403.68	1.54	-55.83	0.01
15.	UAHS-4	369.69	0.55	-50.26	0.11
16.	UAHS-5	350.60	0.19	-40.35	0.29
17.	UAHS-6	326.71	-0.59	5.43	1.10
18.	UAHS-7	370.65	-0.02	14.04	1.25
19.	UAHS-8	392.67	1.47	-41.98	0.26
20.	UAHS-9	370.88	1.33	-30.04	0.47
21.	Varsha Upahar	417.39	0.51	-52.65	0.07
22.	Arka Anamika	376.22	0.99	-27.14	0.52
23.	Parbhani Kranti	359.89	1.26	-53.69	0.05
24.	Pusa Swani	355.54	1.29	93.03	2.64

CONCLUSIONS

The study demonstrated the effectiveness of combining Eberhart–Russell and AMMI models for stability analysis in okra. Arka Anamika, Parbhani Kranti, UAHS-11, UAHS-3, and Varsha Upahar were identified as stable and widely adapted genotypes, suitable for cultivation across seasons. Genotypes UAHS-17, UAHS-18, and UAHS-19 showed superior performance under favorable environments and can be recommended for high-input or Kharif-specific cultivation. These findings provide valuable guidance for varietal recommendation and future okra breeding program.

FUTURE SCOPE

The stable and high-yielding okra genotypes identified in this study offer significant potential for future research and breeding programs. These genotypes can be further evaluated using molecular markers to facilitate marker-assisted selection for improved adaptability and yield. Extending trials across additional locations and multiple seasons would provide more robust insights into genotype stability under diverse environments. Moreover, assessing these genotypes for tolerance to abiotic stresses such as drought, heat, and salinity can support the development of climate-resilient cultivars. Integration with optimized agronomic practices and advancement for large-scale seed production will enable their targeted cultivation and contribute to enhancing okra productivity across varied agro-ecological zones.

Contributions. Conceptualization, B.M.D. and S.N., methodology, S.N., V. R. and B.M.D., software, S.N., formal analysis, S. N., investigation, data curation, S. N., writing-original draft preparations. S. N., B.M.D., supervision, B.M.D. All authors have read and agreed to the published version of the manuscript.

Acknowledgements. The authors express their sincere gratitude to the Director of Research, KSNUAHS, Shivamogga, for providing essential research facilities.

Conflict of Interest. The authors declare no conflicts of interest.

REFERENCES

Birhanu, C., Mekbib, F., Lule, D., Bekeko, Z., Girma, G., Tirfessa, A., Ayana, G. and Mengiste, T. (2023). Genotype by environment interactions and stability for grain yield and other agronomic traits of sorghum in Ethiopia. *Research Square, 1*(1), 1–15.

Eberhart, S. A. and Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, *6*, 36-40.

Elkhalifa, A. E. O., Alshammari, E., Adnan, M., Alcantara, J. C., Awadelkareem, A. M., Eltoum, N. E., Mehmood, K., Panda, B. P. and Ashraf, S. A. (2021). Okra (*Abelmoschus esculentus*) as a potential dietary medicine with nutraceutical importance for sustainable health applications. *Molecules*, *26*(3), 696.

Haq, I. U., Azam, N., Ashraf, M., Javaid, M. M., Murtaza, G., Ahmed, Z., Riaz, M. A., Iqbal, R., Rahman, M. H. U., Alwahibi, M. S., Elshikh, M. S., Aslam, M. U. and Arslan, M. (2023). Improving the genetic potential of okra (*Abelmoschus esculentus* L.) germplasm to tolerate salinity stress. *Scientific Reports*, *13*, 21504.

Hossain, M. A., Sarker, U., Azam, M. G., Kobir, M. S., Roychowdhury, R., Ercisli, S., Ali, D., Oba, S. and Golokhvast, K. S. (2023). Integrating BLUP, AMMI and GGE models to explore GE interactions for adaptability and stability of winter lentils (*Lens culinaris* Medik.). *Plants*, *12*(11), 2079.

Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A., Wondaferew, D., Gelaw, T. A. and Astatkie, T. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*, *10*(12), e32918.

Olivoto, T. and Dal'Col Lúcio, A. (2020). *metan*: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, *11*(6), 783–789.

Panda, S., R. N. K., Pavani, S. L., Ganesan, S., Singh, P. K., Sah, R. P., Subudhi, H., Mahender, A., Anandan, A. and Ali, J. (2023). Multi-environment evaluation of rice genotypes: Impact of weather and culm biochemical parameters against sheath blight infection. *Frontiers in Plant Science*, *14*, 1280321.

Patel, A. A., Vekariya, R. D., Patel, A. I. and Singh, A. G. (2023). Insights into phenotypic stability of okra [*Abelmoschus esculentus* (L.) Moench] hybrids evaluated under multi-environments. *Biological Forum – An International Journal*, *15*(2), 1185–1194.

Rani, R., Raza, G., Ashfaq, H., Rizwan, M., Shimelis, H., Tung, M. H. and Arif, M. (2023). Analysis of genotype × environment interactions for agronomic traits of soybean (*Glycine max* [L.] Merr.) using association mapping. *Frontiers in Genetics*, *13*, 1090994.

Rodrigues, P. C., Monteiro, A. and Lourenço, V. M. (2016). A robust AMMI model for the analysis of genotype-by-environment data. *Bioinformatics*, *32*(1), 58–66.

Smith, A., Ganesalingam, A., Lisle, C., Kadkol, G., Hobson, K. and Cullis, B. (2021). Use of contemporary groups in the construction of multi-environment trial datasets for selection in plant breeding programs. *Frontiers in Plant Science*, *11*, 623586.

Sood, S., Bhardwaj, V., Kumar, V. and Gupta, V. K. (2020). BLUP and stability analysis of multi-environment trials of potato varieties in sub-tropical Indian conditions. *Heliyon*, *6*(11), e05525.

Taherian, M., Saeidnia, F., Hamid, R. and Nazeri, S. M. (2024). Identification of high-yielding and stable cultivars of wheat under different sowing dates: Comparison of AMMI and GGE-biplot analyses. *Heliyon*, *10*(20), e39599.

Singh, J. and Nigam, R. (2023). Importance of okra (*Abelmoschus esculentus* L.) and its proportion in the world as a nutritional vegetable. *International Journal of Environment and Climate Change*, *13*(10), 1694–1699.

Venkatesh, D., Srinivas, J., Lakshminarayana, D., Nagaraju, K., Sai Krishna Nikhil, B. and Sathish, G. (2023). Evaluation of hybrids for growth, yield and yield attributes in okra (*Abelmoschus esculentus* L. Moench). *Biological Forum – An International Journal*, *15*(10), 536–543.

How to cite this article: Sandeep N., Dushyantha Kumar B.M. and Vishal Reddy (2025). Deciphering Yield Stability and Genotype × Environment Interaction in Okra (*Abelmoschus esculentus* L. Moench) under Multi-season Evaluation. *Biological Forum*, *17*(5): 163-167.