Indian J. Genet. Plant Breed., (2025); 85(4 Suppl.) : 734-744
https://doi.org/10.31742/ISGPB.85.suppl.6
ISSN: 0975-6906
www.isgpb.org

RESEARCH ARTICLE

Univariate parametric and nonparametric techniques for analyzing fiber quality and yield stability in Sea Island cotton (*Gossypium barbadense L.*)

K. Baghyalakshmi[*], A. Shanmugam, A.R. Priyanka, G. Sarathapriya, K. Subashree, T. Radhamani[1] and S. Manickam

Abstract

The techniques used to evaluate the stability and adaptability of genotypes across environments and to study genotype-by-environment interactions (GEIs) are ever-evolving. In this sense, employing multiple approaches to measure the nature of the GEI from multiple aspects is frequently preferable rather than relying solely on a single analysis. A panel of 50 *Gossypium barbadense* genotypes was assessed over three years at the research sites using a randomized full-block design. The results of the additive main effects and multiplicative interaction (AMMI) model indicated that the number of bolls (NB), single plant yield (SPY), fiber length (UHML), and fiber strength (FS) were significantly impacted by genotype, environment, and GEI. Based on the multiplicative effects analysis of AMMI into interaction principal components (IPCs), the studied traits had two significant components. The AMMI model predicted that the stable genotypes for NB were G30 (ICB13), G10 (ICB35), and G31 (ICB176), while those for SPY were G38 (ICB16), G34 (ICB244), G19 (ICB73), G29 (ICB207), and G41 (CCB11A). Genotypes, G23 (ICB262), G29 (ICB207), G7 (ICB220), and G21 (ICB143) for UHML and G19 (ICB73) and G39 (ICB39) for FS were considered to be stable. In this study, for yield traits, the E1 environment better differentiated the genotypes, whereas for quality traits, all three environments showed their discriminativeness. In terms of identifying highly stable and high-yielding genotypes, all of the SSI models were performed, which revealed that genotype G41 (CCB 41), an advanced breeding line, had good stability across environments with relatively high yields coupled with good fiber quality.

Keywords: AMMI, GGE, GEI, Stability, parametric and nonparametric indices

Introduction

One of India's most significant cash crops and the world's most important crop for natural textile fiber is cotton. *Gossypium hirsutum* and *Gossypium barbadense*, two allotetraploid species that have developed separately, are responsible for more than 90% of the annual production of commercial fiber (Baghyalakshmi et al. 2024). *G. barbadense* produce the best fiber quality because of its high strength, shiny nature, fineness, and extra-long staple (ELS) fiber. In comparison to *G. hirsutum, G. barbadense* cultivars are low-yielding with narrow adaptability, vulnerable to sucking pests and manual harvesting is challenging due to its noticeable pointy boll edges. Hence, significant efforts have to be made in cotton breeding to increase production while addressing issues related to *G. barbadense* genotypes. One of the primary causes of biotic and abiotic stresses, which negatively impact cotton production and quality, is climate change. Because of the direct and indirect effects of abiotic stress, productivity suffers from severe repercussions that are intensifying due to sudden changes in environmental conditions. Screening of the available germplasm for these stresses is the first step in the breeders' goal of developing more stable genotypes.

It is more crucial than ever to investigate the possibility of genotypes with high stability across seasons and habitats

[*]ICAR-Central Institute of Cotton Research, Regional Station, Coimbatore 641 003,Tamil Nadu, India

[1]Centre for Plant Breeding and Genetics Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

***Corresponding Author:** K. Baghyalakshmi, ICAR-Central Institute of Cotton Research, Regional Station, Coimbatore 641 003,Tamil Nadu, India, E-Mail: kauverik@gmail.com

How to cite this article: Baghyalakshmi K., Shanmugam A., Priyanka A.R., Saradhapriya G., Subashree K., Radhamani T. and Manickam T. 2025. Univariate parametric and nonparametric techniques for analyzing fiber quality and yield stability in Sea Island cotton (*Gossypium barbadense* L.). Indian J. Genet. Plant Breed., **85**(4 Suppl.): 734-744.

Source of support: Nil

Conflict of interest: None.

Received: July 2026 **Revised:** Oct. 2026 **Accepted:** Nov. 2025

in light of climate change. Cotton yield is a quantitative trait that is strongly affected by changes in climatic conditions. In upland cotton (*Gossypium hirsutum* L.), yield traits are influenced by both additive and non-additive effects, with significant contributions from genotype × environment interactions, whereas fiber quality traits are largely controlled by main genetic effects (Zhang et al. 2019). In breeding schemes, taking into account the impact of the GEI improves selection efficiency and facilitates the identification of high-yielding genotypes with both general and specific adaptability (Vaezi et al. 2019). Here, the role of multi-environmental experimental trials plays a significant role. In cotton, empirical multivariate approaches such as the GGE biplot have been widely used to evaluate genotype performance and stability across multiple environments, facilitating the identification of high-yielding and stable genotypes (Yehiaand ElHashash 2022).Two empirical and biological models comprise the grouping of the multivariate approaches. Among them, empirical models such as the GGE biplot approach and the additive main effect and multiplicative interaction model (AMMI) (Gauch 1988) are significant. Due to various concepts, including the "which-one-where" pattern in datasets, the selection of optimal genotypes for use in a variety of environments, the identification of mega-environments, and the assessment of the discriminating power of test environments, these methods are capable of efficiently interpreting GEI effects (Gauch et al. 2008).

The AMMI model is one of the most popular univariate and multivariate models for analyzing the impacts of GEI on a wide range of plant species. This model is a unique fixed-effect model that integrates principal component analysis (PCA) and integrated analysis of variance (ANOVA). Additionally, this model includes a graphical tool for finding the best testing settings and evaluating yield performance and stability at the same time (Gauch 1988). The aforementioned research was carried out using a range of cultivated cotton germplasms to determine the best genotype by evaluating the effect of GEI on the production of seed cotton and the plants' capacity to adapt to different environmental factors. As *G. barbadense* grows only in the southern region of India, it has been evaluated for three years in a single location to study the stability of the changing climate.

Materials and methods

Plant materials and trial

Fifty genotypes of *G. barbadense* were used in the experiment; they were chosen from the germplasm maintained at the ICAR Central Institute for Cotton Research (CICR), Regional Station, Coimbatore. Based on several characteristics, including yield and fiber quality attributes, the first selection was determined (Table 1). The field experiments were conducted under three environments, E1, E2, and E3, at the station's old farm for three consecutive years, 2019-20, 2020-21 and 2021-22. The sowing was performed from July 19 to July 21 during the three years. A randomized complete block design (RBD) was used for the experiment with two replications each. Seeds were sown on ridges with 90 cm apart in rows and keeping 45 cm distance between the plants. All other recommended agronomic practices were followed until the maturity of the crop. Weather parameters such as temperature, relative humidity, and rainfall data were recorded for all three years during all the cropping seasons (Table 2). Harvesting was carried out on the 140th and 160th days after sowing.

Morphological trait evaluation and phenotypic data collection

Various crop intervals were used to record morphological observations. Ten randomly chosen and tagged plants at different growth stages in each field replication were used to obtain all phenotypic data from each plot. Recording of agronomic characters on plant height (cm) (PH), number of monopodia (NM), number of sympodia (NS), number of bolls per plant (NB) and weight of a single boll (g) (SBW), and fiber quality traits namely, upper half mean length (UHML, mm), fiber strength (g/tex) (FS) and fiber fineness (μ) (FF) was done. Only the traits contributing to yield and quality, namely, the number of bolls, single plant yield, fiber length and fiber strength, were analyzed. At the ICAR-Central Institute for Research on Cotton Technology, Regional Station in Coimbatore, the fiber quality attributes were examined, and the results were obtained in HVI (High Volume Instrument) mode.

Statistical analysis

Analysis of variance, AMMI (Additive Main effects and Multiplicative Interaction) and GGE (Genotype-by-Environment) were analyzed with R software using the "Metan" package (Olivoto et al. 2020). Correlations between the traits were estimated using the "corrplot" package (Wei et al. 2017).

Results and discussion

The yield of grown varieties/hybrids of cotton has reached its variability plateau as one or more parents involved in the cotton breeding program have the same parentage (Baghyalakshmi et al. 2023). Unveiling the variation and novel traits existing in germplasm collections and utilizing them in breeding programmes could be the ideal way to address this issue. Impeding climate change and the evolution of minor pests and diseases into major ones allowed breeders to mine novel genotypes in the germplasms to prevent the crop from becoming genetically vulnerable to recently discovered diseases and pests and to improve its stability across the cultivated environment. In the present study,

Table 1. List of genotypes used in the study

Code	Genotype	Acc. Name	Collections	Code	Genotype	Acc. Name	Collections
G1	ICB 174	Sudan VS	Exotic	G26	ICB 34	SILS 7	Exotic
G2	CCB 141	Suvin x (Suvin x Giza 70)	Indigenous	G27	ICB 96	24/2 W	Exotic
G3	ICB 264	26-1-3.	Exotic	G28	ICB 198	EC 97633	Exotic
G4	ICB 290	S.I (Seaberry)	Exotic	G29	ICB 207	EC 98254	Exotic
G5	ICB 1	Alleppo	Exotic	G30	ICB 13	ISLAND	Exotic
G6	ICB 124	ERB 4488	Exotic	G31	ICB 176	SUVIN	Indigenous
G7	ICB 220	EC 104729	Exotic	G32	ICB 46	82/2 R	Exotic
G8	CCB 143 B	Suvinx (SuvinxGiza 70) S	Indigenous	G33	ICB 273	GIZA 129	Exotic
G9	ICB 284	EC 136455	Exotic	G34	ICB 244	EC 136451	Exotic
G10	ICB 35	SILS 5-53/5	Exotic	G35	ICB 161	SIA 2	Exotic
G11	CCB 28	Advance breeding lines	Indigenous	G36	ICB 200	EC 97635	Exotic
G12	CCB 25	Advance breeding lines	Indigenous	G37	ICB 183	EC 9260	Exotic
G13	CCB 29	Advance breeding lines	Indigenous	G38	ICB 16	SUDAN 6-5-3	Exotic
G14	ICB 194	EC 97628	Exotic	G39	ICB 39	T 9-77	Exotic
G15	ICB 58	EC 136456	Exotic	G40	CCB 26	Advance breeding lines	Indigenous
G16	ICB 53	BARBADENSE	Exotic	G41	CCB 11 A	Advance breeding lines	Indigenous
G17	ICB 28	136x181 BK (B)	Exotic	G42	ICB 177	TADLA 2	Exotic
G18	ICB 184	EC 9261	Exotic	G43	ICB 75	EC 154784	Exotic
G19	ICB 73	EC 136450-73 WI	Exotic	G44	ICB 255	EC 154788	Exotic
G20	ICB 258	EC 111264	Exotic	G45	ICB 99	32/2 R	Exotic
G21	CCB 143	Suvin x (Suvin x Giza 70)	Indigenous	G46	ICB 129	GIZA 7-1461	Exotic
G22	ICB 40	MINAXI	Exotic	G47	CCB 11	Advance breeding lines	Indigenous
G23	ICB 262	19/2.	Exotic	G48	ICB 61	PIMA 2	Exotic
G24	ICB 77	EC 193907 B	Exotic	G49	CCB 64	Advance breeding lines	Indigenous
G25	ICB 199	EC 97634	Exotic	G50	ICB 86	2 5 3	Exotic

the yield and quality traits of fifty *G. barbadense* genotypes were investigated across three environments. All the traits were significantly different among genotypes, environments and genotype × environment interactions, indicating the presence of significant variability among genotypes, the considerable influence of environment, and the interaction of genotype with environment on the expression of the trait. Among the different traits, only four major yield and quality contributing traits, *viz*., number of bolls (NB), single plant yield (SPY), UHML and fiber strength, were considered for further stability analysis.

A violin plot was drawn for all four traits to visualize the variability within the seasons (Fig. 1). The width of each violin represents the density of the data points; wider sections represent higher densities of data, while narrower sections denote lower densities. The graphs show variations in distribution, spread, and central tendencies, providing important information on how meteorological parameters affect genotype expression. The results indicate that environment 2 showed uniform variability over the years and was stable for all the traits.

Combined ANOVA

A combined analysis of variance was carried out for the traits NB, SPY, UHML and FS. The results revealed highly significant differences ($P < 0.01$) for genotype, environment and the GXE interaction (GEI) for all the studied traits except for UHML. UHML had significant differences ($P < 0.05$) for the environment and highly significant differences ($P < 0.01$) for genotypes and GEI. According to present findings, significant genotypic, environmental and GEI effects were also reported for seed cotton yield (Jamil et al. 2023), number of bolls, UHML and FS (Shahzad et al. 2019; Rehman et al. 2022). The significant environmental differences implied that the trials were conducted in different climates, which had an impact on the yield and fiber quality of the studied cotton genotypes. A significant GEI shows that the yield and quality attributes of the studied cotton genotypes vary with environment, which decreases the correlation between a trait's genotype and phenotype and, in turn, decreases the effectiveness of genotype selection and, ultimately, slows crop improvement. Thus, reducing the GEI is critical. Therefore, stability analysis would be the ideal way to reduce

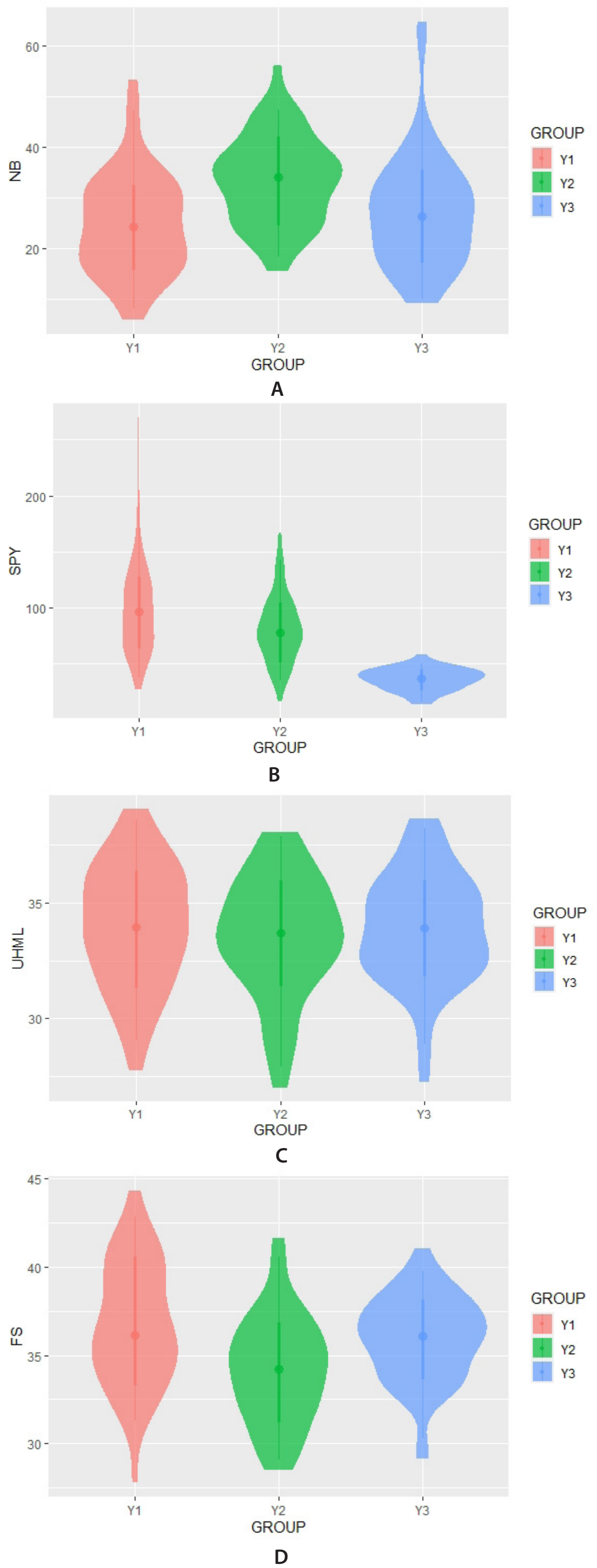

Fig. 1. Violin plots of yield and fiber trait of each environmental condition A. Number of bolls per plant, B. Single Plant Yield (g), C. Fiber length (mm), D. Fiber Strength (g/tex)

the magnitude of the GEI and lead to the selection of stable genotypes with wider adaptations.

AMMI analysis of variance

Phenotypic variance components,*viz.*, genetic, environmental, and GEI variances, were estimated for the studied traits (Fig. 2). Among the variance components, the GEI had a greater contribution to the total phenotypic variance for all the studied traits than to the genotypic and environmental variance. Among the traits studied, single-plant yield had the highest GEI component of variance (0.86), followed by NB (0.65) and total phenotypic variance. In the case of genotypic variance, UHML (0.40) and FS (0.35) exhibited greater genetic variance than SPY and NB. For all the studied traits, environmental variance contributed the least to the phenotypic variance. NB was found to have greater environmental variance than the other traits. Selection efficiency could be high for SPY, UHML and FS, where genetic variance-to-environment ratios are greater. This would lead to more precise identification and selection of favorable genotypes (Kari et al. 2025a). The error variance from the AMMI with the lowest mean of squares for all studied traits was not significant, which indicates that the model is accurate. Greater GEI variances than genotypic variances indicate greater differences in genotypic performance across environments (Kari et al. 2025a). Overall, the findings showed that genes play a significant role in generating genotype diversity among the studied genotypes concerning fiber quality attributes rather than yield attributes, which are highly influenced by environmental and GEI interactions. Studies in cotton by Mohammed et al. (2025) revealed that genotype × environment interaction (GEI) accounted for a substantial proportion of the interaction sum of squares, explaining 58.77% for boll weight, 68.20% for seed cotton yield, and 77.13% for lint yield, highlighting the strong

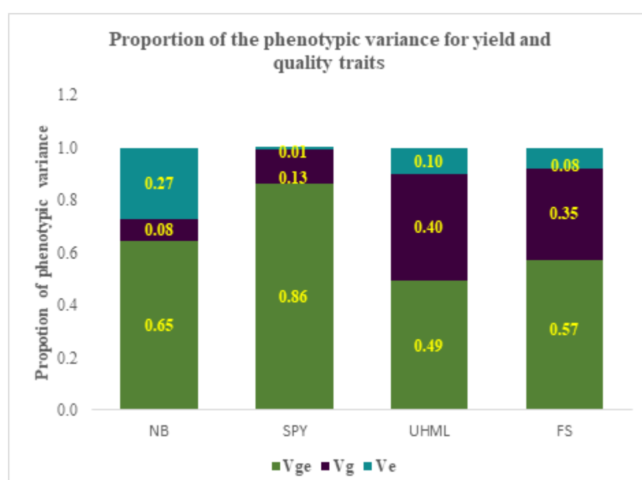

Fig. 2. The proportion of phenotypic variance explained by genetic, environmental and GXE interaction variances for all four tested traits in the cotton genotypes

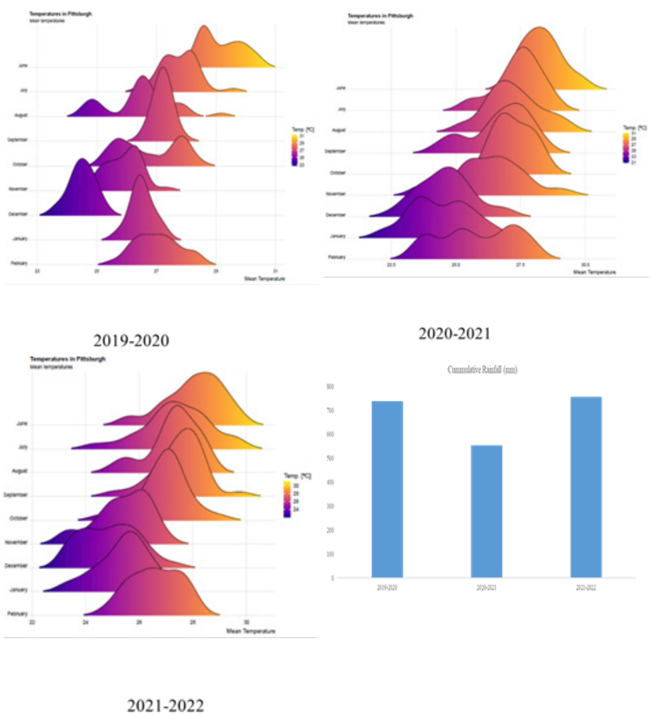

Fig. 3. Mean temperature (C) during the cropping period for all three years and bar graph showing Cumulative rainfall received over the three years

influence of GEI on yield-related traits across environments. In contrast to our results, Yehia et al. (2024), reported that GEI variance had less of an effect on phenotypic variance, which resulted in minimal yield variations between environments. In cotton multi-environment trials, the environment is often the predominant source of phenotypic variation. Studies have reported that environmental effects can account for 67–90% of the total variance in seed cotton or lint yield, with genotype and genotype × environment interactions contributing much smaller proportions (Meredith and Bridge 2012; Jamil et al. 2022; Mundakochi et al. 2025).

After further subdivision of the GEI, the first two interaction principal component axes (IPCAs) were found to be statistically significant. The best projected model is the AMMI model, which has two major IPCAs (Annicchiarico et al. 2006). The results of the present study revealed one to two significant IPCAs for each of the studied traits (Table 2). IPCA1 had a maximum share of 42.28%, while IPCA2 had a share of 39.03% of the total GEI variance of NB. For SPY, two statistically significant principal components, namely, IPCA1 and IPCA2, accounted for 68.25% and 28.67% of the GEI variance, respectively. The mean yield across the investigated genotypes varied from 36.03 to 99.67 g/plant. The IPCA1 of UHML had 65.02%, while the IPCA1 of FS had a 63.58% contribution to the total GEI effect. Rehman et al. (2022) reported that the total GEI effect can be divided into two components, with 90.45% and 9.55% contributions to cotton yield. Shahzad et al. (2019) identified two significant principal components contributing 90.3% and 84.7% of the total GEI effect on the number of bolls and seed cotton yield, respectively. Orawu et al. (2017) and Abro et al. (2022) identified two significant principal components contributing greater than 70% of the total GEI effect on seed cotton yield. The results of our study clearly indicated that using biplots in interactions was highly effective, as the first two IPCA components explained a major contribution to the total GEI effect. The results obtained for genotype stability based on these two IPCA components were thus very reliable. Several studies have also shown that two PCAs accurately predict the GEI (Rehman et al. 2022).

During the cropping season, the pattern of rainfall primarily determines how characteristics manifest. Temperature (21-33 °C) and relative humidity (68-78%) variation was observed to a little extent during the season for all three years (Fig. 3). However, there was a significant change in the amount of rainfall received at various stages of the crop. During the first year (2019-2020), the highest rainfall was observed during the vegetative (221.3 mm) and flowering (246.9 mm) stages. In the second year, the average rainfall was 100 cm during the vegetative, flowering, and boll formation periods. In the third season, the highest rainfall (268 mm) was observed during the flowering and boll formation stage, and the rainfall continued until harvest, indicating its impact on crop yield. Hence, there was greater yield loss during the third season due to squares and boll shedding. Traits such as fiber length and ginning percentage were better suited to all environments, indicating that genotype predominates in determining the expression of the two features and that the environmental factors had less impact.

Additive main effects and multiplicative interaction 1 biplot for tested traits

The stable genotypes identified for NB were G30, G10, and G31, while G38, G34, G19, G29, and G41 were identified as stable genotypes for SPY. Genotypes such as G23, G29, G7, and G21 for UHML and G19 and G39 for FS were considered stable genotypes (Fig. 4). Genotypes with an IPCA 1 score of zero are more adaptable across environments. Among the genotypes studied, G42 was found to have a greater mean yield than the other genotypes, making it superior in terms of yield, while genotype G41 exhibited stable yield performance along with good fiber quality across the environment. The high-yield genotypes differed from season to season, as shown by the AMMI1 biplot, which revealed the impact of temperature variations and variations in rainfall patterns during the crop period on the seed cotton yield of cotton genotypes. PC1 vectors with the same sign and score but apart from the zero lines of the biplot suggested that genotypes were adaptable to a particular environment, while genotypes with PC1 scores

Table 2. Multiplicative effects analysis of variance of the AMMI model for yield and quality traits of cotton genotypes

Source of variation	Df	Sum of squares	Mean of squares	Relative variance (%)	Cumulative variance (%)
Number of bolls (NB)					
IPCA 1	50	12007.78	240.16**	42.28	42.28
IPCA 2	48	5796.03	120.75**	39.03	81.31
Single plant Yield (SPY)					
IPCA 1	50	124132.30	2482.65**	68.25	68.25
IPCA 2	48	43506.74	906.39**	28.67	96.92
Upper half mean length (UHML)					
IPCA 1	50	556.47	11.13**	65.02	65.02
IPCA 2	48	186.70	3.89**	25.46	90.48
Fibre strength (FS)					
IPCA 1	50	634.00	12.68**	63.58	63.58
IPCA 2	48	512.89	10.69**	21.16	84.74

next to the zero lines of the biplot indicated that genotypes were suitable for all environments. On the other hand, if a genotype and environment attain the same sign on the PCA axis, there is a positive interaction; if not, there is a negative interaction. A genotype and environment have a minor interaction influence when their PCA1 score is close to zero and the results were comparable to those of Fathi et al. (2018) and Mohammed et al. (2025)

Which-won-where polygon view of the GGE biplot

All genotypes are enclosed within the polygon, which is created by joining the signs of the genotypes that are furthest from the biplot origin. The perpendicular lines divide the polygon into sectors. The visualization of the macro environments is aided by these sections. In every investigated scenario, genotypes positioned near the polygon vertex in a biplot segment lacking any environmental indicator are deemed to have low performance (Kari et al. 2025b). Figure 5 shows a polygon view of the GGE biplot (which-won-where) pattern for NB, SPY, UHML and FS. The percentage of genotype + GEI variation was 81.31%, 96.92%, 90.48%, and 84.74% for NB, SPY, UHML and FS, respectively. For NB, SPY, UHML, and FS, the environmental indicators were arranged into 2, 2, 2, and 3 segments of a biplot, with a different genotype winning in each section (Fig. 5). Conversely, if the environment is divided into multiple sections, the genotypes on the vertex of each section perform better in all the environments of that section. All genotypes will perform better if all environments fall into a single section and genotypes across the environments indicated (Hasan et al. 2022). With regard to all the traits studied, this result validates the existence of a unique interplay between genotype and environment. The GGE biplot was divided into 6 to 8 sectors for the studied traits based on 50 genotypes and three environments. The G20 genotype had the greatest number of bolls per plant and was highly stable in E3, while the G36 and G42 genotypes performed best in E2 and E1. For SPY, Environments E2 and E3 comprised and formed a mega-environment, with the genotype G42 being the winning genotype in this mega-environment with a relatively high yield. For the UHML genotypes G40 and G41 in E1 and E2, genotype G2 in E3 was predicted to be the most stable and best performing line. Genotypes, G24 and G41 in E2 and genotypes G11 and G16 in E1 were predicted to be the winning genotypes for FS. The best genotype would be the one that is closest to the origin; however, genotypes inside the polygon, especially those near the biplot origin, were less responsive than genotypes on the vertices (Kari et al. 2025b). According to Yan and Tinker (2006), the vertex genotypes with the greatest distance from the origin in their direction were the most responsive genotypes. Similarly, Ali et al. (2018) reported that genotypes located at polygon vertices were more responsive to environmental interaction and are identified as better performers.

Ranking of genotypes based on their mean performance and stability

It has been shown that the PC2 measure of instability must approximate the GE effects connected to each genotype if PC1 of a GGE biplot approximates the genotype main effects. The cosine of the angle between the average environment coordinate (AEC), also known as the average environment axis (AEA), and the environment vector roughly equals the correlation coefficient between the genotype mean value over the environment and the genotype values in that environment (Yan et al. 2007). A smaller angle between the vector and the AEC of the test environment indicates a better environment than does a larger angle. The direction

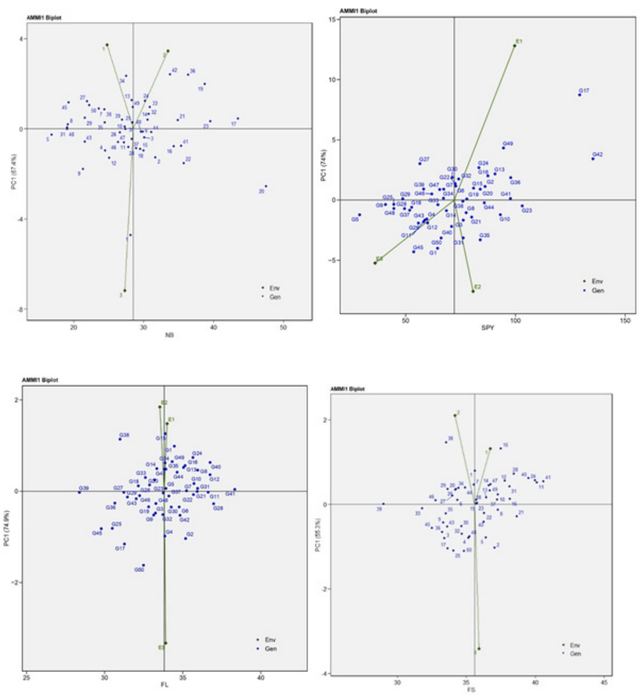

Fig. 4. **AMMI1 biplot for A. Number of bolls per plant, B. Single plant yield (g), C. UHML (mm) and D. Fiber strength (g/tex) vs. principal component 1 (PC1)] of 50 cotton genotypes evaluated in three test environments during 2019–2022**

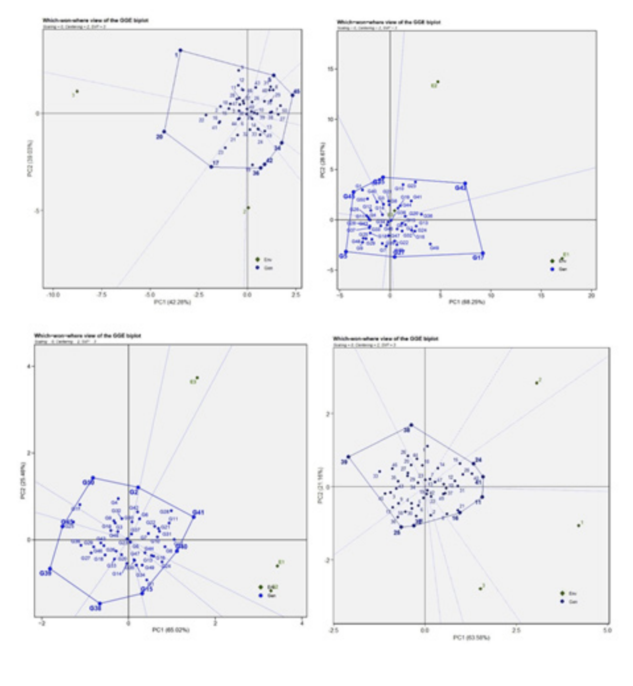

Fig. 5. **The genotype main effect and GEI effect of 50 cotton genotypes under three years are displayed in the "which-won where" pattern of the GGE biplot polygon view for A. Number of bolls per plant, B. single plant yield (g), C. UHML (mm) and D. fiber strength (g/tex). The biplots were based on Centering =0, SVP=2, and Scaling=2**

of the AEC abscissa line is shown by its arrow, the average value of the environment is indicated by a small concentric circle and the discriminating ability is estimated by the test environment vector's length. The length of each environmental vector provides an indication of how well it discriminates between genotypes in the surrounding environment. The GGE biplot's "mean vs. stability" pattern in our investigation showed 81 to 96% G + G x E fluctuation for the yield-attributing traits and 84 to 90% for the quality traits (Figure 6). Greater GEI effects and decreased stability are indicated by moving in either direction away from the biplot origin or the AEC ordinate. The AEC ordinate is used to divide the genotypes with below-average means and those with above-average means. The abundances of the genotypes G5, G31, G45, G48, etc., were greater than the average at the same time that the abundances of G31 and G48 were close to the AEC coordinates; hence, these genotypes are stable throughout the environment for the NB trait. Similarly, G42, G17, and G23 had high above-average means, but the stability of G41 was better than that of the abovementioned genotypes for SPY. Considering the fiber quality traits, most of the genotypes showed similar patterns of stability across the environment based on their distance from the AEC.

Spearman's rank correlation among various stability and simultaneous selection indices estimated for yield data of 50 cotton genotypes

The relationship between each pair of AMMI stability

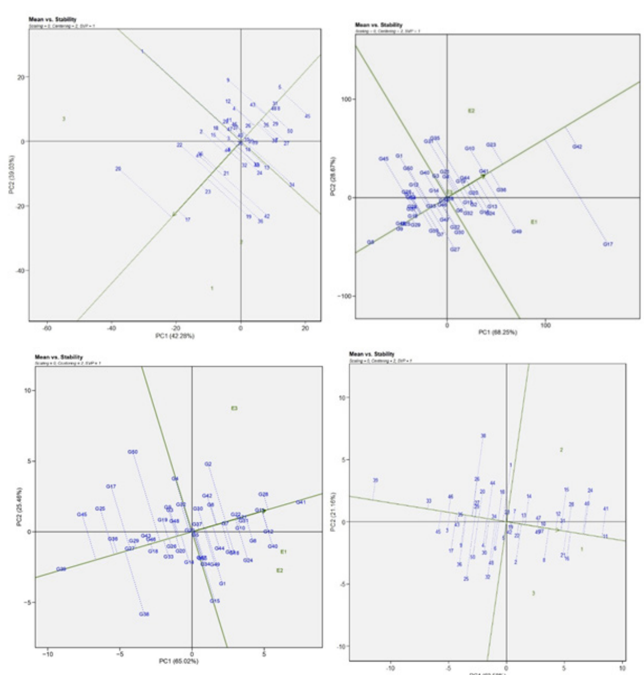

Fig. 6. **GGE biplot showing the interaction effect's "mean vs. stability" pattern for A. number of bolls per plant, B. single-plant yield (g), C. UHML (mm) and D. fiber strength (g/tex) of 50 cotton genotypes evaluated in three test environments during 2019–2022**

parameters was estimated using Spearman's rank correlations, which revealed a strong association among the estimated AMMI-based indices. The results demonstrated a significant association for ZA with almost all the parameters, though at a relatively lesser magnitude for DZ, EV, and FA (Fig. 7). Many indices, such as the ASV, ASI, and MASI, had 100% associations with the AVAMGE. Similarly, the DA was highly correlated with the AVAMGE, ASV, and ASI. A lesser magnitude of correlation was observed between ASI/ASV and DV/EZ and between DZ/EV and MASI/MASV. These results will guide the selection of stable genotypes based on the ranks exhibited by each index. All the stability factors showed a significant positive correlation, suggesting that the extremely stable genotypes remained nearly constant, regardless of the index, suggesting small variations in the computation. Using the same set of stability measures, Baxevanos et al. (2015) reported that multiple AMMI-based stability indices were significantly correlated in cotton. All the other parameters implied nearly identical computations, but the stability parameters, such as ASTAB, AVAMGE and Za were quite critical. These findings concur with previous cotton research, where multiple AMMI-based stability indices, such as ASV, ASI, ASTAB, AVAMGE, and ZA, displayed similar trends in ranking stable genotypes across environments (Kari et al. 2025a). Overall, the strong concordance among the indices supports their use in guiding the selection of stable cotton genotypes across environments.

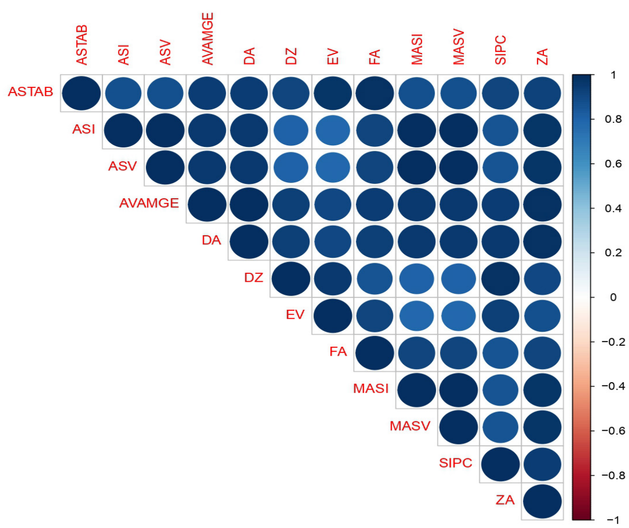

Fig. 7. Spearman's rank correlation between multiple stability and simultaneous selection indices obtained for each of the four attributes of fifty genotypes of cotton assessed in three different test environments

(ASI, AMMI Stability Index; ASV, AMMI stability value; ASTAB, AMMI-based stability parameter; AVAMGE, sum across environments of the absolute value of GEI modeled by AMMI; DA, Annicchiarico's D parameter; DZ, Zhang's D parameter; EV, average of the squared eigenvector values; FA, stability measure based on fitted AMMI model; MASI, genotype-environment modified AMMI Stability Index; MASV, modified AMMI stability value; SIPC, sum of the absolute values of the IPC scores; ZA, absolute value of the relative contribution of IPCs to the interaction)

The number of genotypes used in the study is large; hence, selecting stable genotypes and high-yielding genotypes from biplots that are adaptable to a particular location becomes cumbersome. Hence, the genotypes were selected based on the stability parameters. According to the ASI and ASV estimates, the genotypes, viz., G34 followed by G38, are the most stable, while G34 followed by G19, according to the SPIC stability parameters for SPY (Table 3). These variations show how different estimation techniques vary depending on whether they consider each of the significant PCs or just the first two PCs. Similarly, the two most stable genotypes were selected based on the stability parameters for various traits. The genotypes G31 and G10 for number of bolls per plant, G34 and G38 for single plant yield, G27 and G23 for UHML and G19 and G13 for FS performed stably across the years.

Promising genotypes for the studied traits

The yield and quality parameters of the top five genotypes were selected based on the stability index and are listed in Table 4. Most of the high-yielding genotypes did not show stable performance across the environment except for G41, which performed well in terms of average stability and improved yields and fiber quality in all three environments.

Annually stable genotypes guarantee sustainable harvests with minimal volatility. Simultaneously, it is often recognized that farmers or breeders would rather use a cultivar with an above-average yield and average stability than a highly stable genotype.Genotype selection based solely on mean grain yield in evaluation trials will mislead plant breeders to select the incorrect genotype, which may not persist over time due to its poor stability, in the effort to select the highest yielders. Therefore, a plant breeder must identify a genotype that produces a high yield and consistently performs for a cultivar to last longer in the farmer's fields. The results obtained indicate that the AMMI model is an effective method for analyzing the GEI in multiple cotton environmental experiments. This study considered several stability parameters, including ASV, ASTB, AVAMGE, DA, DZ, EV, and FA, and demonstrated that each has the same potential for identifying stable genotypes. When pinpointing stable, high-yielding genotypes, all of the SSI models performed essentially the same; any of these may serve as a substitute strategy. In conclusion, genotype G41 (CCB 41), an advanced breeding line, had good stability across the environment, with relatively high yields coupled with good fiber quality.

Table 3. AMMI stability indicesand AMMI values for all four traits of cotton genotypes

code	NB			SPY			UHML			FS		
	ASI	ASV	Bolls per plant	ASI	ASV	Yield (g/ plant)	ASI	ASV	Fibre length (mm)	ASI	ASV	Fibre strength (g/tex)
G1	3.18	9.77	28.1	2.97	11.44	64.5	0.78	3.10	34.5	0.57	1.28	35.6
G2	0.86	2.65	31.7	0.86	3.30	86.2	0.79	3.13	35.2	0.59	1.31	37.1
G3	0.32	0.97	30.1	1.23	4.76	76.2	0.37	1.49	33.3	0.54	1.21	33.4
G4	0.66	2.03	24.5	1.21	4.65	59.6	0.76	3.02	33.9	0.47	1.04	35.2
G5	0.27	0.83	16.8	1.34	5.15	29.0	0.07	0.29	33.9	0.55	1.22	36.4
G6	0.38	1.16	29.9	0.87	3.34	72.8	0.33	1.32	34.8	0.55	1.22	34.4
G7	0.60	1.85	23.6	1.12	4.32	67.3	0.16	0.64	35.2	0.29	0.65	35.6
G8	0.14	0.44	19.2	0.81	3.11	77.6	0.43	1.70	36.0	0.43	0.97	37.3
G9	1.22	3.74	21.3	0.53	2.04	40.8	0.40	1.59	33.1	0.30	0.67	33.3
G10	0.09	0.28	27.3	1.19	4.60	93.1	0.13	0.52	35.7	0.16	0.36	37.3
G11	0.62	1.89	27.8	1.35	5.19	58.2	0.12	0.48	36.6	0.46	1.02	40.1
G12	0.88	2.72	25.1	1.40	5.42	60.0	0.27	1.08	36.7	0.34	0.75	37.8
G13	0.88	2.70	28.3	1.61	6.20	90.7	0.39	1.56	35.1	0.10	0.22	36.4
G14	0.71	2.18	30.6	0.65	2.51	68.6	0.37	1.48	33.3	0.29	0.66	36.6
G15	0.79	2.44	29.5	0.73	2.83	80.9	0.94	3.76	33.9	0.78	1.74	37.5
G16	0.60	1.83	34.3	1.49	5.76	87.5	0.43	1.72	35.2	0.54	1.21	38.2
G17	0.80	2.46	43.5	6.47	24.94	129.3	0.87	3.46	31.3	0.60	1.34	33.6
G18	0.66	2.03	30.0	0.60	2.30	52.7	0.21	0.84	32.2	0.41	0.93	35.7
G19	1.38	4.25	38.7	0.51	1.96	77.9	0.26	1.02	32.8	0.08	0.18	35.7
G20	1.72	5.29	47.5	0.71	2.74	84.0	0.23	0.91	33.2	0.27	0.59	34.3
G21	0.28	0.86	34.9	1.06	4.10	80.1	0.05	0.18	35.9	0.24	0.53	38.7
G22	1.06	3.26	35.8	1.17	4.49	72.5	0.07	0.26	35.7	0.12	0.27	36.3
G23	0.23	0.72	39.5	1.01	3.90	103.1	0.03	0.12	33.7	0.14	0.32	35.8
G24	0.83	2.56	30.2	2.00	7.71	83.4	0.56	2.22	35.6	0.46	1.02	40.0
G25	0.46	1.40	28.4	0.45	1.73	44.6	0.64	2.55	30.5	0.65	1.45	34.1
G26	0.42	1.29	26.6	1.42	5.48	55.8	0.12	0.47	32.9	0.43	0.96	34.2
G27	0.91	2.81	21.9	2.26	8.70	56.5	0.02	0.08	31.2	0.15	0.33	34.0
G28	0.73	2.25	28.9	0.52	2.01	49.5	0.21	0.84	37.0	0.40	0.90	38.4
G29	0.33	1.01	21.6	0.34	1.29	48.6	0.12	0.46	31.5	0.22	0.48	33.7
G30	0.49	1.50	27.4	1.49	5.73	71.2	0.29	1.17	34.3	0.34	0.76	34.6
G31	0.03	0.09	19.1	2.44	9.39	76.2	0.09	0.34	35.9	0.27	0.61	38.1
G32	0.47	1.45	30.7	1.30	5.00	74.1	0.39	1.54	33.7	0.58	1.31	34.7
G33	0.78	2.38	30.9	0.40	1.52	64.7	0.23	0.92	32.6	0.23	0.51	31.8
G34	1.59	4.89	27.5	0.15	0.58	67.2	0.51	2.05	33.9	0.31	0.69	34.4
G35	0.51	1.56	24.4	2.51	9.68	84.0	0.37	1.47	33.9	0.21	0.46	33.5
G36	1.62	4.97	36.4	1.42	5.47	97.8	0.22	0.87	30.7	0.50	1.11	33.3
G37	0.48	1.47	28.3	0.66	2.53	51.8	0.08	0.34	34.1	0.15	0.33	37.2
G38	0.58	1.80	24.4	0.21	0.79	76.0	0.86	3.41	31.0	0.86	1.92	33.6
G39	0.27	0.82	26.9	0.83	3.22	58.2	0.09	0.35	28.4	0.34	0.77	29.0
G40	0.68	2.08	29.6	1.62	6.26	70.9	0.47	1.88	36.8	0.35	0.78	39.5

Contd....

G41	0.52	1.60	35.4	0.35	1.36	97.7	0.04	0.16	38.3	0.31	0.70	40.6
G42	1.73	5.30	33.8	2.99	11.53	135.3	0.40	1.58	34.8	0.28	0.63	36.3
G43	0.41	1.25	21.6	1.26	4.86	58.8	0.14	0.56	32.0	0.36	0.81	33.6
G44	0.12	0.36	31.1	0.33	1.25	85.8	0.33	1.31	34.6	0.39	0.87	34.9
G45	1.18	3.63	19.3	3.19	12.29	53.6	0.61	2.45	29.8	0.32	0.72	32.5
G46	0.45	1.38	26.4	0.44	1.71	61.9	0.26	1.02	32.2	0.21	0.48	32.8
G47	0.53	1.63	27.2	0.71	2.75	65.5	0.38	1.52	33.8	0.33	0.73	36.8
G48	0.29	0.90	19.1	0.72	2.76	44.6	0.21	0.83	33.3	0.45	1.00	35.2
G49	0.79	2.42	28.4	3.20	12.35	94.6	0.49	1.94	34.3	0.36	0.81	36.7
G50	0.81	2.50	22.2	2.33	8.98	66.1	1.21	4.83	32.5	0.63	1.41	34.8
Mean	0.7	25.5	28.5	2.38	9.17	72.1	0.36	1.42	33.8	0.378	25.5	35.6

Table 4. List of the top 5 ranking genotypes for all traits studied

	Stable Genotypes	High-performing genotypes
NB	G31, G10, G44, G8, G23	G20, G17, G23, G19, G36
SPY	G34, G38, G44, G29, G41	G42, G17, G23, G36, G41
UHML	G27, G23, G41, G21, G22	G41, G28, G40, G12, G11
FS	G19, G13, G22, G23, G27	G41, G11, G24, G40, G21

Authors' contribution

All authors have contributed equally.

References

Abro S., Rizwan M., Rajput M., Sial M. and Deho Z.A. 2022. Evaluation of upland cotton genotypes for stability over different locations using AMMI and GGE Biplot analysis. Pak. J. Bot., 1: **54**(5): 1733-9. http://dx.doi.org/10.30848/PJB2022-5(1)

Ali I., Khan N.U., Farhatullah Z.B., Bibi Z., Ali S. and Khalil I. A. 2017. Genotype by environment and GGEbiplot analyses for seed cotton yield in upland cotton. Pak. J. Bot., **49**(6): 2273–2283.

Annicchiarico P., Russi L., Piano E. and Veronesi F. 2006. Cultivar adaptation across Italian locations in four turfgrass species. Crop sci., **46**(1): 264-72. https://doi.org/10.2135/CROPSCI2005.0047.

Baghyalakshmi K., Manickam S., Amutha M., Sampathkumar A., Yamuna M. G. and Prakash A. H. 2023. Site regression and multivariate analysis for genetic diversity in *Gossypium barbadense* accessions. Elect. J. Plant Breed., **14**(3): 775–786. https://doi.org/10.37992/2023.1403.088

Baghyalakshmi K., Priyanka R.A., Sarathapriya G., Ramchander S. and Prakash A.H. 2024. Genetic improvement of fiber quality in tetraploid cotton: an overview of major QTLs and genes involved in and edited for the quality of cotton fibers. J Cotton Res., **7**: 33. https://doi.org/10.1186/s42397-024-00196-9

Baxevanos D., GoulaS C., Tzortzios S. and Mavromatis A. 2015. Interrelationship among and repeatability of seven stability indices estimated from commercial cotton (*Gossypiumhirsutum* L.) variety evaluation trials in three Mediterranean countries. Euphytica, **161:** 371–382. https://doi.org/10.1007/s10681-007-9586-0

Fathi S. M., Ranjbar G. A., Zangi M. R., KazemiTabar S. K. and Najafi Z. H. 2018. Analysis of stability and adaptation of cotton genotypes using GGE biplot method. Trakia Journal of Sciences, 1: 51-61. https://doi.org/10.15547/tjs.2018.01.009.

Gauch H.G. 1988. Model selection and validation for yield trials with interaction. Biometrics, **44**: 705–715

Gauch H.G., Piepho H.P. and Annicchiarico P. 2008. Statistical analysis of yield trials by AMMI and GGE: further considerations. Crop Sci., **48**: 866–889. https://doi.org/10.2135/cropsci2007.09.0513

Hasan M.J., Kulsum M.U., Rahman M.H., Akter A. and Paul A.K. 2022. Genotype × environment interaction and yield stability analysis of cotton using GGE biplot methodology. Bangladesh J. Agricult. Res., **47**(2): 143–156.

Jamil M., G. Sarwar I. Akhtar G. Ahmad and S. Ahmad. 2022. Performance stability assessment in upland cotton strains throughout cotton-growing belt in Pakistan. Sarhad Journal of Agriculture, **38**(4): 1361-1369. https://dx.doi.org/10.17582/journal.sja/ 2022/38.4.1361.1369

Jamil M., Saeed M., Abdullah M., Faheem U., Hayat K., Ahmad S., Ahmad G., Hussain A., Hussain F., Akhtar I. and Javed K. 2023. Performance evaluation of Upland cotton genotypes in terms of seed cotton yield under inconsistent environmental conditions. Biol. Clin. Sci. Res. J., **1**: 226. https://doi.org/10.54112/bcsrj.v2023i1.226

Kari B., Priyanka A.R., Shanmugam A., Sarathapriya G. and Manickam S. 2025a. BLUP and AMMI synergy: a comprehensive approach for *Gossypium barbadense* genotype stability and yield assessment, N.Z.J. Crop Hort. Sci., https://doi.org/10.1080/01140671.2025.2491587

Kari B., Priyanka A.R., Shanmugam A., Sarathapriya G. and Manickam S. 2025b. A Multi-Model Stability Analysis Employing AMMI and BLUP-Based Simultaneous Selection for *Gossypium barbadense* Genotype Yield Stability. J. Cotton Sci., **29**: 1–11 (2025)

Meredith W. R., Jr. and Bridge, R. R. 2012. Variance components of lint yield in regional cotton tests. J. Cotton Sci., **25**: 205–212.

Mohammed A., El-Hashash E., El-Sayed A. and Mohamed A. 2025. Genotype × environment interaction and yield stability of Egyptian cotton genotypes under soil moisture deficit conditions. Int. J. Agric. Sci., https://doi.org/10.21608/svuijas.2025.376987.1462.

Mundakochi M., Alagesan S., Nallathambi P., Narayanan M. B., Dhashnamurthi V. and Ramalingam T. Stability analysis of cotton hybrids for yield and fiber quality using GGE biplot, WAASB, and MTSI approaches. J. Cotton Res., **8**(40). https://doi.org/10.1186/s42397-025-00236-y

Olivoto T. and Lúcio A.D. 2020. metan: An R package for multi-environment trial analysis. Methods Ecol. Evol., **11**(6): 783-9. https://doi.org/10.1111/2041-210X.13384

Orawu M., Amoding G., Serunjogi L., Ogwang G. and Ogwang C. 2017. Yield stability of cotton genotypes at three diverse agro-ecologies of Uganda. JPBG, **05**(03): 101-114.

Rehman H.U., Farooq U., Bhutta M.A., Ahmad S., Akram M., Shahid M.R., Hussnain H., Shahid M., Iqba M.M., Raza A. and Iqbal M. 2022. Genetic variability and performance of cotton (*Gossypiumhirsutum* L.) genotypes for yield related agro-morphologic and fiber quality traits under water deficit natural environment. Sarhad J. Agric., **38**(2): 657-68. https://doi.org/10.17582/journal.sja/2022/38.2.657.668

Shahzad K., Qi T., Guo L., Tang H., Zhang X., Wang H., Qiao X., Zhang M., Zhang B., Feng J. and ShahidIqba. M. 2019. Adaptability and stability comparisons of inbred and hybrid cotton in yield and fiber quality traits. Agronomy, **9**(9): 516. https://doi.org/10.3390/agronomy9090516

Vaezi B., Pour-Aboughadareh A., Mohammadi R., Mehraban A., Hossein-Pour T., Koohkan E., Ghasemi S., Moradkhani H. and Siddique K.H.M. 2019. Integrating different stability models to investigate genotype × environment interactions and identify stable and high-yielding barley genotypes. Euphytica, **215**: 63. https://doi.org/10.1007/s10681-019-2386-5

Wei T., Simko V., Levy M., Xie Y., Jin Y. and Zemla J. 2017. Package 'corrplot'. Statistician, **56**(316): 24. Accessed on October 12, 2023.

Yan W. and Tinker N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci., **86**(3): 623–645. https://doi.org/10.4141/P05-169

Yan W., Kang M. S., Ma B., Woods S. and Cornelius P. L. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., **47**(2): 643–653. https://doi.org/10.2135/cropsci2006.06.0374

Yehia W. M. B., Zaazaa E. E. D. I., El-Hashash E. F., Abou El-Enin M. M. and Shaaban, A. 2024. Genotype-by-environment interaction analysis for cotton seed yield using various biometrical methods under irrigation regimes in a semi-arid region. Arch. Agron. Soil Sci., **70**(1): 1–23. https://doi.org/10.1080/03650340.2023.2287759

Yehia W.M.B. and ElHashash E.F. 2022. Lint yield stability of different cotton (*Gossypium barbadense* L.) genotypes using GGE biplot under normal and drought irrigation conditions. J. Plant Prod., **13**(5): 175–182. https://doi.org/10.21608/jpp.2022.142446.1123

Zhang Y., Shahzad K., Li X., Qi T., Guo L., Tang H., Zhang X., Wang H., Zhang M., Zhang B., Qiao X., Xing C. and Wu J. 2019. Genetic analysis of yield and fiber quality traits in upland cotton (*Gossypiumhirsutum* L.) cultivated in different ecological regions of China. J. Cotton Res., 2, Article 14. https://doi.org/10.1186/s42397-019-0031-4.