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RESEARCH ARTICLE

A comprehensive study on the stability of desi cotton (*Gossypium arboreum* L.) genotypes under rainfed conditions using AMMI and GGE biplot analysis

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Abstract

The present study aims to assess the stable and adaptable cotton genotypes under rainfed vertisol conditions using Additive Main effects Multiplicative Interaction and Genotype and Genotype × Environment (GGE) biplot analyses. Seventeen cotton genotypes were evaluated for seed cotton yield at the Agricultural Research Station, Kovilpatti, over three years (2020, 2021 and 2022), treated as distinct environments. Seed cotton yield was subjected to pooled ANOVA, AMMI and GGE biplot analysis, revealing significant variation between genotypes, environment and GEI, with the climate and G × E interaction accounting for 33.8 % and 27.8 % of the total variation, respectively, in seed cotton yield. Based on AMMI I analysis, the genotypes G5 (TKA 0856) and G13 (TKA 1336) were found to have overall adaptability in all the environments (years) studied and considered stable genotypes. GGE biplot was plotted for seed cotton yield using PC1 and PC2, accounting for 70.2% and 26.2 %, respectively, explaining 96.4 % of the total GEI variance. The winning genotypes identified for three mega-environments are G2 (TKA 0612), G16 (TKA 1104) for the first, G6 (TKA 1035), G13 (TKA 1336) for the second and G11 (TKA 1326), G4 (TKA 0848) for the third respectively. The genotype G6 (TKA 1035) was chosen as the most ideal genotype based on mean vs. stability analysis. Among the test environments, E1 was considered the most discriminating environment suitable for selecting widely adapted genotypes.

Keywords

adaptability; genotype × environment interaction; *Gossypium arboreum;* rainfed; stability

Introduction

The Asiatic cotton *Gossypium arboreum* L. is a diploid, short-staple ($2n=2x=26$) Old World cotton. In India, at the time of Independence, Asiatic (Desi) cotton varieties occupied 97 % of the total cotton area and only 3 % was occupied by the New World allotetraploid *G. hirsutum* cotton. The desi cotton acreage has been reduced to 3 %, primarily replaced by *G. hirsutum* (1). Bt cotton hybrids introduced in 2002 in India replaced the *G. arboreum* cultivars, resulting in a shortage of short-staple cotton, the raw material for absorbent cotton (2).

Although *G. hirsutum* cultivars contribute to the majority of Indias' current cotton production, they are highly susceptible to biotic and abiotic stresses. *G. arboreum* is known for its invaluable characteristics unavailable in upland cotton varieties, such as adaptability to extreme environmental conditions and suitability to low rainfall regions. *G. arboreum* is robust and adapts quickly to diverse climatic conditions. This indigenous species can grow well in sub-optimal conditions and marginal soils and is tolerant to abiotic and biotic stresses (3). Cultivating diploid Old World cotton is environmentally friendly and cost-effective (4). Although there is a sizeable reduction in *desi* cotton cultivated area due to the arrival of new world cotton hybrids and Bt cotton in India, short-staple cotton is in great demand for surgical purposes and denim. A significant yield increase is crucial to meet the demand, which necessitates the identification of stable, high-yielding desi cotton genotypes.

The trials were performed under the performance of any crop can be influenced by three factors: genotype, environment and interaction. The environment highly influences seed cotton yield and its contributing traits in cotton. Knowledge of G × E interaction and stability parameters offers valuable guidance in identifying the genotypes suitable for wider adaptability and specific environmental conditions such as rainfed environments. Stability in the yield of a particular genotype has to be assessed before it is recommended for a given situation.

Numerous methodologies have been developed to study the stability of cultivars across test locations. Among them, the AMMI and GGE models are extensively used to assess the stability of genotypes. In both models, biplots display the main effect of the genotype and GEI, the two primary sources of variation (5, 6). Biplots graphically depict the relationship between genotypes, environments and their interaction, highlighting the stable genotypes unaffected by the environments. AMMI and GGE biplot analyses combine Genotype (G) and Genotype × Environment (G × E) to evaluate genotype and mega-environment. GGE biplot analysis explains more about genotype combined with GEI and deals with essential aspects such as mega-environment assessment and evaluation of test environment and genotype. The present investigation aims to identify promising cotton *G. arboreum* genotypes with stable seed cotton yield over years under rainfed vertisol conditions using GGE and AMMI biplot analysis.

Materials and Methods

The study included advanced breeding lines and four check varieties. The trials were performed under rainfed conditions during 2020, 2021 and 2022, considering three separate environments. Seeds of 17 *G. arboreum* genotypes were sown during the *rabi* season using a randomized block design (RBD) with three replications and a 45 × 10 cm spacing. Each genotype was planted in six rows of 6 m length. Standard crop management practices for rainfed cultivation were followed in all three years. Seed cotton yield per plot was recorded at physiological maturity and extrapolated to a per-hectare basis.

Statistical analysis

Seed cotton yield was subjected to pooled ANOVA using the Agricolea package, keeping the genotypes as fixed variables and the environments (seasons) as random variables. Stability analysis to determine the stability of genotypes over the years was carried out in terms of mega-environment analysis, genotype evaluation and test-environment evaluation by AMMI and GGE biplot analyses using the PB Tools software package (5, 6). The AMMI analysis separates G from GE first and then puts them together again, whereas GGE biplot analysis deals with G+GE directly. The AMMI model is a hybrid model involving both additive and multiplicative components of a two-way data structure. The AMMI model separates the additive variance from the multiplicative variance and then applies principal component analysis (PCA) to the interaction portion to extract a new set of coordinate axes explaining the interaction pattern in more detail. In AMMI and GGE models, Biplots display Genotype and Genotype × Environment, the primary variation sources. Both models are used for the evaluation of genotypes and the mega-environment analysis. GGE biplot is utilized to evaluate the test environments, utilizing discriminative power and representativeness.

Results and Discussion

Genotype performance varies across locations and seasons due to differences in growing environments. Breeders face challenges while selecting or recommending the varieties for particular environments because of Genotype × Environment interaction. Repeating the experiments at different places or over the years is crucial to give valid recommendations considering variation in location to location or over seasons. Undertaking multi-environment yield trials is a prerequisite for assessing and selecting stable and superior genotypes (7, 8).

Pooled ANOVA

The primary and interaction effects between different sources of variations were ascertained by the Pooled ANOVA and were presented in Table 1. The pooled ANOVA revealed significant ($p < 0.05$) differences between genotypes, environment and G×E interaction for seed cotton yield. Based on Pooled ANOVA, environmental and G×E interaction were identified as the primary contributors to yield heterogeneity, accounting for 33.8 % and 27.8 % of the total sum of squares. Significant G × E interactions were also reported in earlier studies for seed cotton yield (9, 10).

AMMI Biplots

In the AMMI 1 biplot, the displacements along the x-axis indicate variation in main effects, whereas differences in interaction effects were indicated by displacements along the y-axis. Both main effects and IPCA1 scores of genotypes and environment were plotted against each other (Fig. 1A). The AMMI 1 biplot for seed cotton yield highlighted differences in main and interaction effects among the three environments consistent with the research findings (11). Three environments, E1, E2 and E3, were positioned in three different quadrants, *viz*., IV, I and II, respectively. Among the three, environment E1 was placed distantly from the origin, followed by E3, which showed a moderate interaction effect with the rest of the environments for seed cotton yield. Environments E1 and E2 highly interacted with seed cotton yield under rainfed conditions. In the AMMI1 biplot, genotypes with PC1 scores near zero were suitable for all environments and considered stable since they have small interaction effects. In the present study, the genotypes G5 (-0.41) and G13 (0.45) showed PCA 1 scores close to zero for seed cotton yield (Fig. 1 and Table 2). Hence, these genotypes were found to have general adaptability to all the environments (years) studied and recognized as stable genotypes. If the genotypes and environment represent the same sign on the PCA axis with positive interaction, they are adapted to that particular environment. Environment E1 and the genotypes G1, G2, G5, G6, G7, G14, G15, G16 had negative signs and the remaining genotypes and environments E2 and E3 had positive PCA 1 scores. Hence, E_1 is favourable for the genotypes G1, G2, G5, G6, G7, G14, G15, G16 whereas E2 and E3 are the favourable environments for the remaining genotypes studied. (Fig. 1 and Table 1).

AMMI 2 biplot depicted PCA1 and PCA2 scores (Fig 2). AMMI 2 biplot helps in an easy understanding of the interaction pattern. PCA 1 and PCA 2 denote the first and second principle components and are used to generate a graphical representation of the data. IPCA1 scores of genotype and environment are plotted in the abscissa and IPCA2 scores of genotype and environment are plotted in the ordinate. A higher PC1 score indicates greater yielding ability, whereas a lower PC2 value denotes stability. AMMI 2 biplot involves the detection of genotypes with adaptability based on G×E interaction. The genotypes near the origin have low interaction with the environmental conditions and broader adaptation. From the AMMI 2 biplot, it was inferred that the entries G5, G13 and G8 had broader adaptations for seed cotton yield. They showed good performance across various environments because of the less impact of G x E interaction on these genotypes (Fig. 2 and Table 2). Research indicates similar observations (12). The genotypes positioned far from the origin have large G × E interactions and are sensitive to environmental interaction. Consequently, entries G11 and G4 were more interactive with environmental conditions as they were found to be placed away from the origin. The three environments did not form distinct groups on the plot or clusters near the origin, indicating varied interaction patterns with the genotypes. The lines connected to the origin by the vector are indicative of the interactive forces. Since all the environments had long spokes, they indicate their strong interaction. Environment E3 had a high IPCA 2 score, followed by E2. Environment E3 had a negative IPCA 2 score and recorded a lower yield, whereas E1 had a low IPCA 2 and a higher seed cotton yield.

Among the three environments (years), environment E1 (Year 2020) was considered the highest yielding environment since it had a shorter spoke and shorter angle with the abscissa and is less interactive and ideal for selecting genotypes with high mean performance and adaptability and environment E3 (Year 2022) as the poor yielding environment for seed cotton yield as it had longer spoke and had greater angle with the abscissa. This is also confirmed by the mean performance of the genotypes (Fig 2 and Table 2). The AMMI 2 analysis revealed that GEI less influenced genotypes G11, G2, G17 and G12 and showed broader adaptation to different ranges of locations.

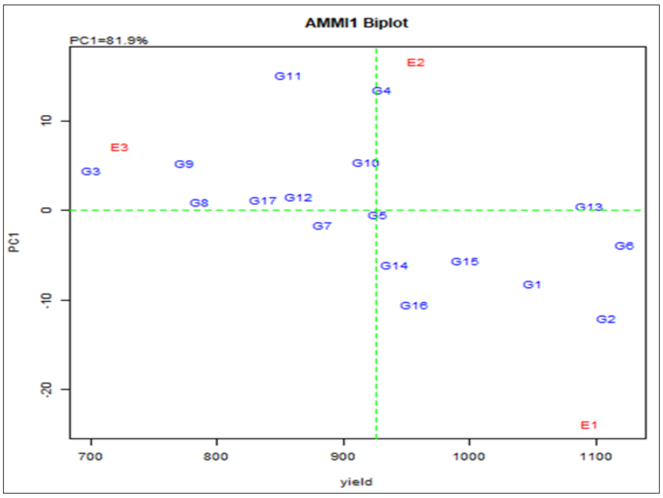

Fig. 1. AMMI 1 biplot for seed cotton yield.

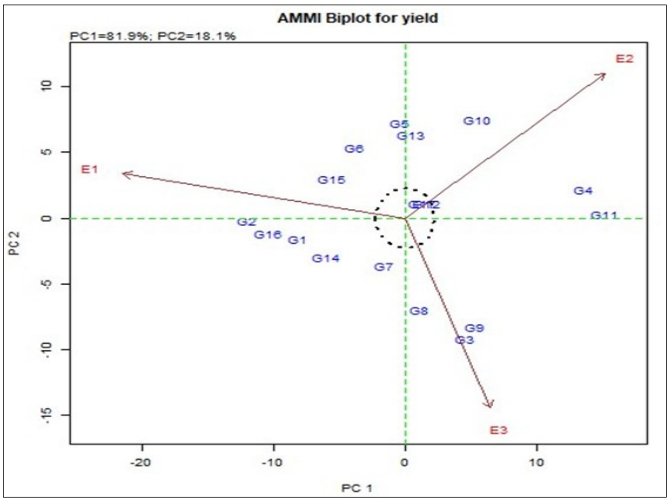

Fig .2. AMMI 2 biplot for seed cotton yield.

Table 1. Pooled ANOVA for stability (AMMI) for seed cotton yield

Source	Df	Sum of squares	Mean sum of squares	Percentage sum of squares
Genotypes	16	2107698	131731*	19.7
Environment	2	3607581	1803790*	33.8
G × E interaction	32	2969486	92796*	27.8
IPCA 1	17	1620531	95325	15.2
IPCA 2	15	359126	23941	3.3
Total	82	10664422	-	100

GGE biplot

Table 2. Estimates of stability parameters (AMMI) for seed cotton yield

Genotype/ Environment code	Genotype / Environment	Yield		
		Mean	PC1	PC2
G1	TKA 0365	1050.33	-8.22	-1.59
G2	TKA 0612	1108.11	-12.00	-0.19
G3	TKA 0822	699.89	4.45	-9.18
G4	TKA 0848	930.22	13.50	2.13
G5	TKA 0856	926.78	-0.41	7.25
G6	TKA 1035	1123.00	-3.84	5.37
G7	K 12	884.00	-1.61	-3.65
G8	PA 255	786.56	1.02	-7.03
G9	RG 8	773.89	5.28	-8.30
G10	TKA 0945	917.67	5.48	7.52
G11	TKA 1326	856.89	15.12	0.28
G12	TKA 1332	864.22	1.60	1.14
G13	TKA 1336	1094.67	0.45	6.38
G14	TKA 1033	940.89	-6.01	-3.02
G15	TKA 1034	996.33	-5.59	3.00
G16	TKA 1104	955.78	-10.47	-1.19
G17	TKA 1123	836.00	1.23	1.09
ENV1	Rabi, 2020	1095.76	-23.86	3.80
ENV2	Rabi, 2021	958.88	16.73	12.28
ENV3	Kharif, 2022	723.92	7.13	-16.08

Mega-environment analysis : The GGE biplots' 'Which-won-where' polygon view graphically represents the specific adaptation of genotypes and the differentiation of mega-environment (13, 14). This polygon view consists of an irregular polygon with lines from the biplot origin transecting its sides at right angles (15). GGE biplot for seed cotton yield was generated using the PC1 and PC2, accounting for 70.2 % and 26.2 %, respectively, explaining 96.4 % of the total GEI variance. An ideal environment should have significant PC1 scores to discriminate genotypes amin based on the genotypic main effects (16).

The spokes from the origin partitioned the biplot into various sections. The polygons' vertices are the genotype markers (peak cultivar) and this peak cultivar at each sector was the best genotype for that location. The genotypes placed within the polygon and close to the origin are less affected by the environments than the genotypes at the vertex.

In the present study, the genotypes G3, G16, G2, G6, G13, G4 and G11 were found at the vertices of the polygon are located far from the origin of the biplot (Fig. 3). These genotypes were adjudged as specially adapted genotypes since they were more responsive to environmental variations. The lines that transect the sides of the polygon divide the biplot into five sectors. The three testing seasons (environments) falling in three sectors indicated that different genotypes won in various environments. These sectors are denoted as mega-environments with different winning cultivars. A mega-environment is an environment or sub-region in which a specific cultivar or group are adapted particularly. Genotypes in sectors without environmental indicators were considered poor performers across all environments and the environments tested were unfavourable for those genotypes (7). The first mega-environment (ME 1) was represented by E1, with G2 (TKA 0612) as the top-performing genotype, followed by G16 (TKA 1104). The second mega-environment (ME2) was represented by E3, where G6 (TKA 1035) performed best, followed by G13 (TKA 1336). The third mega-environment (ME3) was represented by E2, with G11 (TKA 1326) and G4 (TKA 0848) as the winning genotypes.

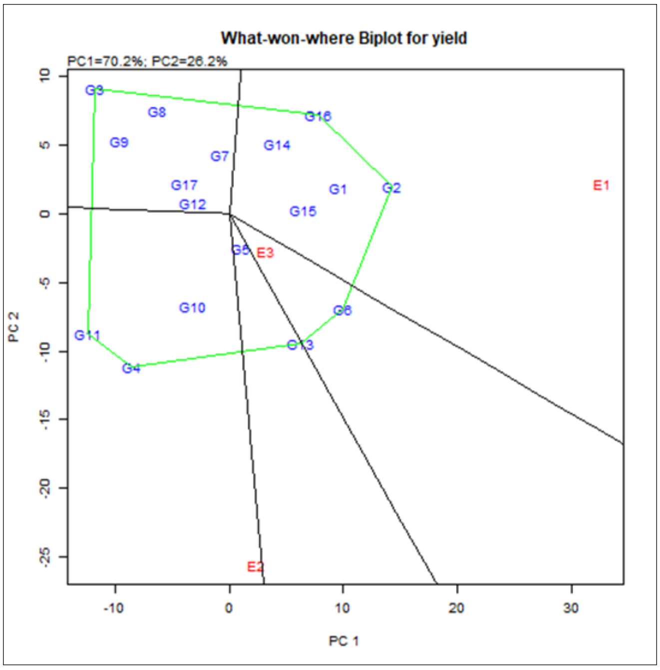

Fig. 3. Which-won-where pattern of GGE biplot polygon view of *G. arboreum* genotypes for seed cotton yield.

Mean vs. stability analysis for selection of ideal genotypes : High mean and stable performance are the indicators of ideal genotype. Fig. 4 depicts the mean performance and stability of the genotypes using Average Environment Coordination (AEC). The biplot graph constitutes the straight lines, the AEC abscissa (horizontal) and the AEC ordinate (vertical). The average environment denotes the average PC1 and PC2 scores of all environments studied and is represented by a small circle. The line with a single arrow passing through this average environment and biplot origin is the Average environment axis or AEC abscissa. In contrast, the axis of the AEC ordinate is a double-arrowed line passing through the biplot origin and is perpendicular to the AEC abscissa. The AEC ordinate separates genotypes based on the average yield, i.e., the genotypes located on the right side of the AEC

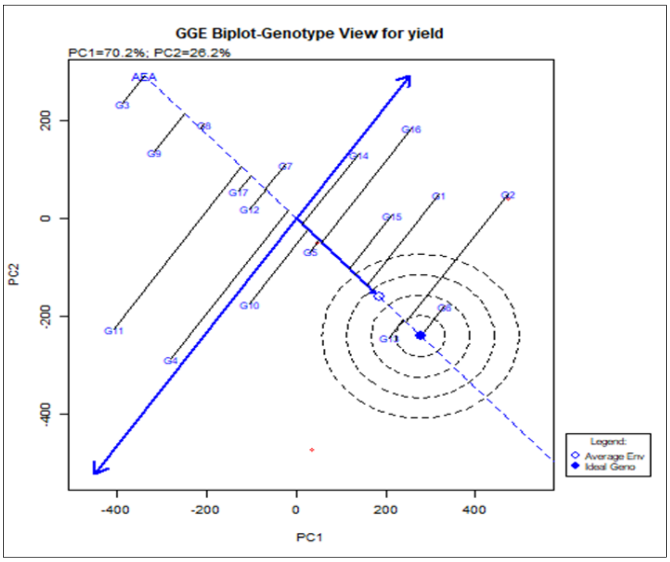

Fig. 4. Mean vs. stability pattern of GGE biplot.

ordinate have a higher yield than the average yield. In contrast, those on the left recorded lower yields than average. The arrow on the axis of the AEC abscissa points towards the greater mean and ranks the genotypes based on their mean performance. Based on this, G6 (TKA 1035) is the ideal genotype. The other genotypes are ranked as G6 > G2 > G13 >G1 > G15> G12 > G16 > G5 >G10> G14 > G4 > G2 > G7 >G17 > G11> G8 >G9 >G3 based on mean. AEC ordinate is a measure of the stability or instability of the genotypes. Dispersion of a genotype along the AEC ordinate is indicative of its stability. Thus, G8 (PA 255) was the most stable genotype since it was present on the AEC abscissa and had zero projection onto the AEC ordinate. In contrast, the less stable cultivars tend to have a higher absolute projection length. Accordingly, G11 (TKA 1326) and G4 (TKA 0848) were the most unstable genotypes, followed by G2 (TKA 0612) and G16 (TKA 1104). The genotypes G2 and G16 recorded higher yields despite low stability because they are located far away from the AEC line on the biplot (17).

***Identification of ideal environment*:** An ideal test environment should be representative of a mega-environment and also should discriminate the genotypes. A perfect test environment can be identified using the discriminating power and the representativeness view of the GGE biplot. The 'Discriminating power vs. Representativeness' view (Fig. 5) of the GGE biplot evaluates each test environment based on two criteria: their ability to provide unique information about genotypes (discriminating power) and their representative of the mega-environment. This is decided based on the length of the environment vector and the angle between the "average-environment axis" and the environment vector (15). The environment having longer vectors differentiates the genotypes more when compared to other environments. The environment with very short vectors is less discriminating and denotes indifference to the performance of the genotypes. The environment at the biplot origin is not discriminating and provides no information about the genotype differences. In this study, the test environment E1 was identified as the most discriminating environment, which provided much information about the dissimilarities of genotypes and is adjudged as a good test environment for identifying widely adapted genotypes. Representativeness is assessed based on the angle between the "average-environment axis" and the environment vector. The smaller the angle between an environment and the AEA, the greater its representativeness of the mega-environment compared to environments with more prominent angles. Accordingly, among the three environments, environment E3 had a smaller angle with the AEA and is declared highly representative, which can provide unique details about the genotypes tested.

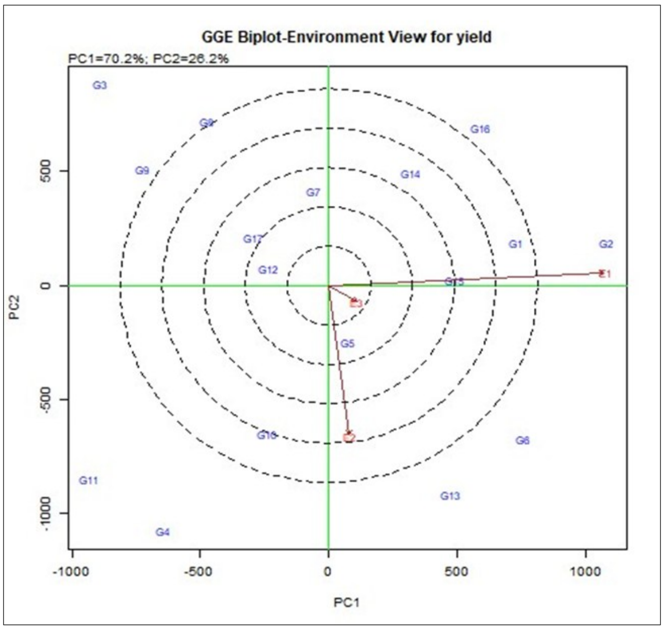

Fig. 5. Discriminativeness vs. representativeness pattern of GGE biplot.

Conclusion

The diploid Old World cotton *G. arboreum* is tolerant to biotic and abiotic stresses and is the source of short-staple cotton, which satisfies surgical cotton needs. With a sizeable area already occupied by *G. hirsutum* hybrids, any increase in *G. arboreum* cultivable area depends on improved seed cotton yield and yield stability to develop high-yielding varieties. AMMI and GGE Biplot analysis for seed cotton yield in desi cotton genotypes indicated the effectiveness of these two models in providing greater insight into the nature and the magnitude of G × E interaction. The analysis revealed that Environment and G × E interaction was the leading cause of heterogeneity for seed cotton yield. G5 (TKA 0856) and G13 (TKA 1336) were found to have general adaptability to all the environments (years) studied and are considered stable genotypes based on AMMI analysis. The GGE biplot model indicated that the three environments in the study belonged to distinct mega-environments. Genotypes G2 (TKA 0612) and G16 (TKA 1104) are identified as the best performers in the first mega-environment, G6 (TKA 1035) and G13 (TKA 1336) in the second and G11 (TKA 1326) and G4 (TKA 0848) in the third. G6 (TKA 1035) was identified as an ideal genotype by manifesting greater mean performance and stability. Among the testing seasons (environments), season 1 (2020) was the most discriminating and is considered a good test environment for selecting widely adapted genotypes.

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Authors' contributions

SA analyzed the data and wrote the first draft of the research paper. SHR conducted the experiments and recorded the observations. PY and NA assisted in writing the research paper and corrected the final draft. KB coordinated the field experiments and arranged for the literary search.

Compliance with ethical standards

Conflict of interest: The authors declare no conflict of interest.

Ethical issues: None

References

1. Prakash AH, Sabesh M. Contribution of AICRIP on cotton in changing Indian cotton Scenario. Int Cotton Res Asso. 2022;1 (11):22–29.
2. Blaise D, Venugopalan MV, Raju AR. Introduction of Bt-cotton hybrids in India: Did it change the Agronomy? Indian J Agron. 2014;59:1–20. https://doi.org/10.59797/ija.v59i1.4534
3. Verma SK, Tuteja OP, Monga D, Waghmare VN. GMS-CISG 20 - A new genetic male sterile line of diploid cotton (Gossypium arboreum L.) with marker trait. J Cotton Res Develop. 2020;34:46–49.
4. Blaise, Kranthi K, Saxena S, Venugopalan M, Mohan P. Productivity and fibre attributes of absorbent Asiatic cotton (Gossypium arboreum) cultivars in rainfed central India. Indian J Agric Sci. 2022;92(3):300. https://doi.org/10.56093/ijas.v92i3.122542
5. Gauch HG, Zobel RW. Identifying mega-environments and targeting genotypes. Crop Sci. 1997;37:311–26. https://doi.org/10.2135/cropsci1997.0011183X003700020002x
6. Yan W, Kang MS. GGE biplot analysis: A graphical tool for breeders, geneticists and agronomists. Boca Raton: CRC Press; 2003 https://doi.org/10.1201/9781420040371
7. Khan MMH, Rafii MY, Ramlee SI, Jusho M, Mamun MA. AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (Vigna subterranea L. Verdc.) genotypes under the multi-environmental trials (METs). Sci Rep. 2021;11:22791. https://doi.org/10.1038/s41598-021-01411-2
8. Lee SY, Lee HS, Lee CM, Ha SK, Park HM, Lee SM, et al. Multi-environment trials and stability analysis for yield-related traits of commercial rice cultivars. Agric. 2023;13:256. https://doi.org/10.3390/agriculture13020256
9. Farias FJC, Carvalho LP, Filho SJL, Teodoro PE. Biplot analysis of phenotypic stability in upland cotton genotypes in Mato Grosso. Genet Mol Res. 2016;15(2):1–10. http://dx.doi.org/10.4238/gmr.15028009
10. Suinaga FA, Bastos CS, Rangel PLE. Phenotypic adaptability and stability of cotton cultivars in Mato Grosso state, Brazil. Pesq Agropec Trop. 2006;36:145–50.
11. Baraki F, Zenawi G, Belay Y, Teame G, Zerabruk G, Assefa A, et al. Parametric and non-parametric measures to identify stable and adaptable cotton (Gossypium hirsutum L.) genotypes. J Nat Fibers. 2024;21(1):2317426. https://doi.org/10.1080/15440478.2024.2317426
12. Samak ANR, Rajeswari S, Ravikesavan R, Subbalakshmi LN, Ganapathy S, Kini AV. Comparison of AMMI and GGE biplot analysis to assess the adaptability and stability of bt cotton genotypes. Int J Curr Microbiol App Sci. 2020;9(9):267–81. https://doi.org/10.20546/ijcmas.2020.909.333
13. Tinker YWNA. Biplot analysis of multi-environment trial data: principles and applications. Can J Plant Sci. 2006;86:623–45. https://doi.org/10.4141/P05-169
14. Rakshit S, Ganapathy KN, Gomashe SS, Swapna M, More A, Gadakh SR, et al. GGE biplot analysis of genotype × environment interaction in rabi grain sorghum. [Sorghum bicolor (L.) Moench]. Ind J Genet. 2012;74(4): 558–63. https://doi.org/10.5958/0975-906.2014.00889.X
15. Yan W, Kang MS, Ma B, Woods S, Cornelius PL. GGE biplot vs. AMMI analysis of genotype-by environment data. Rev and Interpretation. Crop Sci. 2007;47:643–53. https://doi.org/10.2135/cropsci2006.06.0374
16. Yang RC, Crossa J, Cornelius PL, Burgueño J. Biplot analysis of genotype × environment interaction: proceed with caution. Crop Sci. 2009;49:1564–76. https://doi.org/10.2135/cropsci2008.11.0665
17. Hashim N, Rafii MY, Oladosu Y, Ismail MR, Ramli A, Arolu F, Chukwu S. Integrating multivariate and univariate statistical models to investigate genotype-environment interaction of advanced fragrant rice genotypes under rainfed condition. Sustain. 2021;13(8):4555. https://doi.org/10.3390/su13084555