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A Multi-Model Stability Analysis Employing AMMI and BLUP-Based Simultaneous Selection for *Gossypium barbadense* Genotype Yield Stability

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ABSTRACT

Developing stable, high-yielding Egyptian cotton (*Gossypium barbadense*) cultivars that can adapt to changing weather patterns and rising temperatures is one of the main goals of cotton breeders. Nineteen genotypes of *G. barbadense* were evaluated for stable yield over five consecutive Kharif seasons from 2019 to 2024. Genotype-by-environment interactions contributed 96.2% of the variance, highlighting their importance. Genotypes G3 and G4 consistently performed well under all conditions, with high mean yields, according to the Additive Main Effects and Multiplicative Interaction model. As there were more interactions, the relative performance of genotypic values, the harmonic mean of the relative performance of genotypic values, and the harmonic mean of genotypic values were used to estimate the principal components of Best Linear Unbiased Prediction (BLUP)-based simultaneous selection. Genotypes G10 and G9 exhibited the highest anticipated means for number of bolls. Additionally, based on their stability indices, genotypes G10, G9, G2, and G18, were stable in number of bolls produced. Genotypes G9, G18, and G10 presented more bolls and greater stability based on the weighted average absolute scores of BLUP. BLUP was more accurate in determining the stability of the genotypes. In this study, G2, G3, and G13 cotton genotypes were found to be stable across all the models.

Cotton (*Gossypium* spp.) is an immensely important commercial crop for India's economy. In India, cotton plays a major role in sustaining the livelihood of an estimated six million cotton farmers and 40 to 50 million people engaged in related activities such as cotton processing and trade. *Gossypium barbadense* L., commonly known as Egyptian or Sea Island cotton, is distinguished for its superior fiber qualities such as length, strength, and fineness. *G. barbadense* is typically grown in regions with favorable climatic conditions, including warm temperatures and sufficient water supply, which contribute to its high productivity (Cothren, 1999). Despite its advantages, the productivity of *G. barbadense* can be influenced by various factors, including genotype-by-environment interactions (GEI), which affect its stability and yield across different growing conditions (Smith and Cothren, 1999). Local weather within a region varies greatly from year to year, making it difficult to predict weather patterns. Therefore, obtaining stable and high-yielding cultivars is the main goal of crop breeding. For Sea Island cotton areas across the world, where the crop is cultivated as a variety or used as a male parent for hybrid development, selection for *G. barbadense*'s high stability or adaptability is crucial. Furthermore, the success of any breeding program mainly relies on the extent of genetic diversity present in the population. Advances in breeding and agronomic practices have aimed to enhance cotton yield and fiber quality, with a focus on increasing boll number (Zhao et al., 2019).

Boll number is a primary determinant of cotton yield and directly impacts the crop's overall economic value (Smith and Cothren, 1999). A higher boll count generally corresponds to increased fiber production, which is vital for meeting global textile demands (Cothren, 1999). The stability of boll numbers across varying environmental conditions is equally important for achieving stable and high yields, but GEI often complicates the selection process by causing variable performance across different conditions (Kang, 2002). This underscores the importance of robust statistical methods for analyzing

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GEI and identifying stable, high-yielding genotypes. Stable performance across different environments ensures consistent yield and quality, reducing the risk of poor harvests due to environmental fluctuations. Breeding programs aim to enhance this stability by selecting genotypes that perform reliably across diverse conditions, which is essential for achieving sustainable and predictable cotton production (Smith and Cothren, 1999). Among the statistical approaches used to analyze GEI, the Additive Main Effects and Multiplicative Interaction (AMMI) model and Best Linear Unbiased Prediction (BLUP) model have gained prominence. The AMMI model effectively combines analysis of variance (ANOVA) with principal component analysis (PCA) to separate main effects from interaction effects, offering insights into both the stability and adaptability of genotypes (Gauch, 2013). On the other hand, the BLUP methodology, grounded in mixed-model theory, provides accurate predictions by considering both fixed and random effects, making it a powerful tool in plant breeding for selecting genotypes with desirable traits across environments (Piepho et al., 2008).

AMMI is a fixed-effect model that cannot directly accommodate the structure of a linear mixed model (LMM), which incorporates both fixed and random effects. BLUP enables a mixed model method that first estimates the effects of the ANOVA model before assigning weights (repeatability) to these effects and reducing them to zero means. In recent years, the integration of these models in breeding programs has shown promise, enabling simultaneous selection for performance and stability (Crossa et al., 2021). The strength of both of these methodologies has been merged into a new quantitative genotypic stability measure termed WAASB (weighted average absolute scores of BLUPs), which employs the singular value decomposition of BLUP matrix to examine the GEI effects created by an LMM. AMMI allocates most GEI patterns to the first interaction principal component axis (IPCA), while preserving the majority of random errors in the final IPCA. WAASB analyzes GEI in multi-environment trials (METs) by combining AMMI and BLUP characteristics, taking into account the predicted IPCA. This study aims to use a multi-model approach, employing both AMMI and BLUP-based simultaneous selection, to assess the stability and performance of *G. barbadense* genotypes for the number of bolls. The outcomes of this research will contribute valuable insights into the breeding of more productive and stable *G. barbadense* cultivars, ultimately supporting sustainable cotton production.

MATERIALS AND METHODS

Based on yield and fiber characteristics, 19 *G. barbadense* germplasms were chosen from the Indian Council of Agricultural Research and Central Institute for Cotton Research (CICR) gene banks (Table 1). These lines were selected from 50 germplasm lines maintained at the institute for yield, disease, and fiber traits. The 19 germplasm (18 germplasm lines + 1 variety [ICB 174 - Suvin]) lines showed a low incidence of pest and disease and improved fiber traits when compared to other lines maintained in the gene banks. The BLUP and AMMI studies were performed for the number of bolls per plant stability over the changing meteorological parameters from 2019 to 2024.The trial site is characterized as red loam soil, 427 m above mean sea level, and located at latitude 11.0122° N and longitude 76.9354° E. Using a randomized full-block design, three replications were set up with five rows of each genotype planted in each of the five years. The CICR suggested spacing of 90 by 60 cm was followed (Sabesh, 2023). Filling in the gaps and thinning the plants after 15 d allowed one plant per hill, thereby maintaining 10 plants per row. In each replication, 20 plants were randomly selected and tagged and used for making observations throughout the season. The administration of the suggested fertilizer dose and plant protection measures were followed using proper crop management methods (Sabesh, 2023). Once the bolls burst, the number of bolls on each tagged plant was counted before harvesting. Weather data, such as rainfall and

Table 1. ***G. barbadense* genotypes evaluated during five growing seasons from 2019-2024**

Genotype Code	Genotype	Genotype Code	Genotype
G1	ICB 174	G11	ICB 34
G2	CCB 141	G12	ICB 207
G3	ICB 264	G13	ICB 176
G4	ICB 124	G14	ICB 46
G5	CCB 143 B	G15	ICB 161
G6	ICB 284	G16	ICB 183
G7	CCB 25	G17	ICB 39
G8	CCB 29	G18	CCB 11 A
G9	ICB 28	G19	ICB 99
G10	ICB 258		

high and low temperatures, were obtained for all five crop-growing seasons.

Statistical Analysis. To evaluate differences between genotypes (G), seasons (years), and GEI, the number of bolls was subjected to ANOVA.

AMMI and BLUP. The Gauch et al. (1996) model was used to perform AMMI analysis using the number of bolls per plant data from the 19 experimental lines collected over five consecutive crop years. The average of the squared eigenvector values (EV), Annicchiarico's D parameter (DA), the sum of the absolute values of the interaction principal component (IPC) scores (SIPC), AMMI stability value (ASV), Zhang's D parameter (DZ), AMMI-based stability parameter (ASTAB), the sum across environments of the absolute values of GEI modeled by AMMI (AVAMGE), the stability measure based on the fitted AMMI model (FA), AMMI stability index (ASI), modified AMMI stability index (MASI), and modified AMMI stability value (MASV) were among the various AMMI stability indices (ASTABs) evaluated (Anuradha et al., 2022). Based on AMMI scores, including ASTAB, MASV, and MASI, the nonparametric and parametric simultaneous selection indices, as well as the simultaneous selection indices using the Culling strategy were calculated (Ajay et al., 2020; Rao and Prabhakaran, 2005). The estimation of the harmonic mean of genotypic values (HMGV) to infer both yield and stability, the relative performance of genotypic values (RPGV) to examine the mean yield and genotypic adaptation, and the harmonic mean of relative performance of genotypic values (HMRPGV) to evaluate yield, adaptability, and stability simultaneously were used to study BLUP using the formulas from the de Resende studies (2004, 2016).

Software Used. Using the R packages agricolae (De Mendiburu, 2015) and ammistability (Ajay et al., 2018), ASTABs were calculated (R Core Team, 2018). Using R's lme4 package, BLUP-based stability models such as HMGV, RPGV, and HMRPGV were estimated (Bates et al., 2015).

RESULTS AND DISCUSSION

There are predominantly two approaches taken to find stable, high-yielding genotypes: AMMI-based and BLUP-based. The selected genotypes underwent repeated testing at the same location to find a cultivar that would remain stable in the face of changing weather conditions. The seasons differed in the examined meteorological characteristics (Fig. 1). There was variation noted in the total amount of rainfall received during the crop season for all five growing seasons. The first crop season had the most rainfall, whereas the fourth season had the least. There was a noticeable difference in temperature across the five growing seasons. In 2020-2021 and 2023-2024, a temperature increase was observed during the boll development stage. The highest (65 bolls/plant) and the lowest (6 bolls/plant) seed cotton yields were recorded from Season 3 and Season 1, respectively. The cotton genotypes also differed in the number of bolls developed. The highest number of bolls was recorded from G10 and G9 with 45 and 37 bolls/plant, respectively, whereas the lowest number of bolls was recorded from G13 (16 bolls/plant) and G19 (28 bolls/plant) (Table 2).

Additive Main Effects and Multiplicative Interaction. This approach facilitates the identification of superior and stable genotypes excelling in specific environments and reveals genotypes with consistent performance across environments (Danakumara et al., 2023). AMMI analysis revealed variation ($p <$ 0.001) among the studied genotypes, crop season, and GEIs (Table 3). The majority of the total variation was attributed to genotype, whereas environment and GEI contributed approximately 13.24 and 6.55%, respectively. The first four principal components (PCs) contributed to the GEI. The first PC contributed 57.2% to total GEI, whereas the second, third, and fourth PCs contributed 26, 16.1, and 0.7%, respectively. In the AMMI biplot, strong interactions were represented by long vectors in Seasons 1, 2, 3, and 5, whereas weaker interactions were shown by shorter vectors in Season 4. Season 4 showed PCA1 scores closer to zero. This suggests a better performance of all the genotypes in this growing season. Seasons 1, 2, 3, and 5 had vectors parallel to PC1 (57.2%), indicating a higher contribution to overall variation. Seasons 2, 3, and 4 had a higher average number of bolls than Season 1 and Season 5. Crop seasons 5 and 3 were below-average environments (Fig. 2). G4, G11, G16, G15, G8, and G14 had fewer bolls per plant, aligning with zero scores on the first PCA1 axis. These genotypes were less affected by environmental variations.

The results of AMMI analysis showed that G3 and G4 performed consistently regardless of the growing season. G10, G9, and G18 had a high number of bolls only in seasons 2, 3, and 4. Hence, these genotypes are environment-bound genotypes.

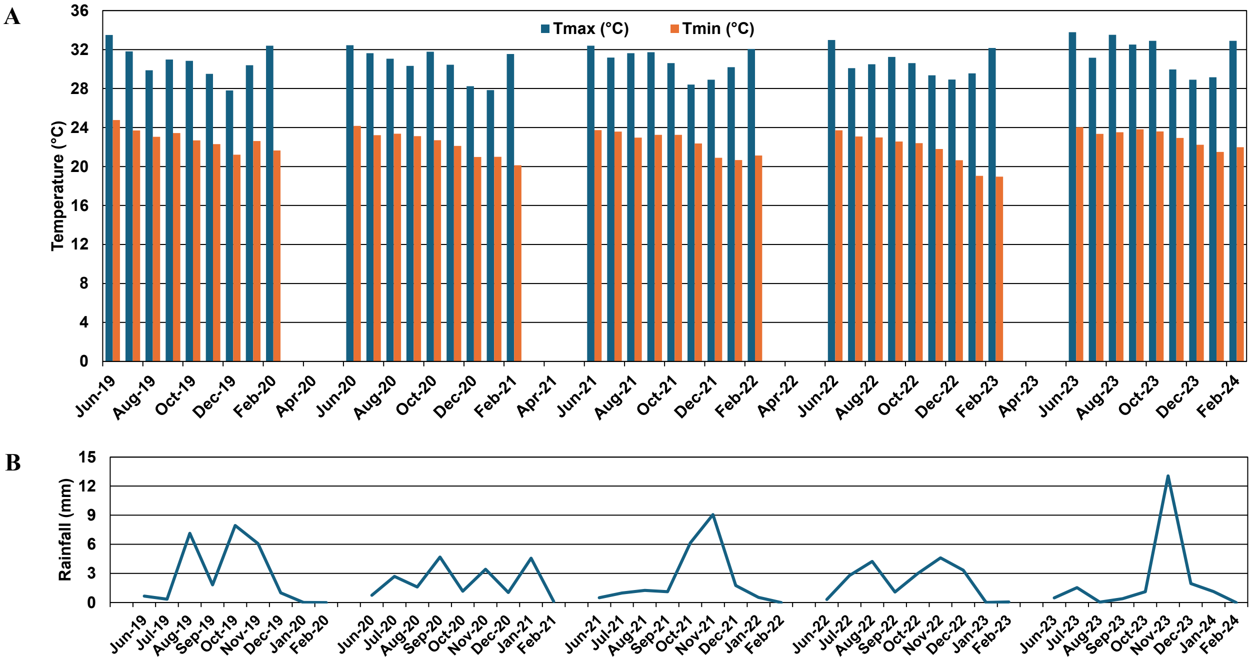

Figure 1. Bar chart illustrating (A) temperature variations and (B) total precipitation for the five crop seasons under test (2019-2024).

Table 2. Mean performance of the genotypes for number of bolls over the seasons

Genotype	2019-20	2020-21	2021-22	2022-23	2023-24	Average
G1	8	14	60	28	44	31
G2	25	33	40	32	29	32*
G3	22	38	32	30	20	28
G4	31	18	30	30	20	26
G5	16	26	17	19	30	22
G6	13	18	33	21	27	22
G7	14	24	33	25	15	22
G8	33	35	18	28	15	26
G9	53	35	39	44	15	37**
G10	33	52	65	48	28	45**
G11	15	35	26	27	25	26
G12	20	31	17	22	10	20
G13	16	15	18	19	12	16
G14	31	38	25	31	17	28
G15	15	46	21	24	20	25
G16	17	27	31	28	25	26
G17	24	29	23	27	20	24
G18	30	41	40	35	18	33*
G19	6	30	9	19	14	16
General Mean				27.69		
CV%				32.15		
SED				4.19		
CD (p = 05) genotypes				8.22		

*Significant under $p = .05$ and **significant under $p = .01$.

Table 3. AMMI analysis for number of bolls of 19 *G. barbadense* genotypes under five test environments

Source	df[z]	MSS[y]	% contribution toward total variation
Environments	4	1145.3	13.24
Rep. (within Environment)	10	0.402	0.01
Genotype	18	735.659	38.28
GEI[x]	72	231.721	6.55
PC[w]1	21	454.335	57.2
PC2	19	228.379	26
PC3	17	158.220	16.1
PC4	15	7.596	0.7
Residuals	180	0.463	
Total	356	144.040	

[z] df, degrees of freedom

[y] MSS, mean sum of squares

[x] GEI, genotype by environment interaction

[w] PC, principal component

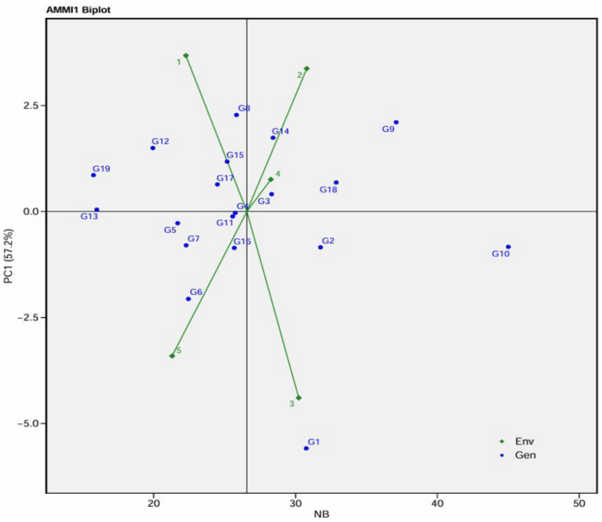

Figure 2. The AMMI biplot [cotton number of bolls vs. principal component 1 (PC1)] for number of bolls of 19 *G. barbadense* genotypes in five test environments between 2019 and 2024.

The number of IPCAs has a major impact on the genotype ranking. The importance of GEI reveals the various responses of genotypes as well as their strengths and weaknesses in various environments. To find promising genotypes across multiple environments, the AMMI model and the genotype main effect plus GEI (GGE) biplot graphical model are frequently employed in tandem. PCA served as the basis for the proposal of this graphical model.

Estimation of AMMI-Based Stability Indices. Stability alone is not a desirable selection criterion for plant selection, hence, simultaneous selection of yield and stability in a single nonparametric index is necessary (Farshadfar et al., 2011; Mohammadi et al., 2007).

The ASI, ASV, MASV, ASTAB, AVAMGE, DA, DZ, EV, FA, MASI, MASV, SIPC, and the absolute value of the relative contributions of IPCs to the interaction (ZA), were analyzed to compare whether they were equally efficient in assessing the stability of genotypes and are presented in Table 4. Based on the results of ASI and ASV, G13, G3, and G17 were stable and G1 was the least stable. The ASI and ASV parameters are helpful when the first two IPCAs account for a large portion of the variation; however, the overall variation described by these parameters is negligible when three or more IPCAs are relevant. Based on MASI values, G13, G3, and G17 were stable, whereas G1 was less stable. Based on the values of MASV, G2, G14, and G17 were stable, and G10 was less stable. MASI and MASV measures are equivalent to plots with all PCA axes for the ranking of genotypes. DA, DZ, ASTAB, and FA showed that G2, G3, and G17 were more stable and that G1 was less stable. Comparing all the stability indices, G2, G3, and G17 were the most stable genotypes.

Several stability parameters, including ASV, ASTAB, AVAMGE, DA, DZ, EV, and FA, revealed each parameter has the same potential for identifying stable genotypes (Anuradha et al., 2022). Comparing all the parameters, G2, G3, and G17 were found to be stable across seasons. The stability parameters almost displayed a similar trend in identifying stable genotypes. Similar results were reported in the study by Cheloei et al. (2020) in rice (*Oryza sativa* L.) using the same set of stability indices.

GEI Biplot: Weighted Average Absolute Scores of BLUP (WAASBY) Index. A clear illustration of the which–won–where pattern can be found in Fig. 3. In the first IPCA, G13 emerged as the dominant performance when considering number of bolls per plant. This performance highlights G13's exceptional adaptability and stability across diverse conditions. By combining mean performance and stability, the WAASB-based simultaneous selection index effectively finds the best genotypes. The WAASB model offers a thorough method for assessing genotype stability and yield by taking into account all IPCAs. The most stable genotypes,

Table 4. Stability indices utilized for ranking genotypes under five test environments

Genotype	ASI	ASTAB	AVAMGE	DA	DZ	EV	FA	MASI	MASV	SIPC	ZA	WAASB
G1	3.199	31.544	87.286	42.086	0.754	0.142	1771.245	3.199	13.642	6.504	0.453	3.358
G2	0.485	1.046	13.977	6.550	0.253	0.016	42.905	0.485	1.961	1.533	0.071	0.520
G3	0.257	1.274	11.054	6.630	0.197	0.010	43.952	0.301	22.862	1.800	0.077	0.497
G4	0.506	7.322	24.695	15.636	0.497	0.062	244.496	0.585	43.106	4.273	0.139	0.822
G5	0.531	9.357	28.221	17.135	0.624	0.097	293.609	0.635	51.138	5.288	0.169	1.019
G6	1.181	5.179	33.976	16.196	0.368	0.034	262.304	1.188	20.016	3.468	0.187	1.342
G7	0.485	2.077	16.590	8.777	0.291	0.021	77.041	0.507	21.616	2.801	0.115	0.769
G8	1.303	6.142	34.083	17.782	0.388	0.038	316.194	1.310	20.688	3.760	0.207	1.488
G9	1.518	17.320	49.079	27.165	0.648	0.105	737.962	1.520	14.186	6.189	0.325	2.211
G10	0.576	14.507	39.130	21.566	0.681	0.116	465.084	0.806	82.727	5.656	0.219	1.364
G11	0.415	2.668	19.888	9.844	0.299	0.022	96.905	0.416	4.888	2.246	0.082	0.507
G12	0.860	2.555	22.606	11.499	0.270	0.018	132.225	0.860	5.434	2.423	0.134	0.971
G13	0.161	1.789	13.903	7.211	0.287	0.021	51.998	0.240	26.068	2.200	0.063	0.364
G14	0.995	3.179	26.635	13.115	0.276	0.019	172.001	0.995	4.161	2.316	0.141	1.045
G15	0.943	10.033	33.206	19.528	0.558	0.078	381.351	0.968	32.371	5.657	0.238	1.557
G16	0.501	1.732	14.563	7.343	0.382	0.036	53.924	0.503	6.998	2.389	0.092	0.638
G17	0.367	1.147	10.895	6.633	0.197	0.010	43.994	0.390	19.255	1.838	0.080	0.537
G18	0.445	3.552	19.256	11.042	0.344	0.030	121.929	0.508	35.976	3.334	0.132	0.852
G19	0.769	8.109	31.215	15.881	0.710	0.126	252.195	0.769	4.760	4.691	0.168	1.105
Mean	0.816	6.870	27.908	14.822	0.422	0.053	292.701	0.852	22.729	3.598	0.163	1.104

^{z}**Abbreviations: ASI, Additive Main Effects and Multiplicative Interaction (AMMI) stability index; ASTAB, AMMI-based stability parameter; AVAMGE, sum across environments of the absolute values of the genotype by environment interaction 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 the fitted AMMI model; MASI, modified AMMI stability index; MASV, modified AMMI stability value; SIPC, sum of the absolute values of the interaction principal component (IPC) scores; ZA, absolute value of the relative contributions of IPCs to the interaction; WAASB, weighted average of the absolute scores of Best Linear Unbiased Predictions (BLUPs)**

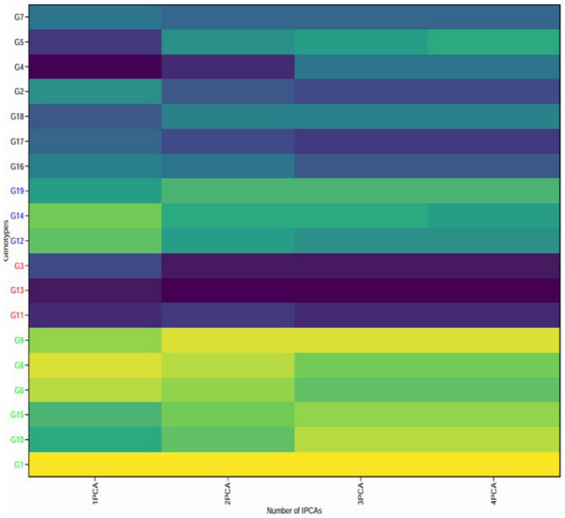

Figure 3. The weighted average of the absolute scores for the best linear unbiased predictions (BLUPs) of the genotype-environment interaction (WAASB) estimation, including the interaction principal component axes (IPCAs).

including G13, G11, and G3 that showed the lowest WAASB values, are highlighted by this method. The significance of several IPCAs for an appropriate assessment is shown by the use of color variations in WAASB figures that group genotypes based on similar stability performances.

The WAASBY index was developed based on the multi-trait stability index (MTSI) which combines stability and trait productivity, facilitating broader adaptations. This method analyzes the GEI effects of an LMM using the singular value decomposition of a BLUP matrix (Vineeth et al., 2022). The analysis included other fiber traits to calculate the MTSI (Table 5). The precise evaluation of genotypes based on performance and stability using the WAASBY index of 100/0 assigns full weight to stability, and 0/100 gives full weight to mean performance. In cluster 1, G7 and G13 exhibited poor productivity and instability and exhibited low rankings for all WAASB:Yield ratios.

Table 5. Plant and fiber characteristics used for calculating the Multi-Trait Stability Index (MTSI) for genotypes grown under multiple environments along with average boll counts

Genotype	Plant height (cm)	Number of monopodial branches	Number of sympodial branches	Single boll weight (g)	Elongation ratio	Fiber length (mm)	Fiber strength (g/tex)	Fiber fineness (µ)
G1	146.57	0	18	5.1	31.43	33.89	35.29	4.78
G2	204.72	5	19	5.1	31.98	34.95	35.90	4.32
G3	165.00	4	23	3.7	30.08	31.73	31.39	4.61
G4	165.95	2	26	3.7	29.82	36.32	39.30	4.61
G5	212.04	4	29	5.4	32.17	39.06	41.12	4.14
G6	188.89	2	26	4.8	36.47	33.30	35.13	4.70
G7	176.14	1	27	4.5	31.29	37.39	40.57	4.11
G8	190.15	1	29	4.5	34.50	35.97	37.52	4.23
G9	147.66	2	26	5.1	31.57	29.02	32.32	4.79
G10	171.13	2	26	3.8	31.71	32.53	34.65	4.04
G11	202.03	1	28	3.7	33.94	32.78	33.17	4.58
G12	215.69	0	28	3.7	29.30	32.06	35.85	4.34
G13	156.63	4	21	4.2	37.18	35.58	40.76	3.92
G14	198.95	1	25	3.9	30.95	32.79	37.84	4.28
G15	144.39	2	14	5.0	31.42	34.16	33.21	4.63
G16	191.88	3	21	4.0	29.84	33.83	39.44	3.46
G17	202.59	3	22	3.9	37.45	27.75	27.80	5.74
G18	197.31	2	27	4.3	32.87	38.81	41.82	3.83
G19	141.68	0	20	4.4	35.27	29.11	32.35	4.35

Cluster 2, G4, G3, G2, G17, G16, G14, and G11 showed good productivity and instability, with low WAASB:Yield ratios. Cluster 3, which comprised G9, G18 and G10, exhibited high productivity and broad adaptability, indicating greater stability with low WAASB scores. In cluster 4, G8, G6, G5, G19, G15, G12, and G1 showed stable but poor yielders with high WAASB:Yield ratios (Fig. 4).

Best Linear Unbiased Prediction (BLUP). The BLUP method uses a mixed-model approach to assess ANOVA model effects, assign weights (repeatability), and reduce them to zero means. The parental lines selection can be enhanced by the estimation of breeding values using BLUP (Bauer et al., 2006). The predicted mean value of BLUP for the number of bolls per plant of the 19 *G. barbadense* genotypes is presented in Fig. 5. Out of the 19 genotypes, seven had higher than the predicted mean value for the number of bolls per plant. Among these, G10 and G9 had the highest predicted mean value. To find multi-environments (ME) and the best performing genotypes within each ME, the AMMI model and the GGE biplot graphical model are frequently employed in tandem. PCA served as the basis for the proposal of this graphical model. The graphical representation of GEI helps breeders evaluate genotype stability and the combination of genotype yield stability with environment without taking into account the limitations of genotypes in different environments. Consequently, using the BLUP approach in this situation could yield more reliable and superior results.

The AMMI model does not make provision for a quantitative stability measurement, which is essential to quantify and rank the genotypes (Ajay et al., 2020). To predict yield, it is necessary to choose between AMMI models and BLUP models. The BLUP has been used in the evaluation of various crops such as rice, corn, cotton, and sugarcane and useful results have been presented (Taleghani et al., 2023). Our results are consistent with Piepho's (1994) findings, which stated that in the context of METs, taking into account intrinsic factors unique to each trial, BLUP has added advantage over the AMMI family in yield prediction (Shimray et al. 2022; Spoorthi et al., 2021).

Estimation of BLUP-based Stability Indices. In breeding programs, estimating the heritability of characteristics is crucial for determining and recom-

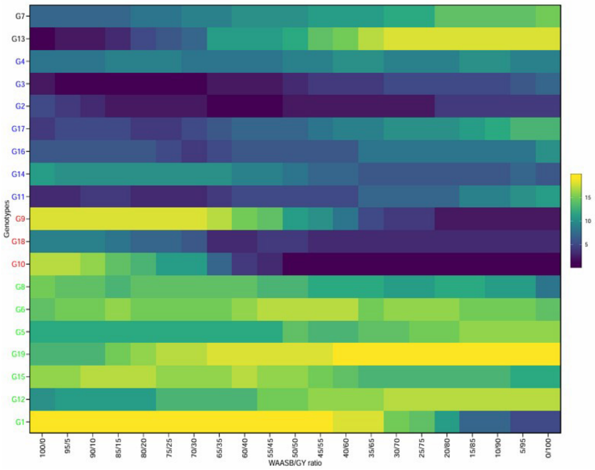

Figure 4. Heatmaps of the WAASBY indices that display genotype rankings based on stability and boll number trait weighted scores. The first component (left side of diagonal line) of the WAASB index to yield ratio (NB) pertains to environmental stability, whereas the second component (right side of diagonal line) relates to number of bolls. Thus, in the genotype ranking, a 0/100 ratio corresponds to stability, whereas the same ratio is also assigned to boll numbers. Moving one unit from left to right in this plot decreases the environmental stability component by 5% and increases the yield component, such that genotypes are ranked solely based on yield (0/100). The first group (green) identifies stable genotypes with optimal yield. The second group (red) identifies poor yielder and instability. The third group (blue) demonstrated high yielder but instability. The fourth group (black) showed poor yield values but with better stability.

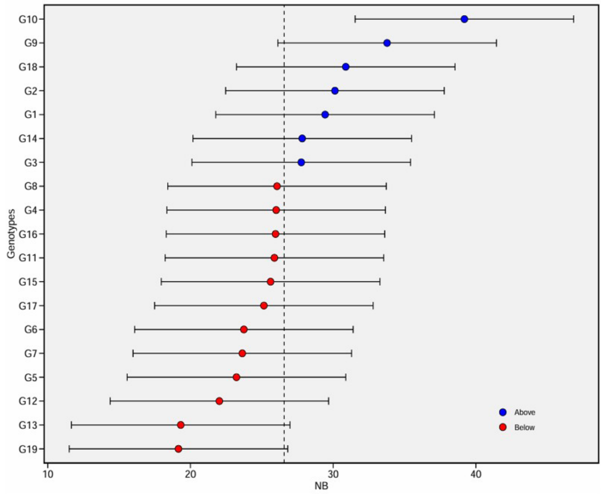

Figure 5. Mean values of best linear unbiased prediction for number of bolls per plant.

mending genotypes (Olivoto et al., 2019). BLUP-based simultaneous selection indices (SSIs) such as HMGV, RPGV, and HMRPGV were estimated for the number of bolls per plant and presented in Table 6. The main advantage of biometric approaches, such as HMGV, RPGV, and HMRPGV, is to disclose the randomness of the genotypic effects and to allow the ranking of genotypes with their performance based on the genetic effects. The BLUP-based SSIs such as HMGV, RPGV, and HMRPGV estimates showed that G10, G2, G9, and G18 exhibited more bolls per plant, with all entries producing above average bolls per plant. The HMGV denotes the phenotypic stability of the principal interaction value (PIV), which adjusts the predicted genetic value to the instability of the cultivated genotypes in the evaluated environments (Borges et al., 2010). The adaptability method of the genotypic values can capitalize the response of genotypes. The adaptation technique of genotypic values (RPGV) was developed to assess the distinct adaptability of each genotype and can capitalize on genotypic responses to improvements in the growing environment. The genetic values predicted by the BLUP technique serve as a basis for the HMRPGV. It provides the ranking of the best genotypes by combining the estimates of stability and adaptability. Although this biometric approach does not undervalue the impacts of the GEI, it does have the advantage of exposing the randomness of the genotypic effects, enabling the ranking of genotypes based on genetic effects.

METs are essential for plant breeding efforts. Thus, predictive accuracy is critical for successful selection, cultivar recommendation, and mega-environment. It concluded that BLUP was the most predictively accurate model. Our findings are consistent with those of Piepho (1994), who concluded that the BLUP surpasses all members of the AMMI family in forecasting Faba bean (*Vicia faba* L.) yield in MET. Olivoto et al. (2019) reported that based on a cross-validation method with four true MET datasets, BLUP had higher predictive accuracy than any other member of the AMMI family.

CONCLUSIONS

Unveiling genotype adaptability and stability using METs of cotton genotypes provided crucial insights into their adaptability and stability under varying environmental conditions. To use the advantages of both AMMI and BLUP, WAASB has been introduced, which is the integration of both methods. The methods RPGV, HMGV, and HMRPGV can be used as selection criteria for investigations into adaptability and/or genotypic stability, as well as addressing a common problem in networks of

Table 6. Best Linear Unbiased Prediction (BLUP)-based ranking of 19 *G. barbadense* genotypes for the number of bolls per plant evaluated in five environments from 2019-2024

Genotype	HMGV[z]	HMGV Rank	RPGV[y]	RPGV Rank	HMRPGV[x]	HMRPGV Rank
G1	18.6	16	1.17	5	0.722	16
G2	31.1	2	1.2	4	1.19	3
G3	26.7	5	1.05	7	1.04	5
G4	24.4	8	0.993	8	0.917	10
G5	20.4	13	0.846	15	0.763	15
G6	20.1	14	0.856	14	0.77	14
G7	20.1	15	0.821	16	0.793	13
G8	23.1	11	0.983	9	0.885	11
G9	30.8	3	1.41	2	1.21	2
G10	41	1	1.66	1	1.62	1
G11	23.8	10	0.959	11	0.923	8
G12	17.5	17	0.741	17	0.685	17
G13	15.6	18	0.607	18	0.596	18
G14	26.4	6	1.07	6	1.02	6
G15	21.8	12	0.928	13	0.854	12
G16	24.6	7	0.97	10	0.949	7
G17	24.1	9	0.931	12	0.919	9
G18	30	4	1.22	3	1.18	4
G19	11.7	19	0.581	19	0.458	19

[z]HMGV, Harmonic Mean of Genotypic Values

[y]RPGV, Relative Performance of Genotypic Values

[x]HMRPGV, Harmonic Mean of Relative Performance of Genotypic Values

competition assays, the variety of variances among settings. A comparison of all the models revealed that the most stable genotypes among those assessed were G2, G3, and G13.

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REFERENCES

Ajay, B.C., J. Aravind, and A.R. Fiyaz. 2018. Ammi stability: Additive Main Effects and Multiplicative Interaction Model Stability Parameters. https://doi.org/10.32614/CRAN.package.ammistability

Ajay, B.C., S.K. Bera, A.L. Singh, K. Narendra, K. Gangadhar, and P. Kona. 2020. Evaluation of genotype environment interaction and yield stability analysis in peanut under phosphorus stress condition using stability parameters of AMMI model. Agric. Res. 9:477–486. https://doi.org/10.1007/s40003-020-00458-3

Anuradha, N., T.S.S.K. Patrol, U. Triveni, P. Jogarao, P K. Priya, M. Elangovan, and S. Pandey. 2022. Assessment of genetic diversity in finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes. Indian J. Plant Genetic Resour. 36(1):105–115. https://doi.org/10.5958/0976-1926.2023.00036.1.14

Bates, D., M. Mächler, B. Bolker, and S. Walker. 2015. Fitting linear mixed-effects models using lme4. J. Stat. Soft. 67(1):1–48. https://doi.org/10.18637/jss.v067.i01

Bauer, A.M., T.C. Reetz, and J. Leon. 2006. Estimation of breeding values of inbred lines using best linear unbiased prediction (BLUP) and genetic similarities. Crop Sci. 46(6):2685–2691. https://doi.org/10.2135/cropsci2006.01.0019

Borges, V., A.A. Soares, M.S. Reis, M.D.V. Resende, V.M.O. Cornélio, N.A. Leite, and A.R. Vieira. 2010. Desempenho genotípico de linhagens de arroz de terras altas utilizando metodologia de modelos mistos. Bragantia 69(4):833–841. https://doi.org/10.1590/S0006-87052010000400008

Cheloei, G., G.A. Ranjbar, N. Babaeian Jelodar, N. Bagheri, and M.Z. Noori. 2020. Using AMMI model and its parameters for yield stability analysis of rice (*Oryza sativa* L.) advanced mutant genotypes of Tarrom-Mahalli. Iran. J. Genet. Plant Breed. 9(1):70–83. https://doi.org/10.30479/ijgpb.2020.13219.1271

Cothren, J.T. 1999. Physiology of the cotton plant. pp. 207–268. *In* C.W. Smith and J.T. Cothren (eds.) Cotton Origin, History, Technology, and Production. John Wiley and Sons, Inc. New York, NY.

Crossa, J., R. Fritsche-Neto, O.A. Montesinos-López, G. Costa-Neto, S. Dreisigacker, A. Montesinos-López, and A.R. Bentley. 2021. The modern plant breeding triangle: Optimizing the use of genomics, phenomics, and enviromics data. Front. Plant Sci. 12:651480. https://doi.org/10.3389/fpls.2021.651480

Danakumara, T., T. Kumar, N. Kumar, B.S. Patil, C. Bharadwaj, U. Patel, N. Joshi, S. Bindra, S. Tripathi, R.K. Varshney, and S.K. Chaturvedi. 2023. A multi-model based stability analysis employing multi-environmental trials (METs) data for discerning heat tolerance in chickpea (*Cicer arietinum* L.) landraces. Plants. 12(21):3691. https://doi.org/10.3390/plants12213691

De Mendiburu, F. 2015. Agricolae: Statistical Procedures for Agricultural Research. R Package Version 1.2-8. https://doi.org/10.32614/CRAN.package.agricolae

De Resende, M.D.V. 2016. Software Selegen-REML/BLUP: a useful tool for plant breeding. Crop Breed. Appl. Biotechnol. 16(4)330–339. https://doi.org/10.1590/1984-70332016v16n4a49

De Resende, M.D.V. 2004. Métodos estatísticos ótimos na análise de experimentos de campo. Embrapa Florestas, Colombo. Available online at https://www.infoteca.cnptia.embrapa.br/handle/doc/305549 (verified 8 April 2025)

Farshadfar, E., N. Mahmodi, and A. Yaghotipoor. 2011. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). Aust. J. Crop Sci. 5(13):1837–1844.

Gauch, H.G. 2013. A simple protocol for AMMI analysis of yield trials. Crop Sci. 53(5):1860–1869. https://doi.org/10.2135/cropsci2013.04.0241

Gauch, H.G., and R.W. Zobel. 1996. AMMI analysis of yield trials. pp. 85–122 *In* M.S. Kang and H.G. Gauch (eds.), Genotype by Environment Interaction. CRC Press, Boca Raton, FL. https://doi.org/10.1201/9780367802226

Kang, M.S. 2002. Genotype-environment interaction: progress and prospects. pp. 221–243. In M.S. Kang (ed.), Quantitative Genetics, Genomics, and Plant Breeding. CABI Digital Library. https://doi.org/10.1079/9780851996011.0221

Mohammadi, R., A. Abdulahi, R. Haghparast, and M. Armion. 2007. Interpreting genotype × environment interactions for durum wheat grain yields using nonparametric methods. Euphytica. 157:239–251. https://doi.org/10.1007/s10681-007-9417-3

Olivoto, T., A.D.C. Lúcio, J.A.G. da Silva, B.G. Sari, and M.I. Diel. 2019. Mean performance and stability in multi-environment trials II: Selection based on multiple traits. Agron. J. 111(6):2961–2969. https://doi.org/10.2134/agronj2019.03.0221

Piepho, H.P. 1994. Best Linear Unbiased Prediction (BLUP) for regional yield trials: A comparison to Additive Main Effects and Multiplicative Interaction (AMMI) analysis. Theor. Appl. Genet. 89:647–654. https://doi.org/10.1007/bf00222462

Piepho, H.P., J. Möhring, A.E. Melchinger, and A. Büchse. 2008. BLUP for phenotypic selection in plant breeding and variety testing. Euphytica. 161:209–228. https://doi.org/10.1007/s10681-007-9449-8

R Core Team. 2018. R: a language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria. Available online at https://www.R-project.org/ (verified 8 April 2025)

Rao, A.R., and V.T. Prabhakaran. 2005. Use of AMMI in simultaneous selection of genotypes for yield and stability. J. Ind. Soc. Agric. Stat. 59:76–82.

Sabesh, M. 2023. Package of practices for cotton cultivation in Tamil Nadu. Cotton Department, TNAU, Coimbatore, Tamil Nadu. Available online at https://cicr.org.in/wp-content/uploads/POP-TN-01.pdf verified (8 April 2025)

Shimray, P.W., C. Bharadwaj, B.S. Patil, S.M. Sankar, N. Kumar, S.P.P. Reddy, T. Singhal, V. Hegde, S.K. Parida, M. Roorkiwal, R.K. Varshney, and P. Verma. 2022. Evaluation and identification of stable chickpea lines for yield-contributing traits from an association mapping panel. Agron. 12(12):3115. https://doi.org/10.3390/agronomy12123115

Smith, C.W., and J.T. Cothren. 1999. Cotton: Origin, History, Technology, and Production. John Wiley & Sons. New York, NY.

Spoorthi, V., S. Ramesh, N.C. Sunitha, and P.V. Vaijayanthi. 2021. Prediction of genotype performance for untested years based on additive main effects and multiplicative interaction and linear mixed models: An illustration using dolichos bean (*Lablab purpureus* L. Sweet) multi-year data. Ann. Appl. Bio. 180(2):224–235. https://doi.org/10.1111/aab.12726

Taleghani, D., A. Rajabi, A. Saremirad, and P. Fasahat. 2023. Stability analysis and selection of sugar beet (*Beta vulgaris* L.) genotypes using AMMI, BLUP, GGE biplot and MTSI. Sci Rep. 13:10019. https://doi.org/10.1038/s41598-023-37217-7

Vineeth, T.V., I. Prasad, A.R. Chinchmalatpure, B.M. Lokeshkumar, S. Kumar, K.T. Ravikiran, and P.C. Sharma. 2022. Weighted Average Absolute Scores of BLUPs (WAASB) based selection of stable Asiatic cotton genotypes for the salt affected Vertisols of India. Indian J. Genet. Plant Breed. 82(1):104–108. https://doi.org/10.31742/IJGPB.82.1.15

Zhao, W., R. Wang, W. Hu, and Z. Zhou. 2019. Spatial difference of drought effect on photosynthesis of leaf subtending to cotton boll and its relationship with boll biomass. J. Agron. Crop Sci. 205(3):263–273. https://doi.org/10.1111/jac.12320