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RESEARCH ARTICLE

Yield stability and jassid resistance in intra-hirsutum hybrids: Multi-environment evaluation using stability tools

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Abstract

Genotype-by-environment interaction (GEI) is a major challenge in developing cotton hybrids with stable performance across diverse agro-ecologies, often resulting in yield and fibre quality instability with significant economic implications. This study evaluated 39 intra-hirsutum cotton hybrids to identify high-performing and stable hybrids with resistance to jassid infestation. Yield was assessed across three locations, while jassid resistance was independently screened under unsprayed hotspot conditions. Based on the jassid injury index, 18 hybrids were classified as resistant and 15 as moderately resistant to jassids. Combined ANOVA results showed that genotype and GEI significantly ($p < 0.01$) influenced seed cotton yield, demonstrating the critical role of stability-focused selection in cotton breeding. Yield stability was assessed using multiple statistical approaches, including stability indices, GGE biplots, Y × WAAS (yield versus weighted average of absolute scores) biplots and WAASBY (weighted average of absolute scores and yield) heat maps to improve the accuracy, reliability and interpretability of the results. GGE biplots highlighted E3 as the most discriminating environment, with hybrids H39, H01 and H25 as the best performers. Across all statistical analyses, H38, H13, H22 and H26 were consistently identified as high-performing and stable hybrids. Robust statistical analyses combined with hotspot screening identified H13, H22 and H26 as superior performers in yield and stability with jassid resistance. These hybrids represent valuable resources for breeding programs aimed at yield stability with jassid resistance in cotton.

Keywords: ASV; cotton; GGE biplot; GSI; hotspot screening; WAASBY

Introduction

Cotton (*Gossypium hirsutum* L., $2n=4x=52$) is an allotetraploid species and a globally important fibre and cash crop. In 2024–25, cotton is cultivated on nearly 77.8 million acres worldwide and continues to serve as a cornerstone of global agriculture and trade, supporting millions of livelihoods and providing about 80 % of the natural fibre used in the textile and apparel industries. *G. hirsutum* contributes to over 90 % of global cotton production (1). Despite its broad adaptability and high yield potential, global cotton yields have declined since the 2017–18 season due to extreme weather conditions linked to climate change and increasing pest pressures and this trend is expected to continue through the 2024–25 crop year, which is projected to experience a slight reduction of 0.12 %, reaching 768 kg/ha of productivity (2).

Cotton is vulnerable to over 160 insect pest species, with sucking pests and bollworm complexes causing significant damage (3). The cotton jassid (*Amrasca biguttula*), a major sap-sucking insect, can cause yield losses of up to 40 % under severe infestation by feeding on plant sap and secreting toxins that impair photosynthesis and cause stunted growth (3–5). Chemical control is still the predominant management strategy, but it has led to pesticide resistance, ecological disruption and health risks. Resistant cultivars offer a sustainable alternative, making field screening under natural infestation essential for identifying genotypes with durable pest tolerance. Hotspot-based natural screening further captures realistic pest pressure, climatic influences and plant–insect interactions, while reducing costs and technical challenges associated with artificial infestation (6).

Genotype × environment interaction (GEI) critically influences hybrid performance stability across environments, necessitating multi-environment evaluation to identify broadly adapted genotypes (7). Several statistical tools quantify stability and adaptability, including the AMMI (additive main effect multiplicative interaction effect) stability value (ASV), which combines the first two AMMI interaction principal components to indicate stability (8). The weighted average of absolute scores (WAAS) further refines this by integrating all significant AMMI interaction effects, while WAASY simultaneously assess yield and stability (9). Additionally, GGE biplot analysis offers a graphical approach to visualise genotype performance, adaptability and test environment discrimination (10). Beyond AMMI-based indices, the genotype selection index (GSI) combines yield and stability parameters to efficiently identify genotypes with superior and consistent performance across environments (11). Therefore, the present study aimed to identify jassid-resistant cotton hybrids exhibiting both high and stable yield across multiple environments using AMMI-based stability parameters, GGE biplot analysis and WAASBY heat maps.

Materials and Methods

Hotspot screening of cotton hybrids for jassid tolerance

Hotspot screening serves as an effective approach for identifying pest-resistant genotypes under intense natural infestation, aiding targeted crop improvement. A total of 39 intra-hirsutum cotton hybrids were developed using a line × tester mating design involving three lines and thirteen testers. These hybrids, along with tolerant (Rasi swift BGII) and susceptible checks (RCH 659 BGII), were evaluated for jassid resistance under hotspot conditions. The choice of these checks was based on their inclusion in the Crop Standards Notification and Release trials, where Rasi Swift (RCH 971 BGII) demonstrated superior performance over the zonal check RCH 659 under unsprayed conditions for sucking pests. Hence, these hybrids were adopted as contrasting checks for the present investigation. The study was conducted at the research farm of Rasi Seeds (P) Ltd. (Lat 11.5971° N, Long 78.5999° E, Attur, Tamil Nadu) during the 2024–25 winter season (September to January) under unsprayed conditions for insecticides to allow natural infestation of sucking pests. Susceptible and tolerant checks were systematically replicated after every ten hybrid (single row) rows with two replications and border rows were planted with the susceptible check to ensure adequate jassid pressure. All other agronomic practices were carried out according to standard recommendations throughout the cropping period (12).

Trait measurement

The jassid injury was assessed following the Indian Central Cotton Committee (ICCC) guidelines and based on resultant symptoms of infestation (13). The Jassid injury grades were presented in Table 1. Jassid infestation was assessed by randomly selecting ten plants per hybrid and counting adults and nymphs on the lower leaf surfaces. Observations were made at 15-day intervals up to 75 days after sowing. The mean injury index was calculated based on visible damage symptoms, following guidelines (13). A leafhopper resistance index was calculated as per Equation 1 (14).

Leafhopper resistant index = (G1 × P1 + G2 × P2 + G3 × P3 + G4 × P4)/(P1 + P2 + P3 + P4) (Eqn. 1)

Where P1, P2, P3 and P4 are the number of plants with G1, G2, G3 and G4 grades. The injury index was used to categorise genotypes into four resistance classes: resistant (0–1.0), moderately resistant (1.1–2.0), susceptible (2.1–3.0) and highly susceptible (3.1–4.0) (14).

Experimental materials and study environment for yield stability

Environmental heterogeneity forms the basis of stability analysis, as it reveals genotype × environment interactions that are pivotal for accurately assessing genotypic adaptability and yield consistency across diverse conditions. This study was conducted at Rasi Seeds (P) Ltd. research farms during the 2024–25 winter season (September-January) across three locations in India (Table 2) (Fig. 1). The same set of hybrids, along with six standard checks (Supplementary table. 1), was evaluated in a randomized block design with two replications at a spacing of 90 cm × 60 cm. Each hybrid was planted in a plot of 131.2 m^2. All the agronomic practices were carried out according to standard recommendations to maintain a healthy crop (12). The seed cotton yield was initially recorded on a per-plot basis and subsequently standardised to kilograms per hectare (kg ha^{-1}) for further analysis.

Statistical analysis

Bartletts' test was conducted using the Bartlett test function ($\alpha = 0.05$) in R (R version 4.5.0) to test homogeneity of variances (15). Combined ANOVA, GGE biplots analysis was carried out using the R-based tool PBMLT (16).

AMMI stability value (ASV)

ASV refers to the distance from the origin in a two-dimensional scatter plot of IPCA1 versus IPCA2 scores. The ASV was calculated as per the standard formula as given in equation 2.

$$ASV = \sqrt{[(SSIPCA1 \,/\, SS\_IPCA2) \times IPCA1]^2 + (IPCA2)^2} \quad \text{(Eqn. 2)}$$

Where SS denotes the sum of squares, while IPCA1 and IPCA2 represent the first and second interaction principal component axes, respectively. The IPCA1 and IPCA2 scores correspond to the genotypic scores derived from the AMMI model (11).

Genotype selection index (GSI)

An important parameter derived from the AMMI analysis is the GSI, which provides a more comprehensive criterion for genotype evaluation by integrating both yield performance and stability.

Table 1. The jassid injury grades based on morphological symptoms

Grades (G)	Symptoms
G1	Leaves exhibiting no signs of crinkling, yellowing, bronzing or drying.
G2	A few lower leaves are showing curling, crinkling and mild yellowing symptoms.
G3	Extensive crinkling and curling of leaves throughout the plant, accompanied by yellowing, bronzing and browning in the middle and lower canopy, with noticeable suppression of plant growth.
G4	Extreme curling, yellowing, bronzing and browning, drying of leaves and defoliation, stunted growth

Table 2. Geographical and climatic profiles of experimental sites involved in stability analysis

Environment	Location	Coordinates	Elevation (MSL)	Annual rainfall (mm)
E1	Attur, Tamil Nadu	Lat 11.5971° N, Long 78.5999° E	244 m	752
E2	Warangal, Telangana	Lat 18.0561922° N, Long 79.6397208° E	266 m	906
E3	Amravati, Maharashtra	Lat 20.93333° N, Long 77.75° E	332 m	1181

MSL: Mean sea level

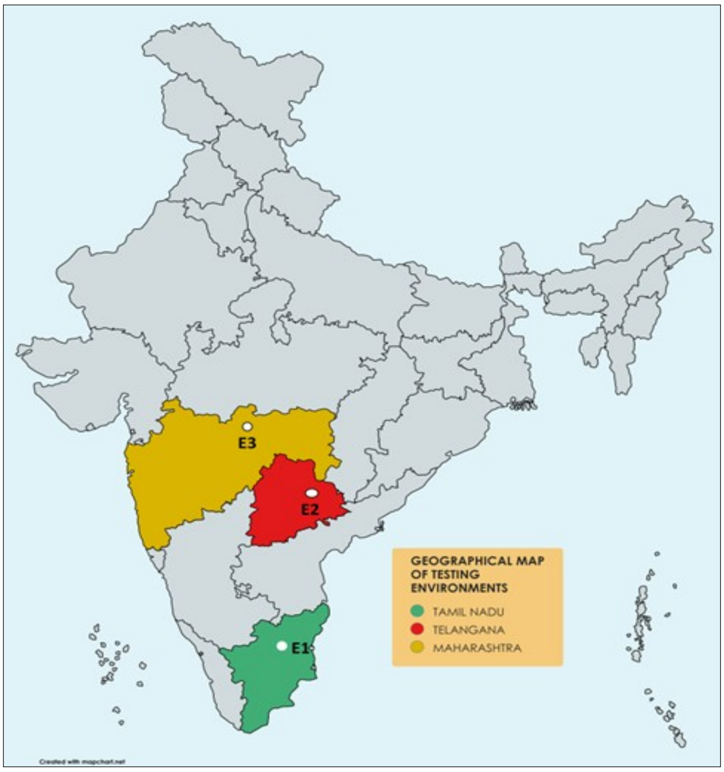

Fig. 1. Geographical maps of experimental locations involved in this study, where E1-Attur, Tamil Nadu, E2- Warangal, Telangana, E3-Amravati, Maharashtra.

$$GSI\ (ASV) = rYi + rASVi \qquad \text{(Eqn.3)}$$

Where, rYi- rank for grain yield and rASVi is the rank for the AMMI stability value. Genotypes with the lowest GSI values are considered to exhibit both high yield potential and greater stability across environments (11).

Weighted average of absolute scores yields (WAASY) index

The WAASY index, provides a comprehensive approach for genotype ranking by simultaneously accounting for both yield stability (WAASB) and mean performance, as outlined in the following model (9).

$$WAASY_i = [(rG_i \times \theta_{\gamma}) + (rW_i \times \theta_s)] / (\theta_{\gamma} + \theta_s) \qquad \text{(Eqn. 4)}$$

Where,

$WAASY_i$ - Superiority index of the *i*th genotype, integrating performance and stability, rG_i - rescaled values (ranging from 0 to 100) for grain yield (GY), rW_i - weighted average of absolute scores from the AMMI model (WAASB), θ⊠ and θ_s are the assigned weights for GY and WAASB, respectively.

Results

Hotspot screening of cotton hybrids for jassid tolerance

Thirty-nine hybrids, along with susceptible and tolerant checks, were evaluated under hotspot conditions. Based on the jassid injury index, the evaluated cotton hybrids were grouped into three categories: 18 hybrids were classified as resistant, 15 as moderately resistant and 6 as susceptible. The detailed classification in relation to the jassid resistance index and injury index is presented in Table 3.

Combined Analysis of Variance (ANOVA) for Yield

A homogeneity test of variances was conducted to assess the uniformity of experimental error across environments. As the test confirmed homogeneous error variances, a combined ANOVA was performed and the results are shown in Table 4.

The highly significant mean squares for environment, genotype and genotype × environment interaction ($p < 0.001$) indicate substantial agro-climatic variation among locations, considerable genetic variability among the hybrids and differential genotypic responses across environments.

AMMI model analysis for seed cotton yield

Mean yield and stability parameters of cotton hybrids evaluated across environments

The mean seed cotton yield (kg ha^{-1}) of 39 hybrids along with 6 standard checks (C01- Rasi swift BG II, C02- US 7067 BG II, C03- Aasha 1 BG II, C04- Akira BG II, C05- Sadhanand BG II, C06- Aadhya BG II) across three locations is illustrated as a box plot in Fig. 2. Among the evaluated environments, E3 demonstrated superior productivity, with seed cotton yields ranging from 1,399 to 3,904 kg ha^{-1}. This was followed by E2, which exhibited a yield range of 1,669 to 3,989 kg ha^{-1}. Although E3 appeared numerically superior, its mean yield (2,688 kg ha^{-1}) did not differ significantly from E2 (2,691 kg ha^{-1}), as the difference was well below the critical difference (CD) ($\alpha = 0.05$). In contrast, E1 showed the lowest performance, with yields varying between 1,255 and 2,863 kg ha^{-1}. The environment-specific mean performance of intra hirsutum hybrids for seed cotton yield (kg/ha) is presented in Supplementary Table 2. Among the evaluated hybrids, H12 (3022 kg ha^{-1}), H19 (2927 kg ha^{-1}), H22 (2871 kg ha^{-1}), H15 (2861 kg ha^{-1}) and H03 (2804 kg ha^{-1}) were identified as the top five performers across environments based on their mean seed cotton yield.

Table 3. Classification of cotton hybrids based on jassid injury index

Genotype code	Jassid injury index	Classification	Genotype code	Jassid injury index	Classification
H01	0.98	R	H22	0.26	R
H02	1.5	MR	H23	0.63	R
H03	1.75	MR	H24	0.76	R
H04	1.25	MR	H25	0.61	R
H05	0.87	R	H26	0.97	R
H06	0.47	R	H27	2	MR
H07	0.61	R	H28	0.67	R
H08	2.5	S	H29	2.94	S
H09	0.83	R	H30	1.25	MR
H10	0.89	R	H31	2.25	S
H11	0.97	R	H32	1.75	MR
H12	0.18	R	H33	2.96	S
H13	0.76	R	H34	2.73	S
H14	0.88	R	H35	2.41	S
H15	1.63	MR	H36	1.23	MR
H16	1.92	MR	H37	1.5	MR
H17	0.93	R	H38	1.75	MR
H18	0.86	R	H39	2	MR
H19	1.43	MR	Rasi swift BGII (check)	0.56	R
H20	1.77	MR	RCH 659 BGII (check)	3.43	S
H21	1.97	MR			

R-Resistant, MR-Moderately Resistant, S-susceptible

Table 4. Combined ANOVA for seed cotton yield

Source	Df	Sum of square	Mean sum of square	F value	Pr(>f)
Environment	2	45706224	22853112	705.845	< 0.001***
Replication (ENV)	3	137355	45785	1.414	0.24
Genotype	44	28556271	649006	20.045	< 0.001***
Genotype x Environment	88	41023085	466171	14.398	< 0.001***
Residuals	132	4273755	32376		

*** represents p-value < 0.001

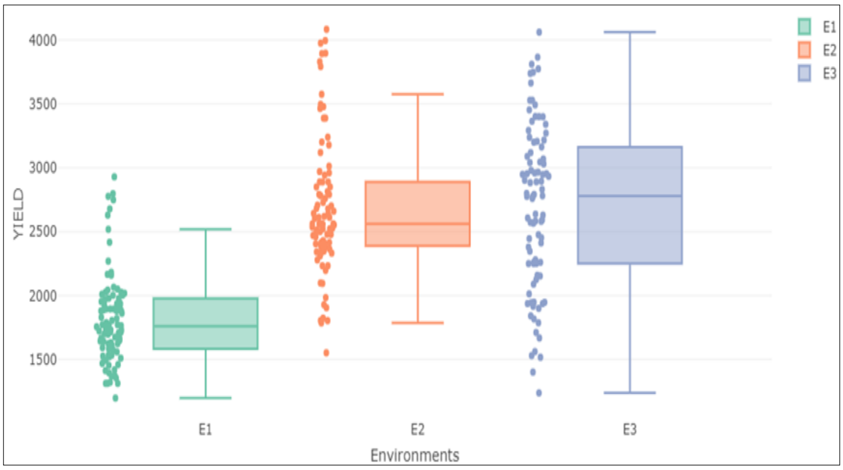

Fig. 2. Mean performance of cotton hybrids in different locations.

AMMI ANOVA

According to the results of the AMMI models' ANOVA, genotype and environment had a significant (p <0.001) impact on seed cotton yield (Table 5). Both IPCA1 (interaction principal component axis) and IPCA2 were statistically significant (p<0.001), explaining 62.7 % and 37.3 % of the genotype × environment interaction variance, respectively. The mean seed cotton yield and stability parameters (ASV, GSI, WAAS and WAASY) of the cotton hybrids evaluated across different environments are presented in Table 6. Based on the ASV, hybrids H13 (3.41), H33 (4.39), H26 (4.92), H05 (5.02), H11 (5.33), H32 (5.39) and H30 (5.7) exhibited lower scores than C01, indicating high stability across environments. Consistently, the WAAS index also identified these hybrids, along with H37, as stable performers, highlighting their potential suitability for cultivation under variable environmental conditions. While stability parameters such as ASV and WAAS are effective in identifying stable hybrids, they do not necessarily account for yield performance. To select hybrids that exhibit both high yield and stability, indices such as GSI and WAASY are more valuable (9). The GSI index, which combines yield and stability rankings, identified hybrids H13 (10), H26 (17), H22 (20), H19 (26), H07 (30), H05 (32) and H38 (33) as superior, exhibiting both high yield and stability compared to the Rasi Swift BG II check (C01). The WAASY index combines mean performance and stability, identifying hybrids H13 (89.42), H22 (84.62), H26 (83.08), H19 (76.94) and H12 (74.94) as stable high-yielding hybrids compared to C01, as they recorded the highest WAASY scores. Based on all stability indices (GSI, WAAS and WAASY) and mean yield, hybrids H13, H19, H22, H26 and H38 were consistently identified as high-yielding and stable across environments.

GGE biplot analysis

GGE biplot analysis effectively visualises genotype performance and stability across multiple environments by combining genotype main effects (G) and genotype-by-environment interaction (GE) into a single biplot (17).

Table 5. Additive main effects and multiplicative interaction - ANOVA

Source	Df	Sum of square	Mean sum of square	F value	Pr(>f)	Proportion	Accumulated
Environment	2	45706224	22853112	499.137	< 0.001***		
Replication	3	137355	45785	1.414	0.24		
Genotype	44	28556271	649006	20.045	< 0.001***		
Genotype x Environment	88	41023085	466171	14.398	< 0.001***		
IPCA1	45	25723865	571641	17.66	< 0.001***	62.7 %	62.7 %
IPCA2	43	15299220	355795	10.99	< 0.001***	37.3 %	100 %
Residuals	132	4273755	32376				
Total	357	160719779	450195				

*** represents $p< 0.001$, IPCA- Interaction principal component axis.

Table 6. Mean yield and stability parameters (ASV, GSI, WAAS, WAASY) of cotton hybrids evaluated across environments

S.no	Hybrids	Mean (kg/ha)	ASV	GSI (ASV)	WAAS	WAASY	Rank (WAAS)	Rank (WAASY)
1	H01	2695	25.30	50	12.05	49.85	39	32
2	H02	2778	15.83	37	8.34	66.63	31	15
3	H03	2804	26.60	46	13.68	48.25	43	34
4	H04	2110	38.63	79	15.54	14.05	44	45
5	H05	2231	5.02	32	2.48	66.22	5	16
6	H06	2461	13.82	45	5.64	63.85	21	19
7	H07	2509	8.73	30	3.81	72.38	11	7
8	H08	2094	16.44	68	8.60	38.58	32	40
9	H09	2672	14.15	39	6.36	69.58	25	10
10	H10	2019	12.07	61	6.06	44.85	24	36
11	H11	2191	5.33	34	2.81	63.46	8	20
12	H12	3022	16.50	35	8.70	74.94	34	5
13	H13	2755	3.41	10	1.80	89.42	1	1
14	H14	2770	15.88	39	7.96	67.66	30	14
15	H15	2861	24.38	42	12.74	53.91	40	28
16	H16	2170	33.12	74	13.28	24.62	41	43
17	H17	2413	15.28	51	7.65	54.64	29	27
18	H18	2404	8.79	37	4.62	65.27	16	18
19	H19	2927	13.51	26	7.12	76.94	27	4
20	H20	2379	11.16	45	4.24	65.71	14	17
21	H21	2156	11.18	51	5.78	51.28	23	30
22	H22	2871	10.29	20	4.38	84.62	15	2
23	H23	2497	11.30	40	4.68	68.79	17	12
24	H24	2549	10.31	35	4.97	69.77	20	9
25	H25	2784	26.58	46	10.16	60.22	37	22
26	H26	2605	4.92	17	1.92	83.08	2	3
27	H27	2444	22.86	58	11.74	41.05	38	38
28	H28	2683	19.40	47	9.19	59.74	35	23
29	H29	2000	31.10	82	13.40	17.43	42	44
30	H30	1995	5.70	49	2.80	55.71	7	25
31	H31	2156	14.16	58	7.47	45.15	28	35
32	H32	2107	5.39	41	2.72	60.45	6	21
33	H33	1813	4.39	46	2.30	50.31	3	31
34	H34	1758	9.84	60	4.69	39.49	18	39
35	H35	2127	7.74	43	3.97	56.73	12	24
36	H36	2407	8.01	34	3.97	67.77	12	13
37	H37	1999	8.85	55	3.43	53.61	9	29
38	H38	2740	12.56	33	6.39	72.16	26	8
39	H39	2601	33.04	58	15.58	33.34	45	41
40	C01	2388	6.21	33	2.34	72.92	4	6
41	C02	2057	7.29	46	3.71	54.90	10	26
42	C03	1963	16.49	76	8.69	33.10	33	42
43	C04	2600	15.18	44	5.67	69.24	22	11
44	C05	2035	10.17	54	4.92	49.61	19	33
45	C06	2338	21.05	63	9.76	44.03	36	37

ASV: AMMI stability value, GSI: Genotype selection index, WAAS: Weighted average of absolute scores, WAASY: Weighted average of absolute scores and yield.

Relationship among environments

GGE biplot analysis revealed that PC1 and PC2 explained 53.0 % and 31.9 % of the variation, respectively, cumulatively capturing 84.9 % of the genotype × environment interaction for yield among the 39 cotton hybrids (Fig. 3). In GGE biplot analysis, a narrow angle between two environments indicates a strong positive correlation and consistent genotype performance, while a wide angle reflects a weak or negative correlation, implying variation in genotype rankings across environments (18, 19). The large angle between E3 and E2 in the GGE biplot indicates a low or negative correlation, suggesting inconsistent genotypic responses across these environments. In contrast, the small angle between E3 and E1 reflects a strong positive correlation, indicating similar genotype performance and ranking patterns. However, their ability to discriminate among hybrids varied considerably.

Discriminativeness vs. representativeness of environments

In GGE biplot analysis, the discriminative ability of an environment is represented by the length of its vector from the origin; longer vectors indicate higher effectiveness in distinguishing among genotypes (20). In Fig. 4, environment E3 exhibited the longest vector, indicating strong discriminative ability and effective differentiation of genotype yield performance. Environment E2 also showed considerable discriminative power with a relatively long vector, while E1 had the shortest vector, suggesting limited ability to distinguish among hybrids, as reflected by their similar yield performance. In the biplot (Fig. 4), the downward-pointing line segment represents the average environment coordinate (AEC) axis. Environments forming larger angles with the AEC axis, such as E3 and E2, are considered less representative of the overall hybrid performance, as they capture unique interaction patterns that necessitate location-specific hybrid recommendations rather than generalised conclusions.

Mean performance vs. stability and hybrid ranking

The hybrids positioned to the left along the AEC axis demonstrate higher mean yields, while the vertical distances either upward or downward from the AEC axis reflect the magnitude of genotype environment interaction (GEI) effects (21). As illustrated in Fig. 5A, hybrids H19, H12, H22, H15, H03, H25, H02, H14, H13, H38, H01, H28, H09, H26, H39, H24, H07, H23, H06, H27, H17, H36 and H18 exhibited mean yields above the overall average. Regarding yield stability, hybrids H30, H36, H33, H38, H22, H09, H13 and H05 showed minimal deviations from the AEC axis, indicating high stability across environments. Followed by hybrids H26, H06, H18, H11, H32, H34, H24 and H35, also closely aligned with the AEC axis, demonstrated lower GE interaction effects. More specifically, the hybrids' ranking was illustrated in the ranking genotypes view of the GGE biplot (Fig. 5B), wherein hybrids situated closer to the centre of the

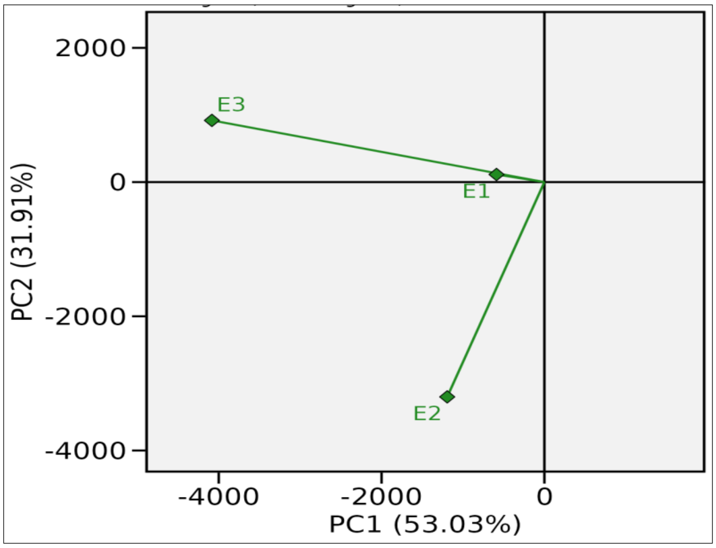

Fig. 3. Interrelationships among the three test environments as depicted in the GGE biplot.

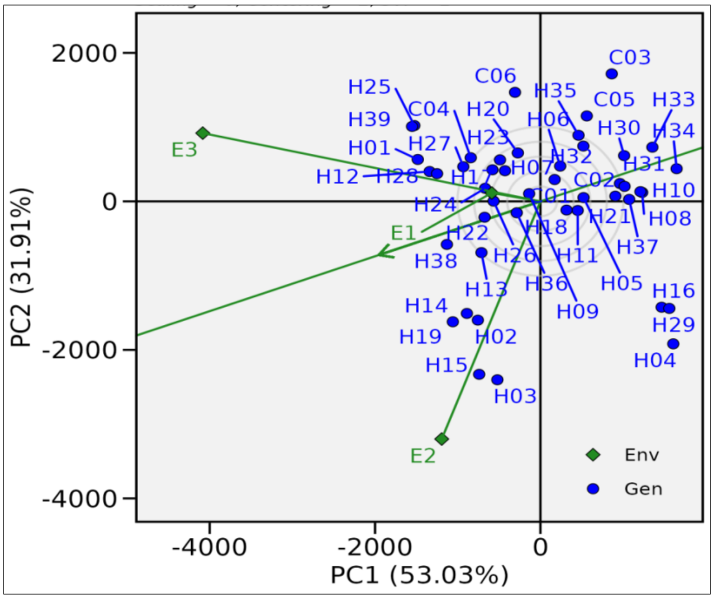

Fig. 4. Discriminativeness vs. representativeness GGE biplot of 3 environments.

concentric circles were indicative of superior overall performance across environments. Based on seed cotton yield, the top ten hybrids were ranked as follows: H38 > H13 > H22 > H28 > H12 > H26 > H24 > H01 > H14 > H27.

Which-won-where polygon view of GGE biplots

The polygon view of the GGE biplot effectively visualised genotype-by-environment interactions and enabled the clear identification of superior genotypes within specific environments (22). In Fig. 6, the dashed lines extending perpendicularly from the edges of the polygon partition the biplot into two distinct sectors. And the hybrids H39, H01 and H25 demonstrated superior performance in the E3 environment, while H15, H03 and H19 were identified as ideal cotton hybrids under the E2 environment.

Genotype ranking using WAAS and WAASY indices

To clearly illustrate the ranking patterns among the evaluated hybrids, a biplot was constructed by plotting seed cotton yield against the WAAS index (Fig. 7A). The biplot classified all hybrids into four distinct quadrants. Quadrant I contained the most unstable hybrids, characterised by below-average seed cotton yield and a strong contribution to GEI. Quadrant II included high-yielding but unstable hybrids, as well as environments with high discriminatory power. Hybrids in Quadrant III were low-yielding but exhibited broader adaptability. Notably, Quadrant IV encompassed the most desirable hybrids, combining above-average yield with high stability, as indicated by low WAAS values suggesting wide adaptability (9).

Based on the results, hybrids H4, H29, H16 and H08, along with environment E1, were positioned in the first quadrant (I), which indicates that the hybrids in this quadrant were low in seed cotton yield as well as low in stability. The second quadrant (II) included hybrids H39, H03, H01, H27, H15, H25, H28, H12 and H02, in association with environments E2 and E3. The hybrids in quadrant II exhibit high-yield but unstable performance across the locations. Hybrids H31, H21, H10, H20, H34, H37, H35, H33, H30, H05 and H11 were grouped in the third quadrant (III), which were low productive and highly stable in performance. The fourth quadrant (IV) comprised hybrids H22, H19, H38, H26, H13, H09, H07, H23, H06 and H24. Quadrant IV holds particular significance, as the hybrids positioned in this quadrant exhibit above-average yield performance coupled with high stability. Among the hybrids evaluated, H14 was positioned at the interface of quadrants II and IV, while H18, H17 and H36 were located on the border of quadrants III and IV.

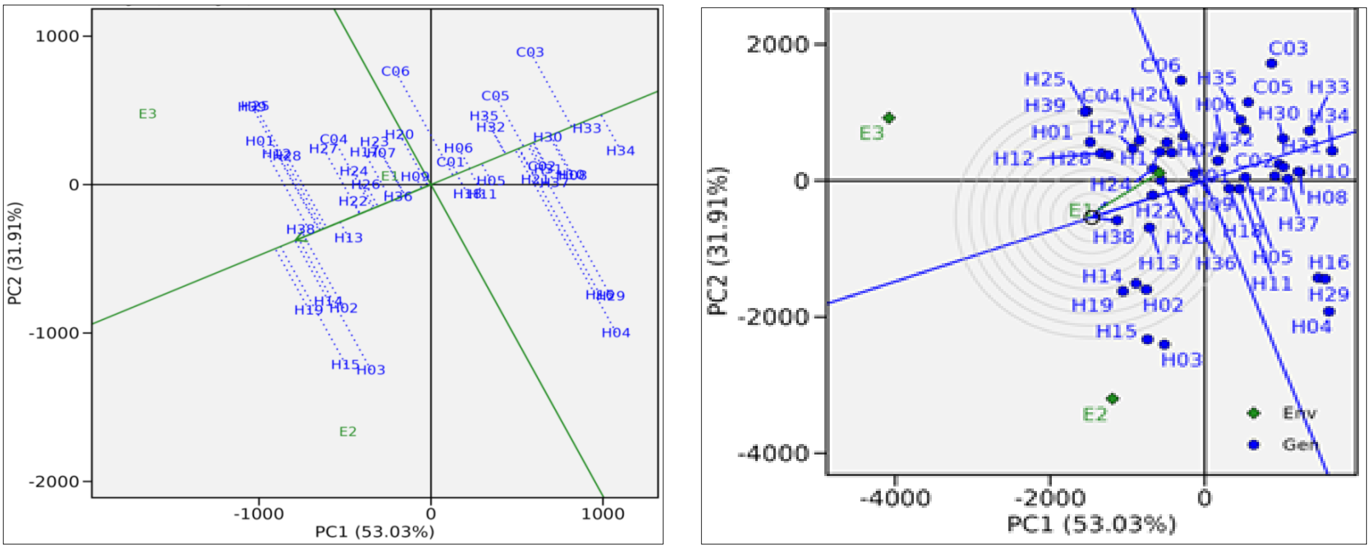

Fig. 5. A. Mean vs. stability view of GGE biplot for 39 intra-hirsutum hybrids**, B.** Genotypic ranking of 39 intra-hirsutum cotton hybrids based on GGE biplot analysis.

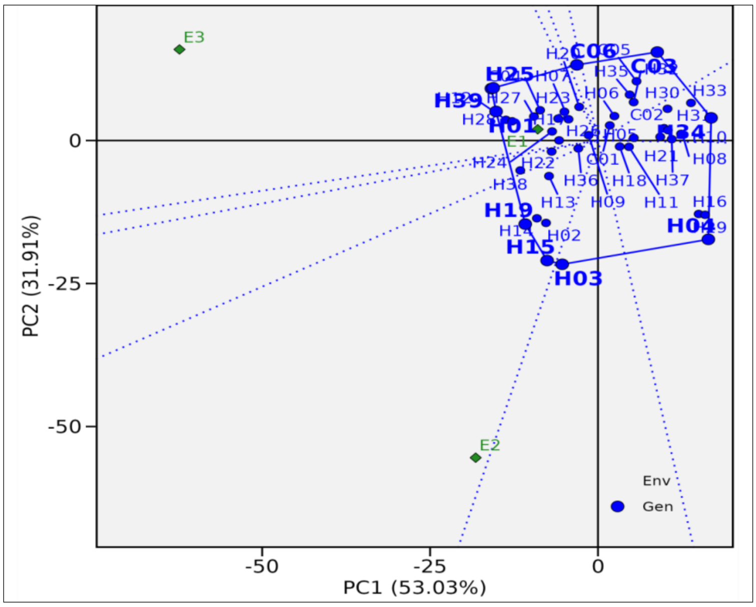

Fig. 6. Which-won-where polygon view of GGE biplot.

The WAASBY heat map (Fig. 7B) classifies cotton hybrids by combining yield and stability (WAASB- weighted average of absolute scores from the BLUPs) under varying weights to identify hybrids with an optimal yield–stability balance. In the heat map, the right side emphasises yield (0/100), whereas the left side places greater weight on stability (100/0) (9). Based on this, group I (highlighted in green) includes hybrids H05, H06, H07, H09, H11, H12, H13, H18, H19, H20, H22, H23, H24, H26, H32, H36 and H38, which demonstrated a desirable combination of high yield and stability. Notably, hybrids H13, H09, H22, H26, H19 and H38 exhibited superior performance across both yield and stability. Group II (highlighted in red) comprises hybrids H10, H30, H33, H34, H35 and H37, characterised by high stability but comparatively lower yield, particularly H30, H33 and H37. Group III (highlighted in blue) comprised hybrids H04, H08, H16, H17, H21, H27, H29, H31 and H39, which exhibited poor stability and low seed cotton yield. Group IV (highlighted in black) included hybrids H01, H02, H03, H14, H15, H25 and H28**,** characterised by high yield but low stability, with H03 and H15 showing particularly poor performance in terms of stability despite their high productivity.

Discussion

Under hotspot field screening, considerable variability in resistance to jassid infestation was observed among the cotton hybrids. A total of 18 hybrids (46 %) expressed resistance with a jassid injury index ranging from 0.18 to 0.98, while 15 hybrids (38 %) exhibited moderate resistance (1.23-2.00). In contrast, six hybrids (15 %) were classified as susceptible, recording higher injury index values between 2.41 and 3.43. Similar resistance categorisation was reported in *G. hirsutum* under natural infestation (6). Consistent variability in jassid resistance among okra genotypes across seasons was found and since jassid is a shared pest of cotton and okra, this evidence further supports the reliability of the present screening approach (6). Among the evaluated hybrids, 18 hybrids exhibited resistance to jassid infestation, reflecting the potential of the parental lines involved in this study. These hybrids could be further evaluated for yield stability across multiple environments and the best-performing, jassid-resistant hybrids may be considered for commercial release.

Combined ANOVA and AMMI analysis showed significant effects of genotype (G), environment (E) and their interaction (GEI) on

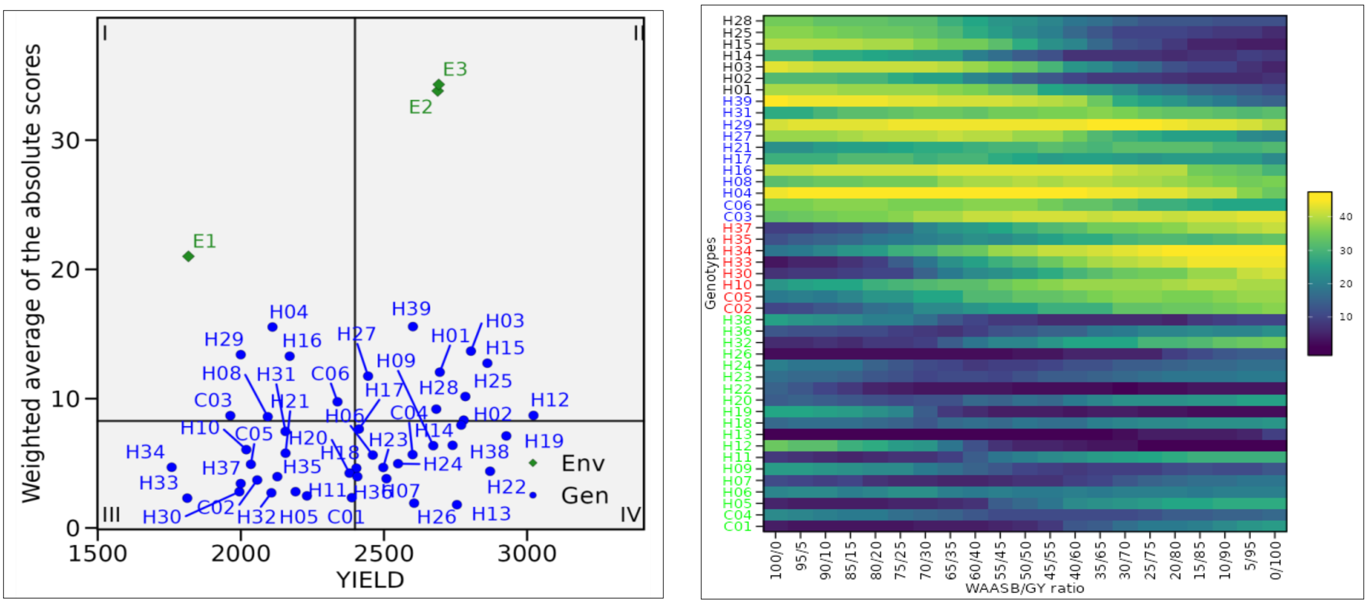

Fig. 7. A. The biplot based on seed cotton yield × WAAS parameters was generated to identify high-yielding and stable cotton hybrids**, B.** WAASBY heat map of 39 cotton hybrids (The different groups of hybrids were highlighted in green, red, blue and black colour).

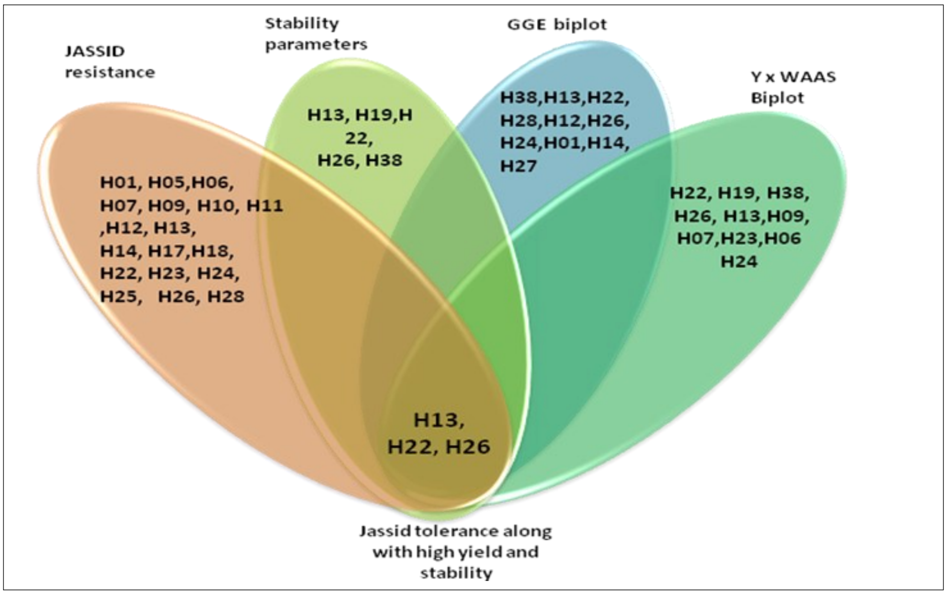

Fig. 8. Venn diagram explaining the selected hybrids in jassid screening, stability parameters, GGE biplot and Y × WAAS biplot.

seed cotton yield, indicating high genetic variability, environmental influence and crossover interactions. This reflects inconsistent performance among the 39 cotton hybrids across locations, underscoring the need for stability analysis to identify high-yielding, widely adapted cotton hybrids. Notably, similar patterns have been observed in earlier cotton studies employing combined and AMMI ANOVA (6, 10, 24). The stability indices (GSI, WAAS and WAASY) and mean yield consistently highlighted that hybrids H13, H19, H22, H26 and H38 were high-yielding and stable across environments. Research has also demonstrated that using multiple stability metrics improved the precision and reliability of genotype selection, reinforcing the value of integrative approaches in GEI analysis (25).

In the discriminativeness vs. representativeness GGE biplot, E3 and E2 showed strong discriminative power with long vectors, while E1 had the shortest vector, indicating limited ability to differentiate hybrids. Similarly, promising sorghum genotypes were successfully identified through GGE biplot analysis, with genotypes located closer to the centre of the concentric circles being ranked higher (20). In the Which-Won-Where GGE biplot, hybrids H39, H01 and H25 showed superior performance in environment E3, while H15, H03 and H19 were ideal for E2 and H12 was suitable for E1. Although these hybrids exhibited limited overall stability, their high performance in specific environments supports their recommendation for targeted, location-specific cultivation. Similarly, research reported that the vertex genotypes in each GGE biplot sector, separated by dashed lines, were top performers (26). Six cotton genotypes located farthest from the origin indicated strong GEI and superior adaptability within their respective environments. The GGE biplot ranked hybrids H38 > H13 > H22 > H28 > H12 > H26 > H24 > H01 > H14 > H27 as the top ten based on combined high yield and stability. Likewise, ideal sorghum genotypes were effectively identified using GGE biplot analysis based on genotypes that were closer to the centre of the concentric circles and had better ranks (20). The strong concordance observed between AMMI and GGE biplot rankings in this study reinforces the robustness of both models in evaluating genotype stability across environments. Thus, either model can be used interchangeably to select high-yielding, stable genotypes (24).

The Y × WAAS biplot identified hybrids H22, H19, H38, H26, H13, H09, H07, H23, H06 and H24 within Quadrant IV, indicating superior yield performance coupled with high stability. This quadrant is critical for selecting broadly adapted, high-performing hybrids. The WAASBY heatmap further validated these findings by highlighting hybrids H13, H09, H22, H26, H19 and H38 as top-performing entries in terms of both yield and stability. A comparable outcome was reported in five durum wheat genotypes in Quadrant IV of the Y × WAAS biplot, demonstrating the models' effectiveness for stability selection (27). Likewise, research employed the WAASBY heatmap to successfully identify barley genotypes combining above-average yield with improved stability across locations (17).

This comprehensive assessment demonstrated that the integration of stability models, including AMMI-based stability parameters, GGE biplots, Y × WAAS and WAASBY, effectively captured genotype-by-environment interactions. The analysis consistently identified hybrids H13, H19, H22, H26 and H38 as both high-yielding and stable. Employing multiple stability models strengthens the selection process by improving the reliability of identifying stable, high-yielding cotton hybrids. The effectiveness of this strategy has also been demonstrated in other crops. Research identified high-performing, stable durum wheat genotypes using a similar analytical framework, reinforcing the broader applicability of integrative GEI analysis (27). Among the highly stable and high-performing hybrids, H13, H22 and H26 also exhibited resistance to jassid (Fig. 8), underscoring their potential for commercial exploitation and as valuable sources in breeding programs targeting seed cotton yield stability and jassid resistance.

Conclusion

The present study successfully identified cotton hybrids with enhanced yield performance, environmental stability and improved resistance to jassid infestation. Hybrids H13, H19, H22, H26 and H38 were consistently superior across environments based on mean yield and stability indices (ASV, WAAS, GSI and WAASY). GGE biplot analysis identified E3 as the most discriminative environment, providing clearer insights into genotype differentiation. Results from the WAASBY heat map, Y × WAAS and GGE biplots further validated the stable performance of H13, H19, H22, H26 and H38. Among the 18 hybrids identified as resistant to jassid, H13, H22 and H26 combined jassid resistance with high yield and stability, making them strong candidates for commercial cultivation and future breeding programs. Further multi-location and multi-season validation will strengthen their suitability for large-scale adoption.

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Authors' contributions

SN contributed to conceptualisation, methodology development, data analysis and writing of the initial draft of the manuscript. JP contributed to conceptualisation and methodology development, carried out necessary corrections and performed final editing of the manuscript. SR contributed to conceptualisation and methodology development and proofread the manuscript. KN contributed to conceptualisation and methodology development and proofread the manuscript. RR, MBN and CN contributed to proofreading of the manuscript. All authors read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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