



RESEARCH ARTICLE

Assessment of genotype by environment interaction for yield stability and sucking pest resistance in cotton (*Gossypium hirsutum* L.) using AMMI, GGE biplot and multi-trait stability index

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Abstract

Cotton (*Gossypium hirsutum* L.) is a major fibre crop underpinning the global textile industry; however, its productivity is increasingly threatened by climatic variability and the resurgence of sap-sucking insect pests. The interaction between genotype and environment ($G \times E$) further complicates the identification of stable and high-yielding genotypes, particularly under rainfed conditions. The present study evaluated 7 cotton genotypes across 9 environments (three locations over 3 consecutive years: 2021–24) in Odisha, India, to assess $G \times E$ interaction for 14 quantitative traits related to yield and sucking pest resistance using advanced statistical approaches. Combined analysis of variance revealed highly significant ($p < 0.01$) effects of genotypes, environments and $G \times E$ interaction for all traits studied. The interaction component was particularly significant for key traits, including seed cotton yield (SCY), lint yield (LY) and populations of major sucking pests, necessitating a comprehensive stability analysis. High broad-sense heritability coupled with moderate to high genetic advance for yield and pest resistance traits indicated the predominance of additive gene action. Stability analyses using the Eberhart and Russell model, additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment (GGE) biplot consistently identified genotype BS 3-17 as superior, exhibiting the highest mean SCY (1978 kg ha⁻¹) and LY (675 kg ha⁻¹), along with the lowest mean populations of aphids (APH) (5.28 per 3 leaves) and jassids (JAS) (1.82 per 3 leaves) across environments. The multi-trait stability index (MTSI) further ranked BS 3-17 as the most desirable genotype (MTSI score = 5.51), indicating its closest proximity to the ideotype. Agronomic validation trials demonstrated that high-density planting (90 × 30 cm) combined with 125 % of the recommended dose of fertilisers significantly enhanced the yield potential of BS 3-17, achieving up to 3114 kg ha⁻¹. These findings establish BS 3-17 as a climate-resilient, high-yielding genotype suitable for commercial cultivation and a promising donor parent for breeding programs targeting yield stability and sucking pest resistance.

Keywords: additive main effects and multiplicative interaction analysis; agronomic optimisation; genotype plus genotype by environment biplot; *Gossypium hirsutum*; multi-trait stability index; sucking pest resistance; yield stability

Introduction

Cotton (*Gossypium* spp.) is the world's most important natural fibre crop and is essential to the agricultural and industrial economies of many developing countries (1). Although India cultivates the largest area under cotton globally, its productivity (yield per unit area) is often lower than the global average. This yield gap is primarily attributed to the predominance of rainfed cultivation, which exposes

the crop to abiotic stresses such as drought, as well as biotic stresses including insect pests (2). The situation in eastern India, particularly in Odisha, is further aggravated by undulating topography and erratic monsoon patterns, leading to frequent moisture stress and fluctuating pest incidence (3). Among biotic stresses, sap-sucking pests such as leafhoppers, aphids (APH), whiteflies (WF) and thrips (THR) pose a serious threat, causing substantial economic losses through direct feeding damage and transmission of viral diseases (4).

For plant breeders, a primary objective is to develop cotton genotypes that combine high yield potential with resistance to insect pests. However, quantitative traits such as seed cotton yield (SCY) are governed by polygenic inheritance and are strongly influenced by environmental conditions (5). Consequently, the relative performance and ranking of genotypes vary across environments, a phenomenon known as genotype $\times$ environment ($G \times E$) interaction. A significant $G \times E$ interaction reduces the correlation between phenotypic performance and genetic potential, thereby complicating the selection of superior genotypes and slowing breeding progress (6). To address this, multi-environment testing is essential to identify genotypes with broad adaptability and stable performance. Traditionally, stability has been assessed using models such as Eberhart and Russell; however, advanced statistical approaches such as additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment interaction (GGE) biplot are now widely used for a more comprehensive analysis of $G \times E$ interaction and genotype performance (7).

In addition, selection in breeding programs requires simultaneous consideration of multiple traits. The multi-trait stability index (MTSI) proposed by previous researchers (8) integrates mean performance and stability into a single index, thereby facilitating the identification of genotypes that are both high-yielding and stable across environments (9). Despite the availability of these analytical tools, their combined application for evaluating yield stability and insect pest resistance in rainfed cotton remains limited. Therefore, the present study was undertaken to estimate genetic parameters, analyse $G \times E$ interaction using stability models, identify superior genotypes through MTSI and determine optimal agronomic practices for the best-performing genotype under rainfed conditions.

Materials and Methods

Plant material and experimental sites

The experimental material comprised 7 cotton genotypes (Table 1), including 6 improved breeding lines (BS 3-17, BS 277, BS 279, BS 144-1, BS 2 and BS-39) and one check variety, Suraj. Seeds were obtained from the All India Coordinated Research Project on Cotton, Bhawanipatna. The field experiments were conducted over 3 consecutive years (2021–22 to 2023–24) at 3 locations in Odisha, namely Bhawanipatna, Keonjhar and Umerkote, representing diverse agro-climatic conditions. Bhawanipatna is characterised by

black soils (Vertisols) with an average annual rainfall of approximately 1300 mm. Keonjhar has red and yellow soils ranging from sandy to silty clay loam, with an average rainfall of about 1400 mm. Umerkote possesses acidic red soils varying from sandy to clay loam, receiving around 1500 mm of annual rainfall. The combination of 3 locations over 3 years constituted 9 environments (E_1 to E_9) for stability analysis.

Experimental design and cultural practices

The main experiment was laid out in a randomised block design (RBD) with 3 replications in each environment. The crop was grown in plots measuring 6.0 m $\times$ 3.6 m, with a spacing of 90 cm between rows and 60 cm between plants. Sowing was carried out during the optimal planting window (June–July). Standard agronomic practices were followed uniformly across all treatments, with a recommended fertiliser dose of 90 : 45 : 45 kg N : P : K ha⁻¹ applied. Bollworm incidence was managed using appropriate plant protection measures, while no insecticidal sprays were applied against sap-sucking pests to allow natural infestation and facilitate evaluation of genotypic resistance.

A separate validation experiment was conducted for the superior genotype BS 3-17 using a split-plot design. Three plant spacings (90 $\times$ 60 cm, 90 $\times$ 45 cm and 90 $\times$ 30 cm) were assigned to main plots, while 3 fertiliser levels (75 %, 100 % and 125 % of the recommended dose) were allotted to subplots, to determine the optimal agronomic conditions.

Data collection

Observations were recorded on 5 randomly selected competitive plants per replication for 14 quantitative traits. Morphological traits included plant height (PH), number of monopodia (NM) and number of sympodia (NS) per plant. Phenological traits comprised days to 50 % flowering and days to boll bursting (Table 2). Yield components included boll weight (BW) and number of bolls (NB) per plant. Economic yield was assessed in terms of SCY, lint yield (LY) and ginning outturn (GOT). Biotic stress was quantified by recording populations of APH, jassids (JAS), WF and THR per 3 leaves at peak infestation using a hand lens.

Statistical analysis

A combined analysis of variance (ANOVA) was performed to evaluate the effects of genotypes, environments and genotype $\times$ environment interaction (10). Genetic parameters, including heritability and genetic advance, were estimated following the procedures described by Burton and Devane (11) and Johnson et al. (12).

Table 1. Description of the seven cotton genotypes and nine testing environments used in the study

Genotype code	Genotype name	Pedigree / Source	Type
G ₁	BS 3-17	Advanced breeding line (AICRP on Cotton, Bhawanipatna)	Test entry
G ₂	BS 277	Advanced breeding line	Test entry
G ₃	BS 279	Advanced breeding line	Test entry
G ₄	BS 144-1	Advanced breeding line	Test entry
G ₅	BS 2	Advanced breeding line	Test entry
G ₆	BS-39	Advanced breeding line	Test entry
G ₇	Suraj	Commercial variety	Check
Environment code	Location	Year	Coordinates
E ₁	Bhawanipatna	2021–22	19.90° N, 83.16° E
E ₂	Keonjhar	2021–22	21.63° N, 85.60° E
E ₃	Umerkote	2021–22	19.66° N, 82.20° E
E ₄	Bhawanipatna	2022–23	19.90° N, 83.16° E
E ₅	Keonjhar	2022–23	21.63° N, 85.60° E
E ₆	Umerkote	2022–23	19.66° N, 82.20° E
E ₇	Bhawanipatna	2023–24	19.90° N, 83.16° E
E ₈	Keonjhar	2023–24	21.63° N, 85.60° E
E ₉	Umerkote	2023–24	19.66° N, 82.20° E

Table 2. List of quantitative traits, their codes, units of measurement and descriptions

Trait code	Trait name	Unit	Description
PH	Plant height	cm	Height from cotyledonary node to apical bud
NM	Number of monopodia	count	Vegetative branches per plant
NS	Number of sympodia	count	Fruiting branches per plant
DFF	Days to 50 % flowering	days	Days from sowing to 50 % flowering
DBB	Days to boll bursting	days	Days from sowing to first boll opening
BW	Boll weight	g	Average weight of single boll
NB	Number of bolls	count	Effective bolls per plant
LY	Lint yield	kg/ha	Yield of fiber per hectare
SCY	Seed cotton yield	kg/ha	Total yield (lint + seed) per hectare
GOT	Ginning outturn	%	Percentage of lint to seed cotton
APH	Aphids	no./3 leaves	Aphid population count
JAS	Jassids	no./3 leaves	Jassid population count
WF	Whitefly	no./3 leaves	Whitefly population count
THR	Thrips	no./3 leaves	Thrip population count

Aphid, jassid, whitefly and thrips populations were recorded as number per three leaves.

Stability analysis was conducted using the Eberhart and Russell model (13), the AMMI model (6) and the GGE biplot approach (7). In addition, the MTSI was computed to identify superior genotypes based on mean performance and stability across traits (8). All statistical analyses were performed using Windostat version 9.50 software, while GGE biplot and MTSI analyses were carried out using R software (14).

Results

Analysis of variance and genetic variability

The combined ANOVA revealed that genotypic differences were highly significant ($p < 0.01$) among the 7 genotypes (G_1 to G_7) for all 14 quantitative traits (Table 3). This indicates the presence of substantial genetic variability, which is essential for effective selection. The effects of environments (E_1 to E_9) were also highly significant for all traits, reflecting the influence of diverse agro-climatic conditions on phenotypic expression. Most importantly, the genotype $\times$ environment ($G \times E$) interaction was highly significant ($p < 0.01$) for most traits, including PH, BW, NB, LY, GOT and all sucking pest populations, namely APH, JAS, WF and THR. This indicates that genotype performance and ranking varied across environments, thereby necessitating stability analysis. Although the $G \times E$ interaction for SCY was comparatively less pronounced, the significant interaction observed in its major components (NB and BW) justifies further stability evaluation.

Estimates of genetic parameters provided further insights

into the nature of variability. High broad-sense heritability ($> 80\%$) was observed for SCY (96.97 %), LY (96.98 %) and JAS (98.77 %). High heritability coupled with high genetic advance as percent of mean was recorded for LY (32.07 %) and SCY (25.12 %), indicating the predominance of additive gene action and suggesting good scope for improvement through selection. Similarly, high genetic advance for pest-related traits indicates strong genetic control. In contrast, traits such as PH exhibited low genetic advance (6.43 %) despite high heritability, suggesting involvement of non-additive gene action (Table 4).

Mean performance of genotypes

Evaluation of mean performance across 9 environments provided preliminary insights into genotype superiority. Genotype BS 3-17 (G_1) consistently outperformed all other genotypes, including the check variety Suraj (G_7). It recorded the highest mean PH (111.72 cm), indicating vigorous growth. Among yield components, G_1 exhibited the highest NB per plant (32.43) along with a substantial BW (4.26 g). Consequently, it achieved the highest mean SCY (1978.04 kg ha⁻¹) and LY (675.41 kg ha⁻¹), significantly surpassing the check variety Suraj (G_7), which recorded 1563.89 kg ha⁻¹ SCY.

In terms of pest resistance, G_1 recorded the lowest mean populations of major sap-sucking pests, with APH (5.28 per 3 leaves), JAS (1.82 per 3 leaves) and THR (1.86 per three leaves). These values were substantially lower than those observed in susceptible genotypes, highlighting its superior inherent resistance to sucking pest complex. The genotype BS 277 (G_2) ranked second in yield performance with a SCY of 1827.22 kg ha⁻¹, whereas the check variety

Table 3. Combined analysis of variance (mean sum of squares) for 14 quantitative traits across 9 environments

Characters	Replication	Environment	Genotype	Genotype $\times$ Environment	Pooled error
df	18	8	6	48	108
PH	52.428*	548.674**	563.359**	117.771**	29.556
NM	0.213**	0.203**	1.497**	0.209**	0.055
NS	0.386	33.960**	21.760**	1.966**	0.373
DFF	1.598	16.847**	168.280**	5.550**	1.425
DBB	2.804	27.688**	157.067**	9.708**	2.076
BW	0.029	5.131**	1.626**	0.108**	0.022
NB	4.472	38.030**	87.188**	11.854**	3.507
LY	1268.783	238193.061**	198884.640**	6000.366**	1792.376
SCY	66637.534**	1888319.997**	1175725.910**	35585.039*	22363.244
GOT	1.188	21.635**	46.686**	4.166**	1.297
APH	0.527	133.826**	120.872**	3.878**	1.133
JAS	0.221	1.316**	30.951**	0.379**	0.162
WF	0.142	0.454**	33.292**	0.473**	0.098
THR	0.353**	10.812**	34.556**	1.181**	0.14

df: degree of freedom; PH: plant height; NM: number of monopodia; NS: number of sympodia; DFF: days to 50 % flowering; DBB: days to boll bursting; BW: boll weight; NB: number of bolls per plant; LY: lint yield; SCY: seed cotton yield; GOT: ginning outturn; APH: aphid population; JAS: jassid population; WF: whitefly population; THR: thrips population. Replication, environment, genotype and genotype $\times$ environment interaction effects were tested using analysis of variance. * and ** indicate significance at $p < 0.05$ and $p < 0.01$ respectively.

Table 4. Genetic variability parameters for 14 quantitative traits in cotton

Trait	GCV (%)	PCV (%)	Heritability (h^2b) (%)	Genetic advance (GA)	GA as % of mean
PH	3.51	3.95	79.10	7.44	6.43
NM	10.71	11.54	86.07	0.42	20.46
NS	5.77	6.05	90.96	1.68	11.34
DFF	5.08	5.16	96.70	4.97	10.28
DBB	2.22	2.29	93.82	4.66	4.42
BW	5.79	5.99	93.36	0.47	11.52
NB	5.75	6.18	86.41	3.20	11.01
LY	15.81	16.05	96.98	171.47	32.07
SCY	12.38	12.57	96.97	416.86	25.12
GOT	3.92	4.11	91.08	2.47	7.71
APH	26.42	26.86	96.79	4.22	53.55
JAS	34.31	34.53	98.78	2.18	70.25
WF	44.74	45.06	98.58	2.25	91.51
THR	33.87	34.46	96.58	2.25	68.56

PH: plant height; NM: number of monopodia; NS: number of sympodia; DFF: days to 50 % flowering; DBB: days to boll bursting; BW: boll weight; NB: number of bolls per plant; LY: lint yield; SCY: seed cotton yield; GOT: ginning outturn; APH: aphid population; JAS: jassid population; WF: whitefly population; THR: thrips population. Replication, environment, genotype and genotype $\times$ environment interaction effects were tested using analysis of variance.

Table 5. Mean performance of 7 cotton genotypes for 14 quantitative traits pooled across 9 environments

Genotype	PH	NM	NS	DFF	DBB	BW	NB	LY	SCY	GOT	APH	JAS	WF	THR
G ₁	111.72	2.03	16.40	48.81	105.44	4.26	32.43	675.41	1978.04	34.12	5.28	1.82	1.12	1.86
G ₂	117.05	2.21	14.67	49.07	108.33	4.45	29.69	606.37	1827.22	33.08	6.34	2.07	1.33	2.31
G ₃	120.77	2.33	15.33	51.26	107.00	4.16	29.67	575.15	1788.93	31.73	5.72	2.24	1.53	2.31
G ₄	112.04	1.80	15.08	46.48	103.44	4.24	28.26	471.41	1573.22	30.00	9.21	4.64	3.06	4.47
G ₅	111.81	1.73	14.04	50.22	106.22	3.93	26.92	478.93	1492.15	32.10	10.09	3.86	3.76	4.20
G ₆	122.85	2.26	13.65	48.89	106.48	3.85	28.82	439.93	1394.30	31.37	8.09	3.30	2.88	3.31
G ₇	114.21	1.92	14.62	43.78	101.15	3.79	27.67	495.63	1563.89	31.52	10.41	3.77	3.57	4.51
Grand mean	115.78	2.04	14.83	48.36	105.44	4.10	29.06	534.69	1659.68	31.99	7.88	3.10	2.46	3.28
SEm $\pm$	1.05	0.04	0.12	0.23	0.28	0.03	0.36	8.15	28.78	0.22	0.20	0.08	0.06	0.07
CD	2.93	0.13	0.33	0.64	0.78	0.08	1.01	22.84	80.68	0.61	0.57	0.22	0.17	0.20
CV	4.70	11.45	4.12	2.47	1.37	3.61	6.44	7.92	9.01	3.56	13.51	12.97	12.70	11.41
Min	111.72	1.73	13.65	43.78	101.15	3.79	26.92	439.93	1394.30	30.00	5.28	1.82	1.12	1.86
Max	122.85	2.33	16.40	51.26	108.33	4.45	32.43	675.41	1978.04	34.12	10.41	4.64	3.76	4.51

PH: plant height; NM: number of monopodia; NS: number of sympodia; DFF: days to 50 % flowering; DBB: days to boll bursting; BW: boll weight; NB: number of bolls per plant; LY: lint yield; SCY: seed cotton yield; GOT: ginning outturn; APH: aphid population; JAS: jassid population; WF: whitefly population; THR: thrips population. SEm $\pm$: standard error of mean; CD: critical difference at 5 % level of significance; CV: coefficient of variation; G₁–G₇: genotypes evaluated in the study.

G₇ performed relatively poorly compared to improved genotypes (Table 5).

Character association and path analysis

Correlation and path analysis

Understanding the relationship between yield and its component traits is essential for effective selection strategies. In the present study, genotypic correlation coefficients were higher than phenotypic correlation coefficients (Table 6, Fig. 1), indicating that strong inherent genetic associations were partially masked by environmental effects. A highly significant and positive genotypic correlation was observed between SCY and LY ($r = 0.995$),

suggesting that selection for LY can effectively improve SCY. Furthermore, SCY exhibited strong positive correlations with NB per plant ($r = 0.872$), BW ($r = 0.762$) and GOT ($r = 0.747$), confirming that yield is primarily governed by sink-related traits. In contrast, PH showed a significant negative correlation with yield ($r = -0.218$), indicating that excessive vegetative growth may reduce assimilate partitioning towards economic yield under rainfed conditions. Notably, the correlations between yield and sucking pest populations were negligible, indicating no significant genetic trade-off between yield potential and pest resistance (Table 6).

To further partition these relationships, path coefficient analysis was performed considering SCY as the dependent

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation matrix of 14 quantitative traits in cotton

Trait	PH	NM	NS	DFF	DBB	BW	NB	LY	GOT	SCY
PH	1	0.947**	-0.429**	0.369**	0.486**	-0.159*	0.037	-0.192**	-0.150*	-0.218**
NM	0.271**	1	0.051	0.435**	0.593**	0.222**	0.521**	0.334**	0.255**	0.314**
NS	-0.163*	0	1	0.035	-0.087	0.580**	0.820**	0.836**	0.481**	0.900**
DFF	0.211**	0.263**	0.02	1	0.907**	0.336**	0.285**	0.298**	0.357**	0.256**
DBB	0.156*	0.228**	-0.065	0.556**	1	0.518**	0.336**	0.345**	0.444**	0.292**
BW	-0.129	0.190**	0.325**	0.302**	0.326**	1	0.601**	0.695**	0.378**	0.762**
NB	0.086	0.165*	0.379**	0.218**	0.192**	0.334**	1	0.885**	0.732**	0.872**
LY	-0.101	0.203**	0.517**	0.205**	0.269**	0.490**	0.544**	1	0.849**	0.995**
GOT	-0.116	0.125	0.238**	0.153*	0.254**	0.270**	0.353**	0.629**	1	0.747**
SCY	-0.092	0.192**	0.478**	0.192**	0.202**	0.502**	0.473**	0.796**	0.417**	1

PH: plant height; NM: number of monopodia; NS: number of sympodia; DFF: days to 50 % flowering; DBB: days to boll bursting; BW: boll weight; NB: number of bolls per plant; LY: lint yield; GOT: ginning outturn; SCY: seed cotton yield. Values above the diagonal represent phenotypic correlation coefficients and values below the diagonal represent genotypic correlation coefficients. * and ** indicate significance at $p < 0.05$ and $p < 0.01$ respectively.

Table 7. Combined phenotypic (P) and genotypic (G) path matrix showing direct and indirect effects of yield components on seed cotton yield

Trait	Level	PH	NM	NS	DFF	DBB	BW	NB	LY	GOT	SCY
PH	P	-0.015	-0.004	0.002	-0.003	-0.002	0.002	-0.001	0.002	0.002	-0.092
	G	0.018	0.017	-0.008	0.007	0.009	-0.003	0.001	-0.003	-0.003	-0.2182**
NM	P	0.008	0.028	0.000	0.007	0.006	0.005	0.005	0.006	0.004	0.1918**
	G	0.041	0.043	0.002	0.019	0.026	0.010	0.023	0.015	0.011	0.3141**
NS	P	-0.009	0.000	0.053	0.001	-0.003	0.017	0.020	0.027	0.013	0.4781**
	G	-0.027	0.003	0.063	0.002	-0.006	0.037	0.052	0.053	0.031	0.8997**
DFF	P	0.004	0.005	0.000	0.020	0.011	0.006	0.004	0.004	0.003	0.1916**
	G	0.021	0.025	0.002	0.056	0.051	0.019	0.016	0.017	0.020	0.2557**
DBB	P	-0.005	-0.008	0.002	-0.019	-0.034	-0.011	-0.007	-0.009	-0.009	0.2017**
	G	-0.055	-0.068	0.010	-0.103	-0.114	-0.059	-0.038	-0.039	-0.051	0.2916**
BW	P	-0.017	0.025	0.043	0.040	0.043	0.132	0.044	0.065	0.036	0.5021**
	G	-0.017	0.023	0.060	0.035	0.054	0.104	0.063	0.072	0.039	0.7616**
NB	P	0.003	0.007	0.015	0.009	0.008	0.013	0.039	0.021	0.014	0.4734**
	G	-0.005	-0.067	-0.105	-0.037	-0.043	-0.077	-0.129	-0.114	-0.094	0.8716**
LY	P	-0.076	0.154	0.392	0.155	0.204	0.370	0.411	0.757	0.476	0.7958**
	G	-0.222	0.385	0.965	0.343	0.398	0.802	0.983	0.854	0.980	0.9951**
GOT	P	0.014	-0.015	-0.029	-0.019	-0.031	-0.033	-0.043	-0.076	-0.121	0.4171**
	G	0.028	-0.048	-0.090	-0.067	-0.083	-0.071	-0.137	-0.159	-0.187	0.7468**

PH: plant height; NM: number of monopodia; NS: number of sympodia; DFF: days to 50 % flowering; DBB: days to boll bursting; BW: boll weight; NB: number of bolls per plant; LY: lint yield; GOT: ginning outturn; SCY: seed cotton yield; P: phenotypic level; G: genotypic level. Values represent direct and indirect effects in path coefficient analysis, with seed cotton yield (SCY) as the dependent variable. * and ** indicate significance at $p < 0.05$ and $p < 0.01$ respectively.

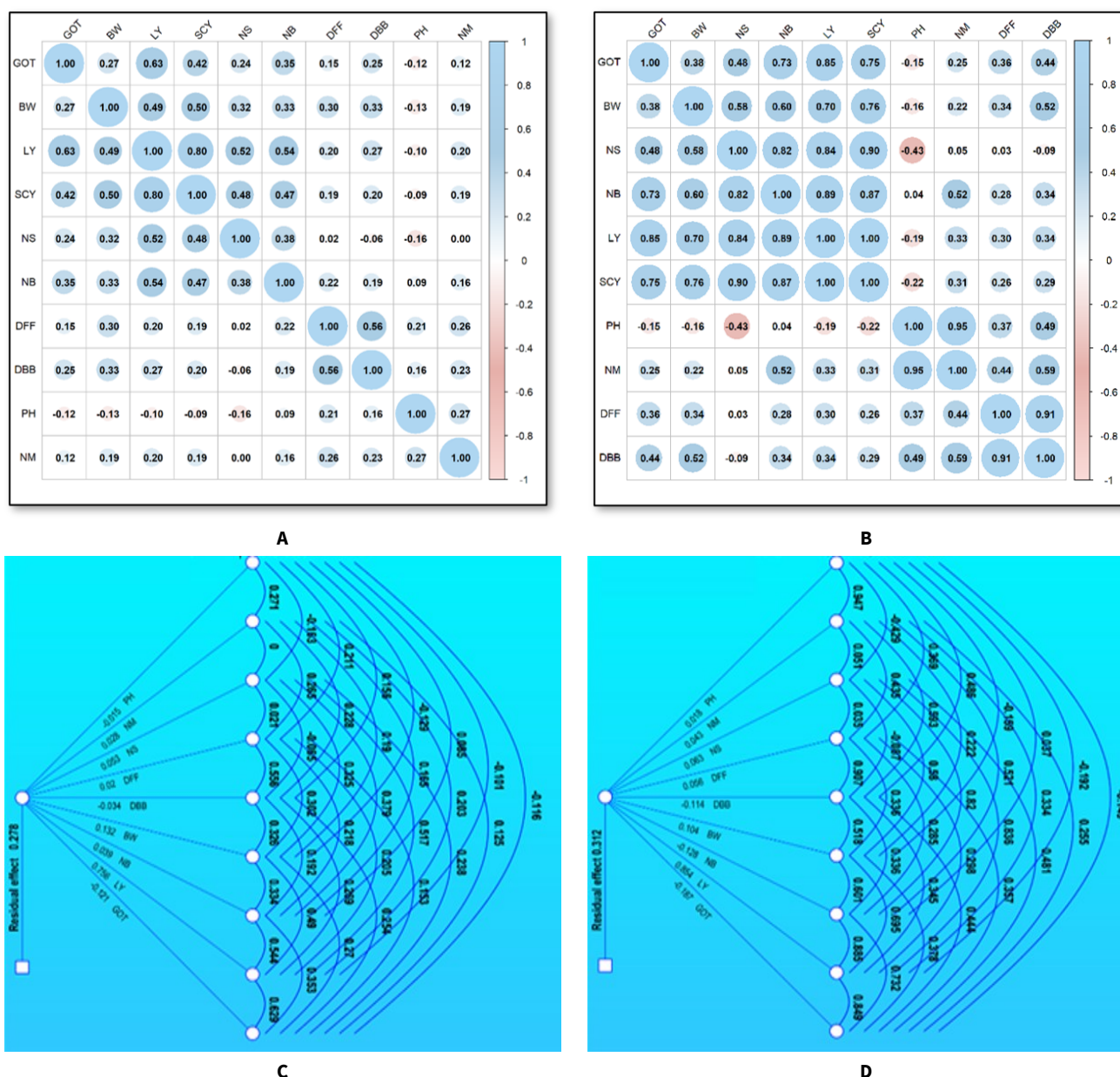


Fig. 1. Correlation and path coefficient analysis of 14 quantitative traits in cotton. (A) phenotypic full-circle correlation matrix; (B) genotypic full-circle correlation matrix; (C) phenotypic path diagram for seed cotton yield; (D) genotypic path diagram for seed cotton yield.

variable (Table 7 and Fig. 1). The results revealed that LY exerted the highest positive direct genotypic effect (0.854) on SCY, confirming its primary contribution. Boll weight also showed a positive direct effect (0.104), indicating its importance as a selection criterion. Although NB per plant exhibited a strong positive correlation with yield, its direct effect was negative (-0.129), suggesting that its influence is mainly indirect through other traits such as LY. The direct effect of PH was negligible (0.018), indicating that its influence on yield is largely indirect. The low residual effect indicates that the selected traits adequately explained the variation in SCY.

Stability analysis

The presence of a significant genotype $\times$ environment ($G \times E$) interaction, as revealed by ANOVA, necessitated a comprehensive stability analysis to identify widely adapted and stable genotypes. The differential performance of genotypes across environments indicates changes in genotype ranking, making selection based on mean performance alone unreliable. Therefore, stability was assessed using complementary models, namely the Eberhart and Russell model, AMMI and GGE biplot approaches.

Eberhart and Russell model

The Eberhart and Russell model partitions $G \times E$ interaction into linear (predictable) and non-linear (unpredictable) components. A stable genotype is characterised by high mean yield, a regression coefficient (b_i) close to unity and a non-significant deviation from regression ($S^2di \approx 0$) (Table 8, Fig. 2). For SCY, the analysis revealed significant differences among genotypes and environments, indicating substantial genetic variability and environmental influence. The significant linear component of $G \times E$ interaction suggests that genotype performance can be predicted based on environmental indices (Table 8, Fig. 3).

Genotype BS 3-17 (G_1) emerged as the most stable and high-performing genotype, recording the highest mean SCY (1978 kg ha⁻¹), significantly exceeding the grand mean. Its stability parameters ($b_i = 1.05$ and $S^2di \approx 0$) indicate wide adaptability and stable performance across environments. This genotype exhibits average responsiveness to environmental changes, performing consistently under both favourable and unfavourable conditions, making it suitable for rainfed cultivation. In contrast, the check variety Suraj (G_7) recorded a lower mean yield (1563 kg ha⁻¹) and exhibited a regression coefficient of 0.91 with a high deviation from regression, indicating poor stability and unpredictable performance across environments. Similarly, genotype BS 144-1 (G_4) showed significant instability despite moderate yield potential. Genotype BS 277 (G_2), which recorded the second-highest yield (1827 kg ha⁻¹), also demonstrated stable performance with $b_i \approx 1$ and non-significant S^2di , making it a suitable alternative genotype. A similar trend was observed for LY, where

BS 3-17 exhibited the highest mean (675 kg ha⁻¹) along with stable performance ($b_i = 1.06$, non-significant S^2di), confirming its superiority.

Additive main effects and multiplicative interaction model analysis

The AMMI model provides a robust framework for partitioning genotype $\times$ environment interaction by separating additive and multiplicative components. The AMMI analysis for SCY revealed that the first two interaction principal component axes (IPCA1 and IPCA2) were highly significant and together explained more than 85 % of the total $G \times E$ interaction variation, justifying the use of the AMMI2 biplot for graphical interpretation. In the AMMI1 biplot, where mean performance is plotted against IPCA1 scores, genotypes positioned further along the positive axis indicate higher yield, while those closer to the zero IPCA1 line exhibit greater stability. Genotype BS 3-17 (G_1) was located farthest along the positive axis with an IPCA1 score close to zero, indicating both high mean yield and superior stability. In contrast, genotype BS-39 (G_6) exhibited higher IPCA scores, suggesting specific adaptation to environments rather than broad stability.

The AMMI stability value (ASV) provided a quantitative measure of stability, with BS 3-17 recording the lowest ASV (0.34) for SCY, confirming it as the most stable genotype. In contrast, the check variety Suraj exhibited a relatively high ASV (2.39), indicating greater sensitivity to environmental fluctuations (Table 9, Fig. 4). The AMMI analysis also identified environment E_7 (Bhawanipatna, 2023–24) as highly discriminating due to its large IPCA score, making it suitable for differentiating genotypic performance. Environments with IPCA scores near zero were less discriminative and represented average testing conditions. For pest-related traits, genotype BS 3-17 exhibited both low mean pest populations and high stability (low ASV) for APH and JAS, indicating a desirable combination of resistance and stability, which is advantageous for breeding programs.

Genotype plus genotype by environment biplot analysis

The GGE biplot methodology enables simultaneous evaluation of genotype mean performance and stability. In the “mean vs. stability” view for SCY, genotype BS 3-17 was positioned farthest along the average environment coordinate (AEC) abscissa, confirming its highest mean performance. Additionally, its minimal projection onto the AEC ordinate indicated high stability across environments, thereby identifying it as the ideal genotype.

Genotype BS 277 was positioned closest to the ideal genotype, indicating its potential as a stable, high-yielding alternative. In contrast, genotypes such as BS 144-1 exhibited shorter projections along the mean axis and larger projections along the stability axis, indicating lower yield and higher instability. These graphical interpretations were consistent with the results

Table 8. Mean performance and stability parameters (Eberhart & Russell) for seed cotton yield (SCY) and lint yield (LY)

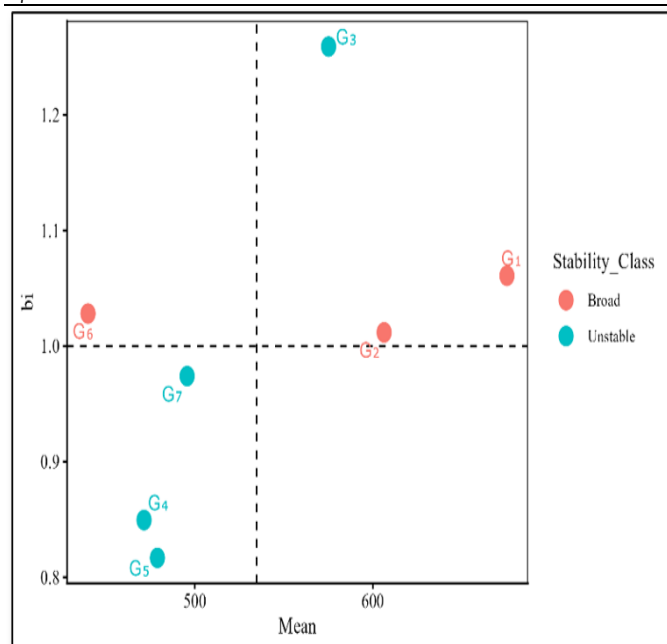
Genotype	SCY (kg/ha)				LY (kg/ha)			
	Mean	b_i	S^2di	Stability	Mean	b_i	S^2di	Stability
G_1	1978.04	1.05	0.00 (NS)	Stable	675.41	1.06	163.54	Stable
G_2	1827.22	1.05	0.00 (NS)	Stable	606.37	1.01	0	Stable
G_3	1788.93	0.99	4708.75**	Unstable	575.15	1.26	1952.92**	Unstable
G_4	1573.22	1.06	5286.88*	Unstable	471.41	0.85	949.12*	Unstable
G_5	1492.15	0.89	10388.25**	Unstable	478.93	0.82	2114.70**	Unstable
G_6	1394.3	1.04	185.31	Average	439.93	1.03	98.51	Stable
G_7	1563.89	0.91	10947.12*	Unstable	495.63	0.97	2724.17**	Unstable

* and ** indicate significance at $p < 0.05$ and $p < 0.01$ respectively.

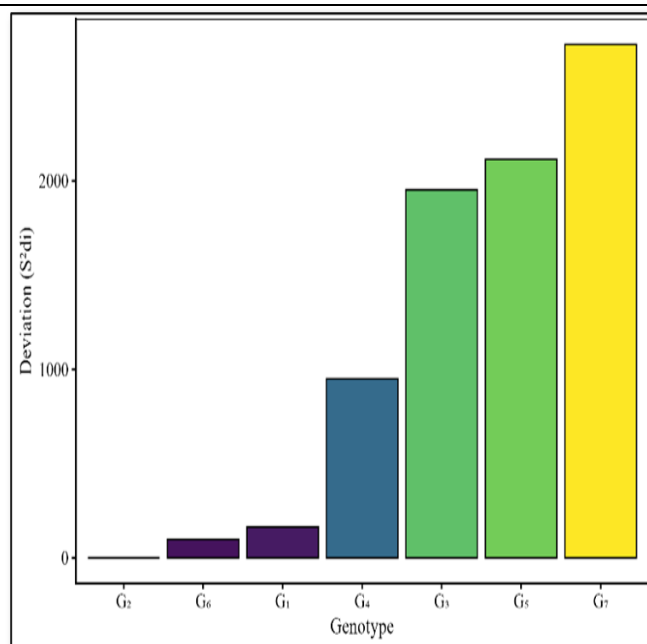
Table 9. Stability parameters including AMMI stability value (ASV), Wricke's Ecovalence (Wi) and genotype selection index (GSI) with their respective ranks for seed cotton yield (SCY), lint yield (LY), number of bolls per plant (NB) and boll weight (BW)

Genotype	SCY					LY				
	ASV	ASV rank	Wi	Wi rank	GSI	ASV	ASV rank	Wi	Wi rank	GSI
G ₁	0.34	1	1543	1	2	6.65	2	5662	3	2
G ₂	1.33	2	4521	2	4	4.29	1	3218	1	3
G ₃	2.06	5	8954	5	6	18.52	7	23949	7	10
G ₄	1.3	4	3876	4	8	13.6	5	12884	4	11
G ₅	2.87	7	14522	7	12	11.54	4	22035	5	9
G ₆	2.01	3	8215	3	10	7.96	3	4943	2	8
G ₇	2.39	6	11245	6	14	18.14	6	23312	6	10

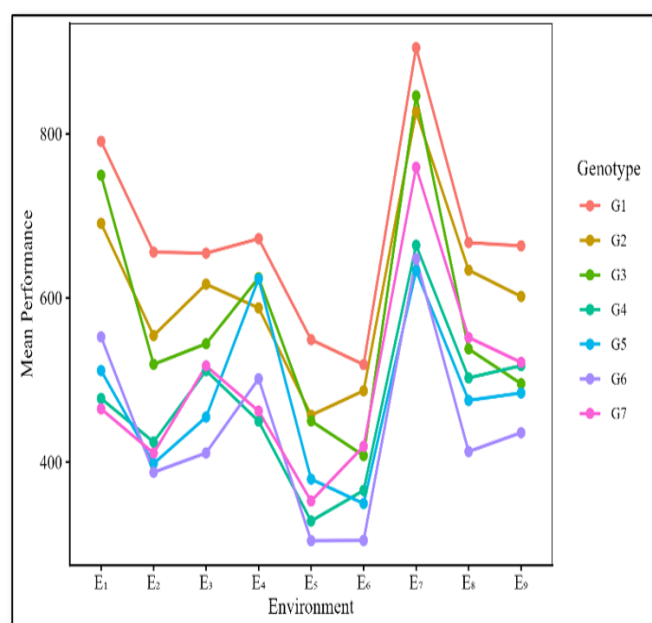
Genotype	NB					BW				
	ASV	ASV rank	Wi	Wi rank	GSI	ASV	ASV rank	Wi	Wi rank	GSI
G ₁	0.25	1	0.18	1	2	0.1	1	0.05	1	2
G ₂	0.88	3	1.15	3	4	0.69	2	0.14	2	3
G ₃	1.31	5	1.98	5	6	0.71	3	0.1	3	6
G ₄	0.05	2	0.08	2	7	1.09	6	0.34	6	7
G ₅	1.25	4	1.84	4	12	0.74	4	0.08	4	9
G ₆	1.09	4	1.45	4	9	0.77	5	0.22	5	10
G ₇	1.22	6	1.67	6	11	0.85	7	0.79	7	14



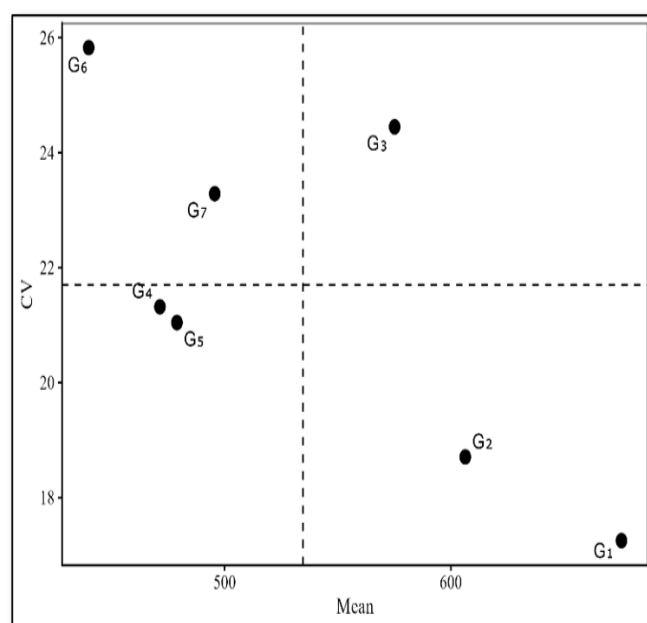
A



B

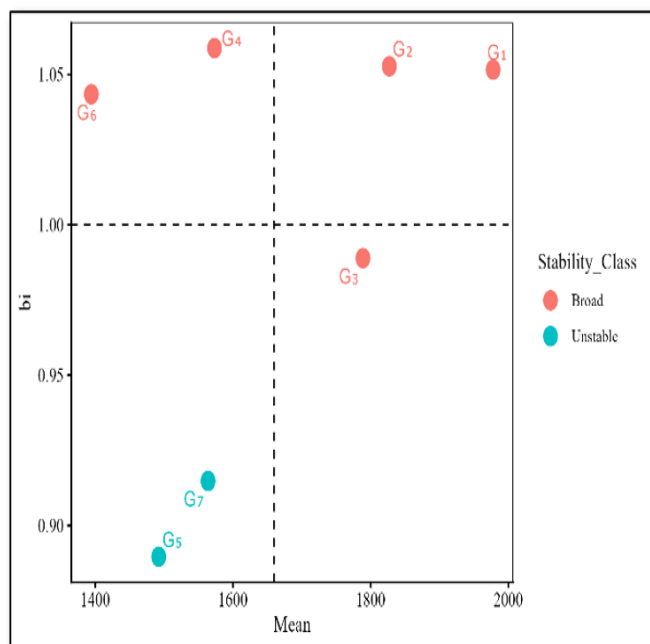


C

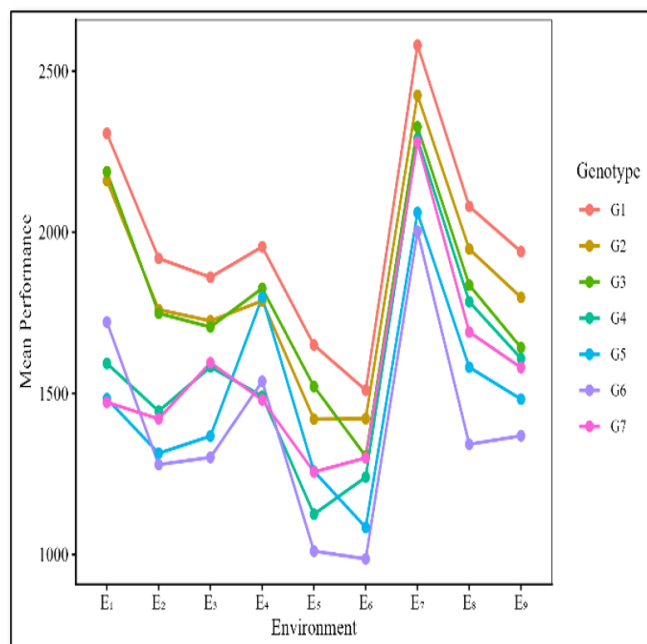


D

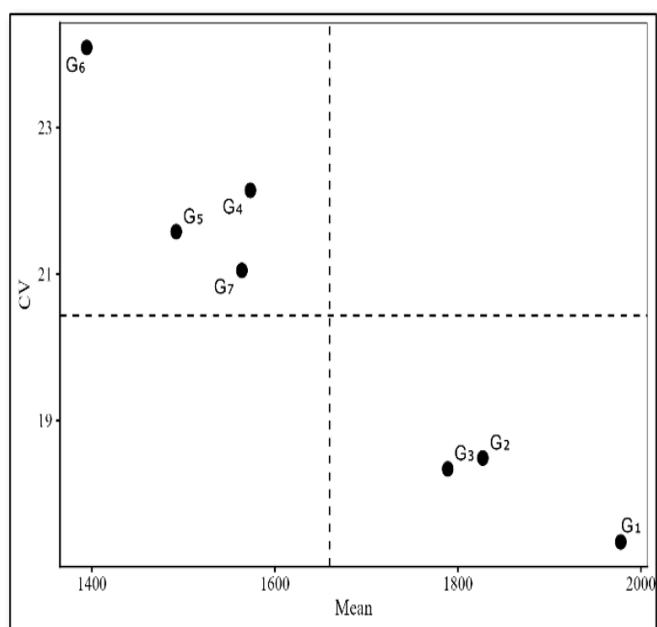
Fig. 2. Stability and adaptability analysis of genotypes across nine environments. (A) adaptation map (mean vs. regression coefficient b_i); (B) stability deviation (S^2di); (C) reaction norms across environments; (D) Francis plot (mean vs. coefficient of variation).



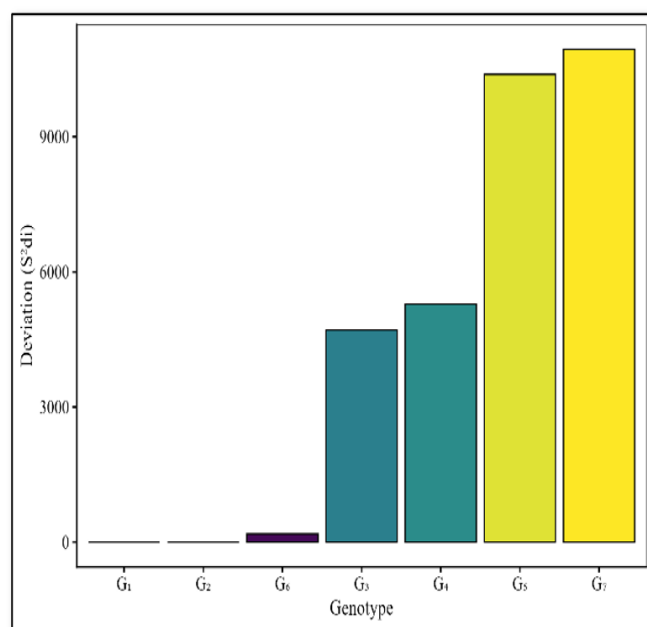
A



B

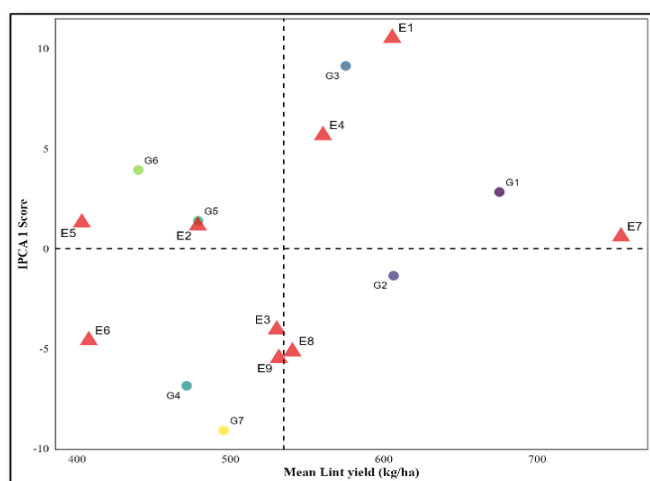


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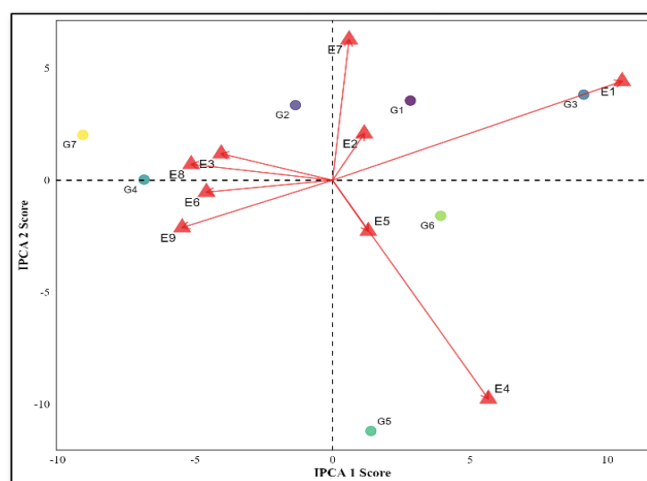


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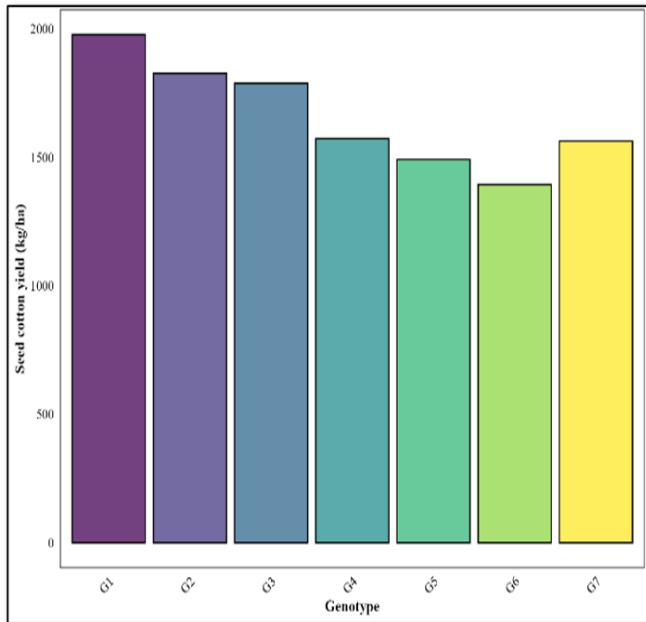
Fig. 3. Graphical visualisation of parametric stability and adaptability for seed cotton yield (kg/ha). (A) adaptation map (mean vs. regression coefficient b_i); (B) stability deviation (S^2di); (C) reaction norms across nine environments; (D) Francis plot (mean vs. coefficient of variation).



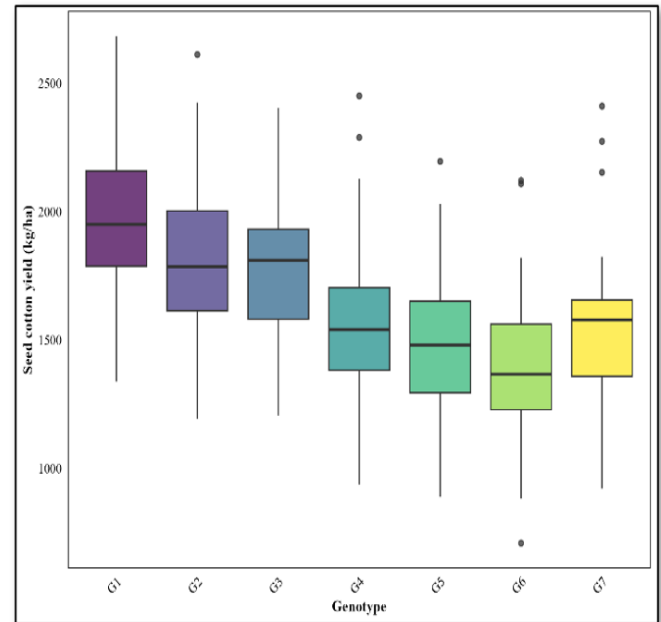
A



B

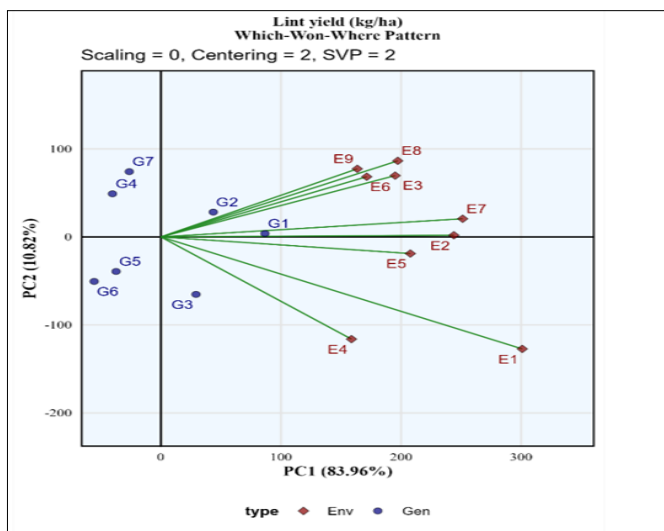


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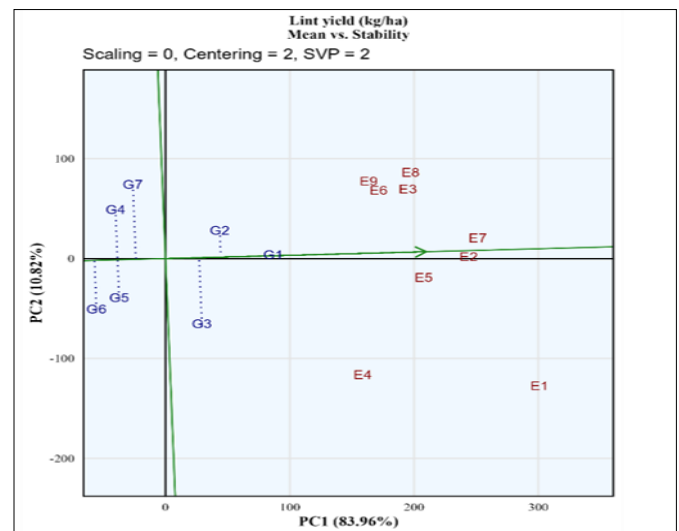


D

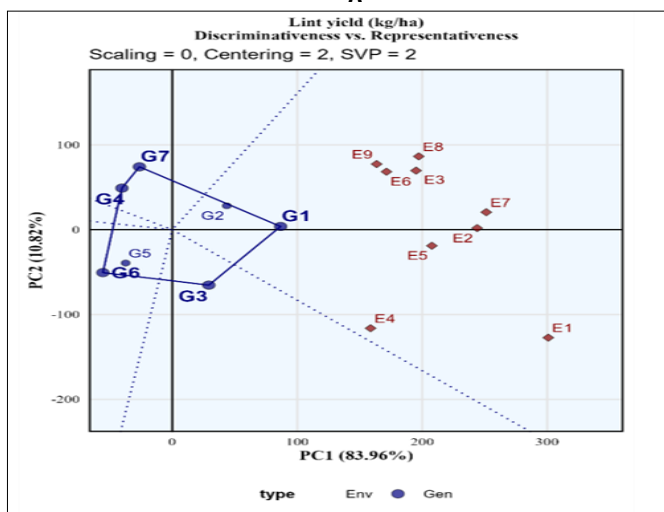
Fig. 4. Additive main effects and multiplicative interaction and yield performance analysis for cotton genotypes. (A) AMMI1 biplot (mean vs. IPCA1 scores) for lint yield (kg/ha); (B) AMMI2 biplot (IPCA1 vs. IPCA2 scores) for lint yield (kg/ha); (C) bar plot comparing mean seed cotton yield (kg/ha) across genotypes; (D) box plot displaying performance distribution and variability of genotypes for seed cotton yield (kg/ha).



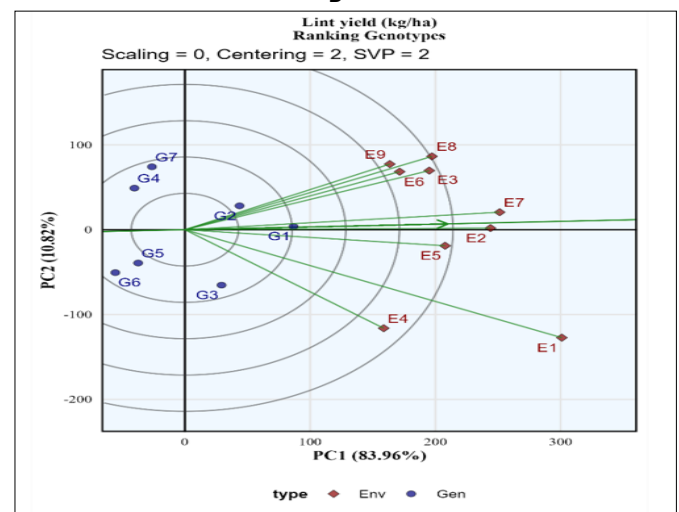
A



B



C



D

Fig. 5. Genotype plus genotype by environment biplot graphical analysis for lint yield (kg/ha). (A) polygon view showing the 'which-won-where' pattern and mega-environments; (B) mean performance vs. stability view using the average environment coordinate (AEC); (C) discriminativeness vs. representativeness of the test environments; (D) ranking of genotypes relative to the ideal ideotype.

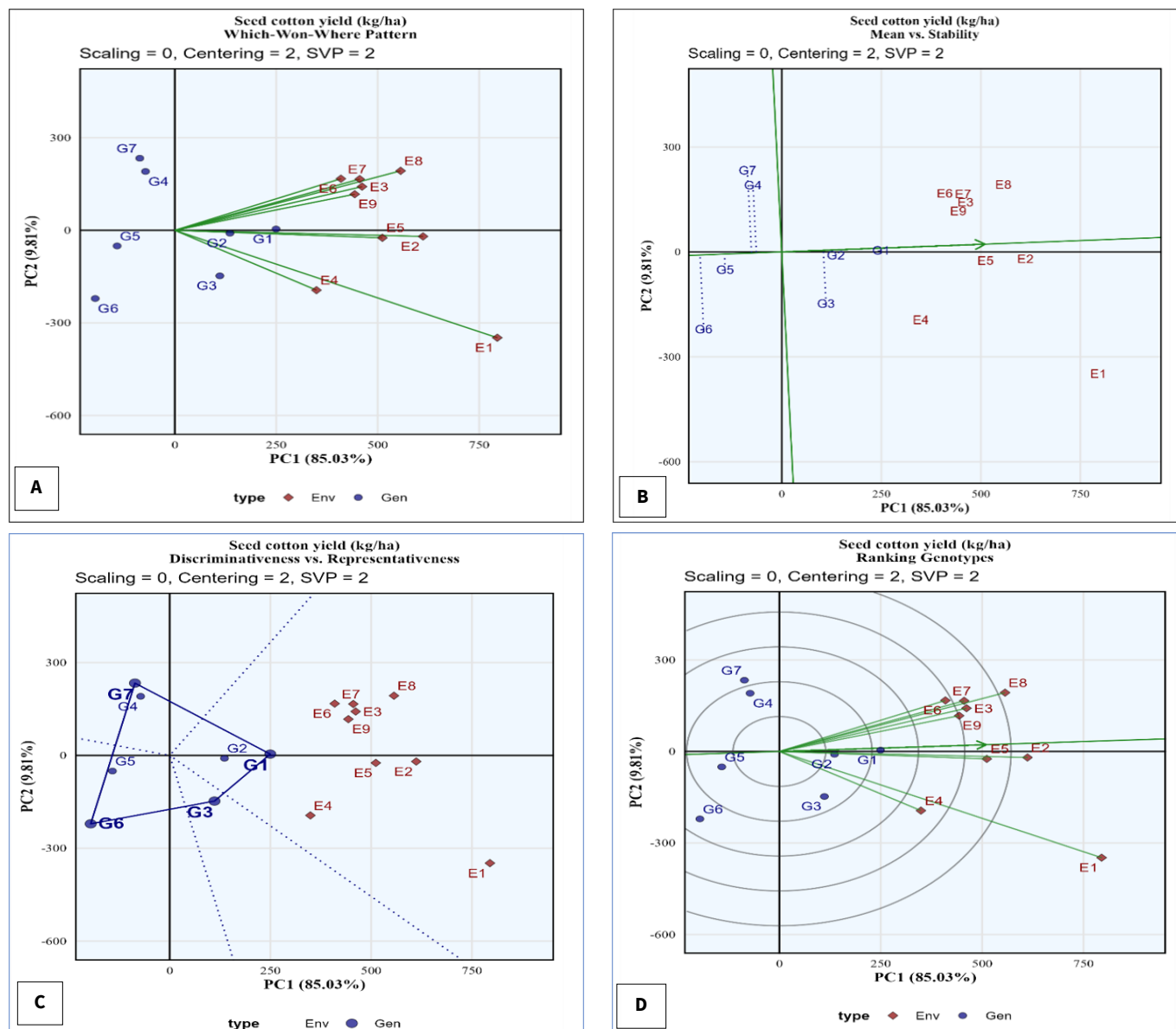


Fig. 6. Genotype plus genotype by environment biplot analysis of seed cotton yield (kg/ha). (A) polygon view illustrating the “which-won-where” pattern and mega-environments; (B) mean performance versus stability based on the average environment coordinate (AEC); (C) discriminativeness versus representativeness of the test environments; (D) ranking of genotypes relative to the ideal ideotype.

obtained from the Eberhart and Russell and AMMI analyses (Fig. 5, 6).

Multi-trait stability index

To identify genotypes combining high yield, stability and pest resistance, the MTSI was employed. Based on a selection intensity of 20 %, genotype BS 3-17 (G_1) was ranked first with the lowest MTSI score (5.51), indicating its closest proximity to the ideotype. It was followed by BS 277 (G_2), which recorded an MTSI score of 5.54 (Table 10, Fig. 7).

The check variety Suraj ranked last with an MTSI score of

10.61, indicating inferior performance in terms of yield stability and pest resistance.

Agronomic adaptability validation

The results of the spacing and fertiliser trial revealed significant effects of agronomic interventions on SCY of BS 3-17 (Table 11). In Bhawanipatna, closer spacing (90×30 cm) combined with 125 % of the recommended dose of fertiliser recorded the significantly highest SCY (3114 kg ha^{-1}). Similarly, under Umerkote conditions, the same treatment combination produced the highest yield (2889 kg ha^{-1}). These results indicate that BS 3-17 responds

Table 10. Ranking of genotypes based on the multi-trait stability index (MTSI)

Genotype	MTSI score	Rank	Selected
G1	5.51	1	Yes
G2	5.54	2	Yes
G6	5.85	3	No
G3	7.64	4	No
G5	8.80	5	No
G4	9.41	6	No
G7	10.61	7	No

Table 11. Combined effect of spacing and fertiliser levels on seed cotton yield (kg/ha) of BS 3-17 at Bhawanipatna and Umerkote

Spacing (cm)	Fertiliser level	Yield (Bhawanipatna)	Yield (Umerkote)	Pooled mean
90 × 60	75 % RDF	2038	1943	1991
90 × 60	100 % RDF	2307	2184	2246
90 × 60	125 % RDF	2400	2262	2331
90 × 45	75 % RDF	2062	1988	2025
90 × 45	100 % RDF	2783	2617	2700
90 × 45	125 % RDF	2980	2664	2822
90 × 30	75 % RDF	2387	2238	2313
90 × 30	100 % RDF	2897	2640	2769
90 × 30	125 % RDF	3114	2889	3002
CD ($p = 0.05$)	Spacing	145	162	-
CD ($p = 0.05$)	Fertiliser	122	135	-
CD ($p = 0.05$)	Interaction	208	236	-

RDF: recommended dose of fertilisers; CD ($p = 0.05$): critical difference at 5 % level of significance.

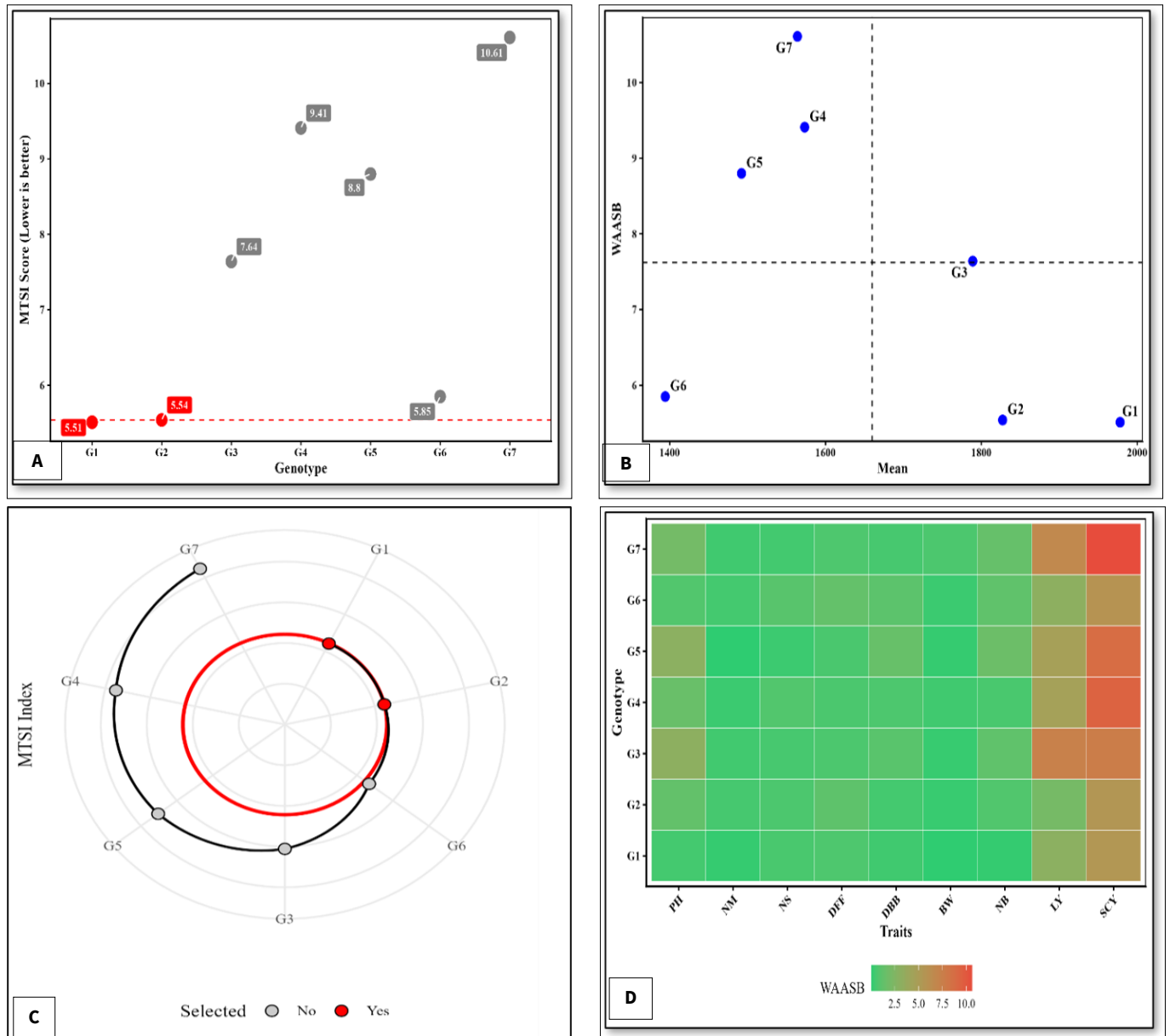


Fig. 7. Multi-trait stability analysis of cotton genotypes. (A) ranking based on multi-trait stability index (MTSL) identifying superior candidates; (B) mean seed cotton yield versus stability (WAASB) biplot; (C) MTSL radar chart illustrating trait contributions to the ideal genotype; (D) stability heatmap based on weighted average of absolute scores (WAASB).

positively to high-density planting and enhanced nutrient application, suggesting this agronomic package for commercial cultivation.

Discussion

The significant $G \times E$ interaction observed for yield and pest-related

traits highlights the complexity of selecting stable genotypes under rainfed conditions (15–19). These findings agree with earlier reports (20–25). Recent studies emphasise that increasing climatic variability necessitates the development of genotypes with high phenotypic plasticity rather than strict stability (26). The superior performance of BS 3-17 across diverse environments indicates its high adaptability and phenotypic plasticity, enabling it to maintain productivity under

stress conditions while efficiently utilising favourable environments (27). This stability may be attributed to efficient assimilate partitioning, which minimises fruit shedding under moisture stress.

The high heritability observed for sucking pest resistance traits (APH, JAS and THR) indicates strong genetic control with limited environmental influence, possibly governed by morphological and biochemical defence mechanisms (23). Previous studies highlighted the importance of such inherent resistance in maintaining yield stability, particularly in non-Bt germplasm (28). The ability of BS 3-17 to resist multiple pests suggests its potential as a component of integrated pest management (IPM) strategies, reducing dependence on chemical control. The negligible correlation between yield and pest incidence further supports earlier findings, indicating that simultaneous improvement of yield and pest resistance is feasible without genetic trade-offs (3).

The strong positive association and direct effect of LY on SCY confirm its importance as a key selection criterion (29). Conversely, the negative association between PH and yield suggests that efficient assimilate allocation is more critical than excessive vegetative growth under rainfed condition. Similarly, previous studies emphasised the importance of compact plant architecture for enhancing yield under such environments (30). The MTSI proved superior to single-trait selection methods by effectively identifying BS 3-17 as the most desirable genotype, eliminating genotypes with high yield but poor stability (8). These findings are consistent with previous researchers, who advocated the use of multi-trait indices to accelerate breeding efficiency (31).

Furthermore, the significant response of BS 3-17 to improved agronomic practices highlights the importance of genotype $\times$ management interaction in optimising productivity. Similar observations were reported previously, emphasising the role of plant density and nutrient management in achieving ideotype-based yield enhancement (32).

Conclusion

This study conducted across multiple environments demonstrated that genotype BS 3-17 is a superior and stable genotype for rainfed conditions of Odisha. It recorded the highest mean seed cotton yield (SCY) (1978 kg ha⁻¹) and lint yield (LY) (675 kg ha⁻¹), while maintaining consistent resistance to major sucking pests. Stability parameters derived from the Eberhart and Russell, additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment interaction (GGE) biplot models consistently identified BS 3-17 as a widely adapted and stable genotype across environments. The multi-trait stability index (MTSI) further confirmed its superiority by ranking it first among all genotypes evaluated. Agronomic optimisation trials indicated that closer spacing planting (90 $\times$ 30 cm) combined with 125 % of the recommended dose of fertiliser maximised yield performance. Therefore, BS 3-17 is recommended for commercial cultivation under rainfed conditions and can be utilised as a valuable donor parent in breeding programs targeting yield stability and sucking pest resistance. Future research should focus on multi-location validation across broader agro-ecological zones and molecular characterisation to further exploit its genetic potential.

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Authors' contributions

SD and BSN conceptualised and designed the research study. JRM, NM and SD carried out the field and/or laboratory experiments and were involved in data collection and curation. BRB, AS and GM performed statistical analysis and interpreted the results. AN, SKP and TP contributed to methodology development and validation of results. KCS, UN and CK provided overall supervision, critical inputs and research guidance. SD, BSN and JRM drafted the original manuscript. All authors read and approved the final 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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