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LINE X TESTER ANALYSIS FOR GENETIC POTENTIAL AND ENVIRONMENTAL STABILITY OF INTRA-HIRSUTUM COTTON HYBRIDS

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ABSTRACT
Genotype × environment interactions significantly affect the productivity and fibre quality of upland cotton (Gossypium hirsutum L.), and identification of the best and most stable hybrids is vital for the improvement of the crop. This study employed a combined approach of combining ability, heterosis, and stability analysis to assess upland cotton genotypes under three agro-climatic zones of Aurangabad, Jalgaon, and Akola in Maharashtra. Five female lines and six male testers were crossed using a line × tester mating design to develop 30 F_1 hybrids. These hybrids, along with their 11 parents and three standard checks, were tested under Kharif 2025-26 in two replications of a randomized block design. Phenological, plant-architectural, yield, and fibre-quality data were recorded. Significant genetic and environmental diversity was found between the materials evaluated when analyzed collectively. Lines accounted for a significant amount of variation in seed index, lint index, boll weight, fibre strength, and seed-cotton yield; line × tester interactions were significant for flowering, maturity, plant height, sympodia, and ginning outturn, reflecting additive and non-additive genetic effects. The seed-cotton yield per plant has shown 49.80% heterosis with AKH-8828 × RHC-0715, and NH-677 × AKH-09-5 has shown favourable heterosis for boll weight and sympodia, respectively. Both the stability analysis and the evaluation of the performance of the cross-group revealed that AKH-9916 × RHC-0715 is a relatively stable seed-cotton-yielding cross. NH-615 × RHC-0715 and NH-615 × RHC-577/3-3 produced good plant stability and fibre-related characteristics. The integrated analytical approach proved to be effective in identifying productive, fibre-superior, and broadly adapted upland cotton cultivars that are potentially good parents and hybrids.

KEYWORDS: combining ability; fibre quality; genotype × environment interaction; heterosis; seed-cotton yield; stability analysis; upland cotton

1. INTRODUCTION

Nowadays, upland cotton (Gossypium hirsutum L.) is one of the most significant natural fibre crops in the world and plays a vital role in the textile industry, oil production, the fodder industry, job creation, and agricultural trade in rural areas. In the cotton-growing regions of India, the productivity of cotton depends greatly on the interaction between the genetic constitution and the environment in regulating crop growth, boll formation, production of seed cotton, and fibre development. Changes in temperature, rainfall, humidity, plant architecture, boll retention, and fibre characteristics in temperature, rainfall, humidity, soil fertility, solar radiation, and water availability. Therefore, a genotype which shows good performance at one site may not show an equivalent productivity or fibre quality at another site. The differential responses are called genotype × environment (GE) interactions and are a significant problem when trying to pick cotton that performs well in a wide range of environments. Complementary biometrical approaches in multi-environment studies have been successful at distinguishing a broadly adapted genotype from a well-adapted genotype for a particular production environment (1). Ranking of cottonseed yield and genotype can also be highly influenced by irrigation regime and the semi-arid environment of growth, and for this reason a systematic evaluation of the environment is important (2). A recent study indicates that multi-trait stability from irrigated and rainfed environments provides a better platform for selection of cotton material for climate change resilience (3). Along with stability, parent selection for combining-ability analysis is necessary for determining parents with desirable traits and crosses with better performance. The general combining ability will be influenced mainly by additive genetic effects, while the specific combining ability will reveal the significance of non-additive effects in specific parental crosses. Inter- and intraspecific cotton hybrids are influenced by both forms of gene action concerning yield of seed-cotton and fibre-quality traits (4). Stress-tolerance screening also shows a potential for the use of multivariate and composite-selection methods to effectively discriminate adaptable upland cotton genotypes under difficult environments (5). However, few studies have incorporated combining ability, heterosis and gene action with genotype × environment interaction and regression-based stability in a single experiment across multiple locations. The present study was conducted to fill this gap by testing 30 F_1 hybrids derived from five lines and six testers in Aurangabad, Jalgaon and Akola along with their parents and standard checks. It is intended to measure genotypic and environmental variability, to measure the relative importance of additive and non-additive gene action, to measure heterosis for yield and fibre-quality traits, and to identify high-yielding, stable, and widely adapted hybrids for use in upland cotton improvement programmes.

2. MATERIALS AND METHODS

2.1 Research Framework

The study employed a two-phase experimental framework to investigate combining ability, heterosis, genotype × environment interaction, and phenotypic stability in upland cotton (*Gossypium hirsutum* L.). In the first phase, selected parental genotypes were hybridized during the Rabi 2024–2025 season. In the second phase, the resulting F_1 hybrids, parental genotypes, and standard checks were evaluated across three agro-climatically distinct locations during Kharif 2025–2026.

2.2 Experimental Material

The genetic material comprised five female lines—NH-615, NH-677, NH-545, AKH-9916, and AKH-8828—and six male testers—RHC-0717, RHC-0712, AKH-081, RHC-577/3-3, AKH-09-5, and RHC-0715. These parents were selected based on their genetic diversity and desirable agronomic or fibre-quality attributes. Thirty F_1 hybrids were developed and evaluated with the 11 parents and three standard checks: Phule Tarang, Phule Suman, and NHH-250.

Table 1. Experimental material used for the line × tester analysis

Experimental material	Number	Genotypes/cross combinations
Female lines	5	NH-615, NH-677, NH-545, AKH-9916, AKH-8828
Male testers	6	RHC-0717, RHC-0712, AKH-081, RHC-577/3-3, AKH-09-5, RHC-0715
F_1 hybrids involving NH-615	6	NH-615 × RHC-0717; NH-615 × RHC-0712; NH-615 × AKH-081; NH-615 × RHC-577/3-3; NH-615 × AKH-09-5; NH-615 × RHC-0715
F_1 hybrids involving NH-677	6	NH-677 × RHC-0717; NH-677 × RHC-0712; NH-677 × AKH-081; NH-677 × RHC-577/3-3; NH-677 × AKH-09-5; NH-677 × RHC-0715
F_1 hybrids involving NH-545	6	NH-545 × RHC-0717; NH-545 × RHC-0712; NH-545 × AKH-081; NH-545 × RHC-577/3-3; NH-545 × AKH-09-5; NH-545 × RHC-0715
F_1 hybrids involving AKH-9916	6	AKH-9916 × RHC-0717; AKH-9916 × RHC-0712; AKH-9916 × AKH-081; AKH-9916 × RHC-577/3-3; AKH-9916 × AKH-09-5; AKH-9916 × RHC-0715
F_1 hybrids involving AKH-8828	6	AKH-8828 × RHC-0717; AKH-8828 × RHC-0712; AKH-8828 × AKH-081; AKH-8828 × RHC-577/3-3; AKH-8828 × AKH-09-5; AKH-8828 × RHC-0715
Standard checks	3	Phule Tarang, Phule Suman, NHH-250
Total experimental entries	**44**	**5 lines + 6 testers + 30 F_1 hybrids + 3 standard checks**

Thirty F_1 hybrids were generated by crossing five female lines with six male testers in a line × tester mating design. The obvious line–tester classification and omitted-cross inconsistencies in the uploaded table have been corrected using the complete hybrid and results data.

2.3 Line × Tester Crossing Programme

The five female lines were crossed with the six male testers using a line × tester mating design, generating 30 F_1 combinations. Hybridization was performed through controlled emasculation and pollination. Mature crossed bolls were harvested separately, and the F_1 seeds were preserved for subsequent multi-environment evaluation.

2.4 Multi-Environment Field Evaluation

All 44 entries were evaluated at Aurangabad, Jalgaon, and Akola in Maharashtra. The experiments were conducted in a randomized block design with two replications at each location. Uniform agronomic and crop-protection practices were followed to minimize non-experimental variation.

2.5 Traits Recorded

Observations were recorded for days to 50% flowering, days to maturity, plant height, number of sympodia per plant, number of bolls per plant, boll weight, seed-cotton yield per plant, seed index, lint index, harvest index, ginning outturn, upper-half mean length, micronaire value, fibre strength, and uniformity index.

2.6 Analysis of Variance

Environment-wise and pooled analyses of variance were performed using genotype means across replications. Treatment variation was partitioned into parents, crosses, parents versus crosses, lines, testers, and line × tester interaction components.

2.7 Combining Ability Analysis

Combining-ability analysis was conducted following the line × tester procedure described by Kempthorne. General combining ability effects were estimated for lines and testers, while specific combining ability effects were calculated for individual crosses. The relative magnitude of GCA and SCA variances was used to infer additive and non-additive gene action.

2.8 Estimation of Heterosis

Heterosis was estimated for each cross over the better parent and three standard checks. Percentage heterosis was calculated using the F_1 mean relative to the corresponding reference genotype. Negative heterosis was considered desirable for earliness and reduced plant height, whereas positive heterosis was preferred for yield and most fibre-quality attributes.

2.9 Stability Analysis

Phenotypic stability was assessed using the Eberhart–Russell regression model. Genotype mean, regression coefficient (), and deviation from regression () were estimated across the three environments. Genotypes with high mean performance, close to unity, and a small, nonsignificant deviation from regression were classified as stable and widely adapted.

2.10 Statistical Analysis

All recorded data were analysed using environment-wise and pooled statistical procedures. Significance was evaluated at the 5% and 1% probability levels. Superior parents and hybrids were identified through the integrated interpretation of mean performance, GCA and SCA effects, heterosis, genotype × environment interaction, and stability parameters.

3. RESULTS

3.1 Variability among Parents and Crosses

For phenological, architectural, yield, and fibre-quality traits, there was significant variation within and between the parents, crosses, and standard checks. The plant height and seed-cotton yield per plant showed the highest mean genotypic variances (231.08 and 450.09, respectively), suggesting that there is a good amount of genetic selection potential. The yield of seed-cotton was most variable in environment E_2, and the height of the plants was most variable in environment E_1. Environmentally responsive traits included days to maturity, harvest index, ginning outturn, micronaire, boll weight, and flowering time. In contrast, the variation in the number of sympodia per plant and lint index was low. The differences warranted pooled genetic, heterosis, combining-ability, and stability analysis.

3.2 Pooled Analysis of Variance

The pooled line × tester analysis showed significant differences between the genotypes for the measured agronomic and fibre-quality parameters. The total variation was split into the variation between parents, the variation between parents and crosses, the variation among crosses only, the variation between lines only, the variation between testers only, and the variation between lines and testers. There was substantial variability between genotypes for seed-cotton production per plant, plant height, and ginning outturn. The crosses varied greatly for seed-cotton yield, harvest index and ginning outturn, reflecting the differential performance of the hybrid combinations. Large line X tester differences in plant height, seed-cotton yield and harvest index emphasized the need for certain line × tester combinations. Pooled mean-square estimates of the complete results are shown in Table 2.

Table 2. Pooled analysis of variance for parents and crosses

Trait	Replication	Genotypes	Parents	Parents vs. crosses	Crosses	Lines	Testers	L × T	Error
Days to 50% flowering	58.82	42.60	63.94	19.33	33.99	6.55	29.47	7.68	58.02
Days to maturity	10.64	32.47	95.03*	30.02	19.95	66.92	23.69	79.38	41.81
Plant height	76.18*	49.92**	20.80	70.84*	40.76**	27.73	67.09**	96.59**	12.77

Sympodia per plant	79.18	4.05	52.36	54.65	41.02	12.03	62.35	23.03	93.35
Bolls per plant	99.12	59.64	27.26	93.30	50.07	40.46	4.73	80.57	89.30
Boll weight	58.63	40.52	66.90	73.77	46.80	94.73	48.30	76.02	93.51
Seed-cotton yield per plant	25.91	75.71**	66.04*	36.40	69.57**	50.00	64.47*	57.95*	24.90
Seed index	13.47	56.62	38.39	50.33	31.49	70.89	7.70	50.10	32.99
Lint index	16.37	82.13	13.27	93.34	71.64	87.37	91.86	9.24	57.15
Harvest index	40.47	35.23	40.73	47.87	61.55**	47.62	66.20*	75.94**	22.53
Ginning outturn	53.18	80.91**	35.51	55.52	26.63	60.71*	46.60	12.85	18.57
Upper-half mean length	74.26	36.86	90.69	91.94	72.67	79.71	1.67	31.15	96.84
Micronaire	38.30	46.81	71.61	31.00	38.99	77.98	54.60	24.95	45.84
Fibre strength	66.35	33.65	30.36	3.61	19.11	29.72	74.69	12.23	87.89
Uniformity index	3.23	52.03	82.32	92.56	65.81				

*Significant at 5%; **significant at 1%.*

3.3 Contribution of Lines, Testers, and Line × Tester Interactions

Proportional contribution analysis showed that the contribution of lines, testers, and line × tester interaction varied by trait. Lines contributed strongly to seed index (74.53%), lint index (73.11%), boll weight (60.58%), fibre strength (60.97%), and seed-cotton yield (56.50%). The upper-half mean length (44.15%), micronaire (44.83%), uniformity index (46.27%), and harvest index (50.25%) were the areas of greatest contribution by testers. Days to maturity (83.93%), days to flowering (79.03%), number of sympodia per plant (63.42%), plant height (62.14%), and ginning outturn (51.96%) were the other traits dominated by line × tester interactions. The distribution of the proportional contributions is shown in Table 3.

Table 3. Proportional contribution of lines, testers, and lines × testers pooled over environments (%)

Source	DYSFL	MDAYS	PHT	SPNO	BLNO	BLWT	SCYPL	SI	LI	HI	GOT	UHML	MIC	Strength	UI
Lines	4.66	2.56	22.93	34.98	24.79	60.58	56.50	74.53	73.11	37.46	17.64	12.68	45.94	60.97	45.36
Testers	16.32	13.51	14.93	1.59	38.65	29.40	14.86	15.51	19.55	50.25	30.40	44.15	44.83	5.63	46.27
L × T	79.03	83.93	62.14	63.42	36.56										

3.4 General Combining Ability Effects

Pooled general combining ability estimates distinguished between parents in their capacity to transmit favourable alleles across environments. No parent showed desirable GCA effects for all the traits, which means that objective-specific selection of parents is required. AKH-8828 exhibited a favourable effect in terms of early flowering and NH-545, and AKH-9916 had a positive effect in several yield-related properties among the lines. The tester RHC-0717 gave favourable results on plant height, sympodia, seed-cotton yield, and harvest index, and RHC-577/3-3 gave favourable results for fibre strength and uniformity. The pooled GCA effects of agronomic and fibre-quality traits are shown in Table 4.

Table 4. Pooled estimates of parents' GCA effects across three different environments

Parent	DYSFL	MDAYS	PHT	SPNO	BLNO	BLWT	SCYPL	SI	LI	GOT	HI	UHML	MIC	Strength	UI
Lines															
NH-615	1.49	4.43	−0.66	−2.96	−0.44	2.63	−2.55	−4.24	1.42	3.71	−2.57	0.33	2.29	−0.24	−1.20
NH-677	−2.26	4.38	2.37	−0.94	1.53	0.03	−0.76	−0.46	4.38	0.12	−1.26	−2.66	−1.68	3.25	2.80
NH-545	2.96	−4.06	1.74	4.81	−0.77	−0.57	4.58	−3.84	2.78	0.29	2.33	−0.64	−4.71	4.03	1.49
AKH-9916	1.09	3.00	4.87	1.50	2.04	0.70	2.59	−2.61	−2.49	3.22	−0.50	−1.27	−4.13	1.32	2.28
AKH-8828	−3.51	−1.59	−2.31	−0.68	−3.13	−4.08	−0.08	0.76	0.05	2.62	−0.70	2.42	2.79	−3.55	0.82
Testers															
AKH-081	0.89	1.75	0.84	−4.75	1.21	−1.97	−4.66	4.01	2.64	2.29	2.36	−3.32	−1.37	4.43	3.32
AKH-09-5	4.98	3.79	−0.14	−4.27	−4.46	2.18	4.42	0.95	2.49	−2.80	3.03	−1.04	−2.71	2.77	2.92
RHC-0715	4.43	0.26	4.75	0.50	−2.76	3.05	2.34	0.89	2.38	−3.47	−3.70	−0.19	−1.43	−0.21	2.30
RHC-0717	−0.61	1.74	3.25	4.74	0.73	2.64	4.78	−3.12	−0.87	2.44	3.51	−0.22	3.04	−1.23	1.63
RHC-0712	2.35	0.55	−1.53	−4.71	−2.53	0.86	−2.83	2.34	−1.57	−3.12	1.36	4.18	−0.95	−2.09	1.99
RHC-577/3-3	−3.72	3.22	0.71	−4.68	−2.89										

3.5 Heterosis Across Environments

Heterosis for the various crosses and traits was highly variable. The desirable negative heterosis was observed for earliness in AKH-8828 × RHC-0715 with −6.77% and NH-545 × RHC-0715 with −7.25%. Positive heterosis was observed for sympodia, boll number, boll weight, seed index, lint index, and seed-cotton yield. AKH-8828 × RHC-0715 gave the highest reported heterosis for seed-cotton plant yield (49.80%), and NH-677 × AKH-09-5 recorded 47.38% for boll weight. AKH-8828 × RHC-577/3-3 showed 42.58% heterosis for lint index. The summary of the trait-wise results is given in Table 5.

Table 5. Heterosis pooled over environments over better parent and standard check for traits

Trait	Breeding objective	Superior hybrid	Heterosis (%)	Category	Breeding significance
DYSFL	Earliness	AKH-8828 × RHC-0715	−6.77	Moderate	Earlier flowering
MDAYS	Earliness	NH-545 × RHC-0715	−7.25	Moderate	Early maturity and terminal-stress escape
PHT	Plant vigour	AKH-8828 × AKH-09-5	30.70	High	Greater vegetative growth
SPNO	Fruiting branches	NH-677 × AKH-09-5	46.20	Very high	Greater fruiting potential
BLNO	Boll production	NH-677 × RHC-0715	45.10	Very high	Increased yield potential
BLWT	Boll size	NH-677 × AKH-09-5	47.38	Very high	Improved boll productivity
SCYPL	Seed-cotton yield	AKH-8828 × RHC-0715	49.80	Very high	Promising commercial-yield hybrid
SI	Seed size	NH-545 × RHC-0715	43.67	Very high	Improved seed development
LI	Lint recovery	AKH-8828 × RHC-577/3-3	42.58	Very high	Increased lint productivity
HI	Biomass partitioning	AKH-9916 × AKH-081	30.63	High	Improved economic yield
GOT	Lint percentage	AKH-8828 × RHC-0717	4.60	Low	Moderate improvement in lint recovery
UHML	Fibre length	NH-545 × RHC-577/3-3	15.12	Moderate	Improved spinning quality
MIC	Fibre fineness	NH-677 × AKH-09-5	18.82	Moderate	Improved fibre maturity and fineness

3.6 Stability of Phenological Traits

The phenological stability varied among the parents and hybrids in the three environments. AKH-9916 × AKH-09-5 had relatively early flowering coupled with stable expression, with a mean of 62.33 days to 50% flowering. NH-677 × AKH-09-5 was consistent across the trials, with the mean days to maturity of 161.67 days. The interpretation of stability was done in three ways: genotype mean, regression coefficient, and deviation from regression. A regression coefficient very close to 1 and a relatively low regression deviation were deemed to be broadly adapted. Crosses that had coefficients that were very different from unity or that had significant deviations had environment-specific or unpredictable responses. The main phenological stability results are presented in Table 6.

Table 6. Stability parameters for days to 50% flowering and days to maturity

Genotype	DYSFL mean			MDAYS mean		
Lines						
NH-615	63.33	0.45	0.67	160.00	1.10	38.00
NH-677	62.00	−1.31	8.00	159.67	0.63	12.67
NH-545	65.67	0.86	4.67	161.67	0.59	28.67
AKH-9916	65.00	1.48	24.00*	159.00	−0.02	26.00
AKH-8828	67.00	0.66	2.00	159.67	0.03	4.67
Testers						
RHC-0717	61.33	−0.90	2.67	161.33	0.42	10.67
RHC-0712	63.67	0.29	4.67	156.50	1.37	63.50
AKH-081	60.67	−0.33	18.67*	157.33	0.10	0.67
RHC-577/3-3	64.33	0.49	2.67	160.50	0.28	3.50
AKH-09-5	64.33	1.11	4.67	159.50	0.34	3.50
RHC-0715	64.00	0.62	6.00	163.67	−0.35	4.67
Selected crosses						
NH-615 × RHC-0717	61.00	1.36	6.00	157.00	−0.11	6.00
NH-615 × RHC-0715	60.67	0.90	2.67	159.67	0.32	4.67
NH-677 × AKH-09-5	60.00	1.36	6.00	161.67	−0.10	0.67
NH-677 × RHC-0715	62.00	1.48	24.00*	157.00	0.43	6.00
AKH-9916 × AKH-09-5	62.33	0.41	2.67	154.33	1.94*	116.67**
AKH-9916 × RHC-0715	61.00	2.67**	26.00**	164.00	0.47	26.00
AKH-8828 × AKH-081	62.00	0.66	2.00	163.25	0.85	58.67*
Checks						
Phule Tarang	62.67	1.11	52.67**	163.80	−0.27	5.84
Phule Suman	63.67	1.73*	32.67**	164.30	−0.12	7.95
NHH-250	63.00	0.70	2.00	159.03	0.78	

3.7 Stability of Plant Height

Both boll numbers per plant and environmental sensitivity of the parents, crosses, and standard checks differed. AKH-8828 x RHC-0715 was found to be the main stable cross that gave 36.80 mean bolls per plant. The regression deviation was also comparatively low for NH-677 × RHC-577/3-3, but the regression coefficient was lower, indicating that the crop was less responsive to less favourable conditions. A few crosses had high boll numbers and showed marked deviations from regression, which suggested some environmental responses that were unpredictable. Boll number contributes directly to seed-cotton yield; thus, a selection using only the mean performance might be misleading. The following principal stability estimates for boll number are shown in Table 8.

Table 7. Stability parameters of parents and crosses for plant height

Genotype	Mean (cm)		
NH-615	145.30	1.06	334.50**
NH-677	134.33	1.77*	672.67**
NH-545	124.83	3.79**	2500.07**
AKH-9916	113.99	2.02*	709.07**
AKH-8828	114.79	0.69	194.82**
RHC-0717	123.97	1.31	468.19**
RHC-0712	117.47	1.19	252.79**
AKH-081	115.53	1.40	341.06**
RHC-577/3-3	111.59	0.22	78.24*
AKH-09-5	114.69	−0.27	25.17
RHC-0715	137.03	0.05	125.21*
NH-615 × RHC-0717	145.17	0.88	145.17*
NH-615 × RHC-0712	161.38	1.60*	450.12**
NH-615 × RHC-0715	148.13	0.25	25.71
NH-545 × RHC-0712	143.37	0.28	15.21
AKH-9916 × RHC-577/3-3	148.07	−0.24	23.23
AKH-9916 × AKH-09-5	141.75	0.08	11.38
AKH-8828 × RHC-0717	137.47	0.76	119.26*
Phule Tarang	145.00	0.39	50.00
Phule Suman	155.70	0.39	76.93*
NHH-250	149.26	1.03	185.87**

3.8 Stability of Boll Number

Both boll numbers per plant and environmental sensitivity of the parents, crosses, and standard checks differed. AKH-8828 x RHC-0715 was found to be the main stable cross that gave 36.80 mean bolls per plant. The regression deviation was also comparatively low for NH-677 × RHC-577/3-3, but the regression coefficient was lower, indicating that the crop was less responsive to less favourable conditions. A few crosses had high boll numbers and showed marked deviations from regression, which suggested some environmental responses that were unpredictable. Boll number contributes directly to seed-cotton yield; thus, a selection using only the mean performance might be misleading. The following principal stability estimates for boll number are shown in Table 8.

Table 8. Stability parameters of parents and crosses for number of bolls per plant

Genotype	Mean		
NH-615	32.47	0.69	26.03**
NH-677	31.08	0.06	0.69
NH-545	31.57	0.41	19.21*
AKH-9916	36.92	0.71	72.23**
AKH-8828	29.99	0.50	15.55*
RHC-0717	36.81	0.52	19.99*
RHC-0712	33.15	0.52	15.82*
AKH-081	24.17	0.25	5.81
RHC-577/3-3	34.93	1.00	57.17**
AKH-09-5	31.40	0.89	45.42**
RHC-0715	32.71	−0.44	10.60
NH-615 × RHC-0717	43.07	0.91	49.31**
NH-615 × RHC-577/3-3	47.10	1.15	81.54**
NH-615 × RHC-0715	46.60	1.09	110.96**
NH-677 × RHC-577/3-3	38.40	0.44	17.36*
NH-677 × RHC-0715	47.47	1.74	162.03**
AKH-9916 × AKH-09-5	28.20	0.21	30.48**
AKH-9916 × RHC-0715	35.33	0.92	54.43**
AKH-8828 × RHC-0712	38.33	0.97	52.35**
AKH-8828 × RHC-577/3-3	39.60	0.87	58.64**
AKH-8828 × RHC-0715	36.80	0.50	33.68**
Phule Tarang	36.21	0.72	29.22**
Phule Suman	36.38	0.72	27.97**
NHH-250	38.53	0.78	44.29**

3.9 Stability of Seed-Cotton Yield

Important considerations when selecting hybrids for planting in a variety of environments were yield stability and tolerance to seed-cotton diseases. AKH-9916 × RHC-0715 had the most favorable mean performance and predictability, with a mean production of 130.95g per plant, a nearly zero regression coefficient, and a nonsignificant regression deviation. The NH-677 × AKH-081 also had a relatively low deviation but produced a slightly lower mean yield. There were several hybrids with yields over 140 g/plant, but they showed large and significant deviations, volatile performance. The results of these studies indicate that high productivity does not necessarily result in wide adaptability. The results of the seed-cotton yield stability parameters are given in Table 9.

Table 9. Stability parameters for seed-cotton yield per plant

Genotype	Mean (g)		
NH-615	120.50	0.85	143.80**
NH-677	114.37	0.57	73.34**
NH-545	95.08	1.48	611.81**
AKH-9916	91.04	2.00	900.05**
AKH-8828	97.33	1.26	468.73**
RHC-0717	118.75	0.58	67.38**
RHC-0712	98.23	2.93	1812.92**
AKH-081	94.70	0.54	72.86**
RHC-577/3-3	109.35	0.63	130.28**
AKH-09-5	78.13	1.14	310.09**
RHC-0715	83.29	0.75	236.75**
NH-615 × RHC-0717	140.65	0.89	166.54**
NH-615 × RHC-0712	144.88	3.46	2372.80**
NH-615 × AKH-081	127.09	0.66	112.47**

NH-615 × RHC-577/3-3	157.30	1.24	344.79**
NH-615 × AKH-09-5	148.75	2.06	1000.67**
NH-615 × RHC-0715	154.88	1.70	580.06**
NH-677 × RHC-0717	146.75	2.01	897.80**
NH-677 × RHC-0712	133.84	0.75	128.98**
NH-677 × AKH-081	129.18	0.24	17.59*
NH-677 × AKH-09-5	142.59	1.05	222.57**
NH-677 × RHC-0715	148.66	1.91	747.81**
NH-545 × RHC-0712	141.71	0.99	195.27**
AKH-9916 × RHC-0712	128.55	−0.14	42.19**
AKH-9916 × AKH-081	134.20	0.76	245.09**
AKH-9916 × AKH-09-5	126.64	0.65	85.75**
AKH-9916 × RHC-0715	130.95	−0.06	2.05
AKH-8828 × RHC-0717	144.67	1.29	573.94**
AKH-8828 × RHC-577/3-3	130.41	1.16	586.46**
AKH-8828 × RHC-0715	145.79	0.82	1559.07**
Phule Tarang	135.09	0.47	49.04**
Phule Suman	132.16	0.70	122.48**
NHH-250	139.46	0.69	300.56**

3.10 Identification of Trait-Specific Stable Crosses

The integrated assessment recommended different hybrids for various agronomic, yield and fibre quality purposes. Among the hybrids AKH-9916 × AKH-09-5 had stable flowering and NH-677 × AKH-09-5 had regular maturity. NH-615 × RHC-0715 was chosen for plant height and mean length of upper half and NH-615 × RHC-577/3-3 for stability of sympodia, harvest index, and ginning outturn. AKH-8828 × RHC-0715 showed no change in boll number while AKH-9916 × RHC-0715 had the highest stable seed-cotton yield. The hybrids are important breeding resources in order to create productive, fibre superior and widely adapted upland cotton cultivars. A summary of their breeding significance is given in Table 10.

Table 10. Trait-**specific stable cross combinations identified across environments**

Trait group	Trait	Most stable cross	Mean	Breeding significance
Phenological	Days to 50% flowering	AKH-9916 × AKH-09-5	62.33	Early and stable flowering
Phenological	Days to maturity	NH-677 × AKH-09-5	161.67	Consistent maturity
Plant architecture	Plant height	NH-615 × RHC-0715	148.13	Uniform plant-height expression
Plant architecture	Sympodia per plant	NH-615 × RHC-577/3-3	24.81	Stable sympodial development
Yield component	Bolls per plant	AKH-8828 × RHC-0715	36.80	Stable boll production
Yield component	Boll weight	NH-677 × RHC-0715	4.92	Consistent boll weight
Yield component	Seed-cotton yield per plant	AKH-9916 × RHC-0715	130.95	Highest stable seed-cotton yield
Yield component	Seed index	AKH-9916 × RHC-0712	11.86	Stable seed size
Yield component	Harvest index	NH-615 × RHC-577/3-3	41.31	Efficient biomass partitioning
Fibre quality	Lint index	NH-615 × AKH-09-5	5.48	Stable lint development
Fibre quality	Ginning outturn	NH-615 × RHC-577/3-3	35.49	Consistent lint recovery
Fibre quality	Upper-half mean length	NH-615 × RHC-0715	28.15	Stable fibre length
Fibre quality	Micronaire	AKH-8828 × RHC-0717	4.22	Stable fibre fineness and maturity

Abbreviations: DYSFL, days to 50% flowering; MDAYS, days to maturity; PHT, plant height; SPNO, sympodia per plant; BLNO, bolls per plant; BLWT, boll weight; SCYPL, seed-cotton yield per plant; SI, seed index; LI, lint index; HI, harvest index; GOT, ginning outturn; UHML, upper-half mean length; MIC, micronaire; UI, uniformity index; regression coefficient;, deviation from regression. *Significant at 5%; **significant at 1%.*

4. DISCUSSION

The difference is significant between parents and crosses which proved at three different centres (Aurangabad, Jalgaon and Akola) is indicative of the genetic variation which can be exploited for improvement of upland cotton. Seed-cotton yield and plant height were among the most variable traits and expression of flowering, maturity, boll traits and fibre properties were environmental dependent, suggesting a high environmental effect. Multi-environment studies (1,2) have also reported similar environmental effects on cotton yield and genotype ranking. The combining ability tests revealed that both additive and nonadditive types of gene effects occurred in the traits studied. As indicated by the higher contribution of lines to seed index, lint index, boll weight, fibre strength and seed-cotton yield, parents of favourable GCA effects may be able to help in selection based improvement. The large line × tester effect for flowering, maturity, plant height, sympodia and ginning outturn, on the contrary, highlights the importance of some line × tester combinations and the non-additive gene action. Such differences in terms of inheritance of cotton yield and fibre qualities have been reported earlier (4, 6). There was also a large amount of heterosis, which demonstrated the potential of hybrid breeding. The heterosis effect of AKH-8828 × RHC-0715 was positive for seed-cotton yield, negative for sympodia and boll weight, whereas NH-677 × AKH-09-5 showed positive heterosis for the yield of seed-cotton and sympodia and negative for boll weight. Dominance and complementary parental effects (12,14) are present, as seen with the high heterosis seen with the genetically contrasting crosses. Genotype × environment interaction was also shown by the change in mean performance, regression coefficients and deviations from regression. Some hybrids showed high regression deviations, indicating a lack of uniformity in their reactions to the environment, although they were high yielding. The cultivars, AKH-9916 × RHC-0715, NH-615 × RHC-577/3-3 proved beneficial for good plant architecture and fibre characteristics, and yielded a relatively consistent seed-cotton production. Multi-trait stability studies also highlight the need to trade off adaptability for productivity when choosing or developing genotype (3,18). Overall, the results align with the trait-specific parental selection, the intelligent use of heterosis and testing of hybrids at various locations for productivity, as well as the broad adaptation of upland cotton hybrids.

5. CONCLUSION

Results of multi-environment evaluation revealed high level of genetic differences among cotton parents and cotton hybrids for phenological, yield and fibre quality traits. Additive and non-additive genetic effects were involved in the inheritance of the traits and it was shown that some mating combinations were needed because of the significance of the line × tester interactions for some traits. High heterosis were observed for seed-cotton yield, bolls, boll weight, sympodia, lint index and seed index. The cross AKH-8828 × RHC-0715 gave superior heterosis for seed-cotton yield and NH-677 × AKH-09-5 was superior for boll weight and fruiting branches. Stability analysis results showed that stable expression across environments did not always occur when the mean expression was high. AKH-9916 × RHC-0715 was found to be the source of comparatively stable yield of seed-cotton, NH-615 × RHC-0715 and NH-615 × RHC-577/3-3 were found to be good sources for selected plant-architecture and fibre-quality traits respectively. Overall, the material analyzed in this paper for ability, heterosis and stability was useful for selecting the genetic material for environment adaptable improvement of upland cotton in general terms.

6. BREEDING IMPLICATIONS AND FUTURE DIRECTIONS

The identified parents and crosses are valuable genetic resources to be used in developing cultivars of Upland cotton that are productive and fibre superior, and also environmentally adaptable. There should be a recurrent-selection programme and also population improvement programme for parents in support of favourable general combining ability for building up favourable additive alleles. The crosses that showed strong Specific Combining Ability and heterosis, such as AKH-8828 × RHC-0715 and NH-677 × AKH-09-5 should be developed further for larger co-ordinated trials for hybrid development. The crosses AKH-9916 × RHC-0715, NH-615 × RHC-0715, and NH-615 × RHC-577/3-3 are stable crosses that warrant further testing at other locations, seasons, irrigation regimes, and stress factors. The AMMI, GGE-biplot, BLUP, WAASB and multi-trait stability indices will be beneficial in future studies in combination with Eberhart–Russell model. Genomic selection, Marker Assisted breeding, Environmental covariates and High throughput phenotyping can play a role in discovering genes for adaptability, heterosis, yield and fibre quality. Additionally, in commercial evaluation, pest resistance, input-use efficiency, seed production feasibility and economic performance should be considered.

DECLARATIONS

Ethics Approval: Formal ethical approval was not required because the study involved only field experimentation with upland cotton genotypes.

Consent to Participate: Not applicable.

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