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HETEROSIS AND COMBINING ABILITY FOR YIELD AND FIBRE QUALITY IN GMS-BASED BT HYBRIDS OF UPLAND COTTON ACROSS THREE ENVIRONMENTS

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ABSTRACT
Cotton hybrid breeding requires simultaneous exploitation of heterosis and informed parent choice. This study quantified heterosis, general combining ability (GCA), specific combining ability (SCA), and the associated gene-action pattern for yield, yield components, and fibre quality in a GMS-based Bt upland-cotton population. Forty F1 hybrids generated by crossing four GMS lines with ten Bt testers were evaluated with 14 parents and four standard checks in a randomized block design with two replications across three environments during *Kharif* 2025–26. Genotypic differences were significant for every studied trait in the pooled analysis. The cross mean for seed-cotton yield was 118.97 g plant−1, compared with 98.71 g for lines, 98.29 g for testers, and 125.86 g for checks. The leading hybrid, GNH-105A × NH22065Bt, yielded 169.57 g plant−1 and expressed 53.59% heterobeltiosis, 34.92% heterosis over NHH 44 BG II, and an SCA effect of 39.52. Other high-value combinations were GNH-101A × NH22160Bt and GNH-111A × NH22037Bt. Non-additive gene action predominated for seed-cotton yield, bolls plant−1, sympodia plant−1, boll weight, seed index, lint index, and uniformity ratio, whereas additive action predominated for flowering time, plant height, ginning outturn, UHML, fibre fineness, and fibre strength. GNH-105A was the strongest female general combiner for yield architecture; NH22037Bt was the strongest tester for yield and boll number; and GNH-101A, GNH-111A, and NH22158Bt contributed complementary fibre-quality effects. The results support a two-stage breeding strategy in which high-GCA parents are used to enrich breeding populations and high-SCA combinations are advanced for hybrid evaluation.

KEYWORDS: *Gossypium hirsutum*; GMS; Bt cotton; heterobeltiosis; line × tester; GCA; SCA; gene action; fibre quality

INTRODUCTION
Upland cotton (*Gossypium hirsutum* L.) supplies the majority of global cotton fibre and remains a major target for yield improvement, fibre-quality optimisation, and adaptation to variable production environments. In cotton, heterosis is expressed as superior F1 performance relative to parental material and commercial checks, particularly for boll number, boll weight, fruiting architecture, and yield. The biological basis of hybrid superiority can involve dominance, overdominance, epistasis, and complementary parental alleles; the practical breeding objective is therefore to identify repeatable and agronomically useful combinations rather than to maximize a single percentage estimate. Shull (1914) established the modern concept of heterosis, while the line × tester framework of Kempthorne (1957) provides a structured means of separating average parental performance from cross-specific deviation.

Combining ability is especially valuable in cotton because the relationship between yield and fibre quality is not always predictable from parental means alone. General combining ability measures the average breeding value of a parent across its crosses, whereas specific combining ability captures the exceptional performance of an individual cross beyond the parental average. In a 4 × 13 cotton line × tester population, Ahuja and Dhayal, 2007 reported significant GCA and SCA effects for most yield and fibre traits and emphasized the importance of non-additive inheritance for seed-cotton yield. Karademir et al., 2009 similarly demonstrated the utility of line × tester analysis for identifying heterotic combinations for yield and fibre quality. Fibre-quality heterosis and combining ability can be trait-specific, so fibre length, fineness, strength, and uniformity must be evaluated alongside yield rather than treated as secondary endpoints (Bolek et al., 2010). Recent Bt-cotton evidence also confirms that heterosis and combining ability can be integrated to identify hybrids with improved fibre yield and quality (Deshmukh et al., 2024).

The present study addresses this breeding problem using four GMS female lines and ten Bt testers evaluated across three environments. The objectives were to quantify pooled heterobeltiosis and standard heterosis, identify superior GCA parents and SCA crosses, and infer whether additive or non-additive gene action predominated for yield and fibre-quality traits. The analysis is intentionally restricted to heterosis and combining ability, excluding the thesis chapters on molecular diversity, stability, and sucking-pest relationships.

2. MATERIALS AND METHODS

2.1 Genetic material and field evaluation

The material comprised four GMS female lines (GNH-101A, GNH-105A, GNH-108A, and GNH-111A), ten Bt testers (NH22158Bt, NH22170Bt, NH22172Bt, NH22160Bt, NH22184Bt, NH22026Bt, NH22037Bt, NH22065Bt, NH22095Bt, and NH22107Bt), their 40 F1 crosses, and four standard checks (NHH 44 BG II, Jadoo BG II, NH 1901 Bt, and NH 1902 Bt). Crosses were produced during *Kharif* 2024–25 at the Cotton Research Station, Nanded, using sterile GMS plants as females and manual pollination with tester pollen. The complete set of 58 entries was evaluated during *Kharif* 2025–26 in a randomized block design with two replications at three environments: E1, Cotton Research Station, Mahboob Baugh Farm, Parbhani; E2, Cotton Research Station, Nanded; and E3, Agricultural Research Station, Somnathpur. Hybrids were planted at 120 × 45 cm and parents at 60 × 30 cm spacing in two-row plots of 2.4 × 6.0 m. The crop received 120:60:60 kg N:P:K ha−1.

2.2 Trait measurement

The study recorded days to 50% flowering, days to maturity, plant height, sympodia plant−1, bolls plant−1, boll weight, seed-cotton yield plant−1, seed index, lint index, ginning outturn, upper-half mean length (UHML), fibre fineness, fibre strength, and uniformity ratio. Five competitive plants were sampled for plant, yield, and fibre-related traits, while flowering and maturity were recorded on a plot basis. Fibre properties were measured using High Volume Instrument procedures. Negative values were treated as favourable for days to flowering, days to maturity, and fibre fineness; positive values were treated as favourable for the other traits.

2.3 Heterosis estimation

Heterobeltiosis and useful heterosis were calculated from treatment means for each environment and for the pooled analysis. For a hybrid mean F1, better-parent mean BP, and standard-check mean SC,
Heterobeltiosis (\%) = 100(F1 - BP)/BP
Useful\ heterosis (\%) = 100(F1 - SC)/SC.
Significance was tested using the thesis error mean square and the t statistic for the corresponding comparison. Directional desirability was defined a priori from the trait biology: negative heterosis for earliness and lower micronaire, and positive heterosis for yield, yield components, ginning outturn, UHML, strength, and uniformity. The estimates follow Fonseca and Patterson (1968) and Meredith and Bridge (1972).

2.4 Line × tester combining ability

Pooled combining-ability analysis followed the line × tester model of Kempthorne (1957) and the design-II framework of Comstock and Robinson (1952). The cross mean-square was partitioned into line, tester, and line × tester components. GCA variance was estimated from the covariance of half-sibs, and SCA variance from the line × tester component. The GCA/SCA ratio was used as the operational indicator of gene action: a ratio greater than 1 indicated predominance of additive effects, whereas a ratio below 1 indicated predominance of non-additive effects. Proportional contributions were calculated as the relevant sum of squares divided by the cross sum of squares × 100. Pooled GCA and SCA effects were estimated with the number of environments included in the divisor.

3. RESULTS

3.1 Genotypic differentiation and pooled performance

Pooled genotype mean squares were significant at $P \leq 0.01$ for all 14 traits, demonstrating sufficient phenotypic differentiation for heterosis and combining-ability inference. The pooled cross mean for seed-cotton yield was 118.97 g plant−1, exceeding the line mean by 20.5% and the tester mean by 21.0%, although it remained below the pooled mean of the four checks (125.86 g plant−1). Crosses exceeded both parental groups for bolls plant−1 (33.25 versus 15.49 in lines and 19.59 in testers) and sympodia plant−1 (18.22 versus 11.34 and 11.07, respectively). The mean cross value for fibre strength was 27.70 g tex−1, higher than the tester mean and checks but lower than the line mean, indicating that high yield and fibre strength were not automatically coupled at the population-mean level.

Table 1. Abstracted pooled performance means for selected traits.

Trait	Lines	Testers	F1 crosses	Checks
Seed cotton yield (g plant−1)	98.71	98.29	118.97	125.86
Bolls plant−1	15.49	19.59	33.25	28.35
Sympodia plant−1	11.34	11.07	18.22	20.16
Boll weight (g)	5.04	4.11	4.90	4.24
UHML (mm)	27.51	25.54	26.95	25.24
Fibre strength (g tex−1)	28.48	26.17	27.70	25.54

Table 2 condenses the pooled variance architecture. The line × tester interaction contributed most strongly to yield (63.22%), bolls plant−1 (59.33%), sympodia plant−1 (61.48%), seed index (57.05%), lint index (47.64%), and uniformity ratio (51.22%). Testers contributed most to ginning outturn (60.45%), UHML (46.82%), and fibre strength (60.50%), whereas lines contributed most to flowering time (46.50%), plant height (53.71%), and fibre fineness (33.59%).

Table 2. Abstracted variance partitioning and gene-action interpretation from pooled line × tester analysis.

Trait	Lines %	Testers %	L × T %	GCA/SCA	Largest source	Interpretation
Days to 50% flowering	46.50	18.00	35.48	1.37	Lines	Additive
Days to maturity	28.22	17.27	54.49	0.39	Line × tester	Non-additive
Plant height	53.71	17.22	29.06	2.01	Lines	Additive
Sympodia plant−1	8.10	30.41	61.48	0.17	Line × tester	Non-additive
Bolls plant−1	8.69	31.96	59.33	0.19	Line × tester	Non-additive
Boll weight	16.14	41.61	42.24	0.81	Line × tester	Non-additive
Seed cotton yield	6.39	30.37	63.22	0.11	Line × tester	Non-additive
Seed index	26.38	16.55	57.05	0.49	Line × tester	Non-additive
Lint index	17.69	34.66	47.64	0.62	Line × tester	Non-additive
Ginning outturn	5.92	60.45	33.61	2.86	Testers	Additive
UHML	25.88	46.82	27.28	2.47	Testers	Additive
Fibre fineness	33.59	39.79	26.61	3.02	Testers	Additive
Fibre strength	18.79	60.50	20.70	4.18	Testers	Additive
Uniformity ratio	35.52	13.25	51.22	0.57	Line × tester	Non-additive

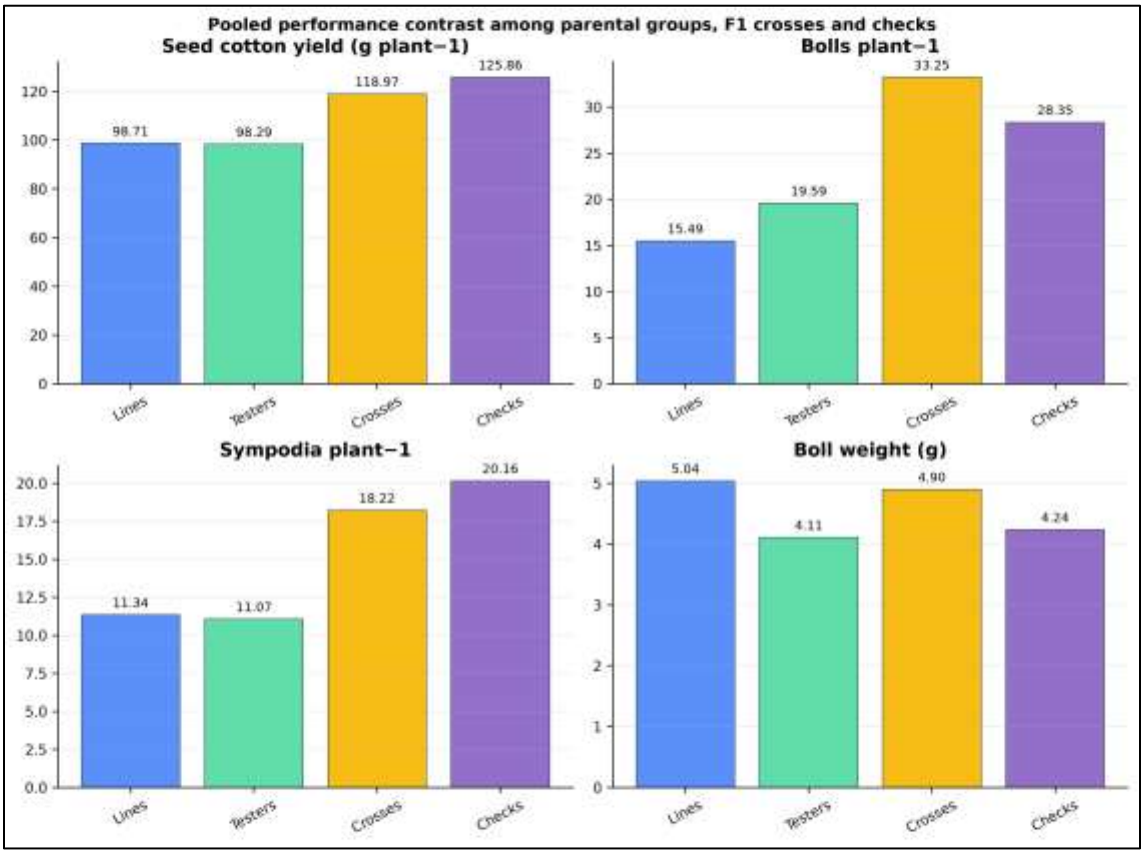

Figure 1. Pooled performance contrast among parental groups, F1 crosses, and checks for selected yield and fibre traits.

3.2 Heterosis for earliness and plant architecture

Earliness was expressed through negative heterosis. Heterobeltiosis for days to 50% flowering ranged from −15.88 to 14.18%, with 23 of 40 crosses favourable in the pooled analysis. GNH-101A × NH22065Bt was the strongest early-flowering combination (−15.88%), followed by GNH-108A × NH22065Bt (−14.31%). For days to maturity, 25 crosses showed favourable heterobeltiosis, and GNH-101A × NH22065Bt again ranked first (−12.32%). The same cross expressed −9.70% heterosis over NHH 44 BG II and −6.32% over NH 1901 Bt. Only GNH-101A × NH22158Bt expressed desirable positive heterobeltiosis for plant height (18.91%).

3.3 Heterosis for yield components and seed-cotton yield

Yield-component heterosis was strongest for bolls plant−1 and sympodia plant−1. Thirty-five crosses showed favourable heterobeltiosis for bolls plant−1, ranging from 3.10 to 158.74%; GNH-108A × NH22158Bt ranked first. GNH-105A × NH22065Bt was the most useful check-relative combination, with 71.53% over NHH 44 BG II, 95.43% over Jadoo BG II, 81.10% over NH 1901 Bt, and 79.10% over NH 1902 Bt. For sympodia plant−1, 28 crosses showed favourable heterobeltiosis, led by GNH-101A × NH22160Bt (131.82%). Only five crosses showed favourable heterobeltiosis for boll weight, led by GNH-111A × NH22172Bt (19.43%). Seed-cotton yield showed economically relevant heterosis: 20 crosses were significantly superior to their better parent, and GNH-105A × NH22065Bt recorded 169.57 g plant−1, 53.59% heterobeltiosis, 34.92% over NHH 44 BG II, 27.51% over Jadoo BG II, 37.23% over NH 1901 Bt, and 39.92% over NH 1902 Bt.

3.4 Heterosis for fibre quality

Fibre-quality heterosis was generally smaller and more trait-specific than yield-component heterosis. Ginning-outturn heterobeltiosis ranged from −15.69 to 7.67%, with four favourable crosses; GNH-111A × NH22037Bt ranked first. UHML heterobeltiosis ranged from −16.06 to 14.04%, and GNH-101A × NH22065Bt was the best better-parent combination. Lower fibre fineness was desirable; nine crosses showed favourable heterobeltiosis, led by GNH-101A × NH22158Bt (−36.51%). Fibre-strength heterobeltiosis was positive in seven crosses, led by GNH-101A × NH22172Bt (17.09%), while GNH-101A × NH22158Bt was most superior over NH 1902 Bt (48.96%). Uniformity-ratio heterobeltiosis was positive in eight crosses, led by GNH-108A × NH22170Bt (3.13%).

3.5 GCA effects and parental selection

GNH-105A was the best female general combiner for yield (7.62), bolls plant−1 (3.54), sympodia plant−1 (1.53), boll weight (0.24), and seed index (0.57). NH22037Bt showed the largest positive effects for seed-cotton yield (19.26), bolls plant−1 (7.79), sympodia plant−1 (2.63), and boll weight (0.34), followed by NH22026Bt for yield (12.12) and NH22095Bt for yield (6.68). GNH-101A combined earliness with positive UHML (1.06) and fibre strength (1.60); GNH-111A was positive for UHML (1.28), lint index (0.35), and uniformity ratio (1.23); and NH22158Bt was strong for UHML (4.63), strength (4.86), and fineness (−0.92), but negative for yield GCA.

3.6 SCA effects and superior cross combinations

Five crosses expressed significant positive SCA for seed-cotton yield. GNH-105A × NH22065Bt was strongest (39.52), followed by GNH-101A × NH22160Bt (36.31), GNH-111A × NH22037Bt (28.85), GNH-108A × NH22158Bt (24.34), and GNH-108A × NH22026Bt (12.88). For bolls plant−1, the corresponding leading SCA effects were 13.79, 12.14, and 11.78 for the first three combinations. For boll weight, GNH-108A × NH22158Bt (1.24), GNH-111A × NH22172Bt (0.66), and GNH-101A × NH22160Bt (0.65) were significant positive specific combiners. Four crosses were significant positive specific combiners for UHML, and only GNH-101A × NH22158Bt was significant positive for fibre strength (1.59). Five crosses were significant positive for uniformity ratio, led by GNH-101A × NH22160Bt (4.36).

3.7 Integrated interpretation of gene action

The GCA/SCA ratio classified flowering time, plant height, ginning outturn, UHML, fibre fineness, and fibre strength as predominantly additive, whereas maturity, sympodia plant−1, bolls plant−1, boll weight, seed-cotton yield, seed index, lint index, and uniformity ratio were predominantly non-additive. The principal implication is that additive traits can be improved through parent-based selection, while non-additive yield traits require preservation and testing of specific hybrid combinations.

Table 3. Abstracted heterosis counts and ranges for the better-parent and principal standard-check comparisons.

Trait	BPH range (%)	BPH n	NHH44 n	Jadoo n	NH1901 n	NH1902 n
Days to 50% flowering	−15.88 to 14.18	23	1	32	4	5
Days to maturity	−12.32 to 8.00	25	24	3	7	7
Plant height	−31.94 to 18.91	1	1	7	1	1
Sympodia plant−1	−2.44 to 131.82	28	3	8	3	4
Bolls plant−1	3.10 to 158.74	35	14	27	17	17
Boll weight	−26.50 to 19.43	5	33	0	33	34
Seed cotton yield	−10.24 to 53.59	20	9	3	8	10
Seed index	−17.53 to 35.30	10	2	0	2	0
Lint index	−42.69 to 30.80	7	7	0	6	0
Ginning outturn	−15.69 to 7.67	4	16	5	4	1
UHML	−16.06 to 14.04	6	16	6	8	22
Fibre fineness	−36.51 to 32.09	9	9	3	3	3
Fibre strength	−23.52 to 17.09	7	16	8	20	29
Uniformity ratio	−6.75 to 3.13	8	4	11	13	12

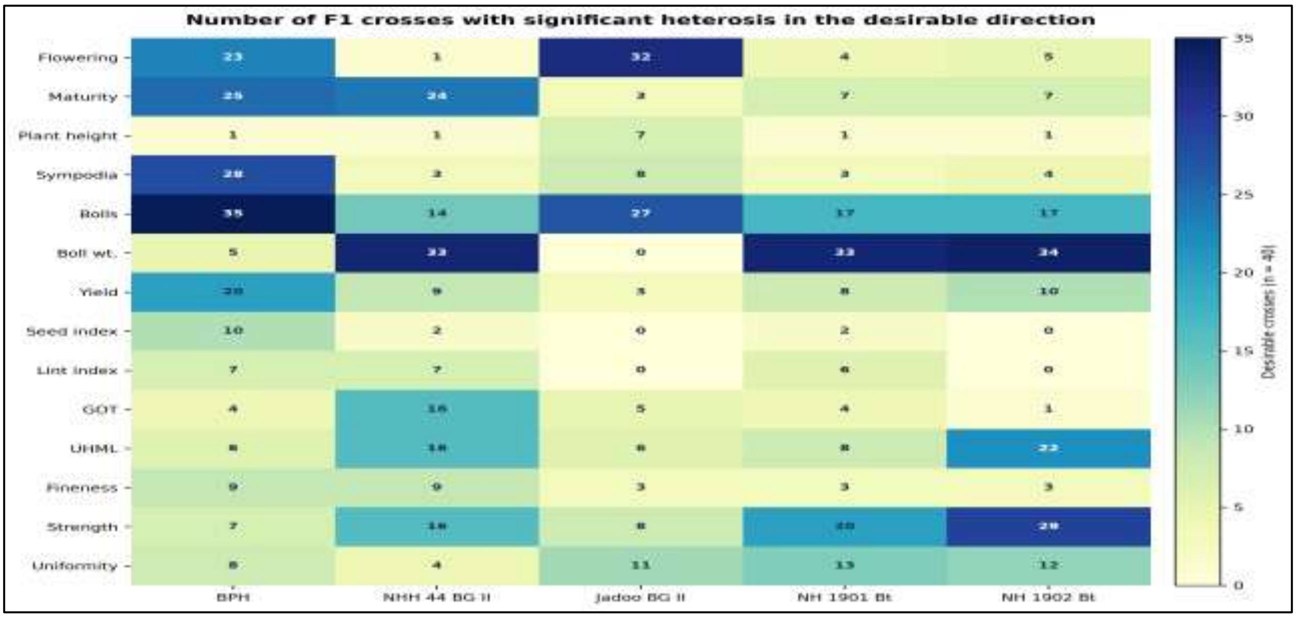

Figure 2. Desirable heterosis counts across better-parent and standard-check contrasts.

Table 4. Trait-indexed GCA sources and breeding interpretation.

Parent	Pooled GCA effects	Breeding interpretation
GNH-105A	Yield +7.62; bolls +3.54; sympodia +1.53; boll weight +0.24	High positive GCA for yield architecture
NH22037Bt	Yield +19.26; bolls +7.79; sympodia +2.63; boll weight +0.34	Strong tester for yield-component accumulation
NH22026Bt	Yield +12.12; bolls +5.22; sympodia +2.56; GOT +2.31	Broad yield and ginning-value combiner
NH22095Bt	Yield +6.68; bolls +2.79; sympodia +2.63; boll weight +0.39	Positive yield-component GCA; fibre-strength +0.58
GNH-101A	Early flowering −2.81; early maturity −3.01; UHML +1.06; strength +1.60	Earliness and fibre-strength source
GNH-111A	UHML +1.28; uniformity +1.23; lint index +0.35	Fibre-length and uniformity source
NH22158Bt	UHML +4.63; strength +4.86; fineness −0.92	Strong fibre-quality tester; poor yield GCA

Table 5. Leading candidate crosses integrating pooled performance, heterosis, and SCA.

Cross	Yield (g plant−1)	Yield BPH %	Yield vs NHH44 %	Bolls BPH %	SCA yield
GNH-105A × NH22065Bt	169.57	53.59	34.92	115.84	39.52
GNH-101A × NH22160Bt	160.27	53.09	27.52	113.16	36.31
GNH-111A × NH22037Bt	163.46	51.20	30.05	112.80	28.85
GNH-108A × NH22158Bt	129.99	34.62	3.43	158.74	24.34
GNH-101A × NH22158Bt	115.41	25.71	-8.17	153.49	5.69

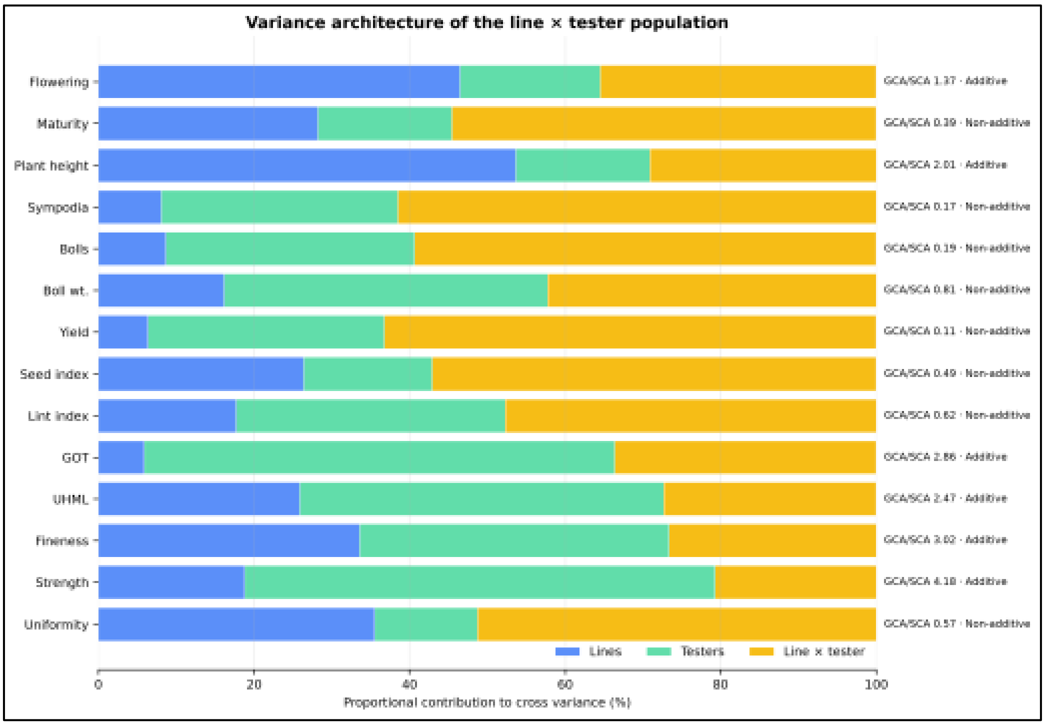

Figure 3. Proportional variance contributions and GCA/SCA interpretation.

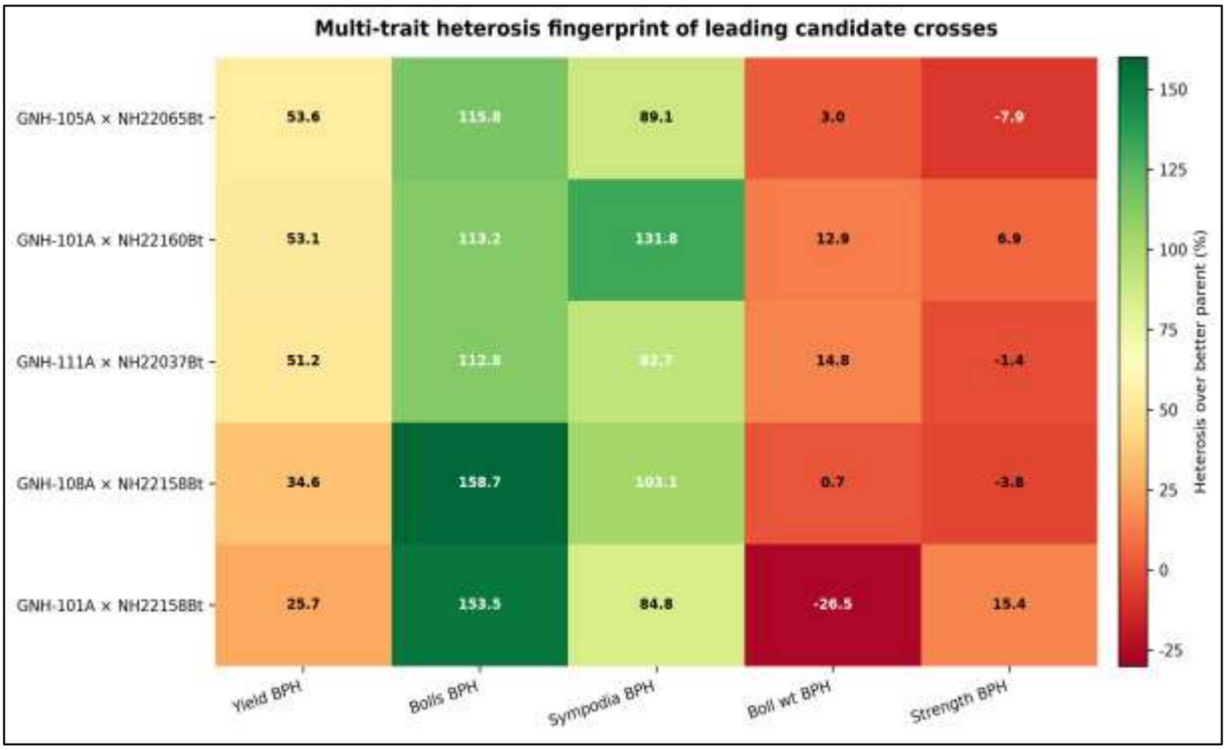

Figure 4. Multi-trait heterosis fingerprint of leading candidate crosses.

4. DISCUSSION

The central result is that heterosis was strongest for fruiting architecture and boll production, while the most valuable yield response occurred when high-SCA combinations were formed between parents with complementary GCA profiles. GNH-105A was a high-GCA female for yield architecture, and NH22065Bt formed the best cross with it, indicating that high parental GCA is useful but not sufficient to predict the top hybrid. Cross-specific non-additive effects must be measured directly.

GNH-105A × NH22065Bt combined high sympodial branching, the highest boll number, high seed-cotton yield, and positive heterosis across all four commercial checks. GNH-101A × NH22160Bt provided a complementary ideotype with high yield and boll number, strong sympodial heterosis, positive boll-weight heterosis, and favourable uniformity. GNH-111A × NH22037Bt was similarly attractive for yield and boll production and contributed positive ginning-outturn heterosis. These candidates should be advanced as a small, trait-indexed set rather than as a single universal winner.

Fibre-quality results place an important boundary on the interpretation of hybrid vigour. The cross with the largest yield heterosis was not the best for fibre strength, whereas GNH-101A × NH22158Bt combined moderate yield heterosis with strong UHML, fineness, and strength advantages but poor boll-weight performance. This trade-off supports a multi-trait selection index and is consistent with the trait-specific rankings reported by Ahuja and Dhayal, 2007, Karademir et al., 2009, and Bolek et al., 2010.

The pooled design represents average performance across the sampled environments, not universal adaptation. Stability was treated separately in the thesis and is outside the scope of this article. Future work should validate the leading crosses in larger multi-location trials, estimate realized hybrid-seed economics, and test whether the observed yield–fibre trade-offs remain under farmer-field conditions.

5. CONCLUSIONS

The 4 × 10 GMS-based Bt mating design generated substantial heterosis and exploitable combining-ability variation in upland cotton. The strongest commercial breeding candidate was GNH-105A × NH22065Bt, which combined 169.57 g $plant^{-1}$ seed-cotton yield, 53.59% heterobeltiosis, 34.92% heterosis over NHH 44 BG II, and the highest pooled SCA effect for yield (39.52). GNH-101A × NH22160Bt and GNH-111A × NH22037Bt were complementary high-yielding candidates. GNH-105A, NH22037Bt, NH22026Bt, NH22095Bt, GNH-101A, GNH-111A, and NH22158Bt were useful trait-specific GCA sources. Non-additive gene action predominated for the principal yield components, whereas additive effects were more important for several fibre-quality traits. The recommended breeding strategy is to use high-GCA parents to improve the population base, retain specific combinations with strong SCA for hybrid development, and apply a yield–fibre-quality index before advancement.

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