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COMPARATIVE EVALUATION OF YIELD, MORPHOLOGICAL TRAITS, AND FIBER QUALITY IN FOUR UPLAND COTTON (GOSSYPIUM HIRSUTUM L.) GENOTYPES

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Gossypium hirsutum; seed cotton yield; plant architecture; genotype evaluation; broad-sense heritability; fiber length; fiber strength; ginning outturn; selection criteria

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Abstract
Cotton improvement depends on identifying genotypes that combine high seed cotton yield, useful plant architecture, and desirable fiber quality. This study compared four upland cotton (Gossypium hirsutum L.) genotypes–42011 (MM-58 × 15006), 42027 (21018 × 21012), 42033 (IUB-13 × 21012), and 42034 (AR-3 × 15008) at The Islamia University of Bahawalpur, Pakistan. Genotype means, broad-sense heritability estimates, and trait-association information were consolidated to examine yield ranking, plant architecture, and fiber-quality contrasts. Genotype 42011 had the highest reported seed cotton yield (145.49 g plant $^{-1}$), boll number, monopodial branch number, ginning outturn, and fiber strength. Genotype 42027 had the greatest plant height and sympodial lengths at the third and sixth nodes, whereas genotype 42034 had the longest reported fiber length (30.13 mm), the highest sympodial branch count, but the lowest yield (79.75 g plant $^{-1}$). Descriptive calculations placed 42011 approximately 26.2% above the four-genotype mean yield and 82.4% above 42034. The reported heritability estimates and trait associations should be verified against the original data before publication. The findings provisionally identify 42011 as a candidate for further yield-oriented testing and 42034 as a possible source of longer fiber, subject to confirmation of the two-year experimental design, year-wise results, and multi-environment performance.

INTRODUCTION

Upland cotton (Gossypium hirsutum L.) is a major source of natural textile fiber and an important cash crop in many production systems. Cotton breeding must improve productivity while retaining fiber properties required by spinning and textile markets. Seed cotton yield is a complex quantitative character influenced by boll production, plant architecture, lint proportion, genetic background and environmental conditions. Consequently, selecting genotypes only based on yield in a single trial may overlook important trade-offs involving fiber length, fineness and strength (Tamboli et al., 2025a).

Genetic variability provides the raw material for selection, while heritability describes the proportion of phenotypic variance attributable to genetic differences in a defined population and environment. Broad-sense heritability includes

additive, dominance and epistatic genetic effects; therefore, it is not interchangeable with narrow-sense heritability and should not automatically be interpreted as a prediction of response to selection in sexually reproducing populations. Estimates are sensitive to the tested material, replication, environmental heterogeneity, measurement error, and the model used to partition variance (Scarpin et al., 2025; Bista et al., 2026).

Correlation analysis can identify traits that vary together and can help formulate hypotheses about indirect selection. However, correlation does not establish causation, and estimates from small samples or restricted genotype sets can be unstable. Published cotton studies have reported associations among yield, boll number, branching, plant height, and fiber properties, but the direction and magnitude of these relationships can vary with genetic material and environment (Polat et al., 2026a; Hussain et al., 2026; Yao et al., 2026). Trait associations should therefore be checked against the experimental unit and underlying observations.

The present study consolidates the thesis results into one integrated assessment of four cotton genotypes. The objectives were to: (i) compare the genotypes for seed cotton yield and key morphological and fiber traits; (ii) summarize the broad-sense heritability estimates reported in the thesis; (iii) interpret the contrasting trait profiles in a breeding context; and (iv) identify statistical and reporting issues that must be resolved before the findings are submitted to a journal (Dimitrova et al., 2026a; Shahzad et al., 2019).

Materials and Methods

Experimental site, material and design

The field experiment was conducted during the two study years of the cotton season at the experimental field of the Department of Plant Breeding and Genetics, Faculty of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur, Pakistan. Four upland cotton genotypes were evaluated in a randomized complete block design (RCBD) with three replications. The genotypes and parentage provided in the thesis are listed in Table 1. Seeds were dibbled at 30 cm within rows and 75 cm between rows. The thesis states that standard agronomic and crop-management practices were applied uniformly across the experiment.

Traits recorded

Five plants from each replication were sampled for trait measurements. Recorded traits included node of first fruiting branch, monopodial branches per plant, sympodial branches per plant, sympodial length at the third node, sympodial length at the sixth node, bolls per plant, plant height, flower petal spot, stem colour, ginning outturn, fiber length, fiber fineness, fiber strength and seed cotton yield per plant. Plant height was measured from the plant base to the top at maturity. Sympodial lengths were measured in centimetres; fiber length and strength were assessed using a high-volume instrument (HVI), according to the thesis. Ginning outturn was calculated as lint weight divided by seed cotton weight multiplied by 100.

Flower petal spot and stem colour were coded categorically in the thesis (petal spot present/absent and red/green stem). Because these are categorical traits represented by numeric codes, their means and variance-based statistics require special caution: arithmetic means of category codes do not have the same interpretation as means of continuous measurements. Before journal submission, the coding scheme and appropriate analysis for these traits should be explicitly justified.

Statistical analysis:

Statistical analysis was based on a randomized complete block design (RCBD), using analysis of variance (ANOVA), least significant difference (LSD) tests at the 5% significance level, and Pearson correlation coefficients estimated in Statistix 8.1. Broad-sense heritability was calculated as $H^2 = Vg/Vp$, with $Vg = (MSg - MSe)/r$ and $Vp = Vg + Ve/r$. Genotype means, a yield bar chart, and a standardized trait heat map were used to summarize the results. Because the raw plant-level data and complete statistical output were unavailable, the reported estimates remain provisional; inconsistencies in some variance components, heritability values, and correlation coefficients require verification before final publication.

Table 1. Genotypes and parentage

Genotypes	Parentages/Cross
42011	MM-58 × 15006
42027	21018 × 21012
42033	IUB-13 × 21012
42034	AR-3 × 15008

Results

Genotype means and yield ranking

The reported seed cotton yield ranking was 42011 > 42027 > 42033 > 42034. Genotype 42011 yielded 145.49 g plant^{-1}, approximately 10.6% more than 42027, 39.4% more than 42033, and 82.4% more than 42034, based on the reported means. The yield advantage of 42011 coincided with the highest reported boll number, monopodial branch number, ginning outturn, and fiber strength (Chapara et al., 2025) (Bilal et al., 2024). This combination makes it the strongest candidate for further yield-oriented evaluation in this four-entry trial, although it does not establish superiority across environments.

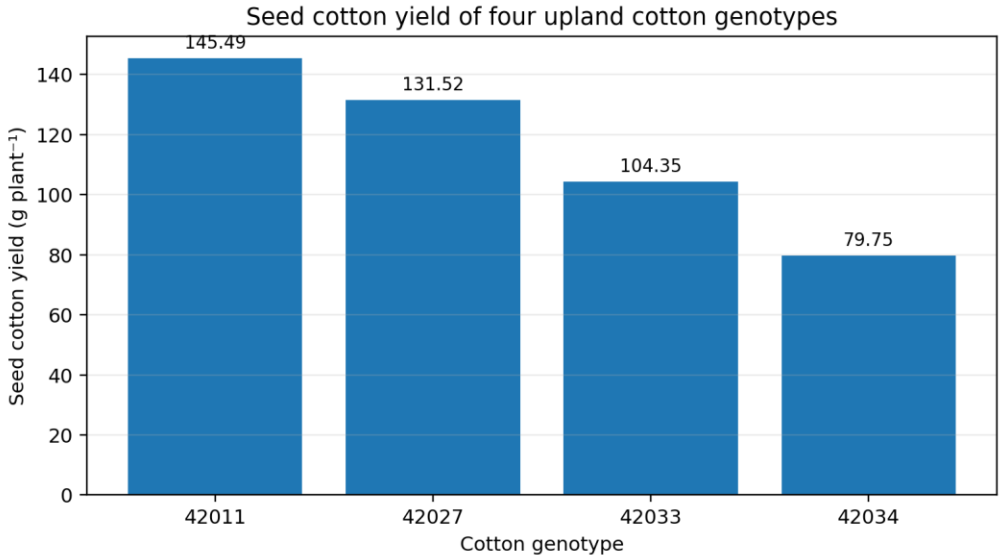


Figure 1. Seed cotton yield per plant for the four genotypes. Bars show means only; uncertainty intervals are not shown because replicate-level data were unavailable for recalculation.

Morphological and fiber trait profiles

Genotype 42027 was the tallest entry (181.79 cm) and had the longest sympodial structures at the third and sixth nodes (26.69 and 37.57 cm, respectively). Genotype 42034 had the highest reported sympodial branch number (31.18 plant^{-1}), closely followed by 42027 (30.94 plant^{-1}), but its seed cotton yield was the lowest (Makhmadjanov et al., 2023). This contrast indicates that a high count of a single architectural trait does not necessarily translate into the highest yield in this small set. Genotype 42011 had 28.09 sympodial branches

plant^{-1} and combined relatively high branching with the highest boll number and yield (Younas et al., 2025).

Fiber traits showed a different ranking from yield. Fiber length increased from 28.69 mm in 42011 to 30.13 mm in 42034 (Rani Chapara et al., 2022). In contrast, fiber strength was highest in 42011 (28.53 g tex^{-1}) and lowest in 42034 (23.72 g tex^{-1}). Ginning outturn was also highest in 42011 (41.14%) and lowest in 42034 (37.56%) (Gaikwad et al., 2025a). These contrasting profiles emphasize that the most suitable parent or candidate genotype depends on the breeding objective and the minimum fiber-quality standards of the intended market.

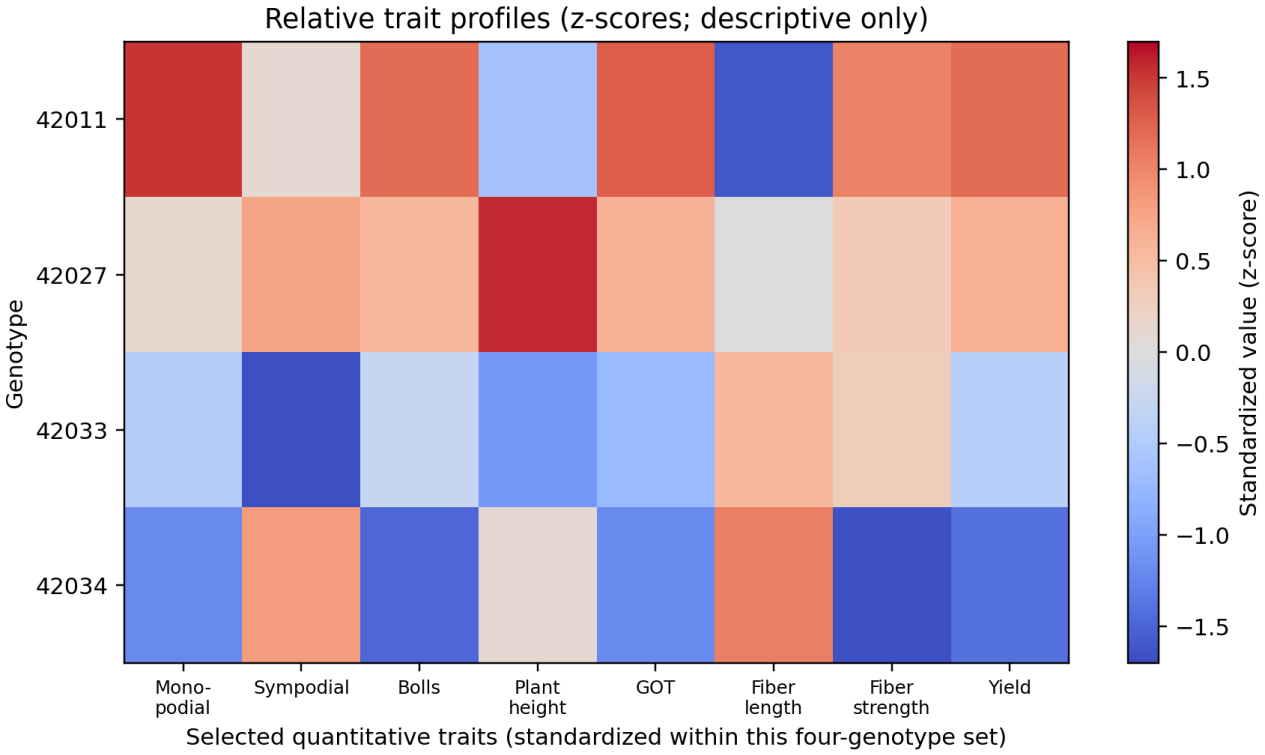


Figure 2. Standardized profile for selected quantitative traits. Z-scores are calculated across the four genotypes separately for each trait; red/blue shading indicates values above/below the four-genotype mean, not significance.

Table 2. **Genotype means for morphological, yield and fiber traits**

Trait	42011	42027	42033	42034
Node of first fruiting branch	5.543	5.387	4.567	4.533
Monopodial branches plant^{-1}	2.043	1.493	1.250	0.960
Sympodial branches plant^{-1}	28.093	30.940	20.537	31.180
Sympodial length at 3rd node (cm)	24.867	26.687	15.167	8.553
Sympodial length at 6th node (cm)	35.713	37.567	18.807	15.440
Bolls plant^{-1}	51.177	45.557	37.940	27.217

Plant height (cm)	135.360	181.790	125.460	150.540
Flower petal spot score[1]	2.000	2.000	1.837	1.827
Stem colour score[2]	1.077	1.000	1.220	1.000
Ginning outturn (%)	41.140	40.193	38.240	37.563
Fiber length (mm)	28.690	29.557	29.857	30.130
Fiber fineness (µg inch^{-1})	4.610	4.550	4.407	4.097
Fiber strength (g tex^{-1})	28.533	27.287	27.243	23.720
Seed cotton yield plant^{-1} (g)	145.490	131.520	104.350	79.750

Heritability estimates

The broad-sense heritability values ranged from 0.94 to 0.99. Values of 0.99 were reported for sympodial branch number, both sympodial lengths, plant height, fiber strength, and seed cotton yield; 0.98 was reported for monopodial branches, boll number, ginning outturn, and fiber fineness (JN et al., 2025a). The highest and lowest values are close together, so the estimates imply little differentiation in reported heritability among traits. However, the arithmetic inconsistencies in the variance table mean these estimates should not be presented as validated evidence until recalculated from the original mean squares and experimental design (Fernández-González & Isidro y Sánchez, 2025) (Naik et al., 2025).

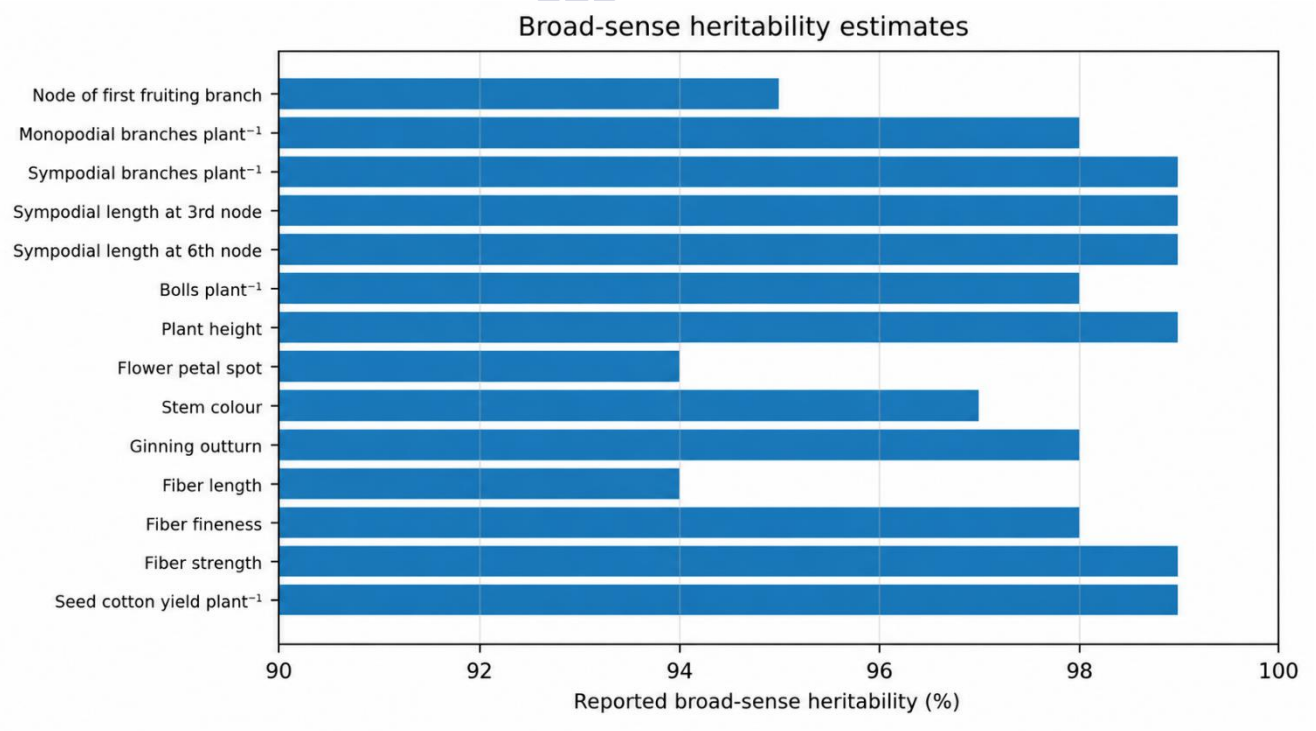


Figure 3. Broad-sense heritability estimates as reported in the thesis. These estimates are provisional and require recalculation because some variance components are internally inconsistent.

Table 3. Variance components and broad-sense heritability as reported

Trait	Genotypic Variance	Phenotypic Variance	Environmental Variance	H^2
Node of first fruiting branch	0.27	0.28	0.04	0.95 (95%)
Monopodial branches plant^{-1}	0.21	0.21	0.01	0.98 (98%)
Sympodial branches plant^{-1}	24.62	24.69	0.23	0.99 (99%)
Sympodial length at 3rd node	72.23	72.40	0.52	0.99 (99%)
Sympodial length at 6th node	129.30	129.43	0.40	0.99 (99%)
Bolls plant^{-1}	106.35	107.52	3.51	0.98 (98%)
Plant height	603.48	605.26	5.34	0.99 (99%)
Flower petal spot	0.01	0.01	0.00	0.94 (94%)
Stem colour	0.01	0.01	0.00	0.97 (97%)
Ginning outturn	2.75	2.77	0.09	0.98 (98%)
Fiber length	0.37	0.39	0.06	0.94 (94%)
Fiber fineness	0.05	0.05	0.00	0.98 (98%)
Fiber strength	4.29	4.29	0.01	0.99 (99%)
Seed cotton yield plant^{-1}	852.67	852.78	0.33	0.99 (99%)

Trait associations with yield

Additional descriptive comparison and selection priorities

A comparison of the reported means helps distinguish traits that co-occurred with high yield from traits that were maximized in different genotypes. Genotype 42011 yielded 145.49 g plant^{-1}, while the arithmetic mean of the four genotype yields was 115.28 g plant^{-1}. Thus, 42011 was approximately 26.2% above the four-genotype mean. Genotype 42027 was approximately 14.1% above the mean, whereas 42033 and 42034 were approximately 9.5% and 30.8% below it, respectively (Tamboli et al., 2025b) (Masood et al., 2026) (Dimitrova et al., 2026b). These are descriptive contrasts calculated from reported means and do not indicate statistical significance.

The yield range between the highest and lowest entries was 65.74 g plant^{-1}. Genotype 42011 produced approximately 82.4% more seed cotton per plant than 42034 ("Genetic Variability for Yield Related Traits in Some F1 Crosses of Upland Cotton," 2025). The same two genotypes differed in fiber length by 1.44 mm, with 42034 having the longer fiber, but 42011 exceeded 42034 in ginning outturn by 3.58 percentage points and fiber strength by 4.81 g tex^{-1} (Gaikwad et al., 2025b). This illustrates that genotype choice depends on the intended selection objective: 42011 appears more promising for yield and strength, whereas 42034 may be of interest as a source of longer fiber, subject to verification of fiber-test methods and statistical differences.

The trait profile also shows why a single plant-architecture measure should not be used as a substitute for yield. Genotype 42034 had the highest sympodial branch count (31.18 plant^{-1}), yet its boll number (27.22 plant^{-1}) and yield were lowest. Genotype 42011 had fewer sympodial branches than 42034 but the greatest reported boll number (51.18 plant^{-1}) and yield. A plausible breeding interpretation is that branch number alone does not reveal how many fruiting sites set and retain harvestable bolls. This explanation remains a hypothesis because boll retention, boll weight, fruiting efficiency, and plant-level covariation were not provided in the available data (Chang et al., 2025) (Ai et al., 2026).

The yield ordering broadly follows the boll-number ordering: 42011 ranked first, followed by 42027, 42033 and 42034 for both traits. That parallel ranking is consistent with boll number being a useful candidate trait for further evaluation. It does not, however, prove that boll number caused the

yield differences. The reported perfect correlation of 1.0000 must be recalculated from the original observations, and the analysis should account for the replicated design and the distinction between sampled plants and experimental plots.

A practical selection strategy would therefore use a staged, multi-trait approach. First, confirm that the yield advantage of 42011 is statistically supported by the original block-level analysis. Second, evaluate whether its fiber length meets the relevant end-use specification (Wang et al., 2026). Third, consider complementary crosses between a high-yield/high-strength entry and a longer-fiber entry only if the fiber-length advantage and other quality attributes are verified. Selection should ultimately be based on the target market's minimum fiber standards and replicated performance across environments rather than on a single trait maximum (Ribeiro et al., 2018).

Table 4. Descriptive contrasts calculated from the reported genotype means.

Descriptive indicator	Reported/derived value	Interpretation
Mean seed cotton yield across four genotypes	115.28 g plant^{-1}	Arithmetic mean of the four reported genotype means
42011 yield relative to four-genotype mean	+26.2%	Descriptive advantage; significance must be tested from original data
42027 yield relative to four-genotype mean	+14.1%	Above the descriptive mean
42033 yield relative to four-genotype mean	−9.5%	Below the descriptive mean
42034 yield relative to four-genotype mean	−30.8%	Lowest reported yield
Yield gap: 42011 versus 42034	65.74 g plant^{-1}; 82.4% higher for 42011	Largest contrast among the four entries
Fiber-length gap: 42034 versus 42011	1.44 mm	42034 had longer reported fiber
Fiber-strength gap: 42011 versus 42034	4.81 g tex^{-1}	42011 had greater reported fiber strength
Ginning-outturn gap: 42011 versus 42034	3.58 percentage points	42011 had the higher reported ginning outturn

Discussion

A yield-oriented candidate and the contribution of reproductive traits

Genotype 42011 ranked first for seed cotton yield and also had the highest reported boll number, monopodial branch number and ginning outturn. This alignment is biologically plausible because yield is the outcome of several linked components, including the number of fruiting sites that develop into harvestable bolls and the proportion of seed cotton converted to lint. Earlier cotton studies have frequently examined boll number, branch traits and plant architecture as potential contributors to yield (Subhashini et al., 2023) (ZHANG et al., 2020) (Wen et al., 2019). Nevertheless, the present experiment cannot establish which trait caused the observed yield ranking. Genotype means from four entries provide a useful initial comparison, but the contribution of individual traits should be tested using the verified plant-level data and a design-appropriate statistical model.

Plant architecture should be interpreted in context

Genotype 42027 was tallest and had the greatest sympodial lengths at the measured nodes, yet its yield was below that of 42011. Genotype 42034 had the highest sympodial branch count but the lowest yield (Madhu et al., 2026; Yan et al., 2019). These findings suggest that cotton selection should not

rely solely on plant height or branching traits, as yield also depends on boll retention, boll weight, and environmental conditions. Plant architecture influences canopy structure, light interception, and resource allocation, but excessive vegetative growth may reduce productivity under certain conditions. Further studies should include additional yield components, such as boll weight, fruit retention, and harvest index, to better explain yield differences. Mixed models and regression analysis using individual-plant data could help clarify these relationships while accounting for genotype and block effects.

Yield and fiber quality represent a multi-trait breeding objective

The trait profiles reveal a potential yield–quality contrast: 42011 had the highest yield, ginning outturn and fiber strength, whereas 42034 had the longest fiber but lower yield and fiber strength. This pattern is relevant to breeding because growers and processors require both adequate productivity and fiber properties suited to end use (Rasheed et al., 2020). The longest fiber should not automatically be considered the best overall quality outcome, just as the highest yield does not guarantee the best spinning performance. Fiber length, strength, fineness, and ginning outturn should be assessed together against target specifications (Smith et al., 2026).

Interpreting broad-sense heritability

The thesis-reported H^2 estimates of 0.94–0.99 are very high. In principle, high broad-sense heritability within a defined trial indicates that a large share of the observed phenotypic variance is associated with genetic differences among the tested entries. However, this interpretation depends on correctly estimated variance components and the assumed model. In a small, single-location experiment, environmental variation may be underestimated, and a restricted set of entries may produce estimates that do not generalize to a wider breeding population. Broad-sense heritability also includes non-additive genetic effects, so it does not directly quantify the expected response to selection based on additive genetic variance (Bazaliy & Larchenko, 2026; JN et al., 2025b).

Correlation findings require reanalysis

Trait correlations can support indirect selection when associations are consistent and the correlated trait is easier to measure than yield. However, a perfect boll-number–yield correlation requires verification, as it may result from data construction, limited observations, or transcription errors. Correlations should be recalculated from original paired observations, accounting for replication, sample size, confidence intervals, and potential dependence among variables. Until verified, these results should be interpreted cautiously, and boll number should not be claimed to determine yield alone(Polat et al., 2026b).

Conclusion

Across the four upland cotton genotypes evaluated in the two-year trial, genotype 42011 had the highest reported seed cotton yield (145.49 g $plant^{-1}$), boll number, monopodial branch number, ginning outturn, and fiber strength. Genotype 42027 was tallest and had the greatest sympodial lengths at the third and sixth nodes, while genotype 42034 had the longest fiber and highest sympodial branch count but the lowest yield. These contrasting profiles suggest that selection should consider the combined breeding objective rather than a single trait. The thesis-reported broad-sense heritability estimates were high, but they require recalculation because some variance components are inconsistent. Likewise, the reported perfect correlations between boll number and yield must be checked using raw observations. Genotype 42011 can be prioritized for further yield-focused testing, and the fiber-length profile of 42034 may be useful in parent selection if confirmed. Multi-environment validation and transparent reanalysis are essential before strong conclusions are made.

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