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Heritability, Genetic Advance, and Correlation of Agro-Morphological Traits in Interspecific Simple and Complex Cotton Hybrids

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Abstract This study evaluated phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficients of variation, broad-sense heritability (h^2), and expected genetic gain (GG, GG%) for agro-morphological traits, as well as inter-trait correlations, in interspecific F_1 complex and F_4 simple cotton hybrid populations derived from designated parental forms. Field phenotyping was conducted in a randomized complete block design (RCBD) with three replications for the following traits: boll weight, staple length, lint percentage, 1000-seed weight, main-stem height, number of fruiting branches, number of bolls per plant, and number of open bolls per plant. In the F_1 complex hybrids, GCV approximated PCV and h^2 was high for most traits; notably, the numbers of open bolls and total bolls per plant showed large GG%, confirming their capacity to deliver rapid, reliable selection responses at early generations. Boll weight in F_1 also exhibited high h^2 with appreciable GG%, indicating expanded early-stage potential. Conversely, negative associations of fruiting-branch number with certain yield and quality components underscore the need to regulate plant architecture. Staple length and lint percentage displayed stable inheritance in F1 under low ECV. In F_4 simple hybrids, boll weight was environmentally sensitive (large PCV–GCV, low h^2) and thus required multi-location confirmation; however, positive linkages among open bolls, total bolls, and lint percentage remained strong.

Keywords Cotton (Gossypium spp.), F1 complex hybrid, F4 simple hybrid, PCV–GCV–ECV, Heritability (h^2), Genetic gain (GG, GG%), Number of open bolls per plant

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1. Introduction

Cotton (*Gossypium* spp.) is one of the cornerstone crops of national agriculture and the textile industry; achieving sustained gains in yield and fiber quality remains a primary goal of breeding programs. Under conditions of increasing climate stress, water scarcity, and agronomic heterogeneity, it is essential to broaden genetic variation and to evaluate it rigorously using quantitative-genetic metrics in order to identify high-performing genotypes that are stable across environments [5]. In this context, the phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficients of variation, broad-sense heritability (h^2), and expected genetic gain (GG, GG%) are key diagnostic parameters: the PCV–GCV gap reflects the enviromental share of variation, whereas h^2 indicates the potential genetic response to selection [2], [9], [1].

Interspecific F1 complex and F4 simple hybrid populations derived from designated parents provide a convenient model for revealing genetic architecture and dispersion. At the F1 stage, GCV typically approximates PCV and h^2 is high, enabling rapid and reliable early-generation selection; at the F4 stage, recombinational dispersion broadens, transgressive segregants may emerge, and evaluating G×E effects becomes more important [1], [3]. In cotton, yield-proximal traits—bolls per plant and open bolls per plant—usually show high h^2 and large GG%, while lint percentage and staple length tend to inherit stably under low ECV, allowing early quality control [12], [21]. By contrast, mass-related traits such as single-boll seed-cotton weight are often environmentally sensitive and therefore require decisions based on multi-location, replicated testing [3]. Accordingly, the objective of this study is to perform a systematic assessment of PCV, GCV, ECV, h^2, and GG (GG%) for major agro-morphological traits in F1 (complex) and F4 (simple) hybrid populations, and to characterize the intertrait correlation structure with the aim of identifying genotypes suitable for effective selection.

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2. Materials and Methods

Experimental site, period, and agronomic management

Field experiments were conducted during 2021–2024 at the regional experimental field of the Institute of Genetics and Plant Experimental Biology, Academy of Sciences of Uzbekistan, located in Zangiota district, Tashkent region. The experimental site is situated approximately 0.5 km northeast of Tashkent city at 41°20′ N latitude, 69°18′ E longitude, along the upper terrace of the Chirchiq River, at an altitude of 398 m above sea level.

The soil of the experimental field is classified as typical light gray soil, characterized by low humus content and a medium loamy texture. The terrain is slightly sloped, non-saline, with weak natural infestation by Verticillium wilt, and with deep groundwater levels (7–8 m). The climate of the region is sharply continental, featuring hot summers (June–August), cold winters (especially December–January), 175–185 sunny days, and a frost-free period of 200–210 days. Precipitation mainly occurs in autumn, winter, and spring, whereas summers are dry, necessitating supplementary irrigation for cotton cultivation.

All agronomic practices were carried out according to the standard management protocols adopted at the Institute's experimental farm. In autumn, fields were cleared of cotton residues and deep-plowed to a depth of 35 cm. In early spring, harrowing was performed to conserve soil moisture and suppress early weed emergence. Sowing was conducted in the third decade of April using a 90 × 20 × 1 cm planting scheme, with seeds placed at a depth of 4–5 cm. Inter-row cultivation, weed control, and irrigation were applied in an integrated manner throughout the growing season. Pest control included the application of GXSG against cotton bollworm and BI-58 against aphids at a rate of 2.0–2.5 kg per ton of water.

Table 1. List of *Gossypium* L. species and derived F_1–F_4 hybrids included in the experiment (Origin)

№	*Gossypium L* species	Origin
1	*G.mustelinum* Miers ex Watt	Brasil
2	*G.hirsutum L. subsp. Paniculatum*	Mexico
3	*G.barbadense* ssp. *eubarbadense* "Surxon-9"	Uzbekistan
4	Ssp. *euhirsutum* "Beshqahramon"	Uzbekistan
5	F4 Surxon-9 × *G.mustelinum*	Uzbekistan
6	F4 *Paniculatum* × *G.mustelinum*	Uzbekistan
7	F4 *G.mustelinum* × Surxon-9	Uzbekistan
8	F4 Beshqahramon × *G.mustelinum*	Uzbekistan
9	F4 *G.mustelinum* × Beshqahramon	Uzbekistan
10	F1 (Surxon-9 × *G.mustelinum*) × (*Paniculatum* × *G.mustelinum*)	Uzbekistan
11	F1 (*G.mustelinum* × Surxon-9) × (Beshqahramon × *G.mustelinum*)	Uzbekistan
12	F1 (Beshqahramon × *G.mustelinum*) × (Surxon-9 × *G.mustelinum*)	Uzbekistan
13	F1 (*G.mustelinum* × Beshqahramon) × (*Paniculatum* × *G.mustelinum*)	Uzbekistan

Experimental design and sampling

The experiment was arranged in a randomized complete block design (RCBD) with three replications. For each genotype and hybrid combination, 30 plants were evaluated in total, consisting of 10 plants per replication, selected randomly for phenotypic assessment. Both F1 complex hybrids and F4 simple hybrids, together with their parental forms, were evaluated under identical field conditions.

All quantitative data were subjected to analysis of variance (ANOVA) using the ANOVA statistical software. Phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficients of variation, broad-sense heritability (h^2), and expected genetic gain (GG, GG%) were estimated using standard quantitative-genetic formulas. Trait correlations were calculated using Pearson's correlation coefficient, and the significance of differences was tested at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$.

Measured Traits and Phenotyping

- Single-boll seed-cotton weight (g): mass of clean seed cotton from an opened boll;
- Staple length (mm): determined according to standard GOST/ASTM protocols;
- Fiber yield (%) – lint % = (lint mass / raw cotton mass) ×100;
- 1000-seed weight (g): measured on dried seeds using a laboratory balance;
- Main stem height (cm): from soil surface to the apical growth point;
- Number of fruiting branches (no.): recorded at the end of the vegetative period;
- Number of bolls per plant (no.);
- Number of open bolls per plant (no.).

In the interspecific complex hybrids belonging to the genus *Gossypium* L and differing in genetic origin, we determined agro-morphological and genetic parameters, including phenotypic, genotypic, and environmental coefficients of variation, the broad-sense heritability, and the genetic gain (efficiency) for the studied traits.

Analysis of dispersion of cotton varieties and hybrids [8], [18] was carried out. In this case, the reliability of differences between genotypes for each trait was determined by Fisher's exact test (F), the standard error of the experiment (SD), the standard deviation of the mean (SE) and the least significant difference ($P \leq 0.05$*, $P \leq 0.01$** and $P \leq 0.001$ ***).

The coefficients of phenotypic, genotypic and environmental variances were estimated [2] and the genetic variance was determined based on them.

Genotypic coefficient of variance (GCV) = $\sqrt{V_g}/GM \times 100$

Phenotypic variance coefficient (PCV) = $\sqrt{V_p}/GM \times 100$

Coefficient of variance of the environment (ECV) = $\sqrt{V_e}/GM \times 100$

Where:

Vg = genotypic variance

Vp = phenotypic variance

Ve = environmental variance

GM = mean trait index

The heritability of a trait over a wide range of generations (h2) was determined using this formula.

$$(h^2) = Vg/Vp$$

Where:

h2 = broad heritability

VP = phenotypic variance

Vg = genotypic variance

The level of genetic potential (efficiency) was determined according to the H. W. Johnson formula (for each trait) [9].

$$GG = k.\ h^2\ \sqrt{Vp}.$$

The percentage of genetic potential (efficiency) was determined based on the following formula:

$$GG = GG/GM \times 100$$

Here:

When k = 1.40, the selection activity of the trait in 20%

GG = genetic effect or genetic potential

The correlation coefficient between the traits was determined [20]. Here, when $r < 0.3$, the correlation between the traits is weak, when $r = 0.3\text{-}0.7$, it is moderate, and when $r > 0.7$, it is strong.

3. Results

The genotypic, phenotypic, and environmental coefficients of variation for the studied traits in the parental varieties and their F_4 simple and F_1 complex hybrids are presented in Tables 2–3. In the parental forms and interspecific F_4 simple hybrids, the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) ranged from 5.6% to 26.78% and from 6.15% to 99.49%, respectively.

In the parental forms and interspecific F_4 simple hybrids, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were as follows: for single-boll seed-cotton weight, GCV = 26.78% and PCV = 99.49%; for the number of open bolls per plant, GCV = 22.94% and PCV = 23.87%; and for the number of bolls per plant, GCV = 18.95% and PCV = 19.91%. For the number of fruiting branches, GCV = 9.20% and PCV = 11.25%; and for main stem height, GCV = 10.21% and PCV = 10.68%. For lint percentage, GCV = 10.33% and PCV = 10.60%, while for staple length they were 5.60% and 6.15%, respectively.

Genetic variability and expected response to selection (parental forms + F4 simple interspecific hybrids). Estimates of phenotypic (PCV), genotypic (GCV), and environmental (ECV) variation, together with broad-sense heritability (h^2) and expected genetic gain (GG, GG%), revealed clear contrasts among traits. Fiber-quality attributes were under strong genetic control: staple length (PCV ≈ GCV; ECV low; $h^2 = 0.91$; GG% = 10.51) and lint percentage (PCV ≈ GCV; ECV very low; $h^2 = 0.97$; GG% = 20.75) showed stable inheritance and are amenable to reliable improvement via early-generation selection. Among yield-contributing components, bolls per plant ($h^2 = 0.95$; GG% = 37.22) and especially open bolls per plant ($h^2 = 0.96$; GG% = 45.49) exhibited the largest expected gains, underscoring their utility as primary selection criteria for elevating seed-cotton yield. Main stem height also displayed high genetic determinism ($h^2 = 0.96$; GG% = 20.13), supporting selection for desirable plant stature alongside reproductive capacity. 1000-seed weight combined high heritability (0.94) with moderate gain (GG% = 15.79), indicating comparatively stable expression with incremental improvement potential. In contrast, single-boll seed-cotton weight was markedly environment-sensitive (very large PCV–GCV gap; ECV extremely high; $h^2 = 0.27$; GG% = 14.87), for which multi-environment validation and delayed selection are warranted to avoid confounding by site-year effects. Number of fruiting branches presented high heritability (0.82) but relatively higher ECV, suggesting that architectural optimization should proceed cautiously and in tandem with direct yield components to prevent unfavorable trade-offs.

Overall, in the F_4 simple interspecific population, many yield-proximal traits showed GCV ≈ PCV, high h^2, and substantial GG%. The numbers of open bolls and total bolls per plant emerged as the most effective criteria for accelerating selection. Lint percentage and staple length serve as stable, quality-ensuring filter traits, whereas single-boll seed-cotton weight is environmentally sensitive and should be incorporated into selection decisions only at later stages after multi-environment testing. In the interspecific F_1 complex hybrids, the ranges of GCV and PCV were 5.18%–17.87% and 5.75%–20.66%, respectively.

In the parental lines and interspecific F_1 complex and F_4 simple hybrids, the genotypic (GCV), phenotypic (PCV), and environmental (ECV) coefficients of variation, together with broad-sense heritability (h^2) and expected genetic gain (GG, GG%), are summarized in Tables 2–3.

For the F_1 complex hybrids, the GCV and PCV values were: single-boll seed-cotton weight 17.87–20.66%; open bolls per plant GCV = 17.27% and PCV = 18.16%; bolls per plant 14.94–15.91%; fruiting branches GCV = 5.11%, PCV = 8.40%; main stem height GCV = 9.35%, PCV = 10.50%; lint percentage GCV = 8.49%, PCV = 8.69%; and staple length GCV = 5.18%, PCV = 5.75%. The proximity of GCV to PCV for most traits and the generally low–moderate ECV indicate that much of the phenotypic variance is attributable to genotypic effects. Accordingly, h^2 was high for most traits and GG% was appreciable.

Among yield-proximal traits, open bolls per plant ($h^2 = 0.95$; GG% = 33.88) and bolls per plant ($h^2 = 0.94$; GG% = 28.95) showed the highest expected genetic gains. Single-boll seed-cotton weight in F1 also exhibited a strong selection signal ($h^2 = 0.86$; GG% = 31.88). Quality traits were under stable genetic control: lint percentage ($h^2 = 0.98$; GG% = 17.12) and staple length ($h^2 = 0.90$; GG% = 9.64). The closeness of PCV and GCV—particularly for lint percentage, 1000-seed weight, bolls per plant, open bolls per plant, and staple length—implies a relatively small environmental share, enabling efficient selection already at the F1 stage ($h^2 \approx 0.89\text{–}0.98$). In practice, the yield-proximal traits (open bolls and total bolls per plant) can form the core of early selection.

Table 2. Genotypic, phenotypic, and environmental coefficients of variation, broad-sense heritability, and genetic gain for agro-morphological traits in parental forms and interspecific F_4 simple cotton hybrids

Morphological and economic characteristics of parental forms and interspecific F4 simple hybrid plants	PCV (%)	GCV (%)	ECV (%)	h^2	GG	GG (%)
Cotton weight per boll (g)	99,5	26,8	95,8	0,3	0,6	14,9
Fiber staple length (mm)	6,1	5,6	2,7	0,9	3,4	10,5
Fiber yield (%)	10,6	10,3	2,0	0,9	6,7	20,7
1000 seed weight (g)	8,6	8,1	2,9	0,9	16,7	15,8
Head stem height (cm)	10,7	10,2	3,1	0,9	18,0	20,1
Number of yielding branches (pcs)	11,2	9,2	6,5	0,8	2,8	15,5
Number of bolls per plant (pcs)	19,9	18,9	6,1	0,9	8,5	37,2
Number of opened bolls per plant (pcs)	23,9	22,9	6,6	0,9	7,2	45,5

Table 3. Genotypic, phenotypic, and environmental coefficients of variation, broad-sense heritability, and genetic gain for agro-morphological traits in parental forms and interspecific F_1 complex cotton hybrids

Morphological and economic characteristics of parental forms and interspecific F1 complex hybrid plants	PCV (%)	GCV (%)	ECV (%)	h^2	GG	GG (%)
Cotton weight per boll (g)	20,7	17,9	10,4	0,9	1,5	31,9
Fiber staple length (mm)	5,7	5,2	2,5	0,9	3,1	9,6
Fiber yield (%)	8,7	8,5	1,8	0,9	6,0	17,1
1000 seed weight (g)	10,8	10,2	3,3	0,9	21,1	20,1
Head stem height (cm)	10,5	9,3	4,8	0,9	16,8	17,2
Number of yielding branches (pcs)	8,4	5,1	6,7	0,6	1,0	6,4
Number of bolls per plant (pcs)	15,9	14,9	5,5	0,9	6,4	28,9
Number of opened bolls per plant (pcs)	18,2	17,3	5,6	0,9	5,9	33,9

While single-boll weight appears more stable in F1 (h^2= 0.86; GG% = 31.88) than in F4, confirmation across locations and years remains advisable. For fruiting branches, $h^2$was lower (0.61) and ECV higher (6.66%), so architectural decisions should be made cautiously.

Literature aligns with these patterns: higher genetic variance underpins successful selection for economic traits [19] whereas strong environmental effects depress genetic variance [11]. The low GCV/PCV observed for staple length suggests the need to source broader genetic variability for further improvement. In medium-staple cotton, moderate GCV/PCV for boll weight supports gains in yield and its components via selection [16].

Across parental lines and their F_4 simple and F_1 complex hybrids, the environmental coefficient of variation (ECV) ranged from 2.04% to 95.84% (F4 and parents) and from 1.85% to 10.37% (F_1). The highest ECV values were recorded for single-boll weight (95.81% in F_4; 10.37% in F_1), followed by open bolls per plant (6.59% and 5.61%, respectively; see Tables 2–3), confirming strong environmental sensitivity of these traits.

Moderate to high GCV/PCV in early generations is widely recommended to facilitate selection for yield and its components [13]. Consequently, heritability coupled with high genetic advance is critical for improving yield-related traits in medium-staple cotton [6], especially when PCV ≈ GCV, signaling limited environmental interference. In our study, $h^2$was high for staple length, lint percentage, 1000-seed weight, main stem height, bolls per plant, and open bolls per plant (Tables 2–3), whereas single-boll weight and fruiting branches showed lower h^2. Similar magnitudes of broad-sense heritability for yield and its components have been reported in medium-staple cotton [15]. Large genetic variance for yield-related traits can drive effective improvement when gene action is favorable [17], [4]. Here, open bolls per plant combined high h^2 with high GG%, indicating predominance of additive effects and strong transmissibility.

Where heritability is driven mainly by non-additive effects, genetic advance tends to be low; with stronger additive effects, genetic advance is higher [7], [10]. Traits showing both high $h^2$and high GG% are therefore prime targets for selection and are typically less environment-sensitive due to a larger additive component [14]. In our material, genetic gain spanned 10.51–45.49% (parents + F4) and 6.42–33.88% (F_1), with the highest values for open bolls per plant (45.49% and 33.88%, respectively; Tables 2–3).

Correlation analysis revealed, in parents and F4 simple hybrids, a moderate positive association between staple length and 1000-seed weight (r = 0.65*). Bolls per plant correlated moderately/strongly and positively with lint percentage (r = 0.68*) and main stem height (r = 0.79*). Open bolls per plant correlated strongly and positively with lint percentage (r = 0.84**), main stem height (r = 0.79*), and bolls per plant (r = 0.94***; see Table 3).

Table 4. Correlations for agro-morphological characters in cotton: F_4 simple hybrids (upper triangle) and F_1 complex hybrids (lower triangle), both including parental forms

Morphological and economic characteristics of cotton genotypes	Cotton weight per boll	Fiber staple length	Fiber yield	1000 seed weight	Head stem height	Number of yielding branches	Number of bolls per plant	Number of opened bolls per plant
Cotton weight per boll		-0,21	0,77	0,15	0,47	-0,26	0,53	0,62
Fiber staple length	0,36		0,01	0,65*	0,19	0,36	0,11	0,17
Fiber yield	0,55	0,29		0,003	0,53	-0,09	0,68*	0,84**
1000 seed weight	0,51	0,61*	0,03		-0,02	0,14	0,05	0,02
Head stem height	0,39	0,74	0,50	0,23		0,57	0,79*	0,79*
Number of yielding branches	-0,77*	-0,20	-0,64*	-0,28	-0,19		0,35	0,21
Number of bolls per plant	0,16	-0,32	0,24	-0,19	0,15	0,22		0,94***
Number of opened bolls per plant	0,55	0,06	0,68*	-0,14	0,60*	-0,29	0,74*	

Note: Significant differences at $P \leq 0.05$ (*), $P \leq 0.01$ (**), and $P \leq 0.001$ (***).

In the parents and F1 complex hybrids, fruiting branches showed moderate to strong negative correlations with single -boll weight (r = −0.77*) and lint percentage (r = −0.64*). Conversely, open bolls per plant correlated moderately to strongly and positively with lint percentage (r = 0.68*), main stem height (r = 0.60*), and bolls per plant (r = 0.74*). A moderate positive correlation was also observed between staple length and 1000-seed weight (r = 0.61*). Notably, in F_1 complex hybrids the negative correlations of fruiting branches with single-boll weight and lint percentage were stronger and statistically significant compared with F4 simple hybrids.

These F_1-stage trade-offs (especially the negative links between branching and both boll mass and lint percentage) suggest that indiscriminately increasing branching may penalize yield and quality. Thus, at early generations a "fewer, more efficient branches" architecture is preferable. At the F_4 stage, the positive "cluster" among yield components accelerates the selection response: open bolls per plant tends to drive overall yield and aligns positively with lint percentage. Positive links involving plant height may support boll setting but should be balanced against agronomic risks (e.g., lodging). Within the quality block, the positive association between staple length and 1000-seed weight indicates the possibility of maintaining quality while sustaining favorable biometric attributes. Overall, F_1 requires a cautious balance between architecture and yield/quality, whereas in F_4 the positive clustering of yield components speeds selection and enables yield improvement while maintaining fiber quality.

4. Discussion

This study compared variation and inheritance parameters for key agro-morphological traits in parental forms and interspecific F_1 complex and F_4 simple hybrid populations. At the F_1 stage, most traits exhibited GCV ≈ PCV with low–moderate ECV and high h^2, indicating that a large share of phenotypic variance is genotypic and that early-generation selection can be both rapid and reliable. By contrast, in the F_4 population single-boll seed-cotton weight showed very high ECV (≈95%) and low h^2, revealing strong environmental sensitivity and arguing for decisions based on later-stage, multi-location testing. In sharp contrast to boll mass, traits such as lint percentage, staple length, 1000-seed weight, main-stem height, bolls per plant, and especially open bolls per plant combined high h^2 with small PCV–GCV gaps and appreciable GG%, marking them as priorities for early selection.

These patterns are consistent with classical quantitative-genetic principles: PCV reflects total (phenotypic) dispersion whereas GCV isolates the genotypic component; thus a small PCV–GCV gap implies a limited environmental share [5]. High h^2 accompanied by substantial GG% typically signals the predominance of additive gene action, predicting good response to straightforward mass selection [9], [1]. Conversely, low h^2 with a large PCV–GCV difference implicates stronger environmental and G×E effects, for which designs with more replications and sites are warranted [2]. Our F_4 boll-mass example fits this latter scenario; although F_1 showed a more favorable signal ($h^2 = 0.86$; GG% = 31.88), confirmation across environments remains prudent.

Yield-proximal components—open bolls per plant and bolls per plant—consistently delivered the largest expected gains (F_4: 45.49% and 37.22%; F_1: 33.88% and 28.95%), providing a robust early-selection core for yield improvement. Among quality traits, lint percentage (F_1 $h^2 = 0.98$; F_4 $h^2 = 0.97$) and staple length (F1 $h^2 = 0.90$; F4 $h^2 = 0.91$) remained under stable genetic control against low ECV, allowing them to function as early filter criteria that safeguard a minimum quality threshold during yield-oriented selection. Correlation analysis further supported indirect selection: open bolls per plant correlated strongly and positively with lint percentage, plant height, and bolls per plant, simplifying simultaneous improvement of yield and fiber traits. At the same time, in F_1 the number of fruiting branches showed negative associations with certain yield/quality components (e.g., boll mass and lint percentage), highlighting the need to regulate plant architecture rather than increase branching indiscriminately.

Overall, the evidence suggests a staged strategy: leverage high-heritability, high-GG% traits (especially open bolls and total bolls per plant) for early-generation advancement, apply quality filters via lint percentage and staple length, and defer decisions on environment-sensitive traits such as boll mass to multi-environment, later-generation trials. This integrated approach aligns with quantitative-genetic expectations and maximizes the likelihood of achieving concurrent gains in yield and fiber quality under variable production environments.

5. Conclusions

This study revealed differential expression of agronomic traits (phenotypic divergence) across combinations. Specifically, in F_1 complex hybrids lint percentage reached up to 39%, 1000-seed weight up to 133.6 g, main-stem height 100–115 cm, and number of fruiting branches 14–16. In F_4 simple hybrids, lint percentage ranged 22–38%, 1000-seed weight 78–122 g, main-stem height 70–120 cm, and fruiting branches 13–19. These contrasts confirm that hybrid genetic components and their heritable potential play a decisive role in shaping phenotypic differences.

Overall, the results indicate that complex (F_1) hybrids possess genetic advantages over simple (F_4) hybrids for several key traits, supporting their preferential use in breeding programs. Leveraging these genetic gains—while validating environment-sensitive traits in multi-environment trials—should enhance breeding efficiency and deliver genotypes with improved yield and fiber quality.

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