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EVALUATION OF F₁ AND F₂ HYBRID POPULATIONS THROUGH MORPHOLOGICAL TRAITS IN MEDIUM-STAPLE COTTON (*GOSSYPIMUM HIRSUTUM* L.)

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SUMMARY

This study aimed to evaluate the inheritance patterns, heterosis, and phenotypic variability among the F₁ and F₂ populations for key morpho-agronomic traits in medium-staple cotton (*Gossypium hirsutum* L.). Six parental genotypes and their 30 F₁ and F₂ diallel hybrids received evaluation through plant height and fruiting branch number. Several F₁ hybrids showed considerable positive heterosis, while F₂ populations displayed expanded phenotypic variability and moderate-to-high heritability, revealing stable transmission of favorable traits. High heritability and superior performance were particularly notable in cross combinations such as Yulduz × T-1391, Niso × T-1336, and Guliston × Niso. These hybrids, therefore, became recommendable as promising breeding material for improving yield components and earliness in medium-staple cotton. The study revealed positive overdominance for plant height in 10 hybrid combinations, while heritability ranged from 0.40 to 0.71 for plant height and from 0.53 to 0.87 for fruiting branches. The identification of significant variation and heterotic effects was successful across hybrid populations, indicating strong breeding potential.

Keywords: Cotton (*G. hirsutum* L.), F₁ and F₂ populations, plant height, fruiting branches, heterosis, inheritance, genetic variability

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Key findings: The cotton (*G. hirsutum* L.) hybrids Niso × Yulduz, Niso × Guliston, Yulduz × T-1336, and Yulduz × T-1391 consistently showed superior performance for plant height and the number of fruiting branches. Therefore, these promising combinations can be a desirable source for improving yield and earliness in medium-staple cotton. treatment 6 mM L⁻¹ concentration notably enhanced the grain and oil yields and carbohydrates.

INTRODUCTION

In cotton (*Gossypium hirsutum* L.), the plant height and other morpho-agronomic traits do not directly determine the yield performance, as productivity depends on the interaction between the genotype potential and agronomic management. Nevertheless, an evaluation of plant architecture, fruiting branch number, and boll formation remains crucial for recognizing productive parental genotypes and their hybrid combinations (Qahhorov, 2013; Choriev *et al.*, 2015).

Key morpho-agronomic traits, such as plant height and the number of fruiting branches, are the widely used indicators in cotton breeding because they contribute to plant architecture, earliness, boll formation, and overall productivity. Previous studies have demonstrated substantial variation for these traits among cotton genotypes, making them useful indicators for the identification of superior parental lines and hybrid combinations.

In cotton cultivars, genetic variability plays a decisive role in the inheritance of economically important traits and also determines the effectiveness of selection in segregating populations of advanced generations. Previous studies have reported moderate-to-high heritability for yield components, such as total boll number and opened boll number, suggesting the beginning of an efficient selection from the early segregating generations, including F₂ and F₃ (Usmonov *et al.*, 2016). From a breeding perspective, genetic variability provides the fundamental basis for selection because increased variation enhances the probability of identifying superior recombinants with desirable agronomic traits. In segregating generations, particularly F₂ populations, the presence of broad phenotypic variability and heritable variation enables breeders to select

promising genotypes for improving yield potential, plant architecture, and earliness. Therefore, the assessment of genetic variability is both crucial for understanding inheritance patterns and for its direct application in practical cotton breeding programs.

In cotton crops, early maturity has shown itself to be largely associated with boll maturation and opening stages, which are highly sensitive to existing environmental conditions (Simongulyan, 1991). More broadly, recent studies applying multivariate statistical approaches and integrative biological analyses enunciated the crucial role of assessments based on genetic diversity and complex biological interactions in improving crop productivity and stability (Jabborova *et al.*, 2025).

Currently, regular monitoring of phytopathogenic diseases prevents the further spread of damages to cotton crops in Uzbekistan (Makhmudov *et al.*, 2026). These methodological advances support the use of comprehensive genetic evaluation of hybrid populations in breeding programs. Therefore, an evaluation of inheritance patterns, heterotic effects, and phenotypic variability across the parental genotypes and F₁ and F₂ populations appeared essential for identifying superior hybrid combinations and improving breeding efficiency.

Although previous studies have highlighted the importance of genetic variability and heritability in cotton breeding, the reported inheritance patterns and dominance effects have varied considerably among different genetic backgrounds and environmental conditions. Furthermore, limited information is available regarding the comparative genetic behavior of plant height and fruiting branch number in reciprocal F₁ and F₂ hybrid populations. Consequently, a clear understanding of the inheritance mechanisms governing these traits remains incomplete,

highlighting the need for further investigation to support efficient cotton breeding strategies.

Therefore, based on the above discussion, the consequent study aimed to analyze the various genetic parameters and key morpho-agronomic traits in F_1 and F_2 diallel hybrids of cotton. This will identify the promising breeding material for improvement in seed cotton yield and early maturity.

MATERIALS AND METHODS

Plant materials and site conditions

The experiments on cotton (*G. hirsutum* L.), conducted during 2022–2024, took place at the Durmon Experimental Research Station, Institute of Genetics and Experimental Plant Biology, Academy of Sciences, Uzbekistan. The experimental field had the characteristics of typical non-saline sierozem soil with a groundwater depth of 7–8 m. Standard agronomic practices, including irrigation, fertilization, and crop protection, succeeded in uniform application to all the experimental subplots to minimize environmental variations.

Parental materials, comprising six cotton genotypes, included cultivars Yulduz, Niso, Guliston, and SSB-Klaster-1, and the breeding lines T-1336 and T-1391. All genotypes have a vegetation period of approximately 110–115 days. All the genotypes sustained crossing using a full diallel design, with F_1 and F_2 populations obtained for further evaluation.

Experimental design and traits measurement

The experiment layout was in a randomized complete block design (RCBD) with three replications. Each genotype underwent planting in two rows with a spacing of 90 cm × 20 cm and one plant per hill. The data recorded on randomly selected competitive plants consisted of the following traits—plant height and the number of fruiting branches.

Genetic and statistical analyses

In F_1 populations, the dominance coefficients' calculation used the Wright formula (Beil and Atkins, 1965), with heterosis percentage estimated according to Fonseca and Patterson (1968). The coefficient of variation and variability classes reached calculations using standard procedures, and broad-sense heritability (h^2) in F_2 populations entailed estimation following Allard and Bradshaw (1964). All the recorded data based on various variables underwent the analysis of variance (ANOVA), following Dospekhov (1985), while the comparison and separation of mean differences employed the significance test ($p \leq 0.05$).

RESULTS AND DISCUSSION

Knowledge about the hybridization ability, inheritance pattern, genetic variability, heterotic effects, and dominance relationship of traits was essential for the successful development of new cotton (*G. hirsutum* L.) hybrids. The detailed knowledge of these breeding processes in F_1 and subsequent segregating populations improves breeding efficiency and supports the selection of suitable parental genotypes. Previous studies conducted across diverse regions have consistently emphasized the importance of inheritance analysis and heterosis evaluation in cotton improvement programs (Ahsan *et al.*, 2015; Ruan *et al.*, 2020).

The identification of genotype groups differing in particular traits within varietal populations provides authentic insights into their genetic background and a comprehensive assessment of population structure and, therefore, requires simultaneous evaluation of multiple morphological and agronomic traits. Among these important traits, plant height represents an influential component of plant architecture and adaptive potential, which may indirectly contribute to yield stability and breeding values. Moreover, multi-generation

selection plays a crucial role in stabilizing the favorable morpho-agronomic traits and identifying promising genotypes for future breeding programs (Ergashev, 2020).

In the latest study, among the parental genotypes, plant height ranged from 109.6 cm (Niso) to 118.2 cm (line T-1336), revealing substantial genetic diversity for this trait among the initial breeding materials (Table 1). This result exhibited that the parental genotypes possess sufficient genetic divergence, which is a prerequisite for obtaining new productive cross combinations. Standard deviation values observed in the F_1 populations (0.53–0.77 cm) were generally higher than those of the parental genotypes, suggesting an increased level of potential phenotypic variability for plant height in hybrid populations. Such an enhancement in phenotypic variability in F_1 populations reflects the contribution of genetic recombination and dominance effects influencing the traits' expression. This could enhance the probability of identifying promising segregants in subsequent generations, which is crucial for cotton breeding programs. In the 4×4 diallel cross of upland cotton, partial dominance of additive genes was noticeable for traits, such as plant height, the number of fruiting branches, and the number of bolls per plant (Sarwar *et al.*, 2011).

According to this study, the dominance coefficient (h^2) reflects the phenotypic expression of F_1 hybrids relative to their parental genotype values (Table 1). The calculated h^2 values with a wide range indicate diverse inheritance patterns for plant height among the studied hybrid populations. In the concerned study, the dominance coefficient (h^2) calculation was according to the method of Beil and Atkins (1965) and served to evaluate the degree and direction of dominance in F_1 hybrids relative to the parental mean values. Positive h^2 values indicate partial or complete dominance toward increased trait expression, whereas negative values signify dominance toward reduced trait expression. Values exceeding ± 1.0 represent overdominance, suggesting the presence of heterotic effects in hybrid populations.

Therefore, the dominance coefficient provides valuable information regarding the genetic control and inheritance pattern of plant height in cotton hybrids. In F_1 hybrids, the highest plant height was evident in the F_1 hybrids T-1336 $\times$ Niso (121.2 cm), Guliston $\times$ T-1336 (120.4 cm), Guliston $\times$ Niso (119.5 cm), and T-1391 $\times$ Niso (119.3 cm). Meanwhile, relatively short-stature plants resulted in F_1 hybrids Niso $\times$ Yulduz and SSB-Klaster-1 $\times$ Guliston, with values of 95.1 and 98.3 cm, respectively. The presented results confirmed earlier findings that inheritance under overdominance leads to increased productivity in hybrid populations (Krishnamurthy and Henry, 1979). The inheritance patterns observed in this study were generally consistent with earlier reports describing the genetic control of plant height in cotton. The occurrence of partial dominance, overdominance, and substantial heritable variation indicates the involvement of multiple genes governing trait expression. The relatively high heritability estimates and diverse dominance patterns observed in the presented study further confirm the complex polygenic inheritance of plant height and highlight its potential for effective improvement through selection in segregating generations.

Based on the dominance classification, plant height inheritance was with a positive overdominance (heterotic effects) in 10 hybrid combinations, partial positive dominance in four cross combinations, partial negative dominance in four cross combinations, and negative overdominance in 13 cross combinations. These confirm the complex polygenic control of this trait. Positive heterosis for plant height was clearly noteworthy in F_1 populations involving Guliston $\times$ Niso, T-1391 $\times$ Niso, Niso $\times$ T-1391, and Guliston $\times$ SSB-Klaster-1, enunciating that these parental genotypes possess the robust genetic potential for improving plant height in hybrid populations. In contrast, negative heterosis occurred in F_1 populations Guliston $\times$ T-1336, Niso $\times$ Yulduz, SSB-Klaster-1 $\times$ Guliston, Yulduz $\times$ SSB-Klaster-1, T-1336 $\times$ Yulduz, Yulduz $\times$ Niso, and Yulduz $\times$ T-1336,

Table 1. Genetic analysis of the plant height in parental genotypes and F₁ hybrids of cotton.

No.	Parental genotypes and F ₁ populations	Plant height (cm)	S	h ²	Heterosis (%)
1	Namangan-77 (standard)	114.±0.9	2.9		
2	Yulduz	114.3±0.4	2.3		
3	Niso	109.6±0.4	2.6		
4	Guliston	110.8±0.4	2.6		
5	SSBK	112.9±0.4	2.6		
6	T-1336	118.2±0.5	3.1		
7	T-1391	116.0±0.5	3.2		
1	Yulduz × Niso	105.9±0.6	3.5	-2.6	-5.2
2	Niso × Yulduz	95.1±0.5	3.9	-7.5	-15.0
3	Yulduz × Guliston	116.9±0.6	3.3	2.9	4.1
4	Guliston × Yulduz	108.5±0.6	2.9	-2.4	-3.4
5	Yulduz × SSB K-1	104.2±0.6	3.4	-8.7	-7.7
6	SSB K-1 × Yulduz	114.4±0.6	2.2	1.5	1.3
7	Yulduz × T-1336	110.3±0.6	3.7	-2.7	-5.0
8	T-1336 × Yulduz	109.2±0.7	3.9	-3.2	-5.9
9	Yulduz × T-1391	116.2±0.6	3.7	1.1	1.1
10	T-1391 × Yulduz	115.3±0.6	3.6	0.6	0.3
11	Niso × Guliston	108.6±0.6	3.4	-2.7	-1.5
12	Guliston × Niso	119.5±0.6	3.9	15.5	8.4
13	Niso × SSB K-1	112.3±0.6	2.9	1.3	1.4
14	SSB K-1 × Niso	112.8±0.6	3.2	1.7	1.9
15	Niso × T-1336	108.1±0.7	3.1	-1.3	-5.1
16	T-1336 × Niso	121.2±0.7	4.2	-1.7	-6.4
17	Niso × T-1391	118.6±0.5	3.4	1.8	5.1
18	T-1391 × Niso	119.3±0.7	3.7	2.0	5.8
19	Guliston × SSB K-1	115.5±0.6	3.6	7.0	3.8
20	SSB K-1 × Guliston	98.3±0.6	3.3	-21.7	-11.7
21	Guliston × T-1336	120.4±0.6	3.3	-6.0	-19.4
22	T-1336 × Guliston	113.9±0.6	3.4	-0.2	-0.5
23	Guliston × 1391	112.6±0.6	3.8	-0.3	-0.7
24	T-1391 × Guliston	115.1±0.7	3.6	0.6	1.5
25	SSB K-1 × T-1336	117.8±0.6	3.8	-0.1	-0.3
26	T-1336 × SSBK	110.1±0.6	3.9	-4.9	-4.3
27	Guliston × 1391	112.6±0.6	3.8	-0.3	-0.7
28	T-1391 × Guliston	115.1±0.7	3.6	0.6	1.5
29	T-1336 × T-1391	117.5±0.7	4.0	0.4	0.3
30	T-1391 × T-1336	114.4±0.6	3.6	-2.5	-2.3

suggesting that dominance of alleles had an association with reduced plant height in these populations. Consequently, modern cotton breeding increasingly relies on both classical and population genetics approaches to identify genotypes that can rapidly adapt to diverse regional environments. In cotton cultivation, the compact plant architecture seemed beneficial since shorter plants allow higher planting density and often contribute to improved flowering and boll opening performance (Boboev *et al.*, 2000). In *G. hirsutum* L. breeding, a positive correlation was remarkable between the main stem height

and yield-related traits in F₂ populations (Naveed *et al.*, 2004).

In F₂ populations, plant height widely varied from 86 to 90 cm (observed in cross combinations T-1336 × Yulduz, Guliston × Niso, Niso × SSB-Klaster-1, T-1336 × Niso, Niso × T-1391, Guliston × SSB-Klaster-1, and Guliston × T-1336) to 131–135 cm (recorded in F₂ populations T-1391 × Yulduz, Niso × T-1336, and T-1391 × Niso). In F₂ hybrids, the trait values extended beyond the parental range (90–130 cm) in both directions, detailing an obvious transgressive segregation and recombination of alleles controlling the plant

height. The coefficient of variation (CV) ranged from 3.5% to 6.5% in the F₂ hybrids, reflecting moderate to relatively high genetic variability. Compared with the parental genotypes (CV = 2.0%–2.7%), variability increased approximately two- to threefold, demonstrating the considerable effect of genetic recombination in segregating populations.

For plant height, the parental genotypes entailed distribution across four phenotypic classes, whereas the F₂ populations showed a broader distribution, covering six to nine classes, ranging from 86 to 135 cm (Table 2). The widest distribution (nine classes) resulted in the hybrid T-1336 × Niso, while several cross combinations, including Niso × Yulduz, Yulduz × SSB-Klaster-1, Yulduz × T-1336, Niso × Guliston, and SSB-Klaster-1 × Guliston, provided six classes. Most cross combinations displayed the highest frequency, with ranges of 106–110 cm and 111–115 cm, although some crosses also produced lower-height classes (86–95 cm), confirming broad segregation patterns. Broad-sense heritability values were relatively high ($h^2 = 0.40$ – 0.71), indicating that genetic factors play a primary role in determining plant height (Table 2).

The highest heritability surfaced in the F₂ population Guliston × Yulduz ($h^2 = 0.71$), suggesting robust genetic control and the highest selection efficiency for the said trait. In contrast, the lowest heritability was apparent in the F₂ hybrid Guliston × T-1391 ($h^2 = 0.40$), implying a comparatively considerable environmental influence in the trait expression. In cotton hybrid breeding, special attention is vital to economically important traits and the genetic regulation of morphological characteristics, inheritance of favorable parental attributes, variability in segregating populations, and stabilization of desirable phenotypes. Among these traits, the development of fruiting branches was particularly valuable because their number significantly affects boll formation and, ultimately, seed cotton yield. In cultivar and breeding line evaluation, increased numbers of fruiting branches were in association with more bolls, which ensures the key role of sympodial branches in cotton breeding programs. These present studies confirmed previous

observations that fruiting branches' development has a considerable impact on the formation of the number of bolls per plant in cotton (Dadajonov *et al.*, 2017).

Among the parental genotypes, the number of fruiting branches ranged from 9.8 (SSB-Klaster-1) to 12.7 (T-1391), exhibiting substantial genetic differentiation among the parental material for the said trait (Table 3). The observed standard deviation values in the F₁ populations (1.0–2.1 branches) were higher than those of the parental genotypes, suggesting an increased level of genetic variability in hybrid populations. The dominance coefficient (h^2) values widely ranged from -0.3 to 10.6 among the F₁ hybrids, demonstrating diverse inheritance patterns for the number of fruiting branches. The highest number of sympodial branches per plant emerged in F₁ populations Yulduz × T-1336 (14.5), Niso × Yulduz (13.8), Niso × Guliston (13.3), and Niso × SSB-Klaster-1 (13.1), whereas relatively lower values for the said trait occurred in the F₁ hybrid SSB-Klaster-1 × Niso (10.1).

Based on the dominance classification, the number of fruiting branches showed an inheritance with positive overdominance (heterotic effects) in 11 hybrid combinations, partial positive dominance in 12 combinations, partial negative dominance in two cross combinations, and absence of parental dominance in two F₁ populations. The results revealed that the number of fruiting branches in cotton was in the control of a complex genetic system with a robust tendency toward positive heterotic effects in many crosses. This suggests better prospects for selecting productive genotypes with improved branching capacity in breeding programs. Past studies revealed both F₁ and F₂ populations provide important information on the inheritance of morphological and yield-related traits and help define efficient breeding strategies (Islomov and Xudoyqulov, 2008; Singh *et al.*, 2018).

For fruiting branches per plant, the positive heterosis resulted in numerous F₁ populations. These involved Niso × Guliston, Niso × SSB-Klaster-1, Yulduz × T-1336, SSB-Klaster-1 × Guliston, Niso × Yulduz, T-1336 × SSB-Klaster-1, Guliston × SSB-Klaster-1,

Table 2. Genetic analysis of the plant height in parental genotypes and F₂ populations of cotton.

No.	Parental genotypes and F ₂ populations	N	Classes (cm)										Mean SE	±	S	CV (%)	h ²
			86-90	91-95	96-100	101-105	106-110	111-115	116-120	121-125	126-130	131-135					
1	Namangan-77 (andoza)	30					26.6	33.5	23.3	16.6			114.8±0.9	2/9		3.4	
2	Yulduz	30					3,3	63.3	26.6	6.8			114.3±0.4	2.3		2.0	
3	Niso	30				3,3	60	30	6.7				109.6±0.4	2.6		2.4	
4	Guliston	30				3,3	50	40	6.7				110.8±0.4	2.6		2.3	
5	SSB K-1	30				6,6	23.3	56.6	13.5				112.9±0.4	2.6		2.3	
6	T-1336	30						16.6	63.3	16.6	3.5		118.2±0.5	3.1		2.6	
7	T-1391	30					10	30	56.6	3.4			116.0±0.5	3.2		2.7	
1	Yulduz × Niso	100		8	9	34	37	5	4	2	1		108.3±0.6	4.4		6.0	0.59
2	Niso × Yulduz	100		2	20	61	1	12	4				103.2±0.6	4.5		4.3	0.65
3	Yulduz × Guliston	100		3	4	19	43	25	4	2			108.6±0.6	4.1		3.8	0.53
4	Guliston × Yulduz	100		6	7	8	41	20	10	6	2		113.2±0.8	5.6		8.2	0.71
5	Yulduz × SSB K-1	100			5	17	9	42	24	3			112.4±0.7	4.8		4.3	0.66
6	SSB K-1 × Yulduz	100		6	38	40	9	4	2	1			110.6±0.6	4.3		5.6	0.58
7	Yulduz × T-1336	100			2	4	44	38	8	4			115.6±0.6	4.0		3.5	0.42
8	T-1336 × Yulduz	100	1	20	39	21	10	4	3	2			103.5±0.9	6.1		7.1	0.70
9	Yulduz × T-1391	100		1	1	3	7	29	39	16	4		111.4±0.8	5.3		4.8	0.65
10	T-1391 × Yulduz	100				2	18	35	35	6	3	1	114.5±0.4	4.5		3.9	0.50
11	Niso × Guliston	100			1	19	19	40	19	2			111.3±0.8	5.3		4.7	0.66
12	Guliston × Niso	100	3	21	28	37	7	2	2				107.2±0.8	5.4		6.4	0.70
13	Niso × SSBK	100	1	1	4	11	44	24	15				109.8±0.7	5.2		4.8	0.69
14	SSB K × Niso	100		4	8	15	38	19	12	4			108.7±0.7	5.1		4.7	0.69
15	Niso × T-1336	100				3	6	14	30	36	7	4	120.3±0.7	5.1		4.3	0.59
16	T-1336 × Niso	100	1	3	5	12	32	38	5	3	1		110.3±0.4	4.5		4.1	0.47
17	Niso × T-1391	100	1	3	3	3	11	13	57	9			116.5±0.6	4.2		3.6	0.51
18	T-1391 × Niso	100			2	3	11	26	41	11	4	2	115.4±0.5	5.1		4.4	0.57
19	Guliston × SSB K-1	100	2	4	38	46	3	2	3	2			111.7±0.6	4.3		5.2	0.58
20	SSB K-1 × Guliston	100			1	7	13	63	14	2			112.6±0.6	4.3		3.8	0.49
21	Guliston × T-1336	100	1	1	9	40	35	11	3				105.4±0.6	4.3		4.1	0.55
22	T-1336 × Guliston	100		4	35	29	22	7	2	1			112.4±0.7	5.0		6.5	0.60
23	Guliston × 1391	100		4	6	12	35	33	8	2			110.6±0.6	4.0		3.6	0.40
24	T-1391 × Guliston	100				3	9	49	29	4	5	1	115.6±0.8	5.3		4.6	0.60
25	SSB K-1 × T-1336	100			1	5	8	45	36	3	2		115.6±0.5	3.8		3.3	0.49
26	T-1336 × SSB K-1	100	1		2	46	45	3	2	1			105.7±0.6	4.4		4.2	0.51
27	SSB K-1 × 1391	100			1	5	7	21	45	18	3		117.5±0.7	4.6		3.9	0.51
28	T-1391 × SSB K-1	100			2	6	14	46	22	7	3		113.6±0.6	4.3		3.8	0.47
29	T-1336 × T-1391	100				7	10	57	10	16			114.5±0.8	5.3		4.6	0.57
30	T-1391 × T-1336	100				1	15	30	43	6	2	3	116.5±0.5	5.2		4.5	0.59

Table 3. Genetic analysis of the number of fruiting branches in parental genotypes and F₁ hybrids of cotton.

No.	Parental genotypes and F ₁ populations	Fruiting branches (no.)	S	h ²	Heterosis (%)
1	Namangan-77 (standard)	11.8±0.2	1.3		
2	Yulduz	12.2±0.1	0.8		
3	Niso	10.4±0.1	0.9		
4	Guliston	9.9±0.2	1.2		
5	SSBK	9.8±0.2	1.2		
6	T-1336	11.5±0.2	1.5		
7	T-1391	12.7±0.2	1.3		
1	Yulduz × Niso	11.0±0.2	1.3	-0.3	-2.3
2	Niso × Yulduz	13.8±0.2	1.4	2.7	22.1
3	Yulduz × Guliston	12.8±0.2	1.3	1.5	15.8
4	Guliston × Yulduz	11.4±0.2	1.2	0.	3.1
5	Yulduz × SSB K-1	11.3±0.2	1.5	0.2	2.7
6	SSB K-1 × Yulduz	12.2±0.2	1.1	1.0	10.9
7	Yulduz × T-1336	14.5±0.3	2.1	6.7	22.8
8	T-1336 × Yulduz	12.1±0.2	1.2	0.7	2.5
9	Yulduz × T-1391	12.4±0.3	1.1	0	0
10	T-1391 × Yulduz	12.8±0.2	1.4	-4.0	3.2
11	Niso × Guliston	13.3±0.2	1.6	10.6	31.6
12	Guliston × Niso	12.0±0.2	1.1	6.3	18.9
13	Niso × SSB K-1	13.1±0.2	1.3	10.0	29.7
14	SSB K-1 × Niso	10.1±0.2	1.2	0	0
15	Niso × T-1336	11.5±0.2	1.4	1.0	5.5
16	T-1336 × Niso	12.6±0.1	1.0	2.8	15.6
17	Niso × T-1391	12.6±0.2	1.3	0.9	9.5
18	T-1391 × Niso	12.3±0.3	2.1	0.6	6.9
19	Guliston × SSB K-1	11.8±0.2	1.3	20	20.4
20	SSB K-1 × Guliston	12.0±0.2	1.4	22.1	22.5
21	Guliston × T-1336	11.9±0.2	1.2	1.5	11.2
22	T-1336 × Guliston	11.2±0.3	1.1	0.6	4.6
23	Guliston × 1391	12.4±0.2	1.3	0.7	9.7
24	T-1391 × Guliston	11.9±0.3	1.6	0.4	5.3
25	SSB K-1 × T-1336	11.2±0.2	1.2	0.6	5.6
26	T-1336 × SSBK	12.8±0.2	1.3	2.4	20.7
27	Guliston × 1391	12.3±0.2	1.1	0.7	10.7
28	T-1391 × Guliston	11.9±0.3	1.6	0.4	5.3
29	T-1336 × T-1391	12.5±0.2	1.4	0.6	3.3
30	T-1391 × T-1336	12.3±0.2	1.3	0.3	1.6

Guliston × Niso, Yulduz × Guliston, T-1336 × Niso, Guliston × T-1336, SSB-Klaster-1 × Yulduz, and SSB-Klaster-1 × T-1391. The predominance of positive heterotic responses in these cross combinations indicates that the corresponding parental cultivars and lines possess the considerable genetic potential for increasing the number of fruiting branches in cotton F₁ hybrids. Previous studies also demonstrated the wide phenotypic segregation for fruiting branches in F₂ populations, which represents a valuable genetic resource for selection (Reddy *et al.*, 2020).

For fruiting branches per plant, the detection of negative heterosis was only in the

F₁ hybrid Yulduz × Niso, suggesting dominance of alleles associated with lower branching capacity in this cross combination. However, in its reciprocal cross Niso × Yulduz, a significant positive heterotic effect (22.1%) was evident. This reciprocal difference revealed that parental genetic effects, including possible maternal influence and cytoplasmic contribution, may affect the expression of fruiting branch number. The said cross based on the Niso × Yulduz parental direction could generate F₁ populations with substantially improved fruiting branching compared with parental genotypes. The number of fruiting branches was in a strong positive correlation

with boll number, and, therefore, it directly influenced the seed cotton yield (McCarty *et al.*, 2008).

Hybrid combinations, such as T-1336 × Niso (121.2 cm), Guliston × Niso (119.5 cm), and T-1391 × Niso (119.3 cm), exhibited the highest plant height values, while Niso × Yulduz (13.8 branches) showed the maximum fruiting branches. The F_2 populations widely varied for fruiting branches, which ranged from 5 to 6 branches in cross combinations Yulduz × Guliston, Guliston × Yulduz, Yulduz × SSB-Klaster-1, SSB-Klaster-1 × Yulduz, T-1336 × Yulduz, and Yulduz × T-1391. Varying fruiting branches also included Niso × Guliston, Guliston × Niso, Niso × SSB-Klaster-1, SSB-Klaster-1 × Niso, Niso × T-1336, T-1336 × Niso, Niso × T-1391, Guliston × SSB-Klaster-1, and SSB-Klaster-1 × Guliston. Moreover, some cross combinations (Guliston × T-1336, T-1336 × Guliston, and Guliston × T-1391) expressed up to 21–22 branches, particularly recorded in the F_2 hybrid T-1391 × Niso. In F_2 populations, the trait values deviated beyond the parental range (5–22 branches) in both directions, confirming the presence of transgressive segregation.

The coefficient of variation ranged from 20.7% to 28.4%, indicating the highest level of variability in the F_2 populations. Compared with the parental genotypes (CV = 7.0%–13.4%), variability increased approximately two- to threefold, further confirming the robust recombination effect and the availability of broad phenotypic diversity suitable for selection. In parental genotypes, the trait distribution covered three classes (Yulduz and SSB-Klaster-1) and four classes (Niso, Guliston, T-1336, and T-1391), whereas in the F_2 populations, the class distribution expanded to five to eight classes within the range of approximately 7–20 branches. The narrowest distribution (five classes) resulted in the F_2 hybrid Yulduz × T-1336, while the widest distributions (eight classes) occurred in F_2 populations Yulduz × T-1391, SSB-Klaster-1 × Niso, T-1336 × Niso, and T-1391 × Niso. Most of the F_2 populations showed the highest frequency in the 11–12 and 13–14 branch classes, revealing that intermediate branching levels predominate in segregating populations.

Broad-sense heritability values were relatively highest in many F_2 hybrid populations ($h^2 = 0.62$ – 0.87), indicating that genetic factors play the major role in determining fruiting branches (Table 4). However, the highest heritability values existed in the F_2 populations Yulduz × T-1391 ($h^2 = 0.87$), Guliston × Yulduz ($h^2 = 0.82$), Yulduz × Niso ($h^2 = 0.80$), Yulduz × Guliston ($h^2 = 0.80$), T-1336 × Niso ($h^2 = 0.80$), and Niso × T-1391 ($h^2 = 0.80$). It suggests significant genetic control and the highest selection efficiency for the said trait in these cross combinations. Conversely, the lowest heritability appeared in the F_2 hybrid T-1391 × T-1336 ($h^2 = 0.26$), indicating a comparatively considerable environmental impact on the said trait expression in this cross combination. Past studies on *G. barbadense* showed that some cultivars were more effective than parental sources, emphasizing careful genotype selection in Uzbekistan (Chorshanbiev *et al.*, 2025). Medium-staple cultivars in irrigated areas depend on multiple traits, especially boll number, and monitoring trait inheritance across the generations enhances the breeding efficiency (Ergashev, 2021).

CONCLUSIONS

In this promising study, most F_1 populations showed improved morpho-agronomic traits compared with their parental genotypes, although no single genotype exhibited consistent dominance across all traits, highlighting the importance of trait-specific parental selection in upland cotton (*G. hirsutum* L.). In F_2 populations, variability increased 2–2.5 fold, and superior plants were prevalent in the F_2 populations such as Yulduz × T-1391 and Yulduz × T-1336. Therefore, these F_2 populations were seemingly the valuable breeding material for improving yield and early maturity in medium-staple cotton. Considerable genetic variation, overdominance effects, and moderate-to-high heritability were notable for both plant height and fruiting branch number in cotton hybrids. Positive overdominance for plant height was distinct in 10 hybrid combinations, while broad-sense

Table 4. Genetic analysis of the number of fruiting branches in parental genotypes and F₂ hybrids of cotton.

No.	Parental genotypes and F ₂ populations	N	Class intervals (no.)									Mean SE	±	S	CV (%)	h ²
			5-6	7-8	9-10	11-12	13-14	15-16	17-18	19-20	21-22					
1	Namangan-77 (standard)	30		10	16.8	46.6	26.6					11.8±0.2	1.3		11.2	
2	Yulduz	30				50	36.6	13.4				12.2±0.1	0.8		7.0	
3	Niso	30		6.6	50	40	3.4					10.4±0.1	0.9		8.9	
4	Guliston	30		13.3	46.6	33.3	6.8					9.9±0.2	1.2		12.1	
5	SSB K-1	30		16.7	53.3	30						9.8±0.2	1.2		12.4	
6	T-1336	30			30	30	33.3	6.7				11.5±0.2	1.5		13.4	
7	T-1391	30			3.3	33.3	56.6	6.8				12.7±0.2	1.3		10.8	
1	Yulduz × Niso	100		7	24	36	14	11	6	2		12.0±0.4	2.		23.3	0.80
2	Niso × Yulduz	100		30	16	18	25	7	4			10.5±0.3	2.4		24.2	0.78
3	Yulduz × Guliston	100	1	24	7	23	40	3	2			11.3±0.3	2.5		22.1	0.80
4	Guliston × Yulduz	100	2	29	19	34	12	3	1			10.3±0.4	2.6		25.3	0.82
5	Yulduz × SSB K-1	100	2	14	9	41	25	6	3			11.5±0.3	2.5		20.7	0.76
5	SSB K-1 × Yulduz	100	2	36	13	23	19	4	3			10.0±0.3	2.3		23.5	0.79
7	Yulduz × T-1336	100		32	15	2	29	22				11.4±0.4	2.8		28.4	0.67
8	T-1336 × Yulduz	100	1	29	7	34	27	1	1			10.8±0.3	2.5		23.4	0.76
9	Yulduz × T-1391	100	2	7	8	27	49	2	4	1		12.3±0.3	3.2		18.9	0.87
10	T-1391 × Yulduz	100		13	15	21	35	11	3	2		11.9±0.2	2.4		20.2	0.74
11	Niso × Guliston	100	11	32	17	27	12	1				9.5±0.3	2.5		26.8	0.75
12	Guliston × Niso	100	2	36	24	23	12	3				9.8±0.3	2.3		23.8	0.78
13	Niso × SSBK	100	1	19	7	22	46	5				11.6±0.3	2.4		20.8	0.76
14	SSB K × Niso	100	2	31	43	16	4	2	1	1		9.6±0.3	2.3		23.8	0.76
15	Niso × T-1336	100	12	31	15	24	17	1				9.6±0.4	2.5		28.1	0.73
16	T-1336 × Niso	100	2	16	13	32	28	7	1	1		11.6±0.2	2.6		23.0	0.80
17	Niso × T-1391	100	5	34	1	34	20	4	2			10.3±0.3	2.7		24.9	0.80
18	T-1391 × Niso	100		3	19	26	30	10	5	5	2	12.6±0.3	3.1		24.7	0.75
19	Guliston × SSB K-1	100	4	40	21	23	8	2	2			9.5±0.3	2.2		23.1	0.68
20	SSB K-1 × Guliston	100	5	36	25	23	9	2				9.5±0.3	2.2		23.6	0.67
21	Guliston × T-1336	100	3	46	20	22	8	1				9.2±0.3	2.1		23.2	0.62
22	T-1336 × Guliston	100	2	30	21	37	7	3				10.0±0.3	2.3		22.3	0.76
23	Guliston × 1391	100	4	28	13	23	23	6	3			10.4±0.3	2.3		22.5	0.69
24	T-1391 × Guliston	100	7	32	20	16	20	5				9.8±0.3	2.5		25.6	0.68
25	SSB K-1 × T-1336	100	1	35	29	24	10	1				9.7±0.3	2.0		21.2	0.57
26	T-1336 × SSB K-1	100	4	22	3	23	42	6				11.3±0.4	2.2		24.8	0.62
27	SSB K-1 × 1391	100	4	30	11	32	20	3				10.2±0.3	2.4		23.4	0.73
28	T-1391 × SSB K-1	100	6	16	36	28	10	3	1			10.0±0.3	2.2		22.4	0.53
29	T-1336 × T-1391	100	4	22	6	26	35	4	2	1		11.3±0.4	2.8		25.2	0.74
30	T-1391 × T-1336	100		7	14	32	29	9	7	2		12.5±0.2	2.7		21.6	0.26

heritability ranged from 0.40 to 0.71 for plant height and 0.53 to 0.87 for fruiting branches. These results indicate the studied hybrid combinations possess strong genetic potential and represent promising breeding material for the improvement of key agronomic traits in cotton.

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