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GENETIC ANALYSIS AND INBREEDING DEPRESSION FOR YIELD-RELATED PARAMETERS IN UPLAND COTTON

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SUMMARY

Cotton is a valuable industrial fiber crop grown in many regions worldwide. Four cotton (*Gossypium hirsutum* L.) cultivars, i.e., Ishonch, Navbakhor-2, C-6524, and Tashkent-6, and their F_{1-2} diallel hybrids' cultivation comprised a randomized complete block design with a factorial arrangement and four replications during 2019–2021 in the Tashkent Region, Uzbekistan. Significant ($P \leq 0.01$) differences were notable among the parental genotypes and their F_1 hybrids for boll weight and seed cotton yield. The parental cultivars Ishonch and Navbakhor-2 and their F_1 diallel hybrids showed more stability and performed better than other genotypes. Broad-sense heritability estimates were the highest for boll weight and seed cotton yield while lowest for bolls per plant. Based on this trait's yield, heritability, and variability, the inbreeding depression was positive in the F_2 populations Ishonch × Navbakhor-2 and Navbakhor-2 × Tashkent-6. According to yield, the cultivars Ishonch, Navbakhor-2, and Tashkent-6 were outstanding as positive donors.

Keywords: Cotton (*G. hirsutum* L.), genetic variability, heritability, genetic gain, correlation coefficient, heterosis, inbreeding depression

Key findings: Cotton (*G. hirsutum* L.) cultivars Ishonch, Navbakhor-2, Tashkent-6, and their F_1 diallel hybrids performed better for bolls per plant, boll weight, and seed cotton yield per plant.

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INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is Uzbekistan's foremost cash and industrial crop. Worldwide, *Gossypium hirsutum* L. is the most commonly cultivated species, also called upland cotton, providing 90% fiber production, while *Gossypium barbadense* (Egyptian cotton) produces only 3% of fiber. These tetraploid species are also called the New World cotton (Amanov *et al.,* 2020; Sanaev *et al.,* 2021; Shavkiev *et al.,* 2022). Cotton cultivars belonging to the medium-fiber quality species (*G. hirsutum* L.) are the main cultivated field crop in 77 countries globally, occupying an area of about 32.0 million hectares and growing in various soil and climate conditions. The worldwide cotton trade is approximately USD 20.0 billion yearly (World Markets and Trade, 2022; Shavkiev *et al.,*2023).

Cotton ginning and processing plants and the textile industry are the primary sources of employment for millions of people and constitute a significant share of the gross domestic product of many countries, such as Uzbekistan, Australia, Greece, India, China, and Pakistan (Matniyazova *et al.,* 2022; Muminov *et al.,* 2023). Uzbekistan is the largest cotton-growing country, ranking fifth for cotton production and fourth in exporting cotton raw materials worldwide. About 93% of the country's cotton fields bear upland cotton cultivar plantings (Worldbank.org, 2020; Amanov *et al.,* 2022; Makamov *et al.,* 2023).

Cotton breeders have continued their efforts to develop high-yielding cotton cultivars with improved fiber quality by using existing cotton germplasm (Narimonov *et al*., 2023; Tian *et al*., 2023). Cotton yield-contributing and fiber-quality traits are quantitatively heritable; thus, yield-related components and fiber quality improvement can result from utilizing new cross-combinations developed through appropriate breeding programs (Chorshanbiev e*t al.*, 2023). Cotton breeders have always encouraged genetic variability in the breeding populations and suggested that screening breeding material for tolerance to different biotic and abiotic stresses is an initial requirement. Reports have gone out on vast genetic variability, along with genotypic, phenotypic, and environmental coefficients of variation, among various upland cotton populations for quantitative and qualitative traits (Rejapova *et al*., 2020; Shavkiev *et al*., 2021; Normamatov *et al*., 2023).

Heritability is an effective tool that helps cotton breeders assess the environmental impacts on various traits in a breeding nursery. It is an effective indicator for determining the level at which parental qualities are passed down from generation to generation (Chorshanbiev *et al.*, 2023). Thus, heritability and genetic gain could be powerful tools for plant breeders to select appropriate breeding schemes (Chandio *et al.,* 2003). Abbas *et al.* (2013) provided information on high heritability with genetic gain for yield-component traits in upland cotton. A study reported moderate to high heritability for bolls per plant, boll weight, seed cotton yield, lint percentage, fiber length, and strength in upland cotton genotypes (Nizamani *et al.,* 2017).

Inbreeding depression also correlates to high heterosis in F_1 hybrids. Hence, one has to search for a moderate type of heterosis stable for lesser inbreeding depression at the F_2 level (Soomro and Kalhoro, 2000). Allelic and non-allelic interactions of genes in specific environmental effects will lead to successful heterosis results. The superiority of hybrids over commercial cultivars and genotypes is common as beneficial heterosis (Meredith and Brown, 1998; Khan *et al*., 2007, 2010). It is a fact that without a proper combination of parents, heterosis does not occur. Heterosis can be advantageous for enhancing cotton production by utilizing heterozygosity and getting such cotton hybrids superior to the best parents. The comparison of the performance of the best hybrids with standard cultivars will result in a determination of economic heterosis.

Before initiating any cotton improvement program, information about the genetic potential of various genotypes, heritability, and inheritance pattern of diverse characteristics and degree of association of yield with various morpho-yield traits is crucial for breeders to handle the problem wisely and enhance the seed cotton and lint yields

(Ahmad *et al*., 2008; Makhdoom *et al*., 2010). The availability of some working knowledge about the correlation between the traits can facilitate the desired plants' selection. Further, identifying the characteristics that influence the final productivity, directly or indirectly, is also helpful. Thus, correlation studies can affect cotton plant improvement (Khan *et al*., 2009, 2010b). Therefore, a research project sought to quantify the genetic potential, heritability, inbreeding depression, and yield correlation with various yield-contributing traits in the upland cotton $F_{1\text{-}2}$ populations and their parental genotypes.

MATERIALS AND METHODS

Experimental site and genetic material

The presented study on upland cotton (*Gossypium hirsutum* L.) commenced during 2019–2021 in the Tashkent Region, Uzbekistan (41.389°N and 69.465°E). This region experiences cold winters and long, hot, and dry summers. The annual photoperiod (light/dark) is 16/8 h. This study evaluated the genetic potential and aspects of four upland cultivars, i.e., Ishonch, Navbakhor-2, Tashkent-6, S-6524, and their 12 F_1 diallel hybrids. These parental cultivars have an average fiber production (2.0–2.2 t/hm2) and varied levels of drought tolerance. The parental cultivars and their F_1 and F_2 hybrids, grown in a randomized complete block design, comprised a factorial arrangement and four replications. The cotton genotypes' planting transpired in 50 m long furrows with plant and row spacing of 10 and 60 cm, respectively.

Generally, the temperature rises in April, during the cotton-sowing season, and decreases in late September before harvesting. Information on maximum and minimum temperatures, air humidity, and total rainfall during the study period is available in Table 1. Recorded sunny days were between 180–185 days. Rainfall varied from 0 to 45 mm during the dry season for 5–6 months. The crop requires intensive irrigation throughout the vegetative period. Cotton irrigation followed a 1–2–1 (pre-flowering – flowering – boll opening) sequence with 900 m^3/hm^2 of water applied before flowering, two applications of 1200 m^3/hm^2 each during flowering, and 900 m^3/hm^2 before the boll-opening phases (Xamidov and Matyakubov, 2019). The said sequence is a widely used optimal irrigation protocol in cotton production in Uzbekistan. Soil moisture also contributes to water during seed germination. For crop protection purposes, the insecticides Bi-58 (BASF, Germany) and Hexachloran application controlled sucking (aphids) and chewing (bollworm) insects, respectively. The fertilizers' application ensued during tillage and before irrigation per annum at 250:180:115 NPK kg/ha rate.

Table 1. Maximum and minimum temperatures, air humidity, and the amount of total rainfall during the study period.

Months	Maximum temp. (°C)			Minimum temp. (°C)			Average relative humidity (%)			Total rainfall (mm)		
	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021
April	+28°	+27°	+29°	+5°	+4°	+4°	34%	32%	34%	42.38	3.98	4.38
May	+36°	+33°	+35°	+10°	+8°	+10°	26%	30%	33%	11.25	2.95	3.36
June	+36°	+37°	+38°	+16°	+15°	+16°	19%	25%	30%	6.90	1.15	1.90
July	+42°	+43°	+40°	+20°	+20°	+19°	15%	15%	19%	2.43	0.00	0.12
August	+40°	+39°	+36°	+17°	+17°	+15°	14%	14%	18%	0.08	0.00	0.05
September	+36°	+32°	+30°	+10°	+11°	+10°	15%	22%	21%	1.05	0.36	0.31
October	+28°	+29°	+26°	+6°	+3°	+4°	29%	29%	26%	2.78	2.74	2.55

Data recorded and statistical analysis

Genetic variance and heritability

The study of economic traits of the parental genotypes and their F_1 hybrids had data recorded on boll weight, bolls per plant, and seed cotton yield per plant. These parameters also served to monitor the stress conditions for comparison with irrigated conditions. First, the data underwent analysis of variance (Steel *et al.,* 1997). Genotypic (GCV), phenotypic (PCV), and environmental (ECV) coefficients of variance estimation followed Burton and Devane (1953). Broad-sense heritability calculation employed the technique of Hanson *et al.* (1965), with genetic gain estimated by Johnson *et al.* (1955). Correlation coefficient computation used the formula given by Kwon and Torrie (1964), as follows:

$$V_g = \text{(Genotypes mean squares – Error mean squares)/Number of replications}$$

$$V_e = \text{Error mean squares}$$

$$V_p = V_g + V_e,$$

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

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

$$\text{Environmental coefficient of variation (ECV)} = \sqrt{V_e}/GM \times 100$$

Where:
V_g: Genotypic variance, V_p: Phenotypic variance, V_e: Environmental variance, and GM: Grand mean of the trait.

Broad-sense heritability (h^2) on an entry mean basis attained calculation as:

$$h^2 = Vg/Vp$$

The expected genetic gain (GG) for each trait followed the below calculation:

$$\text{Genetic gain (GG)} = k.\ h^2 \sqrt{vp}$$

The genetic gain (GG) as a percent of mean for each trait used the following computation:

$$\text{Genetic gain (GG)} = GG/GM \times 100$$

Where:
K: 1.40 at 20% selection intensity for a trait, V_P: Phenotypic variance for a trait, h^2: Broad sense heritability for a trait, and GG: genetic gain (expected response to selection).

Dominance coefficient

The dominance coefficient for various traits studied in the cotton F_1 populations had the following calculations according to the *S. Wright* formula given in the research work of Beil and Atkins (1965):

$$hp = \frac{F_1 - MP}{P - MP}$$

Where:
hp: dominance coefficient, F_1: the evaluated arithmetic mean of the hybrid, MP: the evaluated arithmetic mean of both parents, and P: the evaluated arithmetic mean of the best parents.

Mid-parent heterosis

The F_1 heterosis over mid-parent calculation based on percent increase (+) or decrease (-) of F_1 hybrids over its mid-parent value engaged the following formula (Meredith and Brown, 1998:

$$\text{Mid-parent heterosis (MPH)} = ([F_1\text{-MP}]/\text{MP}) \times 100$$

Where:
F_1: the mean value of F_1, MP: the mean value of two parents involved in the cross.

Inbreeding depression

Inbreeding is the mating between individuals related by ancestry. When the individuals are closely related, e.g., in brother-sister mating or sib mating, the degree of inbreeding will be high. The highest degree of inbreeding succeeds by selfing. The main effect of inbreeding is an increase in homozygosity in the progeny, which is proportionate to the degree of inbreeding. The degree of inbreeding in an individual has an expression as the inbreeding coefficient (F). The degree of inbreeding is also proportional to the degree of homozygosity. Defining inbreeding depression may be the reduction in vigor and fertility due to inbreeding. Inbreeding depression calculation as percentage decrease (d) of the trait in F_2 in relation to F_1 used the following equation (Baloch *et al*., 1993):

$$\text{Inbreeding depression} = F_1\text{-}F_2 / F_1 \times 100.$$

RESULTS AND DISCUSSION

Mean performance, dominance coefficient, and heterosis

Analysis of variance (ANOVA) showed that cotton parental cultivars and their F_1 hybrids significantly differed for the traits, bolls per plant, boll weight, and seed yield per plant (Table 2). Along with the reliable differences, there were also unreliable differences. The bolls per plant fell, ranging from 14.80 to 17.35 and 14.50 to 19.20 in cotton parental cultivars and F_1 hybrids, respectively. Among parental genotypes, the cultivars C-6524 (17.35), Tashkent-6 (16.95), and Ishonch (16.45) produced the maximum number of bolls per plant, whereas cultivar Navbakhor-2 (14.80) presented the lowest number (Table 3). Among the F_1 hybrids, the hybrid Tashkent-6 × Ishonch displayed the maximum bolls per plant (19.20), followed by Tashkent-6 × Navbakhor-2 (17.30), and the lowest bolls per plant appeared in the F_1 hybrid Navbakhor-2 × Ishonch (14.50) (Table 1). The bolls per plant's main inheritance happen with negative and positive extreme dominance and negative incomplete dominance. It was also evident that the rate of heterosis was 30% in the combinations of Ishonch × Tashkent-6.

The boll weight ranged from 5.08 to 5.80 g and 5.23 to 6.31 g in parental cultivars and F_1 hybrids, respectively (Table 3). The heaviest boll weight occurred for cultivar Navbakhor-2 (5.80 g), followed by Tashkent-6 (5.75 g) and Ishonch (5.62 g), whereas the lightest boll weight resulted in cultivar C-6524 (5.08 g).Navbakhor-2 × C-6524 (6.31 g) and Ishonch × Navbakhor-2 (6.24 g), followed by Navbakhor-2 × Tashkent-6 (6.22 g) showed the maximum boll weight among F_1 the cross combinations. The lowest boll weight was notable in F_1 hybrids, C-6524 × Tashkent-6 (5.23 g), Tashkent-6 × Navbakhor-2 (5.38 g), and C-6524 × Navbakhor-2 (5.40 g). Boll weight mainly materialized under negative and positive overdominance and positive underdominance conditions. It was also apparent that the rate of heterosis was 16.0% in the cross combinations Ishonch × C-6524 and Navbahor-2 × C-6524.

The seed cotton yield per plant ranged from 57.18 to 63.97 g and 63.79 to 77.48 g in parental cultivars and F_1 hybrids, respectively (Table 3). The parental cultivar C-6524 (63.97 g) displayed the maximum seed cotton yield per plant, followed by two other cultivars, Tashkent-6 (62.40 g) and Ishonch (60.18 g). However, the parental genotype Navbakhor-2 (57.18 g) garnered the lowest seed cotton yield per plant. Among the F_1 hybrids, Tashkent-6 × Ishonch (77.48 g) and its reciprocal (74.15 g) and Navbakhor-2 × Ishonch (75.65 g) showed the optimum seed cotton yield per plant. However, the minimum seed cotton yield per plant manifested in the F_1 hybrid C-6524 × Tashkent-6 (63.79 g) and its reciprocal Tashkent-6 × C-6524 (64.75 g). The seed cotton yield per plant has the most inheriting in positive super dominance cases. It was also noticeable that the rate of heterosis is 14.59% in the F_1 hybrid Tashkent-6 × Ishonch. Overall, the mean performance of the genetic material for various yield-related traits revealed a considerable genetic variability amount. Previous studies on the assessment of cotton germplasm also reported a significant magnitude of genetic variability among the cotton parental genotypes and their hybrid populations for seed cotton yield and its components (Raza *et al.,* 2016; Nizamani *et al.,* 2017).

Table 2. Analysis of variance for various traits in upland cotton.

Source of variation	d.f.	Bolls plant^{-1}	Boll weight	Seed cotton yield plant^{-1}
Replications	3	5.36	5.49	0.93
Genotypes	15	6.97^{NS}	0.51**	121.52**
Error	45	3.02	0.003	32.79

**: Significant at $P \leq 0.01$, *: Significant at $P \leq 0.05$, NS: Nonsignificant.

Table 3. Mean performance, dominance inheritance, and heterotic effects of parental cultivars and their F1 hybrids for various yield-related traits in upland cotton**.**

Cotton cultivars and their F1 hybrids	Bolls plant^{-1}			Boll weight (g)			Seed cotton yield plant^{-1} (g)		
	M±SE	Hp	Heter %	M±SE	hp	Heter	M±SE	hp	Heter
Ishonch	16.45±0.63			5.62±0.06			60.18±3.00		
Navbakhor-2	14.80±0.53			5.80±0.06			57.18±3.38		
Tashkent-6	16.95±0.74			5.75±0.09			62.40±2.32		
C-6524	17.35±0.85			5.08±0.07			63.97±1.73		
Ishonch x Navbakhor-2	15.20±0.69	-0.52	-2.72	6.24±0.02	5.89	9.28	69.07±2.28	6.93	
Ishonch x Tashkent-6	17.00±1.06	1.2	30.0	5.73±0.04	0.69	4.50	74.15±2.86	11.59	
Ishonch x C-6524	15.50±0.54	-3.11	-8.28	5.51±0.08	0.59	16.00	70.74±3.20	4.57	
Navbakhor-2 x Ishonch	14.50±1.02	-1.36	-7.20	5.70±0.07	-0.11	-1.00	75.65±3.63	11.31	
Navbakhor-2 x Tashkent-6	15.40±0.51	-0.44	-2.99	6.22±0.07	-17.8	7.70	65.64±2.39	2.24	
Navbahar-2 x C-6524	16.90±1.29	0.65	5.13	6.31±0.07	2.42	15.99	66.71±4.75	1.81	
Tashkent-6 x Ishonch	19.20±0.73	10	14.97	5.45±0.05	-3.62	-4.13	77.48±2.43	14.59	
Tashkent-6 x Navbakhor-2	17.30±0.92	-1.33	8.97	5.38±0.06	-15.8	-6.84	68.62±2.37	3.38	
Tashkent-6 x C-6524	14.65±0.65	-12.5	-14.57	5.52±0.05	0.31	1.90	64.75±1.94	1.99	
C-6524 x Ishonch	15.20±0.90	0.76	-10.1	5.42±0.06	0.93	1.30	70.24±2.53	1.19	
C-6524 x Navbahar-2	16.20±1.00	0.1	0.77	5.40±0.07	-0.11	-6.49	67.17±2.45	1.94	
C-6524 x Tashkent-6	14.60±0.69	-12.75	-14.87	5.23±0.07	-0.55	-3.42	63.79±1.82	0.77	

Note: M- mean; SE- Standard error; hp- dominance coefficient; Heter %- Mid-parent heterosis.

Genotypic, phenotypic, and environmental variances

In parental genotypes and their F_1 hybrids, the ranges of genotypic, phenotypic, and environmental variances for various traits appear in Table 4. The GCV and PCV values varied from 6.99% to 12.45%.The highest GCV and PCV effects (6.99% and 11.00%, respectively) prevailed, followed by bolls per plant (6.17% and 12.45%, respectively) for seed cotton yield per plant. However, the lowest values of GCV and PCV were evident for boll weight (5.30% and 6.39%, respectively). Khan *et al*. (2010a, b) reported the utmost genetic variability in cotton segregating populations for economically important traits and declared it a prerequisite for successful breeding programs. Adequate information regarding genotypic variances makes selection in breeding populations effective as long as environmental effects mainly influence cotton plant traits (Magadum *et al.,* 2012). The boll weight showed the lowest GCV and PCV values, suggesting limited room for further improvement in these traits. For the attributes with low estimates of GCV and PCV, the breeders should search for the source of the maximum genetic variability for further improvement. Cotton breeders must exploit Uzbek germplasm from diverse sources to identify the genetic variability in the breeding populations.

The ECV ranged from 11.44% to 17.50%, respectively (Table 4). The highest ECV values were prominent for bolls per plant (17.50%), followed by seed cotton yield (11.44%), suggesting that these traits garnered considerable effects from environmental factors. The selection of the genotypes in early generations with moderate to high GCV and PCV were also suggestions for improvement in seed cotton yield and its component traits in upland cotton (Shao *et al.*, 2016). Thus, genetic variability with high heritability estimates is vital in the inheritance and improvement of yield-related traits in upland cotton (Ahmad *et al.*, 2011).

The coefficient of phenotypic variation has the same contribution as the coefficient of genotypic variation. In the presented study, the GCV and PCV for all traits showed close resemblance, indicating that these traits incur less influence from the environment. The highest GCV and PCV were remarkable for the features, boll weight, and seed cotton yield per plant, and effective selection is a suggestion to isolate the most potential cotton lines. Past studies also reported similar observations for yield-related traits in upland cotton populations (Amir *et al.,* 2012; Abbas *et al.,* 2013).

Heritability (broad sense)

The latest investigations revealed the highest heritability (broad sense) came from the boll weight and seed cotton yield (Table 4). However, low heritability (bs) was evident for bolls per plant. The high heritability estimates highlighted the importance of genetic variance, also depicting that the genetic variation among cotton populations for most traits (except bolls per plant) was under control by genetic factors. High heritability is a determinant of genotype flexibility in the selection process. In the existing study, high heritability and genetic gain occurred for boll weight and seed cotton yield per plant, reflecting the dominance of

Table 4. Genotypic, phenotypic, and environmental variances, coefficient of variation, broad sense heritability, and genetic grain for various traits in upland cotton.

Traits	GCV (%)	PCV (%)	ECV (%)	h^2	GG	GG (%)
Bolls plant^{-1}	6.17	12.45	10.7	0.24	1.01	6.31
Boll weight	5.30	6.39	1.06	0.82	0.72	12.82
Seed cotton yield plant^{-1}	6.99	11.00	8.50	0.40	6.17	9.16

GV: Genotypic variance; GCV%: Genotypic coefficient of variance; PV: Phenotypic variance; PCV%: Phenotypic coefficient of variance; EV: Environmental variance; ECV%: Environmental coefficient of variance; h^2: Heritability (broad sense); Genetic gain: GG.

Table 5. Correlation coefficients among the yield-related traits in upland cotton.

Traits	Bolls plant^{-1}	Boll weight	Seed cotton yield plant^{-1}
Bolls plant^{-1}	-		
Boll weight	-0.045^{NS}	-	
Seed cotton yield plant^{-1}	0.763***	0.554***	-

***: Significant at $P \leq 0.001$, NS: Nonsignificant.

additive gene action in the inheritance of these traits. The work of Johnson *et al.* (1955) revealed that high heritability was not always an indication of high genetic gain. However, if the transmission of heredity from generation to generation is mainly due to non-additive gene effects, then the expected genetic gain will be low; if some additive gene effects exist, then the expected genetic gain will be high (Panse, 1957). Preetha and Raveendran (2007) also reported the highest heritability and genetic gain for seed cotton yield and its contributing traits in upland genotypes.

In this study, under water deficit conditions and considering genetic variability, heritability, and genetic gain, selection would be effective for bolls per plant and boll weight besides seed cotton yield per plant for developing high-yielding cotton cultivars. Hence, the pedigree breeding method will be a reward for improving the traits under investigation. Characteristics with high heritability and genetic gain can be beneficial as tools in the selection process, with such features controlled by additive gene effects and less affected by environmental conditions (Panse, 1957). The genetic gain (as percent of means) for various traits ranged from 6.31% to 12.82% (Table 4). A higher genetic gain (as a percentage of the mean) was remarkable for boll weight (12.82%), followed by seed yield per plant (9.16%) and bolls per plant (6.31%). High heritability and genetic gain were evident for seed cotton yield per plant and boll weight, making these traits highly reliable during selection. In recent studies, some genotypes were distinct as potential donors for improvement in different attributes. Reports of high heritability and moderate genetic gain for lint% surfaced in upland cotton genotypes (Shavkiev *et al*., 2021).

Correlation coefficient

The bolls per plant revealed a significant ($P \leq 0.001$) positive association with seed cotton yield; however, the said association was negative with all other traits (Table 5). Boll weight exhibited a significant ($P \leq 0.001$) positive correlation with seed cotton yield. Currently, greater importance should focus on studying the relationship between yield-related traits and seed cotton yield. Past studies indicated the positive correlation of seed cotton yield with bolls per plant and boll weight in cotton (Shavkiev *et al.*, 2020; Zeeshan *et al.*, 2020). Previous studies also reported the positive correlation of seed cotton yield with lint% and boll weight in upland cotton genotypes (Amanov *et al.*, 2020). Tohir *et al.* (2018) mentioned the positive correlation of seed cotton yield with bolls per plant and boll weight in upland cotton.

Inbreeding depression

In the presented experiment, on average, the highest number of bolls per plant occurred in F_2 populations, Navbakhor-2 × Ishonch (19.14±0.84), Navbakhor-2 × Ishonch (19.14±0.84), and C-6524 × Ishonch (18.3±0.81) (Table 6). The highest heritability was also evident in the cross combinations Navbakhor-2 × Ishonch (71%) and C-6524 × Ishonch (74%). In F_2 populations, the determined variation index ranged from 11.21–15.98. For the bolls per plant, the inbreeding depression values in the $F_{1\text{-}2}$ populations Trust × C-6524 and Navbakhor-2 × Ishonch were strongly negative (ID = -27.35 and ID = -32.00, respectively). In the cross combination Tashkent-6 × Ishonch, the inbreeding depression value was intensely positive (ID =

Table 6. Inheritance, variation, and inbreeding depression in F_2 populations for boll per plant in upland cotton.

F_2 populations	Bolls per plant			ID (%)
	M±SE	V (%)	h^2	
Ishonch x Navbakhor-2	15.56±0.52	14.61	0.56	-2.37
Ishonch x Tashkent-6	16.61±0.67	15.44	0.66	2.29
Ishonch x C-6524	19.74±0.51	11.21	0.56	-27.35
Navbakhor-2 x Ishonch	19.14±0.84	14.71	0.71	-32.00
Navbakhor-2 x Tashkent-6	15.78±0.55	14.71	0.56	-2.47
Navbahar-2 x C-6524	17.27±0.60	14.18	0.62	-2.19
Tashkent-6 x Ishonch	15.65±0.56	14.90	0.58	18.49
Tashkent-6 x Navbakhor-2	17.23±0.66	14.71	0.63	0.40
Tashkent-6 x C-6524	15.56±0.44	13.51	0.66	-6.21
C-6524 x Ishonch	18.3±0.81	15.56	0.74	-20.39
C-6524 x Navbakhor-2	15.94±0.66	15.98	0.65	1.60
C-6524 x Tashkent-6	15.81±0.50	14.06	0.54	-8.29

Table 7. Inheritance, variation, and inbreeding depression in F_2 populations for seed yield per plant in upland cotton.

F_2 populations	Seed cotton yield per plant			ID (%)
	M±SE	V (%)	h^2	
Ishonch x Navbakhor-2	91.47±1.78	15.9	0.59	11.06
Ishonch x Tashkent-6	112.83±1.4	13.1	0.66	-1.57
Ishonch x C-6524	111.76±1.04	13	0.61	-12.70
Navbakhor-2 x Ishonch	89.61±1.03	16.8	0.71	-3.16
Navbakhor-2 x Tashkent-6	70.04±1.83	19.2	0.59	13.18
Navbahar-2 x C-6524	95.05±1.3	15.5	0.65	6.02
Tashkent-6 x Ishonch	68.92±1.31	19.8	0.65	-4.22
Tashkent-6 x Navbakhor-2	86.98±1.51	17	0.67	-7.06
Tashkent-6 x C-6524	86.45±1.9	17.9	0.7	-1.27
C-6524 x Ishonch	83.17±1.83	17.7	0.66	-2.77
C-6524 x Navbakhor-2	76.93±1.54	19.2	0.66	-1.67
C-6524 x Tashkent-6	82.2±1.33	16.5	0.62	-8.60

18.49). For bolls per plant, significant inbreeding depression emerged in F_2 populations of upland cotton (Baloch *et al*., 1993; Khan *et al*., 2010a).

In the latest experiment, the highest seed cotton yield resulted in F_2 populations Ishonch × Tashkent-6 and Ishonch × C-6524 (112.83±1.4 and 111.76±1.04 g, respectively) (Table 7). However, the lowest rate of the yield was visible in F_2 populations Navbakhor-2 × Tashkent-6 and C-6524 × Navbakhor-2 (70.04±1.83 and 76.93±1.54 g, respectively). The maximum level of heritability appeared in the cross combinations Navbahor-2 × Ishonch and Tashkent-6 × C-6524 (71% and 70%, respectively). The variation index in F_2 hybrids showed as 13.0%–19.2%. For seed cotton yield, the inbreeding depression in the F_{1-2} cross combination Ishonch × C-6524 was considerably negative (ID = -12.70). In the F_2 cross combination Navbakhor-2 × Tashkent-6 and Ishonch × Navbahor-2, the significant positive inbreeding depression values (ID = 13.18 and ID = 1.06, respectively) surfaced. For seed cotton yield, significant inbreeding depression has also emerged in F_2 populations in upland cotton (Soomro and Kalhoro, 2000; Khan *et al*., 2007).

The F_2 population Ishonch × C-6524 showed the highest value of boll weight (6.21±0.06 g). The maximum level of heritability was 72% in the F_2 cross combination Tashkent-6 × C-6524 (Table 8). In F_2 populations, the variation index emerged

Table 8. Inheritance, variation, and inbreeding depression in F_2 populations for boll weight in upland cotton.

F_2 populations	Boll weight			ID (%)
	M±SE	V (%)	h^2	
Ishonch x Navbakhor-2	5.55±0.06	29.83	0.61	8.51
Ishonch x Tashkent-6	5.82±0.07	27.97	0.61	4.06
Ishonch x C-6524	6.21±0.06	26.31	0.61	-5.75
Navbakhor-2 x Ishonch	5.88±0.06	28.05	0.61	-5.83
Navbakhor-2 x Tashkent-6	5.40±0.08	31.15	0.63	-3.75
Navbahar-2 x C-6524	5.93±0.12	28.67	0.63	-3.56
Tashkent-6 x Ishonch	5.68±0.13	30.14	0.65	-3.06
Tashkent-6 x Navbakhor-2	5.76±0.06	28.47	0.61	-13.12
Tashkent-6 x C-6524	5.59±0.06	29.23	0.72	1.74
C-6524 x Ishonch	5.57±0.07	29.66	0.61	-0.71
C-6524 x Navbakhor-2	5.49±0.11	31.07	0.63	-14.06
C-6524 x Tashkent-6	5.68±0.09	30.19	0.65	-0.54

as 26.31%–31.15%. In F_2 cross combinations C-6524 × Navbakhor-2 and Tashkent-6 × Navbakhor-2, the inbreeding depression values for the boll weight indicated as immensely negative (ID = -14.06 and ID = -13.12, respectively). A starkly positive (ID = 8.51) inbreeding depression was noteworthy in the F_2 combination Ishonch × Navbahor-2. However, the inbreeding depression was positive in the F_2 populations Ishonch × Navbahor-2, Ishonch × Tashkent-6, and Tashkent-6 × C-6524. Reports stated a similar type of inbreeding depression in F_2 populations for various traits in upland cotton (Khan *et al*., 2007, 2010a).

CONCLUSIONS

The parental cotton cultivars Ishonch and Navbakhor-2 and their F_1 hybrids showed more stability and performed better than other genotypes. Broad-sense heritability was the highest for boll weight and seed cotton yield. Based on this trait's productivity, heritability, and variability, the inbreeding depression was positive in the F_2 populations Ishonch × Navbakhor-2 and Navbakhor-2 × Tashkent-6. According to productivity, cultivars Ishonch, Navbakhor-2, and Tashkent-6 were distinctly positive donors. Based on the bolls in the plant, heritability, variability, and inbreeding depression, the F_2 populations Ishonch × Tashkent-6, Tashkent-6 × Ishonch, Tashkent-6 × Navbahor-2, and C-6524 × Navbahor-2 arose to be positive.

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REFERENCES

Abbas HG, Mahmood A, Ali Q, Khan MA, Nazeer W, Aslam T, Zahid W (2013). Genetic variability heritability genetic advance and correlation studies in cotton (*G. hirsutum* L.). *Int. Res. J. Microbiol*. 4(6): 156–161.

Ahmad M, Khan NU, Mohammad F, Khan SA, Munir I, Bibi Z, Shaheen S (2011). Genetic potential and heritability studies for some polygenic traits in cotton (*G. hirsutum* L.). *Pak. J. Bot.* 43(3): 1713–1718.

Ahmad W, Khan NU, Khalil MR, Parveen A, Aiman U, Saeed M, Ullah S, Shah SA (2008). Genetic variability and correlation analysis in upland cotton. *Sarhad J. Agric.* 24(4): 573–580.

Amanov BK, Abdiev F, Muminov K, Shavkiev J, Mamedova F (2020). Valuable economic indicators among hybrids of Peruvian cotton genotypes. *Plant Cell Biotechnol. Mol. Biol*. 21(67-68): 35–46.

Amanov BK, Muminov K, Samanov S, Abdiev F, Arslanov D, Tursunova N (2022). Cotton introgressive lines assessment through seed cotton yield and fiber quality characteristics. *SABRAO J. Breed. Genet*. 54(2): 321–330.

Amir S, Farooq J, Bibi A, Khan SH, Saleem MF (2012). Genetic studies of earliness in *G. hirsutum* L. *Int. J. Agron. Vet. Med. Sci.* 6(3): 189–207.

Baloch MJ, Lakho AR, Soomro AH (1993). Heterosis in interspecific cotton hybrids. *Pak. J. Bot.* 25: 13–20.

Beil GM, Atkins RE (1965). Inheritance of quantitative characters in grain sorghum. *Iowa State J. Sci.* 39(3): 345–358.

Burton GN, Devane EM (1953). Estimating heritability in Fall Fescue (*Festuca arundinacea* L.) from replicated clonal materials. *Agron. J.* 45: 478–481.

Chandio MA, Kalwar MS, Baloch GM (2003). Gene action for some quantitative characters in upland cotton (*G. hirsutum* L.). *Pak. J. Sci. Indus. Res*. 46(13): 295–299.

Chorshanbiev NE, Nabiev SM, Azimov AA, Shavkiev JSH, Pardaev EA, Quziboev AO (2023). Inheritance of morpho-economic traits and combining ability analysis in intraspecific hybrids of *Gossypium barbadense* L. *SABRAO J. Breed. Genet*. 55(3): 640–652. http://doi.org/10.54910/sabrao2023.55.3.4.

Hanson CH, Robinson HF, Comstock RE (1965). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.* 48:314–318.

Johnson HW, Robinson HE, Comstock RE (1955). Estimate of genetic and environmental variability in soybean. *Agron. J*. 47: 314–318.

Khan NU, Basal H, Hassan G (2010a). Cottonseed oil and yield assessment via economic heterosis and heritability in intra-specific cotton populations. *Afr. J. Biotechnol.* 9(44): 7418–7428.

Khan NU, Hassan G, Kumbhar MB, Kang S, Khan I, Parveen A, Aiman U, Saeed M (2007). Heterosis and inbreeding depression and mean performance in segregating generations in upland cotton. *Eur. J. Scien. Res. 17*: 531–546.

Khan NU, Hassan G, Marwat KB, Farhatullah, Batool S, Makhdoom K, Khan I, Khan IA, Ahmad W (2009). Genetic variability and heritability in upland cotton. *Pak. J. Bot.* 41(4): 1695–1705.

Khan NU, Marwat KB, Hassan G, Farhatullah, Batool S, Makhdoom K, Ahmad W, Khan HU (2010b). Genetic variation and heritability for cottonseed, fiber and oil traits in *G. hirsutum* L. *Pak. J. Bot.* 42(1): 615–625.

Kwon SH, Torrie JH (1964). Heritability and interrelationship among traits of two-soybean population. *Crop Sci*. 4: 194–202.

Magadum S, Banerjee U, Ravikesavan R, Gangapur D, Boopathi NM (2012). Variability and heritability analysis of yield and quality traits in interspecific population of cotton (*Gossypium Spp*.). *Bioinfolet* 9(4A): 484–485.

Makamov A, Shavkiev J, Kholmuradova M, Boyqobilov U, Normamatov I, Norbekov J, Khusenov N, Kushakov SH, Yuldasheva Z, Khoshimov S, Buriev Z (2023). Cotton genotypes appraisal for morphophysiological and yield contributing traits under optimal and deficit irrigated conditions. *SABRAO J. Breed. Genet*. 55(1): 74–89. http://doi.org/10.54910/sabrao2023.55.1.7.

Makhdoom K, Khan NU, Batool S, Bibi Z, Farhatullah, Khan S, Mohammad F, Hussain D, Raziuddin, Sajjad M, Khan N (2010). Genetic aptitude and correlation studies in upland cotton (*G. hirsutum* L.). *Pak. J. Bot*. 42(3): 2011–2017.

Matniyazova H, Nabiev S, Azimov A, Shavkiev J (2022). Genetic variability and inheritance of physiological and yield traits in upland cotton under diverse water regimes. *SABRAO J. Breed. Genet*. 54(5): 976–992.

Meredith WR, Brown JS (1998). Heterosis and combining ability of cottons originating from different regions of United States. *Cotton Sci*. 2: 77–84.

Muminov K, Amanov B, Buronov A, Tursunova N, Umirova L (2023). Analysis of yield and fiber quality traits in intraspecific and interspecific hybrids of cotton. *SABRAO J. Breed. Genet*. 55(2): 453–462. http://doi.org/10.54910/sabrao2023.55.2.17.

Narimonov A, Azimov A, Yakubjanova N, Shavkiev J (2023). Scientific basis of cottonseed germination in the Central Region of Uzbekistan. *SABRAO J. Breed. Genet*. 55(5): 1561–1572. http://doi.org/10.54910/sabrao2023.55.5.10.

Nizamani F, Baloch MJ, Baloch AW, Buriro M, Nizamani GH, Nizamani MR, Baloch IA (2017). Genetic distance, heritability and correlation analysis for yield and fiber quality traits in upland cotton genotypes. *Pak. J. Biotechnol*. 14(1): 29–36.

Normamatov IS, Makamov AKH, Boykobilov UA, Achilov SG, Khusenov NN, Norbekov JK, Kholmuradova MM, Yuldashova ZZ, Mirzakhmedov MKH, Kushakov SO, Karabekov OG, Darmanov MM, Asrorov AM, Buriev Z (2023). Morpho-biological traits of upland cotton at the germination stage under optimal and salinity soil conditions. *Asian J. Plant Sci.*22: 165–172.

Panse VG (1957). Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet. Plant Breed.* 17(3): 318–328.

Preetha S, Raveendran TS (2007). Genetic variability and association studies in three different morphological groups of cotton (*G. hirsutum* L.). *Asian J. Plant Sci*. 6(1): 122–128.

Raza H, Khan NU, Khan SA, Gul S, Latif A, Hussain I, Khan J, Raza S, Baloch M (2016). Genetic variability and correlation studies in F4 populations of upland cotton. *J. Anim. Plant Sci.* 26(4): 1048–1055.

Rejapova MM, Azimov AA, Khatamov MM, Kurbanbaev ID, Matniyazova HX (2020). Indicators of abiotic and biotic stresses of local and foreign cotton (*G. hirsutum* L.). *Plant Cell Biotechnol. Mol. Biol.* 21(44): 8–15.

Sanaev NN, Gurbanova NG, Azimov AA, Norberdiev TN, Shavkiev SJ (2021). Inheritance of the plant shape trait of the varieties and introgressive lines of *G. hirsutum* L. in drought conditions. *Plant Cell Biotechnol. Mol. Biol.* 22(25-26): 122–129.

Shao D, Wang T, Zhang H, Zhu J, Tang F (2016). Variation, heritability and association of yield, fiber and morphological traits in a near long staple upland cotton population. *Pak. J. Bot.* 48(5): 1945–1949.

Shavkiev J, Azimov A, Khamdullaev S, Karimov H, Abdurasulov F, Nurmetov K (2023). Morpho-physiological and yield contributing traits of cotton varieties with different tolerance to water deficit. *J. Wildlife Biodivers*. 7(4): 214–228.

Shavkiev J, Azimov A, Nabiev S, Khamdullaev S, Amanov B, Matniyazova H, Kholikova M, Yuldashov U (2021). Comparative performance and genetic attributes of upland cotton genotypes for yield-related traits under optimal and deficit irrigation conditions. *SABRAO J. Breed. Genet*. 53(2): 157–171.

Shavkiev J, Nabiev S, Azimov A, Chorshanbiev N, Nurmetov KH (2022). Pima cotton (*Gossypium barbadense* L.) lines assessment for drought tolerance in Uzbekistan. *SABRAO J. Breed. Genet*. 54(3): 524–536.

Shavkiev J, Nabiev S, Azimov A, Khamdullaev S, Amanov B, Matniyazova H, Nurmetov K (2020). Correlation coefficients between physiology, biochemistry, common economic traits and yield of cotton cultivars under full and deficit irrigated conditions. *J. Crit. Rev.* 7(4):131–136.

Soomro AR, Kalhoro AD (2000). Hybrid vigor (F_1) and inbreeding depression (F_2) for some economic traits in crosses between glandless and glanded cotton. *Pak. J. Biol. Sci.* 3: 2013–2015. https://doi.org/10.3923/pjbs.2000.2013.2015.

Steel RGD, Torrie JH, Dicky DA (1997). Principles and Procedures of Statistics, A Biometrical Approach. 3rd Edition. McGraw Hill, Inc. Book Co., New York, pp. 352–358.

Tohir AB, Rustam MU, Yang H, Shukhrat AH, Sardorbek M, Jaloliddin S, Saidgani N, Zhang D, Alisher AA (2018). Effect of water deficiency on relationships between metabolism, physiology, biomass, and yield of upland cotton (*G. hirsutum* L.). *J. Arid Land* 10(3): 441–456.

Tian Y, Shuai Y, Yang H, Shao C, Wu H, Fan L, Li Y, Chen X, Narimanov A, Usmanov R, Baboeva S (2023). Extraction of cotton information with optimized phenology-based features fromsentinel-2 images. Remote Sens. 15:1988.

World Markets and Trade (2022). United States Department of Agriculture Foreign Agricultural Service Cotton. https://kun.uz/en/news/2021/03/04/uzbekistan-named-sixth-largest-cotton-producer-in-the-world.

Worldbank.org (2020). Policy dialogue on agriculture modernization in Uzbekistan. Cotton-Textile Clusters in Uzbekistan: Status and Outlook, pp. 4.

Xamidov MX, Matyakubov BS (2019). Cotton irrigation regime and economical irrigation technologies. Monography Tashkent.

Zeeshan MK, Wajid AJ, Jay KS, Muhammad IB, Adil AG, Kirshan KM, Muhammad S, Mitho C (2020). Studies on correlation and heritability estimates in upland cotton (*G. hirsutum* L.) genotypes under the agro-climatic conditions of Tandojam, Sindh, Pakistan. *Pure Appl. Biol*. 9(4): 2272–2278.