Online ISSN: 2588-3526

Journal of Wildlife and Biodiversity

Volume 8(4): 107-118 (2024) (http://www.wildlife-biodiversity.com/)

Research Article

Morpho-economic traits of interspecific cotton hybrid and degree of dominance

Mukhlisa Kudratova[1], Abdullah Iskandarov[1], Feruza Rafieva[1], Abdulqahhor Toshpulatov[1], Mukhammad Khidirov[1], Barno Oripova[1], Asiya Safiullina[1], Bunyod Gapparov[1], Ozod Turaev[1,2,3], Dilrabo Ernazarova[1,2], Fakhriddin Kushanov[1,2]

[1]Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan
[2]National University of Uzbekistan named after Mirzo Ulugbek, Tashkent, Uzbekistan
[3]Research Institute of Plant Genetic Resources, National Center for Knowledge and Innovation in Agriculture, Tashkent, Uzbekistan
Email: muxlisaqudratova6@gmail.com

[1]Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan
[2]National University of Uzbekistan named after Mirzo Ulugbek, Tashkent, Uzbekistan
*Email: muxlisaqudratova6@gmail.com

Received: 01 July 2024 / Revised: 15 September 2024 / Accepted: 21 September 2024/ Published online: 21 September 2024.

How to cite: Kudratova, M., Iskandarov, A., Rafieva, F., Toshpulatov, A., Khidirov, M., Barno, O., Safiullina, A., Turaev, O., Ernazarova, D., Kushanov, F. (2024). Characterization of morpho-biological and economic characteristics of interspecific cotton hybrid and degree of dominance, Journal of Wildlife and Biodiversity, 8(4), 107-118. **DOI**: https://doi.org/10.5281/zenodo.

Abstract

This article describes the morphological characteristics of the combinations obtained from the cotton varieties *G. mustelinum* Miers ex Watt and *G. hirsutum* L. types tropical ssp. glabrum var. marie-galante and ruderal ssp. *punctatum* wild tetraploid species by complex hybridization with the cultivated fiber length, fiber yield, boll weight, and 1000 seed weight per plant indicators were determined from valuable economic traits. The results of the level of dominance coefficient in research samples are presented. Based on complex hybridization, genotypes with higher fiber length, fiber output, and 1000 seed weight were formed compared to parental forms in F1 hybrids.

Keywords: *G. mustelinum* Miers ex Watt., *G. hirsutum* L., ruderal form, tetraploid, hybridization, morpho-biological characters, dominance

Introduction

Currently, cotton (*Gossypium* L.) is one of the most important textile crops in the world, producing natural and quality fiber. For example, in 2017/18, the world's cotton production and use were estimated at 25.1 million tons (Adams et al., 2004). As predicted, world cotton production will grow and reach 26.1 million tons in 2026 (Alves et al., 2013). The *Gossypium* genus is represented by more than 50 species, divided after ploidy into two groups: diploid ($2n = 2x = 26$) and tetraploid ($2n = 4x = 52$) (Adams et al., 2004; Ashkani et al., 2015; Muminov et al., 2022; Amanov et al., 2020). Moreover, 45 species are diploid, and five remaining species are tetraploid (Ashkani et al., 2015). Among them, the diploid species such as *G. arboretum* L., *G. herbaceum* L., and tetraploid *G. hirsutum* L. and *G. barbadense* L. are cultivated only (Barroso et al., 2010; Muminov et al., 2022; Shavkiev et al., 2021,2022). Consequently, this kind of diversity of *Gossypium* species is a suitable model for studying the evolution, domestication, and polyploidy, as well as the study of ploidy effect on the most important agronomic traits of cotton (e.g., fiber quality), as well as the expression and inheritance of corresponding genes of interest (Shavkiev et al., 2021; Azimov et al., 2024).

Similar to most plants, the evolution of cotton was characterized by repeating cycles of whole genome duplication (Adams et al., 2004). At the same time, a parallel level of cytogenetic and genomic diversity emerged during the global spread of the cotton, which finally led to the appearance of eight groups of diploids (n = 13) species (groups A-G and K of genomes) (Adams et al., 2004; Khidirov et al., 2023). It should be noted that despite the existence of different types of polyploidy (Adams et al., 2004). the most common type is allopolyploidy, when two differentiated genomes, usually of various species, are combined in one cell nucleus due to hybridization (Adams et al., 2004).

Thus, allopolyploid duplication of the genome leads to numerous of molecular genetic interactions, inter-locus concerted evolution, differences in genomic evolution rates, interlocus transfer of genetic material, and possibly changes in gene expression (Adams et al., 2004). In addition, allopolyploidy may have stimulated the morphological, ecological, and physiological adaptation of cotton through natural selection based on a higher level of variability, such as a result of duplication of the gene set (Adams et al., 2004; Shavkiev et al., 2020; Sanaev et al., 2021).

For the same reasons, genome duplication may have given new opportunities for cotton improvement by directional selection (David et al., 2019). Another critical aspect of allopolyploidy is that not every allopolyploid has to strictly correspond to the concept of the simple summation of the ancestral diploid genomes. In some cases, the fusion of two different genomes is accompanied by significant genomic reorganization and non-Mendelian genetic inheritance (Freire, 2002).

According to molecular genetic data, cotton evolution has amounted to about 10–15 million years after the *Gossypium* diverged from other *Gossypieae* (Fryxell,1992). At the same time, the evolution of eight groups of diploid species (genomic groups A, G, and K) also occurred by the cotton widespread, which led to the arising of parallel levels of cytogenetic and genomic diversity (Guo et al., 2005). It should be noted that molecular genetics and cytogenetic studies show that the species lineages on the genealogical tree of the genus coincide with genomic groups A-G, K, and AD and geographic origin (Guo et al., 2005; Gupta et al., 2005). Currently, we can observe that the varieties created by various methods in the processes of cotton genetics and selection are similar to each other in terms of valuable economic characteristics and morphological indicators. During the growth period, the plant shows certain biological indicators based on the growth conditions, its genetic capabilities and under the influence of external factors. Among these indicators, one of the important tasks is the expansion of research and development works on the creation and introduction into production of new varieties with characteristics of quick ripening, tolerance to diseases and pests, and compatibility with soil and climate conditions (Iqbal et al., 2001; David et al., 2019; Ergashov et al., 2021; Zakirov et al., 2023).

Currently, special attention is being paid worldwide to the identification of the genes controlling them and their effective use in improving valuable economic traits in cotton. Various research projects on this issue are being carried out in Uzbekistan. Each variety has a large number of valuable farm traits, which further increases the quality of cotton. Traditional and molecular-genetic analysis of the inheritance of valuable economic traits in interspecific wild tetraploid species of cotton provides an opportunity to ensure and study their resistance to various abiotic and biotic stress factors (Matniyazova et al., 2022; Makamov et al., 2023; Shavkiev et al., 2023).

The genus *Gossypium* L. has a long history of taxonomic and evolutionary study. The genus Gossypium, belonging to the tribe family *Malvaceae*, contains approximately 46 diploids and 7 allotetraploid species, according to recent data on cotton systematics (Iqbal et al., 2001; Paterson et al., 2012). Here, diploid (n=x=13) species are divided into eight (A to G and K), and tetraploid (n=2x=26) species are divided into one (AD1-AD7) cytogenetic group (Wendel et al., 2010). In about 90 cotton-growing countries worldwide, four types are planted. Of this, *G. hirsutum* L. species occupy more than 90% of the total area of cotton cultivation on earth, followed by *G.barbadense* L. species at approximately 8%, and only 1% of the two diploid species, *G.arboreum* L. and *G.herbaceum* L., belong to the varieties(Muminov et al., 2023).

Upland cotton (*G. hirsutum* L.) is common among all species of the Gossypium family and is an essential raw material for the cotton industry (Brubaker et al., 2010). The center of origin of this species is Guatemala, but it is widespread throughout Central America and the Caribbean.

According to Mauer's (1954) classification, there are four groups of subspecies of G. hirsutum L: ssp. Mexican, ssp. punctum, and ssp. paniculatum and euhirsutum. These four subspecies include several wild forms and their cultivars, such as yucatanense, Richmond, latifolium, palmeri, morbilli, and purpurascens. According to molecular genetic data, the history of cotton evolution has amounted to about 10–15 million years after the Gossypium diverged from other Gossypieae (Adams et al., 2004). At the same time, the evolution of eight groups of diploid species (genomic groups A, G, and K) also occurred by the cotton widespread, which led to the arising of parallel levels of cytogenetic and genomic diversity (Adams et al., 2004). It should be noted that molecular genetics and cytogenetic studies show that the species lineages on the genealogical tree of the genus coincide with genomic groups A-G, K, and AD and geographic origin (Iqbal et al., 2001; Paterson et al., 2012).

The evolution studies of the *Gossypium* have shown that the origination of tetraploid species proceeded by polyploidization of A- (African) and D-genomes (American) diploid species (Iqbal et al., 2001). Alloploidization of these two genomes occurred about 1.5–2 million years ago, resulting in five different genomes: *G. darwinii*, *G. tomentosum*, *G. mustelinum*, *G. hirsutum* and *G. barbadense*, where the last two belong to cultivated species (Paterson et al., 2012). It was also proved that during the polyploidization process, the *G. arboreum* and *G. herbaceum* were as receptors of the A-genome and should be a predecessor because all existing polyploid species contain the cytoplasm of the A genome. At the same time, the D-genome donor appeared as *G. raimondii* (Paterson et al., 2012).

After the occurrence of the predecessor of allotetraploid species, at the initial stage of divergence led to the origination of two evolutionary lines of cotton with AD genomes: the first includes *G. mustelinum* (AD4 genome), the second one – all other species (AD1 – AD3 and AD5 genomes). In other words, the follow-up divergence of the second evolutionary line of AD genomes led to the emergence of recent allotetraploid cotton species such as *G. hirsutum* (AD1 genome), *G. barbadense* (AD2 genome), *G. tomentosum* (AD3 genome), and *G. darwinii* (AD5 genome) (Iqbal et al., 2001; Paterson et al., 2012). One of the important evolutionary events for *Gossypium* was the domestication of four wild species. This selection was based on the length and quality of cotton fiber, which is anatomically specialized unicellular trichomes located on the surface of the epidermis of seeds (Iqbal et al., 2001; David et al, 2019). This sequential process led to the domestication of four species of cotton: two American – *G. hirsutum* and *G. barbadense* and two Afro-Asian – *G. arboretum* and *G. herbaceum* (Iqbal et al., 2001). The homeland of the species G.mustelinum Miers ex Watt is Brazil, mainly distributed in the northeastern regions. This species is one of the five allotetraploids, and interspecific hybrids with cultivated cotton species, in particular *G. hirsutum* L. and *G.barbadense L.*, have been obtained (Sun et al., 2006).

G. mustelinum is commonly known as Brazilian cotton, and no other subspecies have been found in the areas where this species grows (Khan et al., 2020). When studying the levels of crossbreeding of *G. mustelinum* with cultivated species, it was found that the distribution area of the wild species is large. But despite this, the *G. mustelinum* wild type is less susceptible to foreign pollination, and the amount of hybridization with other species is very low. Resident populations of this wild species have not been found (Strygina et al., 2020). The genomes of *G.mustelinum* and *G.barbadense* L. are similar and closely related to producing F1 hybrids with high productivity and reproduction (Rafieva et al., 2022). Freire (2002) made several conclusions based on his experiences obtaining target hybrid forms between *G. hirsutum* L. and *G. mustelinum* L. The analysis of the studied literature shows that it is of urgent importance to effectively use the potential of tetraploid species in genetic selection research to create transgressive recombinants with a new genetic basis by involving wild and semi-wild species in the creation and improvement of cotton varieties.

According to Khalikova et al.(2013) research, in F1 plants obtained by crossing interspecies hybrid lines of *G. tomentosum* x *G. hirsutum* L. and interspecies hybrids of *G. barbadense* species, early ripening of the main valuable economic characters, a "plant productivity, fiber yield and fiber quality indicators are different compared to the parental generations, and in most of the parental forms studied together with F2 plants, the indicators according to the character were relatively positive and It was found that transgressive plants were isolated. Rizaev (1972) crossed the amphidiploid G. hirsutum x G. anomalum with the varieties of G. hirsutum L. and selected plants with complex characters, creating productive forms with some characters of the wild type, up to 35 mm fiber length.

Murotov et al. (1997) stated that by using the genetic potential of the Gossypium genus through complex hybridization, donors with characteristics such as water deficit and salinity tolerance, which were not evident in production varieties, were created. According to Munasov et al. (2003), complex hybridization is vital in forming new forms. Based on the study of the genetic possibility of creating early-early forms, it was found that selection in the third generation and early-early has a great opportunity to isolate valuable traits for the economy, including wilt-resistant plants. Based on this, the main goal of our research is to identify the species *G. mustelinum*, wild ssp. punctatum, and the cultivated tropical var. Description of the morphological and economic characteristics of Marie-Galante forms. It also aims to use these plants as a starting point for creating new cotton varieties. In addition, research consists of obtaining a single recombinant plant that embodies these useful features. it also isolates families and lines with a positive set of signs, studying the character of heredity of valuable economic and morphological characters from these recombinant plants.

Materials and Methods

Plant samples available in the "Unique Object" collection of the "Experimental polyploidy and phylogeny of cotton" laboratory of the Institute of Genetics and Experimental Plant Biology of the Academy of Sciences of the Republic of Uzbekistan were used in the research work. In this case, F1 was obtained by interspecific reciprocal hybridization of wild tetraploid *G.mustelinum* (AD4) with cultivated varieties *G.hirsutum* L. (AD1) with ssp. punctatum (ruderal) and ssp. glabrum var. marie-galante (cultivated tropical form) (F4 *G.hirsutum* ssp. punctatum × *G.mustelinum*) × (F4 *G.hirsutum* ssp. glabrum var. marie-galante × *G.mustelinum*). Degree of dominance of morphological and valuable economic traits in F1 (F4 *G. hirsutum* ssp. glabrum var. marie-galante × *G.mustelinum*) × (F4 *G.hirsutum* ssp. punctatum × *G.mustelinum*) combinations was analyzed. The morphological characteristics of the parental and F1 hybrids were described based on a special classifier (Lemeshev et al., 1989). The dominance coefficient in F1 hybrids determination was according to Griffing (1950):

$$hp = (F1-MP) / P-MP$$

Where:
hp – dominance coefficient;
F_1 – the evaluated arithmetic mean of the hybrid;
MP – the evaluated arithmetic mean of both parents;
P – the evaluated arithmetic mean of the best parents

G. hirsutum L. ssp.punctatum - ruderal (semi-wild) form. The plant bush is upright; the leaves are moderately dense, the height of the main stem is 60.0-70.0 cm, and it is green and moderately hairy. One opened boll weighs 2.5-3.5 g. Fiber is thick, white, fiber length - 27.0-32.0 mm. The plant is not very demanding on short days, heat-loving, medium-growing, resistant to sucking pests. *G. hirsutum* L. ssp. glabrum var. marie-galante is a cultivated tropical form. The plant is upright and branched, has moderate anthocyanin redness, and is hairless. The length of the main stem is 110.0-120.0 cm. The boll is medium, green, egg-shaped. The weight of cotton in one opened bur is 3.0-4.4 g. Fiber length - 27-30 mm, white color. The plant is mesophytic and requires short days. Pest resistant. *G. mustelinum* Miers ex Watt- wild form. The plant is medium-sized, the height of the main stem is (80.0-100.0 cm), weakly hairy, the boll is conical-ovoid, the tip is pointed, covered with black glands, 3-4 hip. The weight of cotton in one opened bur is 1.1-1.8 g. fiber 34.5 mm, light brown, sparse and ripe. The plant is strongly demanding for short days. Susceptible to spider mite. The research samples were subjected to phenological and laboratory analyses using generally accepted methods. The yield elements of the parental and F1 hybrids per plant, in particular the weight of the boll, were calculated. For this purpose, 10 mature bolls were collected from each plant.

Trait measurement and statistical analyses

Data were recorded for the 1000 seed weight, boll weight (g), lint %, and fiber length (mm). The mean data were subjected to analysis of variance according to Steel et al. (1997) to test the null hypothesis of no differences among various F1 hybrid populations and their parental cultivars. In this case, the Fisher criterion (F), the standard deviations (SD), the standard error (SE), and the degree of significant differences ($P \leq 0.05^*$, $P \leq 0.01^{**}$, and $P \leq 0.001^{***}$) determined the reliability of the differences among the genotypes for each trait.

Results

F_4 *G. hirsutum* L. ssp. *punctatum* × *G. mustelinum* is an upright plant; the leaves are moderately dense, the height of the main stem is 90.0-130.0 cm, and it has moderate anthocyanin redness. The total number of joints is 18.0-25.0; the branching is sympodial, unlimited, the first sympodial fruiting branch (hs) is on the 5th-7th joint, sympodial branches (s) are 18.0-25, 0 belonging to type I-II-III. The leaf is medium-sized (12.0 x 18.0 cm), dark green, 3-5-lobed, weakly hairy, 3 nectaries, round, colorless. The length of the leaf band is 10.0-15.0 cm, with an average anthocyanin redness. The flower is medium in size (6.0 cm) with a medium opening, and the length of the flower band is 1.3 cm. Sepals are 3, heart-shaped, tip 8-10-toothed (1.9-3.5 cm), with weak anthocyanin redness, external nectary of the petiole is 3, round, colorless, inner nectary is absent. Bracts are wavy and light green. Petals are 5 (4.5-2.5 cm), wavy yellow. Stamen is cylindrical and orange. The pistil has three columns; it protrudes 0.5 cm from the paternal column. Medium-sized, dark green, egg-shaped, unevenly pitted, sharp-pointed, surface covered with gossypol glands, wide opening, 3-4 cups. The weight of cotton in one open boll is 2.6-2.9 g; the seed is medium ovoid. The fiber is white. The plant requires a short day; all its organs are covered with gossypol glands, and spider mites moderately damage it.

F_4 *G. hirsutum* L. ssp. *glabrum* var. *marie-galante* × *G.mustelinum* - The plant grows upright, and the leaves are of medium thickness. The height of the plant is 110.0-150.0 cm, hairless, green, medium anthocyanin brown, and 2-3 monopodial branches. The total number of joints is 20.0-24.0. hs - in the 8th stanza. The number of sympodial branches is 15.0-22.0. The plant belongs to type I-II-III. The leaf is medium in size (8.0-12.0 cm), the total length is 17.0 cm. Three to five grooves, dark green, hairless. The main veins of the leaf plate are green. There is anthocyanin redness in the leaf band, leaf plate, and junction. Nectardo 1, oval, colorless. The length of the leaf band is 12.0-15.0 cm. The flower is medium-sized, 7.0 cm long, pale yellow, without spots at the base of the flower. Bracts and petals are medium in size (5.0-4.0) cm, and the edges of the sepals have weak anthocyanin redness. The flower is 1.5 cm long and has 3 nectaries. Colorless and dry, covered with gossypol glands. Style is 3.0 cm long, 4-lobed, untwisted, pale yellow; stigma is 0.5 cm longer than the anthers. filament - 0.4-0.6 cm. Bolls are medium-sized, egg-shaped, green and smooth surface, covered with gossypol glands. 4-5 cups, one ball of cotton weighs 3.0 g. The fiber is 33.0-35.0 mm long and white. The plant is demanding for short days, heat-loving, resistant to sucking pests.

Morphological indicators of hybrid combinations obtained with *G.mustelinum* type and *G.hirsutum* L. type varieties

F1 (*G. hirsutum* L. ssp. glabrum var. marie-galante × *G.mustelinum*) × (*G.hirsutum* L. ssp. punctatum × *G.mustelinum*) - the length of the main stem is 110.0-130.0 cm, the plant is upright, branched and compact, the stem is strongly hairy and has moderate anthocyanin redness. The total number of joints is 18.0-25.0, hs - in the 4th joint. The number of monopodial branches is 1-2, and the number of sympodial branches is 18.0-22.0. The plant belongs to type I-II. The total length of the leaf is 23.7 cm. Leaf blade -3-lobed dark green, 10.2 x 11.0 cm, leaf band -13.5 cm. The hairiness is moderate, there are anthocyanin spots on the leaf blade and leaf band. Nectardo 1 soaked. The total length of the flower is 6.6 cm. Petals 6.2 x 3.3 cm, pale yellow, without anthocyanin spots at the base. Bracts are 3 strongly cut, 5.5 x 2.0 cm with 10 teeth. Sepals are 3.3 x 1.4 cm, with 5-toothed gossypol glands. Pistil - 3.5 cm. Stigma 4 pieces. Filaments are located in medium density. Flower 1.5 cm. There are no anthocyanin spots in the green color. The boll is medium ovoid, the surface is green and smooth, covered with gossypol glands, 4-5 cups. The weight of one ball of cotton is 4.9 g. Fiber color - white. The plant is short-day demanding, heat-loving, and resistant to spider mites, but not resistant to aphids.

F1 (*G. hirsutum* L. ssp. punctatum × *G.mustelinum*) × (*G.hirsutum* L. ssp. glabrum var. marie-galante × *G.mustelinum*) - - the length of the main stem is 130.0-150.0 cm, the plant is upright, branched and compact, the stem has moderate pubescence and strong anthocyanin redness. The total number of joints is 17.0-22.0, the first sympodial branch is on the 5th joint. There are 1-2 monopodial branches, the number of sympodial branches is 15.0-20.0. The plant belongs to type I-II. The total length of the leaf is 24.0 cm. The leaf blade is dark green with 5 lobes, 12.0 x 11.5 cm. Leaf band 13.5 cm. Nectardo 1 soaked. The leaf band has anthocyanin spots, it has moderate hairiness. The total length of the flower is 6.5 cm. Petals 5.5 x 4.0 cm, pale yellow without anthocyanin spots. Bracts 5.3 x 3.0 cm with 10 teeth, 5 strongly cut. Sepals are 5-toothed, 3.5 x 3.0 cm, and have gossypol glands. Pistil is 3.5 cm. stigma is 4-lobed. filaments are densely arranged pale yellow. Inflorescence 2.0 cm green with three moist outer nectaries, no anthocyanin spots. Boll is medium, dark green, ovoid, unevenly pitted, with a sharp tip; the surface is covered with gossypol glands, wide opening, 4-5 cups. The seed is medium, ovoid. The fiber is white. The length of the fiber is 33.4 mm. The plant requires a short day; all its organs are covered with gossypol glands, moderately affected by spider mites, and moderately resistant to aphids.

The main economic characteristics of cotton, including fiber length, fiber yield, cotton weight per boll, and 1000 seed weight, are the main requirements for cotton raw materials in industrial production. Therefore, scientists have conducted many studies to isolate the forms with high economic signs and indicators.

In the study, valuable economic traits were studied in the initial samples and their F1 hybrid combinations. In the F4 combinations used as parental forms (F4 *G.hirsutum* ssp.punctatum × *G.mustelinum* and F4 *G.hirsutum* ssp. glabrum var. Marie-Galante × *G.mustelinum*), fiber length values were 33.4 mm, 34.1 mm respectively, and the coefficient of variation was 3.2-4.0%.

According to the fiber yield indicator, it was 30.6% in the combination of F4 *G.hirsutum* ssp. punctatum × *G.mustelinum*, and 32.6% in the combination of F4 *G.hirsutum* ssp.glabrum var. marie-galante × *G.mustelinum*. The variability amplitude is in the range of 24.7-36.1%, and the coefficient of variability is 3.7-5.3%, respectively. In addition, the characteristics of one pod weight and 1000 seed weight were also analyzed in parental forms. The weight of the boll was 4.8 g in the combination of F4 *G.hirsutum* ssp. punctatum × *G.mustelinum*, and 4.6 g in the combination of F4 *G.hirsutum* ssp. glabrum var. marie-galante × *G.mustelinum*. Similarly, the 1000 seed weight traits were 100.8 gm and 99.6 gm respectively (Fig.1).

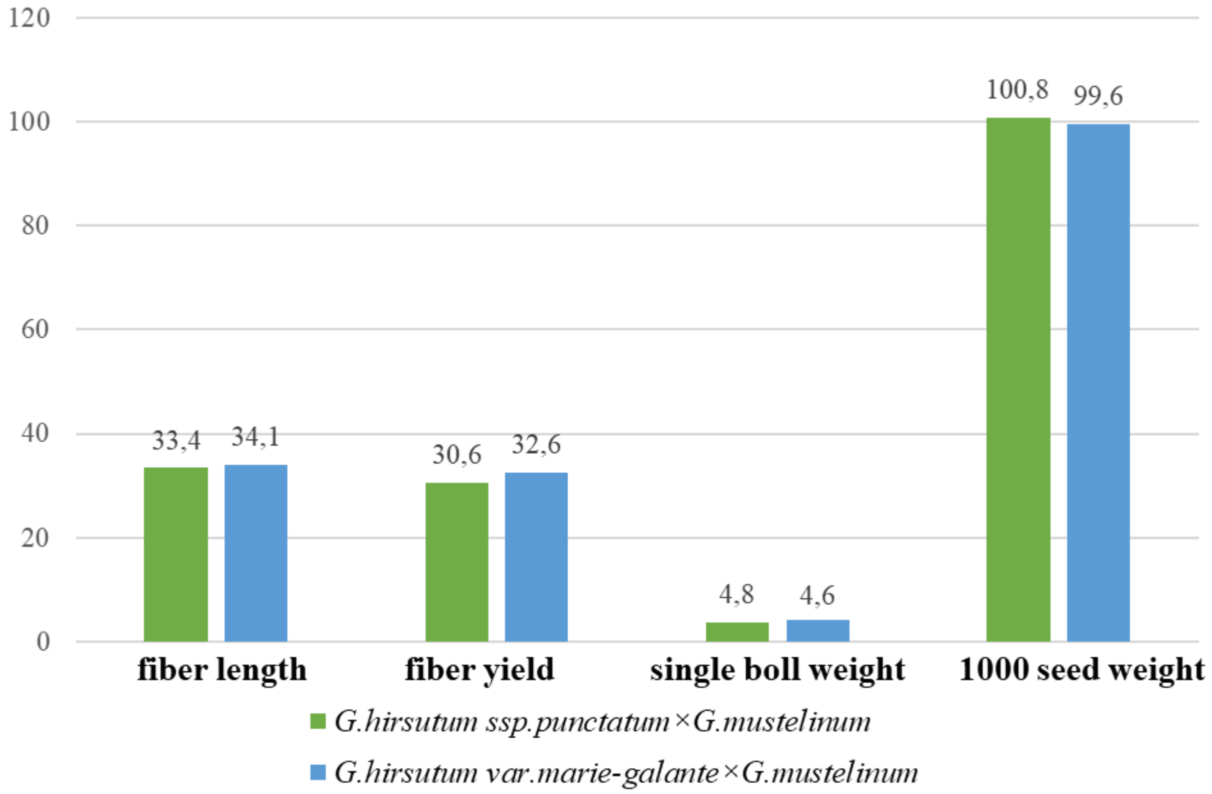

Figure 1. Morpho-yield traits in parents' genotypes

The fiber length indicator of the F1 (*G. hirsutum* ssp. glabrum var. marie-galante × *G.mustelinum*) × (*G.hirsutum* ssp. punctatum × *G.mustelinum*) combination was 33.4 mm. The difference between the samples in terms of fiber length was 30.0–37.0, and the coefficient of variation was 7.9%. In the hybrid generation, the heritability coefficient of the trait was hp=-1, and it was inherited in the state of negative dominance. Fiber yield indicators were analyzed in the offspring obtained from the reciprocal hybridization of parental samples. In this case, the fiber yield of the F1 (*G.hirsutum* ssp. punctatum × *G.mustelinum*) × (*G.hirsutum* ssp. glabrum var. marie-galante × *G.mustelinum*) combination was 37.6%, the fiber yield indicators were the difference between the hybrids was 35.6-40.5, and the coefficient of variation was 4.7%, respectively. In this hybrid form, the inheritance of the character was hp=6, and it was observed that it was inherited in a positive super dominant manner. In the same samples, the weight of the boll was 4.9 g and 4.7 g, respectively, and the coefficient of variation was 2.7% and 4.4%. The degree of heredity for the character being studied is hp=5; hp=4, and it was observed that it was inherited in a positive super-dominant state. Similarly, the heritability of the 1000 seed weight trait was analyzed in F1 generations. In this case, F1 (*G.hirsutum* ssp.punctatum × *G.mustelinum*) × (*G.hirsutum* ssp.glabrum var.marie-galante × *G.mustelinum*) combination had 104.0 g, F1 (*G.hirsutum* ssp.glabrum var.marie- galante × *G.mustelinum*) × (*G.hirsutum* ssp.punctatum × *G.mustelinum*) combination was 97.0 grams. The coefficient of variation in the combinations was 1.7% and 2.0%, and the heritability indicators for the 1000 seed weight marker were hp=6.3 and hp=-5.3, respectively. A state of positive and negative extreme dominance was observed (Fig. 2).

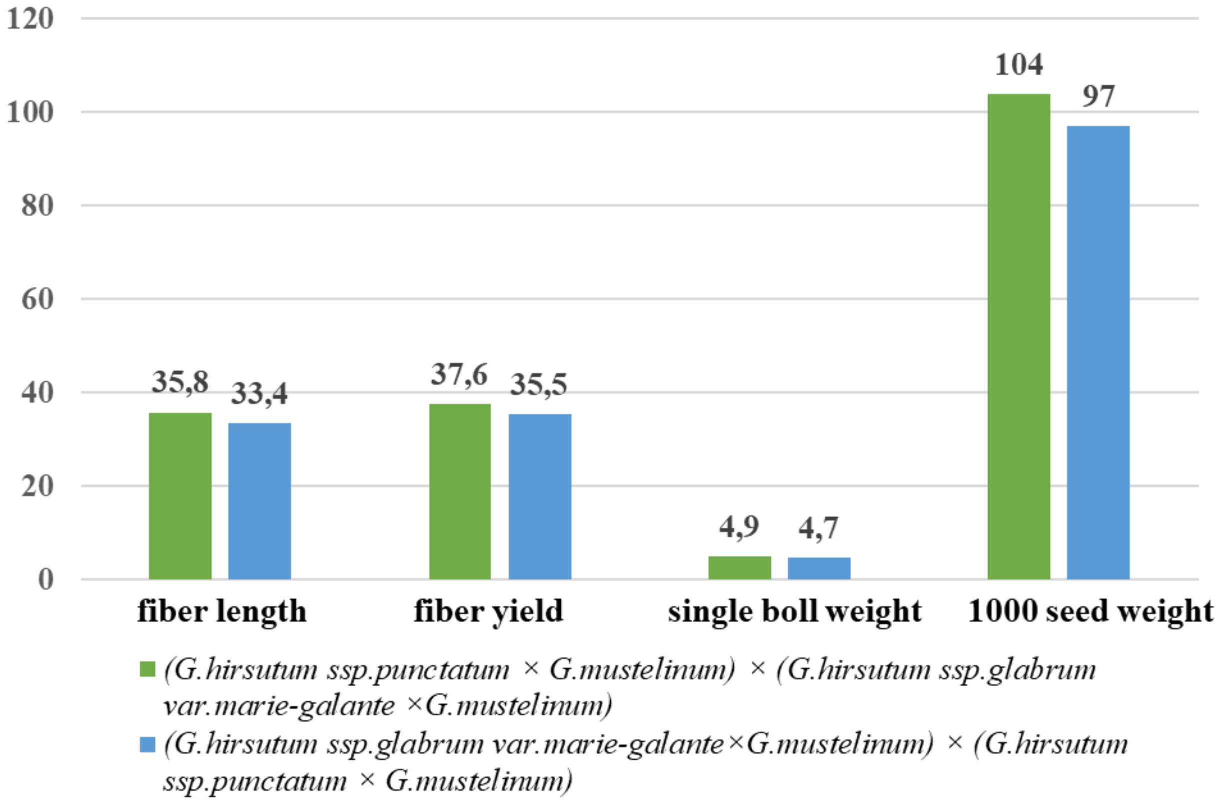

Figure 2. Morpho-yield traits in F1 hybrid combinations

Discussion

Upland cotton is the most widely planted cotton species in Uzbekistan, which shows advances in high yield, high boll setting rate, and wide adaptability. However, its fiber quality cannot meet the requirements of high-end textiles. In addition, upland cotton has a narrow genetic base, so it is not easy to improve the fiber quality of upland cotton under the standard breeding procedure. *G.*

tomentosum has the characteristics of stress resistance and high fiber strength (Hou et al., 2013). Introducing the superior alleles of *G. tomentosum* into upland cotton might enrich the genetic diversity and further improve the potential of fiber quality. At the beginning of the 20th century, the first three-way hybrid was obtained from wild cotton and upland cotton (*G. hirsutum* × Asiatic cotton × *G. tomentosum*). Its fiber quality was excellent, but the yield was relatively low. Through continuous backcrossing, hybridization, and selective breeding, a cotton variety with excellent fiber quality and high yield was cultivated. Subsequently, the favorable alleles derived from *G. tomentosum* regulating non-nectary traits were successfully introduced into upland cotton (Meyer et al., 1978). *G. tomentosum*, as the allotetraploid wild cotton species, shows its special agronomic traits (Liu et al., 2016). Based on the analysis results, it was observed that in the F1 hybrids, hybrid forms with a higher fiber yield were formed compared to the parent forms. By crossing these plants, new donors of the F1 generation were obtained. In the F1 combination, fiber length values were 33.4-34.1 mm, 1000 seed weight traits were 99.6-100.8 g, and fiber yield was 37.6 %. Fiber length and fiber yield in F1 hybrid(*G.hirsutum* ssp. punctatum × *G.mustelinum*) × (*G.hirsutum* ssp. glabrum var. marie-galante × G.*mustelinum*) was higher index.

Conclusion

In F1 hybrid plants, it was found that the fiber length trait was inherited mainly with positive and negative incomplete dominance. Similarly, fiber yield, weight of cotton per boll, and weight of 1000 seeds were also recorded as heritability indicators. Based on the analysis results, it was observed that in the F1 hybrids, hybrid forms with a higher fiber yield were formed compared to the parent forms. By backcrossing these plants, new donors of the F1 generation were obtained. In the F1 combination, fiber length values were 33.4-34.1 mm, 1000 seed weight traits were 99.6-100.8 g, and fiber yield was 37.6 %. Considering the indicators of preservation of the achieved positive state in the F2 generation, fiber yield, fiber length, and 1000 seed weight are recommended as high initial resources for future genetic and selection studies.

References

Adams, K.L., Percifield, R. and Wendel, J.F. (2004). Organ-specific silencing of duplicated genes in a newly synthesized cotton allotetraploid. Genetics, 168, 2217–2226. doi: 10.1534/genetics.104.033522

Alves, M.F., Barroso, P.A.V., Ciampi, A. Y., Hoffmann, L.V., Azevedo, V.C.R., Cavalcante, U. (2013). Diversity and genetic structure among subpopulations of G. mustelinum (Malvaceae). Genetic Molecular Research, 12, 597-609. http://dx.doi.org/10.4238/2013.February.27.9

Amanov, B., Abdiev, F., Shavkiev, J., Mamedova, F., Muminov, Kh. (2020). Valuable economic indicators among hybrids of Peruvian cotton genotypes. Plant Cell Biotechnology and Molecular Biology, 21(67-68), 35-46.

Ashkani, S., Rafii, M. Y., Shabanimofrad, M., Miah, G., Sahebi, M., Azizi, P. (2015). Molecular breeding strategy and challenges towards improvement of blast disease resistance in rice crop. Front. Plant Sci, 6:886. http://dx.doi.org/10.3389/fpls.2015.00886.

Azimov, A., Aliqulov, E., Ergashev, O., Shavkiev, J. (2024). Estimation of dominance and heterosis of morpho-economic traits in intraspecific F1 hybrids of upland cotton, Journal of Wildlife and Biodiversity, 8(3), 162-174. https://doi.org/10.5281/zenodo.11409018

Barroso, P.A.V., Hoffmann, L.V., Batista, C.E., Freitas, R.B., Alves, M.F., Silva, U.C., Andrade, F.P. (2010). In situ conservation and genetic diversity of three populations of G.mustelinum Miers (ex Watt). Genetics Resource and Crop Evolution, 57, 343-349. http://dx.doi.org/10.1007/s10722-009-9472-9

Brubaker, C.L., Bourland, F.M., Wendel, J.F. (1999). The origin and domestication of cotton. In Smith CW, Cothren JT, editors. Cotton: Origin, History, Technology and Production. New York: Wiley, 3-31

David, M. F., Heather, L. M., Deana, N.C. (2019). Gene Pyramiding Using Molecular Markers. 86.

Ergashev, O., Gapparov, B., Sherimbetov, A., Khidirov, M., Ruzmetov, D. (2021). Evaluation of fusarium and verticillium wilt tolerance in upland cotton cultivars. Plant Cell Biotechnology and Molecular Biology, 22(19-20), 94–98.

Freire, E.C. (2002). Fluxo geˆnico entre algodoeiros convencionaise transgeˆnicos. Rev Bras Ol Fibros, 6(1):471–482

Fryxell, P.A. (1992). A revised taxonomic interpretation of Gossypium L. (Malvaceae). Rheedea, 2, 108–165.

Griffing, J. (1950). Analysis of quantitative gene action by constant parent regression and related techniques. Genetics, 35, 303–321.

Guo, W. Z., Zhang, T. Z., Zhu, X. F., and Pan, J. J. (2005). Modified backcross pyramiding breeding with molecular marker-assisted selection and its applications in cotton. Acta Agron. Sin, 31, 963–970.

Gupta, P. K., and Varshney, R. K. (2005). “Cereal genomics: An overview,” in Cereal Genomics. eds. P. K. Gupta and R. K. Varshney (Dordrecht: Springer Netherlands), 1–18.

Iqbal, M.J., Reddy, O.U.K., El-Zik, K.M., and Pepper, A.E. (2001). A genetic bottleneck in the “evolution under domestication” of upland cotton *G.hirsutum* L. was examined using DNA fingerprinting. Theor. Appl. Genet, 103, 547–554. doi: 10.1007/PL00002908

Khalikova, M., Saydaliev, H., Shodieva, O., Khalikova, N. (2013). Some economic characteristics of *G. tomentosum* x *G. hirsutum* L. interspecies hybrid lines and interspecies hybrids belonging to *G.barbadense* species. Journal of Agro Science. Tashkent, 2(26), 6.

Khan, M.A., Wahid, A., Ahmad, M., Tahir, M.T.(2020). World Cotton Production and Consumption: An Overview. In: Ahmad S, Hasanuzzaman M, editors. Cotton Production and Uses. Singapore: Springer Nature Singapore Pte Ltd, . 1-7.

Khidirov, M.T., Ernazarova, D. K., Rafieva, F. U., Ernazarova, Z.A., Toshpulatov, A. Kh., Umarov, R. F. Kholova, M.D., Oripova, B. B., Kudratova, M.K., Gapparov, B. M. (2023). "Genomic and Cytogenetic Analysis of Synthetic Polyploids between Diploid and Tetraploid Cotton (Gossypium) Species" Plants 12(24), 4184.

Lemeshev, N., Atlanov, A., Podolnaya, L., Korneychuk, V. (1989). A comprehensive classification of the genus Gossypium L. 5- 20.

Liu, F., Zhou, Z.L., Wang, C.Y., Wang, Y.H., Cai, X.Y., Wang, X.X., Wang, K.B., Zhang, Z.S. (2016). Collinearity analysis of allotetraploid Gossypium tomentosum and Gossypium darwinii. Genetics and Molecular Research. 15 https://doi.org/10.4238/gmr.15038391.

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 Journal of Breeding and Genetics, 55(1), 74-89.

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 Journal of Breeding and Genetics, 54(5), 976-992.

Mauer, F.M. (1954). Cotton. Origin and taxonomy of cotton. Tashkent, 384.

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.

Munasov, H., Namozov, Sh., Kochkarov, O. (2003). Fiber quality. Uzbekistan Agricultural Journal. Tashkent, 11, 14.

Muratov, U.M., Alikho'jaeva, S.S., Munasov, H. (1997). Use of global samples of cotton in breeding. Journal of cotton and grain production. Tashkent, 4, 12-15.

Paterson, A.H., Wendel, J.F., Gundlach, H., Guo, H., Jenkins, J., Jin, D., (2012). Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibers. Nature, 492, 423–427. http://dx.doi.org/10.1038/nature11798

Pickersgill, B., Barrett, S.C.H., Lima, A.D. (1975). Wild cotton in northeast Brazil. Biotropica, 7, 42-54. http://dx.doi.org/10.2307/2989799

Rafieva, F.U., Ergashev, U.I., Iskadarov, A.A., Toshpolatov, A.N., Abdumominova N.A. (2022). Description of morphobiological characters of G. mustelinum Miers ex Watt G. barbadense ssp. vitifolium f. brasiliense cotton species and their interspecific hybrids. News of UzMU, 3(1), 133-137.

Rajabov, Z., Azimov, A., Shavkiev, J., Narimanov, A., Xotamov, A. (2024). Yield and yield component traits of the new Niyat variety of cotton under field conditions in the Khorezm region of Uzbekistan, Journal of Wildlife and Biodiversity, 8(3), 213-222.

Rizaev, M. M.(1972). Possibility of using G.anomalum W. in cotton breeding. Bulletin of Agricultural Science. Moscow, 4, 20.

Rizayeva, S.M., Ernazarova, Z.A., Ernazarova, D.K., Abdullaev, F.Kh., Amanov, B.Kh., Arslanov, D.M., Muminov, H.A., Abdullaev, A.A. (2013). Study and evaluation of economically valuable traits of varietal diversity of the species *G.hirsutum* L. from various eco-geographical groups. Uzbek Biological Journal, 3:31-34.

Sanaev, N.N., Gurbanova, N.G., Azimov, A.A., Norberdiev, T.N., Shavkiev, J.S. (2021). “Inheritance of the "plant shape" trait of the varieties and introgressive lines of G. hirsutum L. in drought conditions”, Plant Cell Biotechnology and Molecular Biology, 22(25-26), 122-129.

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, Journal of Wildlife and Biodiversity, 7(4), 214-228. DOI: https://doi.org/10.5281/10.5281/zenodo.8304871

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

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

Shavkiev, J., Nabiev, S., Azimov, A., Chorshanbiev, N., Nurmetov, K.H. (2022). Pima cotton (Gossypium barbadense L.) lines assessment for drought tolerance in Uzbekistan. SABRAO Journal of Breeding and Genetics, 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. Journal of Critical Review, 7(4), 131-136.

Strygina, K., Khlestkina, E., Podolnaya, L (2020). Cotton genome evolution and features of its structural and functional organization. Bio. Comm. 65(1):15-27.

Sun, Y., Zhang, X., Huang, C., Guo, X., Nie, Y. (2006). Somatic embryogenesis and plant regeneration from different wild diploid cotton (Gossypium) species. Plant Cell Rep, 25, 289-296.

Wendel, J.F., Brubaker, C.L., Seelanan, T. (2010) The origin and of Gossypium. In: Stewart J.M., Oosterhuis D., Heitholt J.J., Mauney J.R. (eds) Physiology of Cotton. Springer, Dordrecht. 1–18.