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ANALYSIS OF YIELD AND FIBER QUALITY TRAITS IN INTRASPECIFIC AND INTERSPECIFIC HYBRIDS OF COTTON

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SUMMARY

The present study, comprising an evaluation of cotton amphidiploid hybrids and their families for yield and fiber quality traits, commenced from 2007 to 2022 at the Chirchik State Pedagogical University, Tashkent, Uzbekistan. The amphidiploid hybrids' creation was through interspecific hybridization of *Gossypium hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*) and experimental polyploidy, with genetically enriched new genotypes obtained. According to genetic variability, a considerable variation showed based on F_1–F_6 populations belonging to various clusters for the traits boll weight (2.3–6.21 g), 1000-seed weight (67.3–125.529 g), fiber length (24.9–34.4125 mm), fiber yield (31.4%–40.26%), and fiber index (6.3–7.5875 g). Furthermore, among the F_6 *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum)* combination families, the promising genotypes selected gave the highest trait values for boll weight (6.6 ± 0.13 g - Family-41), 1000-seed weight (125.8 ± 3.48 g - Family-59), fiber yield (40.3% ± 0.65% - Family-59), fiber index (8.5 ± 0.23 g - Family-59), and fiber length (34.5 ± 0.16 mm - Family-8). Genotype evaluation using cluster analysis allows the prediction of cotton families with a better combination of traits. Introgressive hybrids created based on the early maturing families, viz., Family-5, Family-8, Family-13, Family-14, Family-41, and Family-59, with high yields and fiber indices attained inclusion in the Cotton Gene Pool, Uzbekistan (Certificate of the Academy of Sciences of the Republic of Uzbekistan No. 4/1255-2635 dated November 26, 2020). The promising families selected based on their best performance included F_5 (*G. hirsutum* L. × F_1 [*G. arboreum* L. × *G. arboreum* L.], Family-5, Family-8, Family-13, Family-14, and Family-59) and F_6 (*G. hirsutum* L. × F_1 [*G. arboreum* L. × *G. arboreum* L.], Family-5, Family-13, and Family-59), with the said cotton gene pool as valuable recombinants benefiting future breeding programs.

Keywords: *G. hirsutum* subsp. *euhirsutum*, *G. arboreum* subsp. *perenne, G. arboreum* subsp. *obtusifolium*, amphidiploid hybrids, F_1–F_6 populations, boll weight, 1000-seed weight, fiber length, fiber yield

Key findings: Results revealed considerable variations were among the primary cotton sources and interspecific amphidiploid F_1–F_6 populations for yield and fiber quality traits. Based on various economic traits, the cotton genotypes showed a relationship with different clusters..

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INTRODUCTION

Currently, it is vital to rationally use the unique genetic resources of available biodiversity of cotton (*Gossypium* L. family) in nature to increase the resistance of cotton cultivars to biotic and abiotic stresses and provide better production with economic benefits to meet the growing demands of world agriculture (Rizaeva *et al.,* 2009; Muminov and Abdullaev*,* 2014, 2015; Abdullaev *et al.,* 2016a, b). Intraspecific diversity and various cultivated diploid species have the genetic potential for precocity, productivity, and resistance to pests and environmental stresses, and eventually, play an imperative role in solving several production problems and boosting the technical crops' industry (Lather *et al.,* 2001; Laghetti *et al.,* 2002; Abdullaev, 2003; Ali *et al.,* 2003; Zhang *et al.,* 2014; Baboev *et al.,* 2017, 2021; Qulmamatova *et al.,* 2022).

After the independence of Uzbekistan, carrying out wide-range reforms persisted in the advancement of cotton growing, with special emphasis on creating new cultivars of precocious and high-yielding cotton. Based on the measures taken in this regard, developing certified high fiber-yielding cotton cultivars progressed on various diploid and tetraploid species. Moreover, nowadays, the research provided more time to use the diploid genotypes in the breeding process for creating cotton cultivars resistant to biotic and abiotic stress factors (Muminov *et al.,* 2011; Abdullaev *et al.,* 2013a, b; Matniyazova *et al*., 2022; Makamov *et al*., 2023). In the action plan strategy for the further development of the Republic of Uzbekistan, the task of "the creation of new breeding cultivars of crops resistant to diseases and pests, adapted to local soil-climatic and environmental conditions" received greater emphasis (The decree of the President of the Republic of Uzbekistan dated February 7, 2017). The scientific research is of particular importance aimed at isolating and implementing recombinants from the intraspecific diversity of *G. arboreum* L. species, resistant to adverse biotic and abiotic factors (Abdullaev *et al.,* 2007; Rizaeva *et al.,* 2009).

At present, effective use of the genetic potential of cultivated diploid (*G. arboreum* L.) species, subspecies, and forms of cotton makes it essential to transfer their unique traits to cultivated tetraploid genotypes (Singh *et al.,* 2001, 2004; Kulkarni *et al.,* 2003). Transferring valuable traits from generation to generation and studying the nature of heredity serve as the basis for producing new cotton cultivars resistant to various stress conditions. Accordingly, the determination and transmission of farm-valuable traits of subspecies of cultivated cotton *(G. arboreum* L.) diploids, generation to generation, and the nature of heredity have a greater scientific and practical importance in creating valuable and high fiber-yielding recombinants with good fiber quality, drought-resistant and early maturing based on hybridization (Rizaeva *et al.,* 2010, 2015; Panchal *et al.,* 2018). Increasing efficiency in cotton selection depends on the characteristics of the cultivars being created. Developing cultivars with high yields and fiber quality, resistant to disease and pests, can achieve such efficiency in cotton.

Factually, cotton cultivars do not retain their traits under the influence of external and internal factors in creating new cultivars. Therefore, breeding methods play an influential role in creating competitive cotton genotypes for the world market. Currently, developing new cotton cultivars use various techniques of hybridization. Numerous scientific studies undertook identifying and transferring of the traits of precocity and resistance to different pests and diseases to cultivated cultivars, with significant improvement achieved in cotton crops (Campbell *et al.,* 2010; Rizaeva *et al.,* 2016; Amanov *et al.,* 2020, 2022; Muminov, 2020, 2021, 2022). Past studies revealed the research work on various farm-valuable traits like yield, seed index, fiber yield, fiber index, and fiber length and strength in many species and subspecies of cultivated diploids and tetraploids of cotton and obtained tangible results (Singh and Singh*,* 1984; Sandhu *et al.,* 1987; Sandhu, 1989; Deshpande *et al*., 2001; Narula *et al.,* 2001; Kulkarni *et al.,* 2003; Singh *et al.,* 2003).

Saidaliev *et al.* (2001) claimed they obtained precocious hybrid forms with a vegetation period of 100 days based on intraspecific and interspecific hybridization of geographically distant, wild autopolyploid *G. tomentosum* and diploid *G. herbaceum.* Similarly, Sirojidinov (2017) reported to acquire a new unique introgressive hybrid F_2C *(G. hirsutum* subsp*. euhirsutum* cultivar Namangan 77 × *[G. arboreum* subsp. *obtusifolium* var. *indicum* × *G. austral]), G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *nanking* [white fiber] × *G. nelsonii*) recombinants based on interspecific hybridization and using experimental polyploidy methods, which were recommended for use as the primary valuable source in cotton crop. Juraev (2008) identified the interrelations of cotton cultivars by their farm-valuable traits complex by dividing various cultivars of *G. hirsutum* L. into clusters using cluster analysis.

Hodges *et al.* (2007) developed a new cultivar based on the transfer of genes of fine-fiber Pima cotton cultivars (resistant to saline soil) to medium-fiber cultivars by backcrossing. This cultivar was more tolerant to saline soils than its parental cultivars, with a higher germination rate in saline soils. Mamarakhimov *et al.* (2000) studied the inheritance of fiber yield in interspecific hybrids and found that cultivars (Acala sj-5, C-6530, MCU-5, 433, Acala 4-42, and C-4727) were involved in hybrids as a mother parent, the sample with higher fiber yield manifested predominance in the F_1s, with the inheritance observed to be intermediate.

Analysis of the above literature showed that the genetic potential of intraspecific diversity of Indo-Chinese cotton species, the hereditary nature of morpho-biological and farm-valuable traits, the degree of correlation, and the possibility of their use in selection have limited studies. Research in this area is one-sided and focuses only on cultural cultivars. Additionally, the current challenges geneticists and breeders face are the study of the inheritance of morpho-biological and farm-valuable traits in hybrids involving intraspecific wild, ruderal, tropical, and subtropical subspecies and types of *G. arboreum* L. species and the transfer of unique and beneficial characteristics to cultural cultivars.

The cluster analysis basis measures the Euclidean distance among the points in a multidimensional space (hybrid, family, line, and cultivars) as a gauge of genetic divergence to distinguish genetically close groups of cultivars. Such a method makes it possible to assess the genetic similarity of the lines and cultivars and plan the breeding program accordingly. The cluster analysis method is the most informative. It allows the classification of genetically close families when the selected traits are correct, identifying differences between families belonging to different clusters and predicting the degree of transgressive separation in hybrids while crossing different types of cotton.

MATERIALS AND METHODS

The progressive research began in 2007–2022 at the Department of Genetics and Evolution Biology, Chirchik State Pedagogical University, Tashkent, Uzbekistan, and the Institute of Genetics and Experimental Plant Biology at the Sciences Academy of the Republic of Uzbekistan, District Zangi-Ota, Tashkent region, Uzbekistan (with an altitude of 398 meters above sea level). The climate characteristics are sharp fluctuations, high temperatures in summer (June, July, August), and a sharp drop in air temperature in winter (especially December and January). Sunny days are 175–185 days, with cooler 200–210 days. It rains in the fall, winter, and spring, with dry air in summer. The cotton crop requires artificial irrigation during the crop season.

The soils of the experimental field are low humus, typical gray soil that is moderately sandy according to the granulometric composition. The terrain is slightly sloping, not saline, and naturally damaged by wilt (verticillium). The volumetric weight of the soil is 1.32–1.33 g/cm^3, with a limited field moisture capacity (LFMC) of -22%. Groundwater is deep (8 m or more). The experiment employed agro-technical measures in a general way, adopted on the experimental base. Applying mineral fertilizers was done three times before sowing, during sowing, and during the growing season (first feeding at the beginning of budding, second at mass budding, and third at flowering - yield accumulation). The annual rate of mineral fertilizers in pure form was 250:180:115 kg NPK ha^{-1}. Sowing in the fields used the scheme 90 × 20 × 1 (the width among rows is 90 cm, the spacing of the nests in rows is 20 cm, and the number of the plants is one per nest) on the third day of April. Seeds sown had a depth of 4–5 cm.

As a primary source, the basis for obtaining the F_1–F_6 populations was on interspecific hybridization of *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*) and *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G.*

arboreum subsp. *obtusifolium* var. *indicum*) used in the experiment (Abdullaev *et al.,* 2010). Research methods used classical approaches of cotton genetics and breeding, interspecific hybridization and comparative morphology, phenological observations, statistical analysis, and cluster analysis through the computer program *Statgraphics* (Dospekhov, 1985; Lemeshev *et al*., 1989).

Fiber yield

Defining the ratio of fiber weight to cotton weight was in %.
The fiber yield calculation used this formula:

$$\text{Fiber yield (\%)} = \frac{\text{Clean fiber x 100}}{\text{raw cotton}}$$

Fiber index

The fiber index defines the fiber weight obtained from 100 cotton seeds in g.
Calculating the Fiber index followed this formula:

$$\text{Fiber index} = \frac{\text{Seed weight x Fiber yield}}{\text{100 - Fiber yield}}$$

RESULTS AND DISCUSSION

Morpho-biological traits of the populations

The F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*) genotype plants grew upright, in compact form, with medium density. The height of the main stem was 50.0–55.0 cm, with average green color, hairiness, and anthocyanin redness. The total number of nodes was 20–25. Branching - sympodial: the first sympodial branch *(hs)* was in the seventh to eighth nodes; monopodial branches (m) were 3–4, sympodial branches were 13–17, and node intervals between two sympodia were 3.0–4.0 cm. The leaves have medium-sized (9.5 cm × 9.0 cm), green-colored, 5-7-lobed, and ovate-lobed. The hairs were weak with no nectar. The leaf stem was 7.0–8.0 cm long, with a light anthocyanin redness, and had two small side leaves. The flowers were medium-sized, bell-shaped, round, and broadly open. Pedicel was short, 0.5–0.6 cm long, with three bracts, whole-hearted shaped with 8-10 toothed, and 0.1-0.2 cm long. Sepals were whole wavy, with green, gossypol glands of medium density and no nectar. The flower petals were 5.0 cm × 4.5 cm in size, yellow in color, with darker anthocyanin spots at the base. The pollen stamens on the style were sparse, the color of the stamens was yellow, and the female ovary had three columns equal to the male. The bolls were medium-sized, green, conical, pointed, and wavy at the base, with four capsules, with each capsule containing 5-6 quality seeds. The boll weight was 2.2-2.4 g, the fiber color was white, and fiber length was 24.0–26.1 mm. Cottonseeds were hard-shelled and small, having a 1000-seed weight of 66.0–69.0 g. Concerning biological and farm traits, the cotton F_1 hybrid plants were medium precocious; branching was type I and not demanding for short days. The polyploidy created with interspecific hybridization with the inclusion of the cultivated, wild, ruderal, tropical, and subtropical subspecies also got support from past cotton studies (Abdullaev *et al.,* 2010; Rizaeva *et al.,* 2010).

In *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak, the plants grew upright spherical shape, with medium density. The height of the main stem was 90.0–100.0 cm, in green color. The first sympodial branch (*hs*) was in the fourth to fifth nodes, and the monopodial branch (m) were 1–2. The leaves were medium-sized (11.0 cm × 10.0 cm), green, with 3–5 claw-shaped veins, weak hairiness, and owned one nectar. The leaf stem was 9.0–9.5 cm long, with moderate anthocyanin redness. The flower was medium-sized, bell-shaped, wavy, and open in medium width. The length of the pedicel was 1.5–2.0 cm. Three bracts were whole, heart-shaped, with 10–11 teeth, with a length of 0.5–1.5 cm. The sepals were whole, star-shaped, light green in color, and covered with gossypol glands of moderate density. In flowers, the size of petals was 4.5 cm × 3.5 cm, whole, wavy, white, without anthocyanin spots at the base. The pollen stamens on the style column were dense and white; female ovary bulges were 0.3 cm relative to the male. The bolls were oval, large, smooth, and green, with 4–5 capsules containing 9–10 quality seeds per capsule. The boll weight was 5.5–6.5 g, and the fiber color was white, with a fiber length of 33.0–38.0 mm. The cottonseeds were medium-sized, and the 1000-seed weight was 118.0–123.0 g. On biological and farm traits, the cultivar Kelajak showed resistance to disease, pests, insects, drought, and soil salinity. Notably, the plant branching belongs to type II. Similar results regarding 1000-seed weight, fiber length, and fiber index in cotton came from previous studies (Deshpande *et al*., 2001; Narula *et al.,* 2001; Zhang *et al.,* 2014).

In F_1 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × [*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*]), the plants grew erect, in a compact shape, with medium density. The height of the main stem was 55.0 cm and green. Hairiness was weak, and anthocyanin redness was medium. The total number of nodes was 20. The first sympodial branch (*hs*) was in the seventh node, with 14 sympodia the sympodia internodes at 2.0–4.0 cm. There are no monopodial branches (m). Leaves were medium-sized (10.0 cm × 13.0 cm), green, with 3–5 claw-shaped veins. Nectars were three, egg-shaped, and colorless. The leaf stem has moderate anthocyanin redness. Flowers were medium-sized, bell-shaped, wavy, and open with medium width. Pedicel length was 0.5–1.0 cm. Bracts were three, whole, heart-shaped, 8–10 toothed, with a 0.2–1.6 cm length. Sepals were whole, wavy, light green in color, and covered with thin gossypol glands. In flowers, the petal size was 4.0 cm × 3.8 cm, whole, wavy, and light yellow, with no anthocyanin spots at the base. The pollen stamens on the style column were dense and in yellow color, and the female ovary bulges 0.1 cm relative to the male. The bolls are oval, medium-sized, and green, with 4–5 capsules. The boll weight was 2.3–7.3 g, the fiber color was white, and the fiber length was 32.0–38.0 mm. The cottonseeds were medium-sized, and the 1000-seed weight was 152 g. Furthermore, the study's use of polyploidy as a result of interspecific hybridization with the inclusion of cultivated and wild species got support from previous cotton studies (Abdullaev *et al.,* 2016a; Muminov, 2022).

The conduct of cluster analysis used the descriptions of studied interspecific *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp*. obtusifolium* var. *indicum*) amphidiploid F_1–F_6 populations as primary information by their various yield and fiber quality traits. Based on this, the parental genotypes and their F_1–F_6 populations underwent analysis by dividing them into four clusters (Tables 1, 2, and Figure 1). The cluster analysis results were used to alternate breeding processes. According to cluster analysis, the first cluster included F_1 *(G. arboreum* subsp*. perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum)* combination, which was involved in the experiment as a male. The various recorded trait values were, i.e., boll weight (2.3 g), 1000-seed weight (67.3 g), fiber yield (31.4%), fiber index (6.3 g), and fiber length (24.9 mm). The indicators of this cluster were the lowest as compared with other cluster trait indicators. Past studies also reported similar findings in newly developed cotton populations by comparing them with standard and check genotypes (Juraev, 2008; Rizaeva *et al.,* 2016; Sirojidinov, 2017).

In the second cluster, the included populations were *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak, F_2 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*), F_6 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-8, Family-14, Family-41, F_1 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*), and the standard check cultivar C-6524. The various recorded variable values were, i.e., boll weight (5.91 g), 1000-seed weight (125.52 g), fiber yield (36.72%), fiber index (7.17 g), and fiber length (34.31 mm). However, only the 1000-seed weight was superior in these populations compared with other cluster indicators. In this cluster, also noted indicators of *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak, F_2 *G. hirsutum* × *(G. arboreum* × *G. arboreum*), F_6 *G. hirsutum* × *(G. arboreum* × *G. arboreum*) Family-8, Family-14, F_1 *G. hirsutum* × (*G. arboreum* × *G. arboreum*), and the standard cultivar C-6524 were closer to each other for various yield and fiber quality variables. The results also authenticated that these cotton populations could be useful in the future breeding program and selection process for further improvement in fiber length and quality traits, as also mentioned in past studies (Singh and Singh*,* 1984; Sandhu *et al.,* 1987; Sandhu, 1989).

In the third cluster, the cotton populations were, i.e., F_3 *G. hirsutum* L. × F_1 (*G. arboreum* L. × *G. arboreum* L.) Family-5, Family-14, Family-41, F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-14, Family-41, F_3 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-59, F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-59, F_3 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-8, Family-13, F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-5, F_5 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-41, and F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-8 and Family-13. The various recorded yield and fiber quality parameter values were for boll weight (4.63 g), 1000-seed weight (101.25 g), fiber yield (38.64%), fiber index (6.39 g), and fiber length (33.54 mm). However, these values

Table 1. Mean performance of primary source and interspecific amphidiploid F_1–F_6 populations for yield and fiber quality traits.

Families	Boll weight (g)	1000-seed weight (g)	Fiber length (mm)	Fiber yield (%)	Fiber index (g)
F_1 (*G. arboreum* subsp. *perenne*) × (*G. arboreum* subsp. *obtusifolium* var. *indicum*)					
	2.3±0.03	67.3±0.37	24.9±0.25	31.4±0.12	6.3±0.08
G. hirsutum subsp. *euhirsutum* cultivar Kelajak					
	5.6±0.11	122.0±0.85	35.6±0.55	38.4±0.40	7.1±0.22
F_1 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
	4.5±0.67	152.0±0.87	35.1±0.54	35.3±0.91	8.2±0.10
F_2 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
	5.7±0.25	112.8±4.03	33.6±0.54	37.6±0.58	6.8±0.27
F_3 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
Family-5	4.8±0.29	99.1±5.03	33.4±0.88	38.8±0.88	6.3±0.34
Family-8	5.1±0.23	105.1±5.28	33.2±0.41	40.0±0.66	7.0±0.30
Family-13	4.8±0.25	102.5±4.36	33.3±0.46	39.7±0.52	6.7±0.25
Family-14	4.6±0.24	92.9±5.13	33.7±0.40	39.6±0.81	6.1±0.36
Family-41	4.2±0.25	89.9±3.69	32.6±0.53	38.8±0.96	5.7±0.32
Family-59	3.5±0.26	84.3±4.73	33.1±0.67	37.2±1.37	5.1±0.48
F_4 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
Family-5	4.8±0.23	107.3±2.09	33.8±0.43	38.9±0.67	6.8±0.16
Family-8	4.5±0.25	109.2±2.48	33.8±0.41	39.5±0.48	7.1±0.14
Family-13	4.9±0.20	107.8±2.46	34.3±0.38	40.0±0.49	7.2±0.15
Family-14	4.7±0.26	106.2±3.07	33.6±0.37	37.5±0.70	6.4±0.19
Family-41	4.8±0.17	107.6±2.63	33.2±0.54	37.4±0.38	6.4±0.18
Family-59	3.9±0.27	100.8±3.71	35.1±0.62	34.6±1.19	5.4±0.34
F_5 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
Family-5	6.1±0.16	106.5±2.24	34.9±0.20	40.9±0.44	7.3±0.10
Family-8	6.0±0.16	109.8±2.40	34.8±0.24	39.8±0.54	7.2±0.19
Family-13	6.2±0.15	109.8±3.66	34.8±0.61	40.6±0.62	7.4±0.08
Family-14	6.4±0.22	109.1±1.62	33.5±0.41	40.3±0.40	7.4±0.18
Family-41	5.6±0.23	103.6±1.73	33.0±0.39	40.4±0.56	6.9±0.15
Family-59	6.4±0.17	111.2±2.00	35.4±0.30	40.9±0.47	7.7±0.23
F_6 (*G. hirsutum* subsp. *euhirsutum* cultivar Kelajak) × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*)					
Control cultivar (C-6524)	6.2±0.16	132.2±1.33	33.3±0.38	33.2±0.28	6.6±0.07
Family-5	6.1±0.17	119.1±3.47	34.0±0.31	39.4±0.65	7.7±0.22
Family-8	6.4±0.15	118.8±2.90	34.5±0.16	38.2±0.75	7.3±0.17
Family-13	6.0±0.18	112.7±1.84	33.8±0.39	39.9±0.72	7.5±0.18
Family-14	6.4±0.17	118.3±2.61	34.1±0.25	37.6±0.66	7.1±0.22
Family-41	6.6±0.13	122.6±2.68	34.0±0.24	36.8±0.60	7.1±0.15
Family-59	6.5±0.15	125.8±3.48	34.1±0.28	40.3±0.65	8.5±0.23

Table 2. Primary source and interspecific amphidiploid F_1–F_6 populations based on clusters for yield and fiber quality traits.

Cluster No.	Boll weight (g)	1000-seed weight (g)	Fiber length (mm)	Fiber yield (%)	Fiber index (g)
1	2.30	67.30	24.90	31.40	6.30
2	5.91	125.52	34.31	36.72	7.17
3	4.63	101.25	33.54	38.64	6.39
4	6.21	113.00	34.41	40.26	7.58

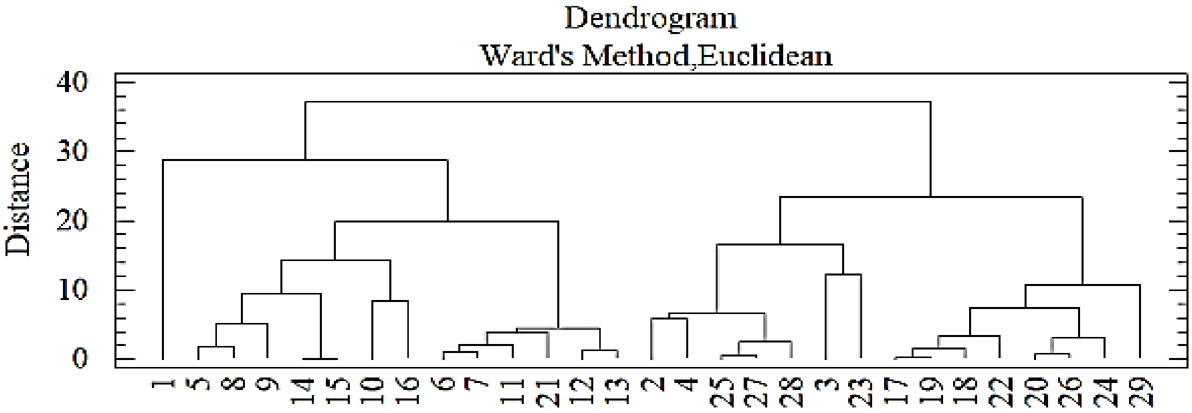

Figure 1. Dendrogram form of division of primary source and interspecific amphidiploid F_1–F_6 populations into clusters on yield and fiber quality traits.

were relatively lower when compared with the traits of the cotton populations of other clusters. The yield and fiber quality traits of the populations, i.e., F_3 *G. hirsutum* × *(G. arboreum* × *G. arboreum*) Family-5, F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-14, Family-41, F_3 *G. hirsutum* L. × F_1 (*G. arboreum* × *G. arboreum*) Family-59, F_4 *G. hirsutum* L. × F_1 (*G. arboreum* × *G. arboreum*) Family-59, F_3 *G. hirsutum* L. × F_1 (*G. arboreum* × *G. arboreum*) Family-8, Family-13, F_4 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-8 and Family-13, included in this cluster, appeared closer to each other. Past research revealed that interspecific hybridization performed better in the creation of cotton hybrids for better seed cotton yield and fiber quality traits (Amanov *et al.,* 2020, 2022; Muminov, 2022).

In the fourth cluster, the included cotton populations were F_5 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-5, Family-13, Family-8, Family-59, and Family-14, F_6 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-13, Family-5, and Family-59, with the trait values of, i.e., boll weight (6.21 g), 1000-seed weight (113.00 g), fiber yield (40.26%), fiber index (7.58 g), and fiber length (34.41 mm). These showed superiority over the cotton populations of other cluster plants by the traits, i.e., boll weight, fiber yield, fiber index, and fiber length. Although, the farm-valuable traits of the cotton populations in this cluster, viz., F_5 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-5, Family-13, and Family-14, F_6 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-13 emerged to be similar to each other. Past studies also revealed significant differences among intraspecific and interspecific populations for various yield and fiber quality traits in cotton (Kulkarni *et al.,* 2003; Rao *et al.,* 2004; Sirojidinov, 2017; Muminov and Khamroyev, 2022).

CONCLUSIONS

Results revealed considerable variations in the primary cotton sources and intraspecific and interspecific amphidiploid F_1–F_6 populations for various yield and fiber quality traits. Given the greater variation, the traits also indicated belonging to different clusters, and this variation showed boll weight ranged from 2.3–6.22 g, 1000-seed weight 67.3–125.52 g, fiber yield 31.4%–40.26%, fiber index 6.3–7.58 g), and fiber length 24.9–34.41 mm. Furthermore, among F_6 *G. hirsutum* subsp. *euhirsutum* cultivar Kelajak × F_1 (*G. arboreum* subsp. *perenne* × *G. arboreum* subsp. *obtusifolium* var. *indicum*) families, the isolated plants showed high indicators according to their traits, viz., boll weight (6.6 ± 0.13 g - Family-41), 1000-seed weight (125.8 ± 3.48 g - Family-59), fiber yield 40.3% ± 0.65% (Family-59), fiber index (8.5 ± 0.23 g - Family-59), and fiber length (34.5 ± 0.16 mm - Family-8). The fourth cluster population families, i.e., F_5 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-5, Family-13, Family-8, Family-59, and Family-14, F_6 *G. hirsutum* × F_1 (*G. arboreum* × *G. arboreum*) Family-13, Family-5, and Family-59, with superior and desirable yield and fiber quality traits, proved also recommended for use in the future breeding program to develop high-yielding cotton genotypes.

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