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# COTTON INTROGRESSIVE LINES ASSESSMENT THROUGH SEED COTTON YIELD AND FIBER QUALITY CHARACTERISTICS

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## SUMMARY

The conducted study, with focus on the earliness and opening rate of bolls, and other economic traits of introgressive cotton lines, was carried out from 2017 to 2019 at the Institute of Genetics and Plant Experimental Biology, and Genetics and Evolution Biology Department, in Chirchik State Pedagogical Institute, Tashkent, Uzbekistan. Overall, the introgressive cotton lines were found to ripen two to 13 days earlier than a standard cotton cultivar C-6524. Particularly, in line L-PCM, the vegetation period took 109 days and matured 12.3 days earlier than a standard cultivar check. According to the boll weight, the selected cotton lines were identified to have the best performance, as well as, good germination ability of seeds. The cotton line, T-138, was found highly resistant to strains of *Fusarium oxysporum* f. sp. *vasinfectum* pathogenic fungi, while the lines, L-PCM and L-138, had 80% to 100% resistance to *Verticillium dahliae* fungi. The cotton lines, L-PCM and L-141, were not infected with *Fusarium solani* fungi. The cluster analysis revealed that according to the economic traits, the first cluster included lines L-24 and L-138 and were found to be closely related to each other. The line, L-PCM, was included in the third cluster, and it was found that this cotton line was among the cultivars with the best performance for all the valuable economic traits. The comparative analysis of cotton lines resulted in a creation of a new medium-fiber cotton cultivar "Niso," with the productivity of 3,830 to 5,650 kg ha$^{-1}$, boll weight of 6.0 to 6.7 g, boll opening at 109.0 to 112.0 days, type IV fiber, 1000-seed weight of 118.0 to 120.0 g, fiber percentage ranging from 36.9% to 41.4%, fiber length at 34.0 to 35.9 mm, and relative tensile strength (34.6 cN/tex). Cotton lines obtained on the basis of intergenomic introgression methods were included in the leading "Cotton gene pool" (Reference of the Academy of Sciences of the Republic of Uzbekistan №4/1255-2473 dated November 12, 2020). These introgressive cotton lines made it possible to enrich the collection of cotton, to evaluate wild cotton species, and to form a system of information and analysis of the electronic database of adaptable stress factors and genetically enriched samples.

**Keywords:** Cotton, introgressive lines, genome, cultivars, earliness, bolls, boll weight, fiber yield, fiber length, and strength

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**Key findings:** Results showed that in the introgressive lines, the boll opening was two to 13 days earlier than standard cotton cultivar C-6524. The selected introgressive lines have shown the best performance for economic characteristics and were found significantly superior to the standard cotton genotype.

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## INTRODUCTION

Cotton researches currently focus on the development of high-yielding and high-fiber cotton cultivars that are resistant to biotic and abiotic stresses, to help meet a country's requirements and boost national economy. Cotton is grown in subtropical and seasonally dry tropical areas in both the northern and southern hemispheres, although most of the world's production takes place north of the equator (Amanov *et al.,* 2020; Sirojiddinov, 2020). Twenty-seven million tons of cotton are produced globally in a year, and the main cotton producing countries are India, China, the United States, Brazil, Pakistan, and Uzbekistan (FAOSTAT, 2020-21). This indicates the need to create new cotton cultivars and involve the wild germplasm in the selection to transfer their beneficial traits to cultivated cultivars, including resistance to different stresses, early maturity, high-yielding, high-fiber, and desirable fiber quality characteristics (Boboyev, 2017; Amanov, 2019; Shavkiev *et al*., 2021). Research in this area is one of the most important and practical directions through genetic principles, the selection to improve the genetic potential of the cotton genotypes belonging to the genus *Gossypium*.

The latest research aimed to improve the economic and quality characteristics of the upland cotton, with particular focus on a wide use of wild species, especially the involvement of interspecific hybridization, obtaining rare genetically enriched hybrids using experimental polyploidy methods, to create new cultivars with high economic and quality traits from the existing germplasm (Chen *et al.,* 2014). Recently, rare amphidiploids, recombinants, families, and lines have been obtained using wild species of cotton, i.e., *G. harknessii* Brandg, *G. klotzschianum* Anderss, *G. raimondi* Ulb., *G. laxum* Phill., *G. bickii* Prokh, *G. australe* F. Mull, and other species. One of the important tasks in the study of these cotton lines is to determine the genetic regulations of the morphological and economic traits, such as, heredity and genetic variability in the cotton genotypes, and association among various traits (Namazov *et al.,* 2005).

Development of new cotton cultivars through interspecific hybridization with the participation of intergenomic cultural and wild species, as well as, the use of experimental polyploidy, has been reported at the national level (Rizaeva, 1996; Rizaeva *et al.,* 2014) and also in other cotton producing countries (Wendel and Cronn, 2003; Benbouza *et al.,* 2010). These newly developed cotton genotypes have created unique hybrid forms with high economic characteristics, and primary sources of resistance to the biotic and abiotic stresses based on the hybridization of wild species with existing cultivars and isolated new genetically enriched genotypes, as well as, recommended primary donors for practical selection. Boboyev (2017) created new interspecific complex hybrids based on the hybridization of complex *(G. thurberi* Tod. x *G. raimondii* Ulbr., and *G. arboreum* L. x *G.hirsutum* L.) amphidiploids with cultural cultivars of *G. hirsutum* L. and *G. barbadense* L., involving 4/5 cotton species, and also determined the formation and variability of main valuable economic traits.

A comparative assessment of the inheritance, degree of variability, and formation of valuable economic traits in polygenomic cotton hybrids was performed using interspecific hybridization and experimental polyploidy methods (Sirojiddinov, 2020; Mangi *et al*., 2022). Research on obtaining introgressive forms using the hybridization of multi-genomic wild cotton species and experimental polyploidy methods, to form morphological features in the introgressive cotton lines based on obtained types of genotypes, as well as, their correlation is of scientific importance (Soomro *et al*., 2008; Srinivas and Bhadru, 2015).

The latest research aimed at creating new cultivars of cotton enriched genetically by studying valuable economic and quality traits of cotton lines obtained under intergenomic introgressive methods, their cluster analysis, and the influence of *Fusarium oxysporum* f. sp. *vasinfectum, Fusarium solani,* and *Verticillium* *dahliae* fungi on seed germination ability of the cotton plant and limb.

## MATERIALS AND METHODS

The study was carried out from 2017 to 2019 at the Institute of Genetics and Plant Experimental Biology, and the Genetics and Evolution Biology Department, Chirchik State Pedagogical Institute, Tashkent, Uzbekistan. Four cotton lines, L-24, L-PCM, L-138, and L-141 obtained under intergenomic introgressive methods, were used for evaluation in the study. Also, standard cultivar, C-6524, was used to compare and analyze the lines obtained by the experimental polyploidy method of three-genome Tashkent-1 x (*G. raimondii* x *G. thurberi*) and Tashkent-1 x (*G.harknessii* x *G.raimondii*) hybrid combinations belonging to *Gossypium* family. For fiber quality traits, the fiber samples of different cotton lines and check cultivar were measured by using HVI equipment at the Republican Center "Sifat", Uzbekistan.

These cotton lines were analyzed according to the methodology of Bipinchandra *et al.* (2016) by studying the effect of mycotoxins isolated from *Fusarium oxysporum* f. sp*. vasinfectum, Fusarium solani,* and *Verticillium dahliae* fungi on seed germination of plant and limb. Furthermore, a cluster analysis was also carried out to characterization of the cotton lines. This analysis is known from multidimensional statistics that the natural measure of the distance of objects from each other is the distance of Mahalanobis. The Euclidean distance is a special case of the Mahalanobis distance. Statistical work of the results of practical research was carried out by the method of Fisher (1934). The correlation analysis for various traits was also carried out among the cotton introgressive lines (SAS Institute Inc., Cory. NC. USA).

## RESULTS AND DISCUSSION

It is a well-known fact that one of the most important indicators of the maturity of cotton is the period from the date of germination to the 50% boll opening. By comparing the results of the years 2017–2019 for the vegetation period in multi-genomic cotton lines, nonsignificant differences were observed among lines for the said trait. The standard cultivar, C-6524, was used as a check genotype, and the vegetation period was 119.4 to 122.1 days. For the said trait, the lines constituted 109.2 to 117.7 days and were found 1.7 to 12.9 days earlier than the standard cultivar C-6524, based on the three years' data. Studying the line, L-PCM over three years, there was a slight change, and during 2018–2019 the said line was found superior over all other cotton introgressive lines in earliness, and its average boll opening rate was ±109.2 days. With the involvement of local and exotic genotypes in the polyploidy methods, the newly developed genotypes revealed the best performance for earliness and yield traits than check cultivars in cotton (Wendel and Cronn, 2003; Benbouza *et al.,* 2010).

In the study based on the results of 2017–2019, a comparative analysis of the first joint of a plant with the fruiting branch (sympodia) was made, but nonsignificant differences were observed in the introgressive lines. In standard cultivar C-6524, the average was 5.1 to 5.5 joints over the years, with a coefficient of variation of 13.5% to 17.3%. In the introgressive lines, for the said trait the average rate was 3.9 to 5.5 joints. In line, L-PCM, the first fruiting branch was noted with 4.2 joints, and the coefficient of variation was 19.0%, which was slightly lower than line, L-138 (6.2 joints) and standard cultivar, C-6524 (5.1 to 5.5 joints). Past studies exhibited that as a result of intergenomic and interspecific hybridization with the inclusion of wild species, the hybrids showed remarkable results for various morphological and yield-related traits in cotton (Rizaeva, 1996; Amanov *et al.,* 2020).

In the lines on average, the boll weight was 5.7 to 7.1 g, whereas in the standard cultivar C-6524, the average boll weight was 5.2 to 5.5 g during 2017–2019 (Table 1). By comparing the standard cultivar, C-6524 with introgressive lines, the cotton lines were found 0.3 to 1.6 g heavier than check cultivar C-6524. In 2017, the boll weight was ranging from 5.8 to 6.4 g in the multigenomic lines. However, the highest boll weight was noted in line L-PCM (6.4 g) with a coefficient of variation (7.86%), and a slightly lower boll weight was observed in line L-138 (5.8 g), but showed +0.6 higher indication than check cultivar C-6524. During 2018–2019, analogue indicators were recorded for boll weight. The cotton lines, L-PCM (6.7 g) and L-24 (7.1 g) with larger bolls, were also recommended to be used in future selection as primary breeding material. With the intergenomic and interspecific hybridization and use of cultivated and wild species, the cotton hybrids performed

**Table 1.** Boll weight in cotton lines obtained through introgressive methods during 2017–2019.

| No. | Lines | Boll weight (g) | | | | Difference by ± default |
|---|---|---|---|---|---|---|
| | | $\bar{X} \pm S\bar{x}$ | Limit | S | V (%) | |
| | | 2017 | | | | |
| 1 | L-24 | 6.1 ± 0.13 | 5.3 – 6.6 | 0.40 | 6.48 | + 0.9 |
| 2 | L-PCM | 6.4 ± 0.16 | 5.6 – 7.3 | 0.50 | 7.86 | + 1.2 |
| 3 | L-138 | 5.8 ± 0.13 | 5.1 – 6.2 | 0.40 | 6.87 | + 0.6 |
| 4 | L-141 | 5.9 ± 0.14 | 5.3 – 6.7 | 0.43 | 7.28 | + 0.7 |
| 5 | C-6524 (Check) | 5.2 ± 0.14 | 4.3 – 5.7 | 0.38 | 8.20 | ± |
| | | 2018 | | | | |
| 1 | L-24 | 5.7 ± 0.14 | 4.7 – 6.4 | 0.46 | 7.98 | + 0.3 |
| 2 | L-PCM | 6.2 ± 0.20 | 5.1 – 7.4 | 0.63 | 10.20 | + 0.8 |
| 3 | L-138 | 5.9 ± 0.23 | 4.9 – 7.5 | 0.72 | 12.15 | + 0.5 |
| 4 | L-141 | 5.9 ± 0.19 | 4.8 – 6.7 | 0.60 | 10.10 | + 0.5 |
| 5 | C-6524 (Check) | 5.4 ± 0.10 | 4.4 – 6.0 | 0.52 | 9.80 | ± |
| | | 2019 | | | | |
| 1 | L-24 | 7.1 ± 0.22 | 6.2 – 8.4 | 0.87 | 10.21 | ± 1.6 |
| 2 | L-PCM | 6.7 ± 0.17 | 5.8 – 7.7 | 0.65 | 9.64 | + 1.2 |
| 3 | L-138 | 6.1 ± 0.20 | 5.0 – 7.6 | 0.79 | 13.00 | + 0.6 |
| 4 | L-141 | 6.9 ± 0.19 | 5.2 – 7.9 | 0.72 | 10.49 | + 1.4 |
| 5 | C-6524 (Check) | 5.5 ± 0.22 | 4.6 – 5.9 | 0.83 | 12.65 | + |

better than standard check cultivars (Boboyev, 2017; Sirojiddinov, 2020).

In the comparative analysis of fiber length during 2017–2019, similar fiber length (33.6–35.9 mm) was noted in lines, and by comparing with the standard cultivar C-6524, the lines were found 0.5 to 2.8 mm higher (Table 2). The longest fibers were observed in line L-PCM (35.9 mm) with a coefficient variation of 4.37%. During the study years 2018–2019, similar mean values were recorded for the fiber length. In 2019, line L-141 showed 33.6 mm with a coefficient of variation of 3.68%, lower than other lines, whereas line L-PCM had the highest fiber length (35.1 mm) among the other lines. The introgressive lines were found superior in fiber length compared with the standard cultivar, which authenticated that these lines fully comply with type IV fiber, and further research is needed to stabilize the lines with enhanced seed cotton yield and fiber length. In previous research works on cotton genotypes concerning the best performance for yield and fiber quality traits, the newly developed interspecific hybrids performed better by having resistance to biotic and abiotic stresses compared with standard check cultivars (Namazov *et al.,* 2005; Rizaeva *et al.,* 2014).

During 2017-–2019, the selected lines exhibited significant differences in lint percentage (Table 3). In 2017, on average, the lines had significantly increased fiber percentage (36.8% to 38.5%) and were found 1.9% to 3.6% higher than standard cultivar C-6524. During 2018, on average, the fiber percentage and coefficient of variation values were 40.3% to 41.7% and 4.00% to 6.10%, respectively, which were recorded with 5.1% to 6.5% more fiber percentage than the check cultivar. The line, L-141 showed the highest lint % (41.7%) with a coefficient of variation of 4.00%. However, lower lint % (40.3%) and coefficient of variation (6.10%) were observed in cotton line, L-PCM. The inclusion of cultivated cotton and wild species and the use of polyploidy confirmed the best performance of the newly developed interspecific hybrids for fiber yield and fiber quality traits compared with the existing check genotypes (Chen *et al.,* 2014; Sirojiddinov, 2020).

For 1000-seed weight, the introgressive selected lines revealed nonsignificant differences over the three years of data. On average, in standard cultivar C-6524, the 1000-seed weight was ranging from 115.6 to 117.0 g, while the coefficient of variation values were 1.2% to 4.2%. In the selected cotton lines, the 1000-seed weight was found to be 109.1 to 120.3 g, and the lines were found 0.3 to 5.5 g heavier than standard check cultivar C-6524. The analysis showed that the degree of variability of multi-genomic cotton lines for the said trait was not significantly different, however, the cotton lines were found stabilized for 1000-seed weight.

**Table 2.** Fiber length in cotton lines obtained through introgressive methods during 2017–2019.

| No. | Lines | Fiber length (mm) | | | | Difference by ± default |
|---|---|---|---|---|---|---|
| | | $\bar{X} \pm S\,\bar{x}$ | Limit | S | V (%) | |
| | | 2017 | | | | |
| 1 | L-24 | 33.6 ± 0.33 | 31.3 - 35.3 | 1.04 | 3.18 | ± 0.5 |
| 2 | L-PCM | 35.9 ± 0.45 | 33.5 - 37.3 | 1.44 | 4.37 | ± 2.8 |
| 3 | L-138 | 34.4 ± 0.28 | 32.6 - 35.2 | 0.89 | 2.65 | ± 1.3 |
| 4 | L-141 | 34.5 ± 0.39 | 32.9 - 36.0 | 1.23 | 3.68 | ± 1.4 |
| 5 | C-6524 (Check) | 33.1 ± 0.43 | 30.2 - 34.6 | 1.34 | 4.23 | ± |
| | | 2018 | | | | |
| 1 | L-24 | 34.5 ± 0.48 | 32.8 - 36.8 | 1.51 | 4.49 | ± 1.0 |
| 2 | L-PCM | 35.4 ± 0.48 | 32.3 - 37.1 | 1.50 | 4.50 | ± 1.9 |
| 3 | L-138 | 34.2 ± 0.28 | 32.1 - 35.1 | 0.88 | 2.59 | ± 0.7 |
| 4 | L-141 | 34.6 ± 0.26 | 32.2 - 36.8 | 0.84 | 2.45 | ± 1.1 |
| 5 | C-6524 (Check) | 33.5 ± 0.26 | 32.3 - 34.8 | 0.79 | 2.42 | ± |
| | | 2019 | | | | |
| 1 | L-24 | 34.1 ± 0.43 | 33.1 - 36.0 | 1.80 | 4.46 | ± 1.2 |
| 2 | L-PCM | 35.1 ± 0.46 | 33.8 - 37.1 | 1.52 | 3.87 | ± 2.2 |
| 3 | L-138 | 33.8 ± 0.46 | 32.0 - 35.2 | 1.59 | 4.52 | ± 0.9 |
| 4 | L-141 | 33.6 ± 0.38 | 32.3 - 35.1 | 1.48 | 3.68 | ± 0.7 |
| 5 | C-6524 (Check) | 32.9 ± 1.32 | 31.1 - 35.8 | 1.26 | 3.82 | ± |

**Table 3.** Fiber percentage in cotton lines obtained through introgressive methods during 2017–2019.

| No. | Lines | Fiber (%) | | | | Difference by ± default |
|---|---|---|---|---|---|---|
| | | $\bar{X} \pm S\,\bar{x}$ | Limit | S | V (%) | |
| | | 2017 | | | | |
| 1 | L-24 | 36.8 ± 0.61 | 34.7 - 39.8 | 2.37 | 5.40 | ± 1.9 |
| 2 | L-PCM | 39.5 ± 0.63 | 36.2 - 41.1 | 1.98 | 5.20 | ± 4.6 |
| 3 | L-138 | 37.3 ± 0.62 | 33.9 - 41.3 | 2.41 | 6.40 | ± 2.4 |
| 4 | L-141 | 38.5 ± 0.52 | 36.4 - 44.1 | 2.03 | 5.20 | ± 3.6 |
| 5 | C-6524 (Check) | 34.9 ± 0.04 | 32.0 - 36.0 | 1.13 | 3.50 | |
| | | 2018 | | | | |
| 1 | L-24 | 40.5 ± 0.71 | 37.3 - 44.0 | 1.98 | 5.50 | ± 5.3 |
| 2 | L-PCM | 40.3 ± 1.01 | 35.5 - 40.5 | 2.26 | 6.10 | ± 5.1 |
| 3 | L-138 | 41.1 ± 0.66 | 36.6 - 41.8 | 1.87 | 5.30 | ± 5.9 |
| 4 | L-141 | 41.7 ± 0.53 | 39.2 - 44.2 | 1.52 | 4.00 | ± 6.5 |
| 5 | C-6524 (Check) | 35.2 ± 0.39 | 31.0 - 37.0 | 1.28 | 4.10 | |
| | | 2019 | | | | |
| 1 | L-24 | 41.0 ± 0.73 | 37.1 - 44.2 | 2.30 | 5.60 | ± 6.3 |
| 2 | L-PCM | 41.4 ± 0.83 | 38.9 - 43.2 | 2.62 | 3.90 | ± 7.0 |
| 3 | L-138 | 40.2 ± 0.66 | 36.6 - 43.0 | 2.08 | 5.10 | ± 5.5 |
| 4 | L-141 | 39.8 ± 0.49 | 37.2 - 41.2 | 1.56 | 3.70 | ± 5.1 |
| 5 | C-6524 (Check) | 34.7 ± 0.27 | 30.4 - 36.5 | 1.42 | 4.80 | |

From 2017 to 2019, by studying the micronaire (мic) in the cotton lines, it was found to be between 4.1 to 4.8 мic. However, in 2017 the best value of micronaire was recorded in line L-24 (4.3 мic), which matched the “base” interval application. Micronaire indication of cotton fiber was within 4.6 мic in two lines out of four, constituting 50.0% of all studied lines. In line L-138, the micronaire was 4.4 мic, which was determined to be equal to the indication of standard cultivar C-6524. In the different genomic lines, no micronaire was found less than 3.4 мic and more than 5.0 мic. During 2018–2019 data, analogue mean values were recorded for the micronaire. In the cotton line L-PCM, there was a slight positive change over the years, and in 2018–2019, this line was recorded with 4.1 мic matching “premium”

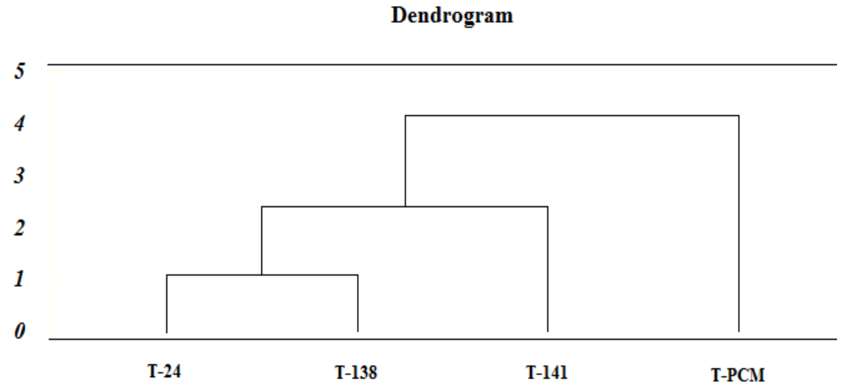

**Figure 1.** Cluster analysis of cotton lines through economic traits.

interval application and was found to be superior to all lines. The micronaire of the lines was significantly more positive than that of the standard cultivar C-6524, which fully complies with the requirements for types III and IV cotton fiber belonging to the medium-fiber cotton cultivars for the micronaire index.

In all the multigenomic cotton lines during 2017, the specific tensile strength ranged between 32.1 cN/tex (T-141) to 35.4 cN/tex (T-138), whereas in the standard cultivar C-6524, the said range was 24.3 to 27.0 cN/tex, and the difference was 7.8 to 11.1 cN/tex. In 2018–2019, lines were observed with positive mean values for the said trait and fully met the requirements of standard cotton fiber. Results revealed that cultivated and wild species of cotton were involved in the production of these lines with the best fiber quality traits, the separation of transgressive forms based on experimental polyploidy, and the proper selection of new lines with high fiber quality. Past studies also reported similar findings in newly developed cotton populations by comparing them with standard check genotypes (Srinivas and Bhadru, 2015; Shavkiev *et al*., 2021).

In this study, the distribution of the cotton lines into different clusters was determined using the Euclidean distance as a measure of genetic proximity in the Statgraphics computer program by using the Ward method for combining. The latest case also showed the availability and scope of increasing the yield at the expense of using the cotton genotypes found in clusters for the hybridization of genotypes. For cluster analysis, the quantitative traits data of multigenomic lines were used. The economic traits of these cotton lines, i.e., boll weight, 1000-seed weight, fiber %, fiber length and strength, and micronaire were determined and analyzed under the field and laboratory conditions. Cluster analysis determined the occurrence of genetic variability among the genotypes to a significant degree to evaluate yield and fiber traits genetically (Heilegiorgis and Mesfin, 2011; Muminov *et al.,* 2020).

In the cotton lines, the highest boll weight was noted in line L-PCM (6.4 g), whereas a lower mean value was recorded in line L-138 (5.9 g). However, on average, the remaining cotton lines were ranging from 6.2 to 6.3 g. After analyzing the economic characteristics of the cotton lines, the clusters were three groups. The minimum number of clusters to which the lines combined was two, and the maximum number was four. After the division of lines into different clusters, the third cluster was found optimal for the determination of the proximity of the cultivars by their valuable economic traits (Figure 1).

Cotton lines, L-24 and L-138, were included in the first cluster and were found closely related for economic traits, although differed for boll weight. The line, L-141, was included in the second cluster and was found superior to other lines and plays an important role in the production of higher seed cotton yield with medium-fiber quality traits. Line L-PCM was included in the third cluster, and it was found the highest among high-yielding cultivars by its valuable economic traits. The results also authenticated that these cotton lines could be used in the future selection process for further improvement in seed cotton yield and its fiber quality traits as also mentioned in past studies (Soomro *et al*., 2008; Wendel and Cronn, 2003).

Cluster analysis was used to determine the degree of diversity of these introgressive lines based on qualitative traits and to combine them according to their relative proximity. In introgressive cotton lines, the fiber quality traits were also used for cluster analysis. In these lines, fiber quality characters, i.e., micronaire, specific tensile strength, and fiber upper half mean length, were determined and analyzed by planting the lines in the same environment. After analyzing the fiber quality characters of the cotton lines, the clusters were three groups . In these groups, it was observed that a 3-cluster analysis was found most effective to determine the proximity of the cotton cultivars based on valuable economic traits. Past research on the creation of cotton hybrids, as a result of intergenomic interspecific hybridization, performed better for yield and fiber quality traits (Amanov, 2019; Amanov *et al.,* 2020; Sirojiddinov, 2020).

In cotton growing, one of the most important tasks is to enhance the resistance to various diseases, insect pests, and abiotic factors. The disease effects on the seed samples of medium-fiber cotton cultivars were also studied. The study showed that plant seeds were infected by mycotoxins isolated from the fungi belonging to *Fusarium* group. Fungal strains viz., 576, 601, and 656 belonging to *F. oxysporum* species isolated from the cotton plant that got infected with fusarium wilt in Bukhara region, Uzbekistan, caused damage to seeds of cotton cultivar, AN-Boyovut-2 from to 8.0% to 35.0%, and adversely affected the germination of cultivar Bukhara-6 from 16.0% to 31.0%. The strain, 595 isolated from the soil, affected the germination of the seeds of cotton cultivars, AN-Boyovut-2 and Bukhara-6 by 100.0% (Sherimbetov, 2016).

The research work was carried out on the resistance degree of the leaves in cotton lines obtained by intergenomic introgressive methods of cotton to phytopathogen fungi *Verticillium dahliae* Kleb. and *Fusarium oxysporum* f. sp. *vasinfectum*. The study analyzed the effect of mycotoxins isolated from micromycetes of *Verticillium dahliae* Kleb., *Fusarium oxysporum* f. sp. *vasinfectum* on seed germination in the cotton lines. It should be noted that the germination of cotton line seeds in the control was 100.0% (Figure 2). The recombinant forms of mycotoxins were isolated with the highest effect on seed germination separated from *Verticillium dahliae* and *Fusarium oxysporum* f.sp. *vasinfectum* micromycetes in cotton hybrids and recommended as a primary source (Sirojidinov *et al.,* 2018; Mangi *et al*., 2022).

The cotton line, L-24 was found moderately tolerant to *Verticillium dahliae*, which was 30.0%. Lines L-PCM and L-138 have 80.0% to 100.0% resistance to mycotoxins of micromycetes. It was also observed that these lines were found resistant to *Verticillium dahliae*. By seed germination, line L-138 was found to be highly resistant to the strains of pathogen fungi (*Fusarium oxysporum* f. sp*. vasinfectum,*). In addition, it was found that the tolerance of cotton lines, L-PCM and L-138, was 80.0 to 100.0% to mycotoxins of micromycetes (*Verticillium dahliae*). It is a well-known fact that diseases not only reduce the seed cotton yield but also affect the quality of fibers and seeds. Therefore, in cotton growing, one of the most important tasks is to study, analyze, and search for the measures to control the nature of fungi and bacteria that are agents of diseases. One of the most common diseases in cotton-growing countries is *Verticillium dahliae* Kleb., infecting not only the cotton crop, but also damaging about 700 other cultivated and wild crop plants. According to past researches conducted on diseases of transgenic cotton plants and ensuring the resistance to the pathogen of the fungus (*Alternaria alternata*), in transgenic wild species of cotton, the resistance was found stronger (Sherimbetov*,* 2016).

The degree of resistance of intergenomic cotton lines to *Fusarium solani, Verticillium dahliae* Kleb., and *Fusarium oxysporum* f. sp. *Vasinfectum,* was analyzed through plant leaf samples by affecting them with biomaterials prepared from phytopathogenic micromycetes specimens. Following the results, leaf samples were found to have a different response to phytopathogen micromycetes of *Fusarium solani, Verticillium dahliae* Kleb., and *Fusarium oxysporum* f. sp. *vasinfectum* (Figure 3). In cotton introgressive lines, L-24, L-138, and L-141, the leaf samples were strongly infected as a result of phytopathogen micromycetes of *Fusarium oxysporum* f. sp. *vasinfectum*. However, in the cotton line L-PCM, the leaf samples got less damage by phytopathogen micromycetes of *Fusarium oxysporum* f. sp. *vasinfectum*. Under the influence of phytopathogen micromycetes, the line L-24 showed weak tolerance to *Fusarium solani*. However, in cotton lines, L-PCM and L-141, the biomaterials of the leaf samples were relatively undamaged as a result of the effect of phytopathogenic micromycetes of *Fusarium solani*, which means that these lines were resistant to *Fusarium solani*.

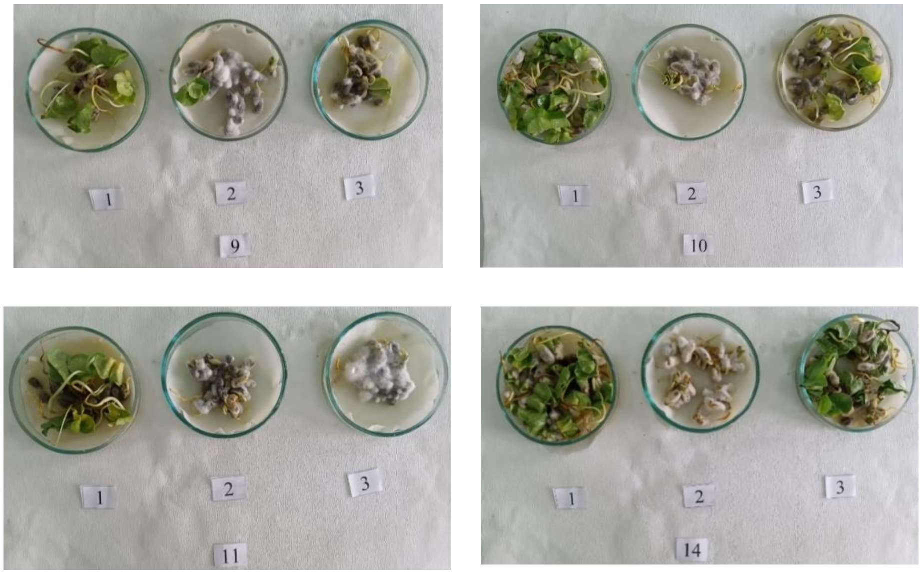

**Figure 2.** Resistance of cotton lines obtained by introgression methods to pathogen fungi (*Fusarium oxysporum* f. sp*. vasinfectum,* and *Verticillium dahliae*). Note: 1. Control, 2. *Fusarium oxysporum* f. sp. *vasinfectum,* 3. *Verticillium dahliae,* 9. T-24, 10. T-PCM, 11. T-141, 14. T-138.

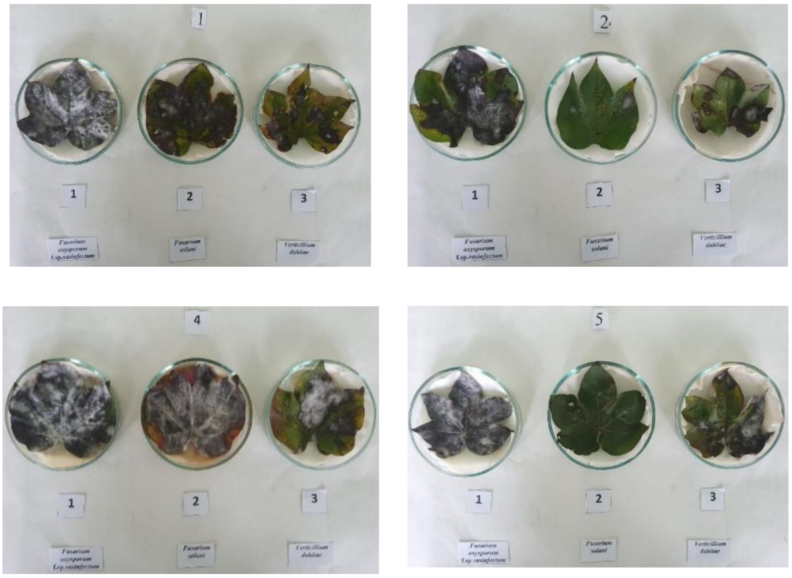

**Figure 3.** Resistance of cotton lines obtained by introgression methods to phytopathogen fungi (*Fusarium oxysporum* f. sp*. vasinfectum, Fusarium solani,* and *Verticillium dahliae*). Note: 1. *Fusarium oxysporum* f. sp. *vasinfectum,* 2. *Fusarium solani,* 3. *Verticillium dahliae,* 1. T-24, 2. T-PCM, 4. T-141, 5. T-138.

The recent study revealed that analysis of valuable economic traits and features of the cotton lines obtained based on introgressive methods, the research was continued to bring the remarkable lines with the greater genetic potential to the varietal level and their introduction into production. Selection of cotton line, L-PCM resulted in the introduction of the new medium-fiber cotton cultivar "Niso," which successfully passed ground control in 2019, and since 2020 it has been tested at the four branches of the cultivar testing center (CTC) and exceeded the standard check cultivar C-6524 (Table 4).

**Table 4.** Cultivar Testing Center (CTC) branches for comparing the improved cultivar "Niso" with standard check cultivars during 2020.

| Cultivars | Average seed cotton yield (kg ha$^{-1}$) | Vegetation period (days) | Boll weight (g) | Fiber (%) |
|---|---|---|---|---|
| Fergana cultivar testing branch | | | | |
| C-8290 (Check) | 4550 | 126 | 6.0 | 35.7 |
| Niso | 5650 | 124 | 6.5 | 36.9 |
| Khatirchi cultivar testing branch | | | | |
| Bukhara-6 (Check) | 4080 | 115 | 6.3 | 33.4 |
| Niso | 4150 | 110 | 6.4 | 37.1 |
| Mingbulok cultivar testing branch | | | | |
| C-6524 (Check) | 4050 | 118 | 5.6 | 35.4 |
| Niso | 4250 | 118 | 6.1 | 36.5 |
| Termez cultivar testing branch | | | | |
| Besh kahramon (Check) | 3750 | 111 | 4.7 | 34.6 |
| Niso | 3830 | 110 | 5.9 | 38.1 |

The medium-fiber cotton cultivar "Niso" was found to be integrated in terms of economic and fiber quality traits, and competitive with regionalized cultivars of medium-fiber cotton in Uzbekistan. The cotton cultivar "Niso" has high seed cotton yield, lint %, and desirable fiber quality traits that fully comply with the requirements of type IV, as well as, resistant to diseases and drought, which confirm its superiority over existing cotton cultivars. Furthermore, as a result of intergenomic interspecific hybridization with the inclusion of cultivated and wild species, the use of polyploidy confirms the work of past researchers in cotton (Namazov *et al.,* 2005; Boboyev, 2017).

Cotton lines based on intergenomic introgression were included in the leading "Cotton gene pool" (Reference of the Academy of Sciences of the Republic of Uzbekistan №4/1255-2473 dated November 12, 2020). These introgressive cotton lines made it possible to enrich the collection of cotton, evaluate wild cotton species, and form a system of information and analysis of the electronic database of adaptable stress factors and genetically enriched samples.

## CONCLUSIONS

Results showed that in cotton introgressive lines, the boll opening was two to 13 days earlier than the standard check cultivar C-6524. Cotton lines selected on the basis of boll weight have shown the best performance and were significantly superior to standard cultivar. Under the influence of the pathogen fungi *Fusarium oxysporum* f. sp*. vasinfectum* on seed germination, line L-138 showed strong resistance, and the lines, L-PCM and L-138, were found to have 80.0% to 100.0% tolerance to fungi *Verticillium dahliae*. The cotton lines, L-PCM and L-141, were not even damaged by *Fusarium* solani, and the leaf samples of lines, L-24 and L-PCM, were not infected with fungi *Verticillium dahliae*. The cluster analysis of economic traits in the cotton lines showed that line L-PCM was included in the third cluster, and this line was also identified as the best performer for economic traits and could be used in the selection process. As a result of these studies, a new medium-fiber cotton cultivar "Niso" has been introduced with economic traits, i.e., plant height (100.0 to 110.0 cm), productivity (3830 to 5650 kg ha$^{-1}$), boll weight (6.0 to 6.7 g), boll opening (109.0 to 112.0 days), weight of 1000-seed weight (118.0 to 120.0 g), fiber (36.9% to 41.4%), fiber length (34.0 to 35.9 mm), relative tensile strength (34.6 cN/tex), and type IV fiber.

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