Variability and inheritance of fiber length and wilt resistance in a complex 4-5 specific and backcross hybridization of cotton

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Abstract

In this paper presents data of researches about fiber length in the 4-5 species. The largest number of plants with the indicated analyzed trait in hybrid combinations, obtained with the participation of the variety Omad, appeared with a number of variations in fiber length at 35.0-36.0 mm and above. Investigation of 4-species hybrids of F2 and back cross hybridization allowed some improvement in the average value of trait when compared with F1. Despite the emergence of transgressive plants with fiber length 36.1-37.0 mm and above, the average trait of composite 5 species hybrids F2 remained almost at the level of F1, i.e. 35.5-36.0 mm. The greatest number of positive recombinants occurred in 5 species back crossing developed with the participation of Termez-31.

Introduction

In breeding of cotton, a wide variability of agronomy valuable traits and development of new forms can be achieved by using various hybridization methods. The hybridization process, however, implemented, leads to the decoding of inheritance, allowing the formation of new flexible genotypes that have the ability to change and adapt to new growing conditions. Hybridization and selection are the main synthetic methods to develop new varieties, and success in this task depends largely on the choice of the method of crossing and the original forms of the genotypes. Therefore, the genetic variability of agronomic traits of crop plants must be increased, by involving genetic resistance to various stress factors, diseases and insects of original forms as well as wild relatives.

The emergence of new diseases, the distribution of insect populations and environmental degradation confront breeders with the challenge of increasing cotton production through the creation of varieties with early maturation, high yields, good yield and quality of fiber, and resistance to diseases and pests, as well as stress factors. The solution to these problems requires the improvement of the genetic basis of the evaluation of existing donors and the use of various methods of hybridization in order to create new genotypes that promote positive polygene recombination in a hybrid organism for use in applied cotton breeding.

The current problems of modern genetics and breeding are to assess the different hybridization methods that involve the genes that control economically valuable traits in order to identify optimal hybridization methods, allowing the development of new genotypes and genetically enriched recombinants. In this regard, research is underway to study the effectiveness of various complexities of hybridization and to generate unique genotypes of basic agronomy valuable traits and prove their effectiveness in creating genetically enriched and unique recombinants.

To solve the above problems, a wide study was deployed on the existing models of cultivated and wild species in the genetic collection of cotton using various hybridization techniques, the identification of donors and the creation of new genotypes for primary selection. However, some aspects of the complex interspecific hybridization of cotton, especially comparative studies to determine the effectiveness of interspecific hybrids obtained by crossing genetically different initial parents and the development of initial materials with complex agronomic traits for practical breeding are not comprehensively covered in the literature.

It is known that hybridization is a major source of genetic variation in populations. The resulting random chromosome segregation at meiosis, involving diverse parental forms, leads to the recombination of genetic materials.1 In the selection of crops, including cotton, different methods of interspecific hybridization are exploited to produce a wide variability in economically valuable traits and to develop nonexistent combinations.

Academicians Abdullaev et al. (1980) noted that the genus Gossypium L. has a huge variety of biological features.2 Most of these species are collected in genetic collections in Australia, Brazil, China, France (CIRAD), India, Pakistan, the USA and...
Uzbekistan. On the basis of cytogenetic differences, genus *Gossypium* includes 46 diploid and 5 allotetraploid species. Uzbek scientists have similar observations. Many wild and ruderal forms have unique biological features that are absent or poorly expressed in cultivated species. A significant role is attributed to backcrossing hybridization for the improvement of agronomic traits. On the basis of hybridization, a composite triple hybrid (*G. hirsutum* L. x *G. herbaceum* L.) x *G. harknessii* with a variety of *G. hirsutum* is valuable for bigger boll size, lint output and fiber length.

In interspecific hybrids of cotton produced by crossing amphidiploids with different varieties starting with F2, there is widespread transgressive variability for all quantitative traits, forming the basis for the selection of new genetic forms by selection. However, he noted that the most widespread variation in fiber output is observed in F2-F3, and in length and resistance to wilt in F2-F3. In composite interspecific hybrids *G. thurberi* Tod. x *G. raimondii* Ulbr. x *G. herbaceum* L., a formative process for agronomical valuable traits to the identification of transgressive forms in subsequent generations is observed due to wide segregation. He found that the fiber output and length in the studied composite interspecific hybrids had less variability compared to productivity and its components. Relatively high variation in fiber output was observed in F1, and in fiber length in F2-F3.

To solve this problem, the scientists of the republic carried out extensive research on transfer of wilt-resistant gene of wild cotton species to cultivars and there is a great success achieved. In particular, the emergence of transgressive plants with fiber length 36,1-37,0 mm and above, the average trait of composite 5 species hybrids F2 remained almost at the level of F1, i.e. 35.5-36.0 mm. The greatest fiber length (36,6 mm) was observed in variety Termez-31 and the shortest one (33,0 mm) in amphidiploids [F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-4727 (G. hirsutum L.)) and [F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-6524 (G. hirsutum L.)]. The longest fiber length (36,6 mm) was observed in variety Termez-31 and the shortest one (33,0 mm) in amphidiploids [F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-4727 (G. hirsutum L.)]. It was concluded that two backcrosses, unlike one, with the variety Omad improved average fiber length and variability. The largest number of plants with values is located in the middle and the right classes in an ordered series, and the average level of initial 4-species hybrid amphidiploids, i.e. 33,1-33,9 mm.

In 5-species hybrids, the average fiber length was 2-3 mm better than in the 4x species. The largest number of plants with the indicated analyzed trait in hybrid combinations, obtained with the participation of the Omad variety, appeared with a number of variations in fiber length at 35,0-36,0 mm and above. Investigation of 4-species hybrids of F2 and back cross hybridization allowed some improvement in the average value of trait when compared with F1. Despite the emergence of transgressive plants with fiber length 36,1-37,0 mm and above, the average trait of composite 5 species hybrids F2 remained almost at the level of F1, i.e. 35,5-36,0 mm. The greatest environmental problems created in the cotton-growing areas for today promoted the appearance of new races of wilt disease. Consequently, it determines the relevance of scientific research and applied investigations in this direction. It is known that wild and semi-wild species, thanks to their distribution in various environmental conditions and long-term natural selection, have an abundance of genetic diversity that contains a lot of outstanding genes that can be used to implement such features as resistance to drought, disease and pest resistance, fine and strong fiber and others.

### Materials and methods

When creating complex 4x species and their back cross progenies - synthetic amphidiploid F0(F0K- 28=F1G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S - 4727, F0 (F0K-28 F1G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S - 6524 and variety Omad of species *G. hirsutum* L.

When creating complex 5x species and their back cross progenies 4x genomic hybrid - F0 (F0K-28 F1G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S - 4727, F0(F0K-28 F1G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S - 6524 and variety Termez -31 of the species *G. barbadense* L. All the experimen-

### Results and Discussion

The staple length of the original cultivars was longer than that of amphidiploids ([F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-4727 (G. hirsutum L.))] and [F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-6524 (G. hirsutum L.)]). The longest fiber length (36,6 mm) was observed in variety Termez-31 and the shortest one (33,0 mm) in amphidiploids [F2(F1(G. thurberi Tod. x G. raimondii Ulbr. x G. arboreum L.) x S-4727 (G. hirsutum L.)]. It was concluded that two backcrosses, unlike one, with the variety Omad improved average fiber length and variability. The largest number of plants with values is located in the middle and the right classes in an ordered series, and the average level of initial 4-species hybrid amphidiploids, i.e. 33,1-33,9 mm.

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number of positive recombinants occurred in 5 species back crossing developed with the participation of Termez-31.

The average value of staple length in complex 4-5 species hybrids was observed to significantly improve among progenies F3 (Table 1).

As a result, the average value of four species hybrids is 34.7 mm, from one and two-fold and back crosses F1, [BC1] (F1K-28 x S-6524)x Omad|x Omad), F1, [BC2] (F1K-28 x S-6524)x Omad|x Omad) at 35.0 mm. It should be noted that the highest average values of the trait (36.0 mm and above) were detected in 5 back cross species hybridization. This data will likely be explained by the influence encountered by recombinants with a length 40.0 mm and above in F1.

However, the performance of the standard deviation and coefficient of variation in F1 hybrids were lower, indicating a relatively rapid stabilization of the trait. The above conclusion is confirmed by the average value of the attribute staple length in composite hybrids F4, due to the appearance of a large number of plants in the right classes of variation series, resulting in mean values of the analyzed trait ranging from 35.0 to 35.5 mm in composite 4 species hybrids and back crosses. Unlike the 4x species hybrids, at 5 species mean values of the attribute staple length (36.4-37.0 mm) were at a higher level. The highest average value of staple length (37.0 mm) was observed in 5 species back cross hybridization F4 {(BC1 (F1K-28) x C- 6524) x Termez-31 x (37.0 mm) was observed in 5 species back cross hybridization. This data will likely be explained by the influence encountered by recombinants with a length 40.0 mm and above in F1.

Study of the variability of the attribute “staple fiber” hybrids F1-F4 shows that composite 4-5 species hybridization promotes positive transgression. The highest variability in a composite trait hybridization occurred in composite 5 species hybrids, which indicates the significant contribution of long-genotype component crossing trait on display. The occurrence of plants with positive transgression composite interspecific hybridization is mainly observed in F4, and since F4 is stabilized on the basis, as in 4 species, and 5 species hybrids.

Further, wilt-resistant plants have been studied in detail at the newly created polygenomatic and backcrossing interspecies cotton hybrids. The results of research of the parental varieties indicate the resistance to wilt of Omad variety in total of 12.6 % and 5.53 % in the strong degree (Table 2). The most intense susceptibility was observed in grade differentiator C-4727 – 34.3 % in total and 15.6 % to a great extent. On the basis of the average values of the characteristic “tolerant to V. dahliae” in complex interspecific hybrids we can talk about the impact of the original genotype of cultivars, that is, depending on the stability of their aforementioned different races of the pathogen. This is confirmed by the highest affection of wilt of 4 species hybrid F1 (K-28) x S-4727, obtained with the participation of the first race of the unstable grade S-4727 in general, and to a great extent as compared with a complex of 4 species hybrid F1 (K-28) x S-6524, created with the participation of the second race of tolerant varieties V. dahliae S-6524. Affection of these hybrids, a total degree was 7.4 % and 19.7 % and a strong 2.2 % and 3.6 %, respectively. As a result of two-fold hybridization with Omad variety of form G. hirsutum L., the affection of wilt is decreased in general and and a large extent, which is apparently due to the relatively high tolerance to the aforesaid pathogen (Table 2).

The conclusion, which refers to the efficiency of selection of resistant plants to wilt in the early generations of interspecies hybrids, created with the participation of grade S-6524, is confirmed by the values of F2 hybrids. It should be noted, that unlike other agronomic characteristics on resistance to wilt, strong differences are not observed depending on genotype and the number of backcrosses. This is confirmed by the appearance of the most tolerant and relatively unstable families and among complex interspecies hybrids and backcrossing F4. Among the plants of F2 combination [(F1K-28 x S-6524) x Omad]) plants were identified with the highest rates of plant susceptibility, both general and a strong degree of affection by wilt. At the F3 the value of the coefficient of variation in the variational series on the analyzed attributes was decreased, especially in the hybrids (BC1 [(F1K-28 x S-4727) x Omad]) x Omad) and (BC2 [(F1K-28 x S-6524) x Omad]) x Omad).

Thus, by studying the tolerance characteristic in V. dahliae complex species hybrids 4-5 obtained with involving amphidiploid F1-K-28 at wilt background can be it concluded, that it is a valuable donor of stability and it can be recommended together with hybrids

| Varieties and hybrids | n  | 10 mm range | M±m  | SD  | CV  |
|-----------------------|----|-------------|------|-----|-----|
|                        |    | 30.1-31.1 | 31.1-32.1 | 32.1-33.1 | 33.1-34.1 | 34.1-35.1 | 35.1-36.1 | 36.1-37.1 | 37.1-38.1 | 38.1-39.1 | 39.1-40.1 | 40.1-41.0 |
| 1. Omad                | 37 | 5           | 2     | 11   | 12   | 7       | 34.9±0.2 | 1.1    | 3.2  |
| 2. Termez-31           | 38 | 1           | 5     | 15   | 9    | 3       | 36.6±0.2 | 1.2    | 3.2  |
| 3. F3[(F1K-28) x S-6524 | 66 | 2           | 5     | 13   | 25   | 10      | 7       | 4     | 2    | 34.7±0.3 | 1.5    | 4.6  |
| 4. F3[(F1K-28) x S-4727 | 76 | 2           | 3     | 4    | 14   | 22      | 14      | 9     | 5    | 3    | 34.7±0.2 | 1.6    | 4.8  |
| 5. F3 BC1 [((F1K-28 x S-6524) x Omad] | 85 | 2           | 6     | 17   | 14   | 22      | 11      | 10    | 2    | 35.0±0.2 | 1.6    | 4.6  |
| 6. F3 BC2 [((F1K-28 x S-4727) x Omad] | 112 | 1        | 2     | 9    | 12   | 23      | 35      | 20    | 8    | 4    | 35.1±0.1 | 1.6    | 4.5  |
| 7. F3 BC3 [((F1K-28 x S-6524) x Omad] | 112 | 4        | 6     | 16   | 23   | 31      | 20      | 8    | 4    | 35.1±0.1 | 1.4    | 4.0  |
| 8. F3 BC4 [((F1K-28 x S-4727) x Omad] | 114 | 3        | 7     | 11   | 32   | 35      | 16      | 6    | 3    | 35.0±0.1 | 1.4    | 4.1  |
| 9. F3 [(F1K-28 x S-6524) x Termez-31] | 85 | 2           | 4     | 9    | 13   | 28      | 14      | 11    | 3    | 2    | 36.5±0.2 | 1.7    | 4.5  |
| 10. F3 [(F1K-28 x S-4727) x Termez-31] | 95 | 2           | 6     | 5    | 23   | 32      | 13      | 9    | 5    | 3    | 36.0±0.2 | 1.7    | 4.6  |
| 11. F3 BC1 [((F1K-28 x S-6524) x Termez-31] | 88 | 4          | 4     | 9    | 13   | 20      | 18      | 6    | 4    | 2    | 36.8±0.2 | 1.8    | 4.9  |
| 12. F3 BC2 [((F1K-28 x S-4727) x Termez-31] | 102 | 1 | 5      | 11   | 13   | 24      | 16      | 9    | 6    | 2    | 36.5±0.2 | 1.7    | 4.7  |
A comparative study of the variability of the characteristic of fiber length at the composite 4-5 species hybridization found that F_1-F_4 demonstrated positive transgression. The highest variability in a composite hybridization was observed among the composite 5 species hybrids, which indicates the significant contribution of long staple genotypes involved in crossing.

It is determined that at composite 4-5 species hybridization the occurrence of the largest number of plants with positive transgression of fiber length is mainly observed in F_3, and starting F_4 is stabilized in both 4 species and 5 species hybrids.

Wild species of cotton, as well as complex polygenomatic hybrids obtained featuring amphidiploid F_1-K-28 are valuable donors of resistance to wilt, that allows to recommend them for use as a breeding material for practical breeding.

created by its participation to be included in genetic and breeding research to create original, hybrid and breeding material for breeding for tolerant to *V. dahliae*.

### Conclusions

A comparative study of the variability of the characteristic of fiber length at the composite 4-5 species hybridization found that F_1-F_3 demonstrated positive transgression. The highest variability in a composite hybridization was observed among the composite 5 species hybrids, which indicates the significant contribution of long staple genotypes involved in crossing.

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