

MOLECULAR GENETIC ANALYSIS OF HEREDITARY OF MORPHOBIOLOGICAL AND ECONOMIC CHARACTERISTICS OF COTTON-PLANT

Komilov Doniyor Jo'raevich¹,
Mirzaolomov Sherzodbek Mirzavalievich¹
1.Namangan State University
Email: dkomilov81@mail.ru

ANNOTATION

The paper presents the results of a study on the study of the morphobiological and economically valuable characteristics of cotton using traditional and molecular genetic methods. As the objects of study was chosen F₂ generation hybrids, derived from hybridization wild-type of cotton *G.hirsutum* ssp. *purpurascens* var. *el-salvador* with the variety "Kupaysin".

Keywords: Cotton, height of plant, hs, monopodia, simpodia, hybridization, hybrid, genotyping, primer, marker.

INTRODUCTION

Today, world scientists are paying special attention to the creation of cotton varieties with high fiber quality, high yield, resistant to biotic and abiotic stresses, as well as improving the existing varieties and increasing their yield [1, 2]. This, in turn, shows the need to effectively use the world's wide variety of cotton gene pool and the potential of wild and semi-wild species in the creation of new, productive varieties. [3].

Taking into account the above, these studies *G. hirsutum* ssp. *purpurascens* var. It was carried out in order to study the morphobiological characteristics of the El Salvador wild form and to use its valuable economic characteristics in the future to create new varieties. Based on the research results, it is possible to identify QTL loci (genetic markers) involved in the appearance of some morphobiological traits of cotton. Identified genetic markers can be used as a main instrument for the use of wild cotton germplasm in selection processes and introgression of unique genes from them into existing cotton varieties.

The main goal of this research is to involve wild varieties of the cotton gene pool in selection processes, to study the inheritance of their morphobiological and valuable economic traits. El Salvadorian wild form of *G. hirsutum purpurascens* subspecies of cotton and "Kopaysin" variety created from this form using radiomutagenesis [6] and hybridization methods were selected as the object of research. Samples were crossed and first and second generation F₁, F₂ hybrids were created.

When analyzing the second generation hybrids in our research, a total of 147 different plants, their parental forms and F₁ hybrids were studied in natural, i.e., field conditions.

In the F₂ generations of each plant, research was conducted on the following parameters and morphobiological characteristics:

1. the beginning and continuation of flowering.
2. Plant height, cm .
3. The height of the first fruit branch.
4. Number of monopodial branches.
5. Number of sympodial branches.
6. Number of joints, pc.
7. Total and number of opened cysts.
8. The shape of the pouch.
9. The number of

hips in the pelvis. 10. Branching. 11. Type of branching. 12. Antionic stain. 13. Hairiness of the stem. 14. The shape of the bush was studied during the growing season.

MATERIALS AND METHODS

Plant samples. In the research works, cotton *G. hirsutum* type *purpurascens* subspecies *el salvador* wild form (photoperiodic), "Kopaysin" variety created from this species by means of radiomutagenesis and crossing methods [4] and F2 generation hybrids created as a result of mutual crossing of these samples were used.

RESEARCH RESULTS

In research works, morphobiological and some economically important traits were studied in F2 generation hybrid combinations of El Salvador wild form and Kopaysin variety. In particular, based on phenotypic observations, the beginning of flowering, the speed of flowering, hs (height of sympodia, or the height of the location of the first harvest branch), plant length, the number of monopodial (vegetative) and sympodial (harvest) branches, the number of joints, the number of total and opened pods are valuable. heritability of economic traits and characteristics was assessed genetically. (Table 1).

According to the results of phenotypic observation, the following indicators were observed in the hybrids of the first and second generation when the average value of the studied characters was obtained:

Hybrids of the first generation (F1): plant height - 120 cm, height of the first harvest branch - 17 joints, number of monopodial branches - 5, number of sympodial branches - 5, number of joints - 21, shape of the pod - ovoid, number of pods - 4-5, number of pods - 13/0 (ie 13 pods and none of them opened), branching - unlimited, type 2-3, anthocyanin spot - moderate, stem hairiness - moderate, stem shape - scattered.

In hybrids of the second generation (F2): plant height - 110 cm, height of the first harvest branch - 8.5 joints. Number of monopodial branches; 64% of plants had 4 branches, and the remaining 36% of plants did not have monopodial branches. The number of sympodial branches is 17, the number of joints is 25. Pocket shape; Out of 145 plants, 112 were ovoid, 23 were conical, and 1 was spherical, and 9 plants were not formed. It was observed that the number of cysts in the formed cyst is 4-5. The number of pods is 15/1 (15 pods and 1 of them is opened), branching is unlimited, type 1-3, anthocyanin spot is intermediate. The degree of pubescence of the stem; strong – 13%, average – 40%, weak (low) – 47%. The shape of the bush; It was found that 12.3% of the plants are scaly, 87.7% of the hybrids are scattered (Table 1).

As can be seen from the table, in the first generation hybrids, plant height, number of pods, anthocyanin spot, number of joints and hairiness of the stem were intermediately inherited compared to both parental samples. According to the type of branching, the number of sympodial branches and the shape of the stem, *G. hirsutum* ssp. *purpurascens* var. It can be seen that the El Salvador wild form predominated. In addition, it was observed that the height of the first harvest branch (hs) and the number of pods in the pod were increased in the F1 generation hybrids compared to the wild type.

It can be observed that the number of monopodial branches in the hybrids of the second generation is reduced compared to the wild form of El Salvador and the hybrids of the F1

generation. The number of sympodial branches was significantly increased compared to the El Salvador wild form and the first generation hybrids. It can be seen that the hybrids of the F2 generation showed a better result even compared to the "Kopaysin" variety. Plant height, number of joints, number of pods, type of branching, stem hairiness (strong, medium, sparse), stem shape, pod shape, first harvest branch (hs) were shown to be inherited intermediately. In conclusion, it can be said that in the hybrids of the first and second generation, the variety "Kopaysin" was dominant in terms of the number of pods and the number of pods. The El Salvador wild form was dominant in the first generation hybrids according to the number of sympodial branches, anthocyanin stain, branching type and stem shape. It can be observed that the percentage of plants with average number of sympodial branches is higher in the second generation hybrids than in the parent and first generation hybrids. This makes it possible to select recombinant plants with a high number of sympodial branches in the second generation hybrids.

In addition, genetic diversity between parental samples was studied based on polymorphism using molecular markers. When the results of the research were analyzed, molecular polymorphism between parental genotypes was determined using microsatellite CH, TMB, BNL, JESPR markers, genotyping of F2 generation hybrids was performed using the identified polymorphic markers.

In order to determine polymorphism, parental genotypes were analyzed using PCR method with 336 microsatellite (or SSR - simple sequence repeat) markers. According to the amplification results, 69 out of 336 SSR primers showed polymorphism between the parental genotypes (Figure 1).

Table 1 Information on morpho-economic characteristics of parental samples and F1 and F2 generation hybrids recorded as a result of phenotypic observations

№	Signs	"increase" variety	El Salvador wild form	F1 generation hybrid	F2 generation hybrids
1.	Plant height, cm	80	175	120	110
2.	Number of monopodial branches, pcs	0	7	5	4
3.	Number of sympodial branches, pcs	15	5 (short and weak)	5	17
4.	The number of joints, pcs	18	26	21	25
5.	Cup shape	ovoid	ovoid	ovoid	conical -23, spherical -1, ovoid -112
6.	The number of groins in the bag, pcs	4-5	3-4	4-5	4-5
7.	Number of pods, pcs	15/7*	-	13/0	15/1
8.	Branching	not limited	not limited	not limited	not limited
9.	Branch type	1-types	2-3 types	2-3	1-3
10.	anthocyanin stain	strong	average	average	intermediate

№	Signs	"increase" variety	El Salvador wild form	F1 generation hybrid	F2 generation hybrids
11.	Hairiness of the stem	strong	rare	Average	strong – 13%, average – 40%, rare (less) – 47%
12.	The shape of the bush	noise	scattered	Scattered	noise – 12.3%, scattered – 87.7%
13.	First harvest branch - hs	4	13-14	17	8,5

* - Total number of cysts/number of opened cysts

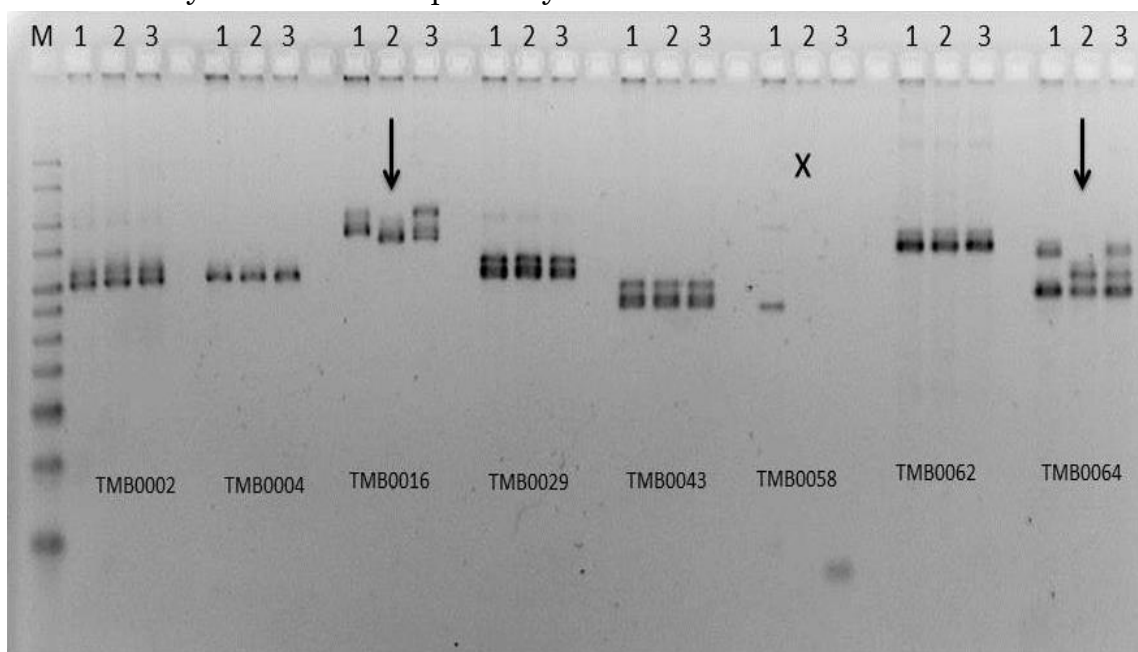


Figure 1. PCR analysis of parental F1 hybrid using TMB primers. 1- *G. hirsutum* ssp. *purpurascens* var. El Salvador; 2) "Payksin" variety; 3) F1 generation hybrid. A polymorphic marker is indicated by the pointer.

Among them, GH polymorphism was observed in 12 out of 48 samples, TMB in 26 out of 144 samples, BNL in 21 out of 96 samples, JESPR in 10 out of 48 samples. It is noteworthy that the group of primers that showed the most polymorphism between the parental samples belonged to the BNL set (Figure 1).

The created hybrid population of F2 generation can be used as a valuable resource for molecular genetic mapping of important morphobiological and economic traits in cotton in the future.

In conclusion, it can be said that in F2 generation hybrids, parameters such as plant height, first harvest branch (hs), number of monopodial branches, and number of sympodial branches were dramatically changed compared to those of the parent samples. In addition, high polymorphism was found between parental samples. This, in turn, is of great importance in the mapping of QTL-loci, which are genetically linked to the above-mentioned morphobiological and valuable economic traits of these polymorphic markers.

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