

Cluster Analysis of Valuable Economic Features of Introgressive Forms

Gafurjon Gulomov^{1,*}, Bekhzod Sirojiddinov²

¹Southern Paxtakor 3/17, 170100, Andijan, Uzbekistan

²Yunusobod District 19/475, 100001, Tashkent, Uzbekistan

Abstract In this article, a comprehensive analysis of introgressive hybrid forms of cotton is more important than a separate analysis of quantitative traits for creating lines and varieties with a complex of valuable economic traits, and many scientific studies have been carried out on the application. Information on the methods of factorial and cluster analysis of local varieties and lines. It has been established that the level of dominance of the cotton weight in terms of the weight of one box, the length of the fibre, the yield of the fibre, and the weight of 1000 seeds is inherited in positive and negative intermediate, dominant and extremely dominant states. In order to maintain the state of positive heterosis achieved in these ranges, it is necessary to continue the work of genetic breeding research in the next generations. During the studies, cluster analysis of valuable farm marks of 10 parent forms, F₁ and F₂ of hybrid plants (cotton weight in one boll, 1000 pieces of seed weight, fiber output and fiber length), which were initially studied for cluster analysis, quantitative marks were used. The indicators of valuable economic marks of these ridges were determined and statistically analyzed in laboratory and field conditions.

Keywords Variety, Line, Hybridization, Cluster, Generation, Heterosis

1. Introduction

Complex analysis of introgressive hybrid forms of cotton is more important than individual analysis of quantitative traits for creating lines and varieties with a set of valuable economic traits. A lot of scientific studies have been conducted on the application of factor and cluster analysis methods in local varieties and ranges. The creation of new varieties has always been of the highest importance [1-5].

If more than two populations are taken to determine plant traits, then it is necessary to divide the genotypes into groups according to their closeness to each other. For this purpose, to determine the level of diversity of these varieties according to their quantitative characteristics and to combine them according to their mutual proximity, the cluster analysis method was used to achieve this goal.

Cluster analysis is a multivariate statistical analysis method that identifies the properties of objects that are similar to each other and divides them into the same groups based on these properties.

In our experiment, the clustering of the lineages was determined using the Statgraphics computer program using Euclidean distance as a measure of genetic closeness, and

Ward's method as a clustering method.

2. Literature Review

Kh. Muminov, Z. Ernazarova, B. Amanov, the primary resources and interspecific amphidiploid F₁-F₆ generation plants belonging to different clusters showed a wide variation in characters, according to the weight of cotton in one boll, 2.3 -6.2125 g., 67.3-125.529 g. by the weight of 1000 seeds, 24.9-34.4125 mm by fibre length, 31.4-40.2625% by fibre yield, 6.3-7.5875 g according to the fibre index. established Also F₆ *G. hirsutum* subsp. *euhrisutum* "Kelajak" variety F₁ (*G. arboreum* subsp. *perenne* x *G. arboreum* subsp. *obtusifolium* var. *indicum*) combination families, 6.6 ± 0.13 g of cotton in one boll. ("Oila-41"), 125.8 ± 3.48 g by weight of 1000 seeds. ("Oila-59"), fibre length 34.5 ± 0.16 mm ("Oila-8"), fibre yield 40.3 ± 0.65% ("Oila-59"), 8.5 ± 0.23 g according to the fibre index. High-performance plants up to ("Oila-59") were isolated. Within the fourth cluster (F₅*G. hirsutum* L. x (*G. arboreum* L. x *G. arboreum* L.) «Oila-5», «Oila-13», «Oila-8», «Oila-59», «Oila-14", F₆ *G. hirsutum* L. x (*G. arboreum* L. x *G. arboreum* L.) "Oila-13", "Oila-5", "Oila -59") is a family with valuable economic traits recommended the use of plants as practical and theoretically valuable donors in genetics and selection research. Samanov Sh.A., et al. in their scientific research, divided the cluster analysis of the valuable economic characters of the

* Corresponding author:

abdulatif20131@gmail.com (Gafurjon Gulomov)

Received: Apr. 27, 2023; Accepted: May 16, 2023; Published: May 22, 2023

Published online at <http://journal.sapub.org/ijge>

introgressive lines of cotton into different groups. According to the characteristics of the cotton weight in one boll, fibre length, fibre yield, and 1000 seed weight, the degree of dominance was determined to be inherited in a positive and negative intermediate, dominant and extremely dominant state. He emphasized that to maintain the state of positive heterosis achieved in these ranges, it is necessary to continue carrying out genetic-selection studies in the next generations [6-12].

3. Material and Methods

Scientific research work was carried out within the scientific research topic of Andijan State University "Genetics and selection of cotton and soybean plants grown in farms of Fergana Valley" (2018-2022). Cotton *G. hirsutum* ssp. *euhiirsutum* (genome AD1) "Bukhoro-6", "Omad", "Genofond-2" varieties, *G. mustelinum* Miers ex Watt, [F₅ Kelajak x (ssp. *nanking* (white fibre) x *G. nelsonii*)], [F₅ Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)], {F₄B₁C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)]}, {F₄B₁C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)] x Namangan 77}, {F₄B₁C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G. nelsonii*)]}, {F₄B₁C [Kelajak x (ssp. *nanking* (white fibre) x *G. nelsonii*)] x Kelajak} introgressive hybrid forms were used.

Cluster analysis is a multivariate statistical analysis method that identifies the properties of objects that are similar to each other and divides them into the same groups based on these properties.

In our experiment, the clustering of the lineages was determined using the Statgraphics computer program using Euclidean distance as a measure of genetic closeness, and Ward's method as a clustering method.

4. Results Discussion

If more than two populations are taken to determine plant traits, then it is necessary to group the genotypes according to their closeness to each other. For this purpose, the cluster analysis method was used to determine the degree of diversity in terms of quantitative characteristics of these varieties and to combine them according to their mutual proximity.

Quantitative traits of the 10 hybrid forms studied and the parental forms were used as a template for cluster analysis. Quantitative characteristics of these hybrid shawls were studied, cotton weight in one bag, weight of 1000 seeds, fibre length, and fibre yield indicators were determined in laboratory and field conditions and statistically analyzed.

According to the results of research, a high indicator on the cotton weight mark in one boll, which is one of the valuable economic signs s [F₅ Kelajak x (ssp. *nanking* (white fiber) x *G. nelsonii*)] in the form of a hybrid (6.0 grams), which is relatively low by this mark *G. mustelinum* (2.0

grams) was observed in hybrid combinations.

A high indicator on the mark of the weight of 1000 pieces of seeds is *G. hirsutum* ssp. *euhiirsutum* "Omad " is in hybrids (115.1 grams), then the low result on this mark is *G. mustelinum* (95.0 grams) was manifested in hybrid combinations.

The average figure in parental hybrid forms on the mark of fiber length from valuable farm mark is 34.4 mm. ni, while the fiber output mark was 37.75%.

The results from analysis of the conducted experiments show that cotton is divided into 3 main groups within the cluster when we analyze the economic characteristics of cotton, i.e. cotton weight per boll, 1000 seed weight, fiber yield and fiber length characteristics, and economic economic characteristics. it became known.

The first main large group consists of parent forms [F₅ Kelajak x (ssp. *nanking* (white fiber) x *G. nelsonii*)], {F₄B₁C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)] x Namangan 77}, {F₄B₁C [Kelajak x (ssp. *nanking* (white fiber) x *G. nelsonii*)] x Kelajak}, {F₄B₁C Kelajak x [Kelajak x (ssp. *nanking* (white fiber) x *G. nelsonii*)]} and it was found that valuable economic markers are close to each other.

The second main large group [F₅ Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)], *G. hirsutum* ssp. *euhiirsutum* «Omad», {F₄B₁C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)]}, *G. hirsutum* ssp. *euhiirsutum* "Bukhara-6", *G. hirsutum* ssp. *euhiirsutum* "Genofond-2" combinations are known to have entered, and entered this second cluster group [F₅ Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)], *G. hirsutum* ssp. *euhiirsutum* "Omad" that the quantitative characteristics of combinations are moderately close, {F₄B₁C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G. australe*)]}, *G. hirsutum* ssp. *euhiirsutum* "Bukhara-6", *G. hirsutum* ssp. *euhiirsutum* "Genofond-2", and the valuable economic traits of the combinations were shown to be very close to each other, *G. hirsutum* ssp. *euhiirsutum* "Bukhara-6", *G. hirsutum* ssp. *euhiirsutum* "Genofond-2" showed that the economic characteristics of the combinations are very close.

Dendrogram

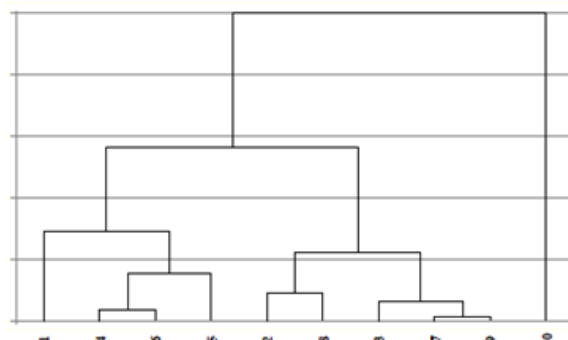


Figure 1. Cluster analysis of economic traits of parental forms (cotton weight per boll, 1000 seed weight, fibre yield and fibre length)

Valuable economic characters of parental forms, when cluster analysis was performed in Statgraphics computer program, only 1 combination, i.e., *G. mustelinum*, was found to have lower valuable economic characters than any of the above 9 combinations, and it was separated into a separate cluster group.

The second main cluster group of F_1 hybrid plants included 27 combinations, these combinations: Bukhoro-6 x { F_4B_1C [Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, Bukhoro-6 x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x Genofond-2, { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]} x *G.mustelinum*, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x *G.mustelinum*, Omad x [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)], Genofond-2 x { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Genofond-2, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Bukhara-6, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Omad, Genofond-2 x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, Bukhara-6 x { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77}, Bukhara-6 x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x *G.mustelinum*, Genofond-2 x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, { F_4B_1C Kelajak x [Kelajak x (ssp. *Nanking* (white fibre) x *G.nelsonii*)]} x Bukhara-6, *G.mustelinum* x [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)], [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x *G.mustelinum*, *G.mustelinum* x { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, *G.mustelinum* x [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)], { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]} x *G.mustelinum*, *G.mustelinum* x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, *G.mustelinum* x { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77}, *G.mustelinum* x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibres) x *G.nelsonii*)] x Kelajak} x *G.mustelinum*, and they were divided into 2 medium and 6 small groups and 9 closely related very small groups. They, in turn, are divided into 6 small groups and 9 very small groups close to each other.

The following combinations belong to the second main large group: [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Bukhoro-6, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x Omad, Genofond-2 x [F_5 Kelajak x (ssp. *nanking*

(white fibre) x *G.nelsonii*)], [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Omad, Bukhara -6 x { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77}, Bukhara-6 x { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x Bukhara-6, Omad x [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)], Bukhara-6 x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Omad, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Bukhara-6, Genofond-2 x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x *G.mustelinum*, Genofond-2 x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, Bukhara-6 x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]} x *G.mustelinum*, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x *G.mustelinum*, Omad x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77} x Genofond-2, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x Genofond-2, Genofond-2 x { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, Genofond-2 x { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77}, { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]} x Bukhara-6, *G.mustelinum* x [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)], *G.mustelinum* x { F_4B_1C Namangan 77 x [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)]}, { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak} x *G.mustelinum*, *G.mustelinum* x { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]}, *G.mustelinum* x { F_4B_1C [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)] x Kelajak}, *G.mustelinum* x { F_4B_1C [Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x Namangan 77}, { F_4B_1C Kelajak x [Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)]} x *G.mustelinum*, *G.mustelinum* x [F_5 Kelajak x (ssp. *nanking* (white fibre) x *G.nelsonii*)], [F_5 Namangan 77 x (ssp. *obtusifolium* var. *indicum* x *G.australe*)] x *G.mustelinum*, and it was found that they were divided into 2 medium and 4 small groups and 10 closely related subgroups.

The purpose of conducting this cluster analysis is that the cluster analysis dendrogram of each of the quantitative traits of the combinations included in the subgroups, i.e. cotton weight per boll, 1000 seed weight, fibre yield and fibre length traits and valuable it was shown that the results of marks are very close to each other. These small closely related combinations will serve as starting material for practical selection if much research is carried out in future research work.

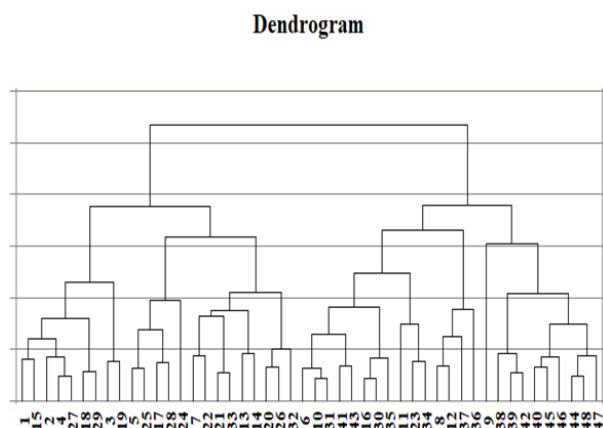


Figure 2. Cluster analysis of valuable economic traits of F₁ hybrid plants (cotton weight per boll, 1000 seed weight, fibre yield and fibre length)

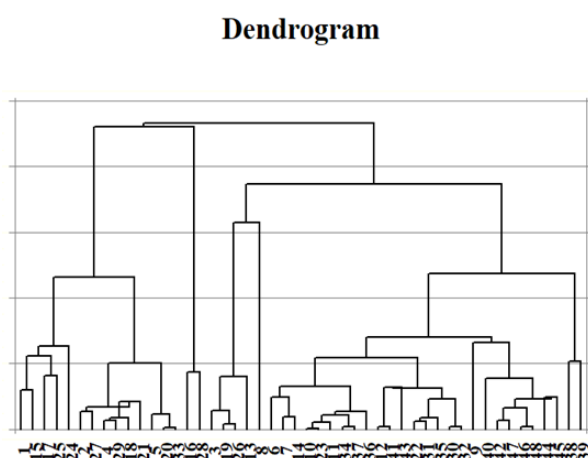


Figure 3. Cluster analysis of valuable economic traits of F₂ hybrid plants (cotton weight per boll, 1000 seed weight, fibre yield and fibre length)

5. Conclusions

The results of the cluster analysis of our research show that the parent, F₁ and F₂ hybrid forms are cluster analyzed and differ from each other in size and shape, but they are distant and partially close to each other in terms of valuable traits. was determined. Quantitative indicators of introgressive hybrid forms according to the result of cluster analysis showed that hybrid forms belonging to the same species are close to each other. In our research, the cluster analysis of hybrid forms of F₂ showed that F₅ Kalajak x (ssp. Nanking (white fibre) x G.nelsonii) x Bukhara-6 had high economic traits. It was found that this line can be used in the process of practical selection as one of the productive varieties with high performance in terms of all economic indicators. Complex analysis of introgressive hybrid forms of cotton is more important than individual analysis of quantitative traits for creating lines and varieties with a set of valuable economic traits. In the selection of initial sources

for the practical selection process or in the evaluation of lines, individual selection for each character is often not a correct conclusion, and cluster analysis is the relationship of these characters to each other and several gives an opportunity to choose varieties or samples consisting of biotypes that are close to each other in terms of characteristics. In addition, when choosing a form for the initial source, it shows that not one type, but one cluster, can be used to transfer a certain character.

REFERENCES

- [1] Hafiz SB, Jehanzeb F, Bibi T, Tariq M. Cluster and principle component analyses of maize accessions under normal and water stress conditions. *Journal of Agricultural Sciences (Belgrade)*. 2015; 60(1): 33-48.
- [2] Muminov K, Ernazarova Z, Amanov B. Cluster analysis of valuable economic traits in amphidiploid cotton hybrid plants. *EurAsian Journal of BioSciences*. 2020 Aug 1; 14(2).
- [3] Abdiev F.R. Application of genetic-statistical methods in the creation of lines and varieties of cotton. Autoref q/x.f.d. (DSc). Tashkent. 2018. pp. 20-23.
- [4] Dospekhov BA. Metodika polevogo opyta [Method of field experience]. Moscow: Agropromizdat. 1985; 351.
- [5] Joraev S.T. Evaluation of combinatorial ability and degree of heterogeneity of cotton cultivars based on cluster and diallel methods. B.f.d. diss. autoref. Tashkent. 2008. S. 16-18.
- [6] Samanov Sh.A. et al. Cluster analysis of valuable economic markers of introgressive ridges. Tashkent. 2022. pp. 21-25.
- [7] Amanov B, Muminov K, Samanov S, Abdiev F, Arslanov D, Tursunova N. Cotton introgressive lines assessment through seed cotton yield and fibre quality characteristics. *Sabrao Journal of Breeding and Genetics*. 2022 Jun 1; 54(2): 321-30.
- [8] Muminov K, Ernazarova Z, Amanov B. Cluster analysis of valuable economic traits in amphidiploid cotton hybrid plants. *EurAsian Journal of BioSciences*. 2020 Aug 1; 14(2).
- [9] Amanov B, Umirova L. Evolution of valuable economic characteristics of systems made by introgressive methods of cotton. *EPRA International Journal of Multidisciplinary Research (IJMR)*. 2022 Dec 19; 8(12): 103-7.
- [10] Dospekhov BA. Methodology polevogo opyta. M.: Kolos. 1985: 316-28.
- [11] Wang GL, Dong JM, Paterson AH. The distribution of *Gossypium hirsutum* chromatin in *G. barbadense* germ plasm: molecular analysis of introgressive plant breeding. *Theoretical and Applied Genetics*. 1995 Nov; 91: 1153-61.
- [12] Zhou T, Wang N, Wang Y, Zhang XL, Li BG, Li W, Su JJ, Wang CX, Zhang A, Ma XF, Li ZH. Nucleotide Evolution, Domestication Selection, and Genetic Relationships of Chloroplast Genomes in the Economically Important Crop Genus *Gossypium*. *Frontiers in Plant Science*. 2022; 13.