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Analysis of Qualitative and Quantitative Signs Collectible Cotton Genotypes

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Abstract

For this study, 77 best varieties of cotton were selected from the collection of the National Gene Bank of Azerbaijan. Due to the fact that the previously studied characteristics of these samples turned out to be incomplete, it was advisable to supplement information on such features and properties as fiber yield, the main qualitative features tested on the HVI (High Volume Instrument) electronic system in accordance with a unified international classification, as well as resistance of plants to wilt. In the process of studying additional traits, a significant divergence of traits was revealed, which made it possible to distinguish from the total number of 15 genotypes characterized by a successful combination of the studied traits. Along with this, it was found that the susceptibility of the main part of the genotypes is zero. In the article under discussion, the definition of correlations between various paired features is considered. In the selected genotypes, a positive or negative orientation of the relationship was established, as well as the degree of relationship, which, depending on the paired traits, varied from a low unreliable to a highly significant value. The results of this study can serve as a basis for enriching the genetic diversity of the collection and subsequent use in various directions.

Keywords: collection, cotton, fiber quality, immunity, correlation

1. Introduction

The biological genus *Gossypium* L. includes 45 diploid and 5 tetraploid cotton species. The species G. hirsutum is the main source of the most commonly used natural fiber, accounting for 95% of the world production [6], thus having a significant impact on the economies of many countries of the world. This species is widely cultivated due to its high adaptability to environmental conditions[2].

Taking into account the demand for natural cotton fiber in the world market, the main task of ongoing selection and genetic research is the creation of new productive varieties and hybrids of cotton, characterized by high fiber quality and resistant to major diseases.To achieve this goal, it is necessary to first study the diversity of the collection, select the necessary source material and use it in various areas of breeding [15, 12].Knowledge of the genetic diversity of the collection is very important for fruitful approaches to improve cotton genotypes [5, 18].

So, A.A. Abdullaev et al. [1] conducted research to assess the biological diversity of cultivated cotton species of the world gene pool, stored at the Uzbek Institute of Genetics and Experimental Plant Biology.The study of varietal diversity of cultivated diploid (*G.herbaceum* L. and *G.arboreum* L.) and tetraploid (*G.hirsutum* L. and *G.barbadense* L.) species of various ecological and geographical groups made it possible to identify a number of promising samples recommended for use in genetic breeding programs as a valuable source material for breeding high-yielding and high-quality cotton varieties.

Seyoum et al.[14] studies have been conducted to assess the genetic diversity and structure of cotton populations at the DNA level. Using 198 simple sequence repeat (SSR) markers, the germplasm of 302 elite cotton accessions from 253 Chinese and 49 different exotic sources was genotyped.The genetic distance of the germplasm ranged from 0.451 to 0.052 (mean 0.270), demonstrating a wide range of genetic diversity. Chinese origin samples showed the highest level of polymorphism, while American origin

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germplasm showed the highest average genetic distance (0.274).The analysis identified three potential subpopulations for the identification and maintenance of beneficial alleles in cotton germplasm.

In different regions of China, samples of 719 collections of *G. hirsutum* L. were evaluated for five qualitative characteristics of cotton fiber for two years.A number of phenotypic data were obtained, after which the elite samples were subjected to further screening using single nucleotide polymorphism markers.Samples from the northern and northwestern regions of China tend to have the highest length (FL), breaking load (FS), and the best micronaire (Mic) fiber. Using genotypic data, 31 elite germplasms were selected over a period of two years by evaluating five traits of fiber quality. These results provide useful information on the feasibility of using high fiber quality genotypes in breeding programs [16].

Nazarova et al. [10] presented the results of studying the collection of cotton genotypes of various geographic origins. A comparative evaluation of 135 cotton samples in field and laboratory conditions was carried out in terms of productive and quality characteristics of the fiber. The correlation between paired features was determined. In particular, a positive correlation of a weak degree (0.15 - 0.22) was found between the yield of raw cotton from one plant and the upper average length (AML), as well as between the average strength (0.30 - 0.38) with a specific breaking load (Str) and (0.32 - 0.44) with micronaire (Mic).In the process of research, constant genotypes, characterized by a complex of qualitative and economic traits, were transferred to the Azerbaijan Genbank for preservation.

Dai et al. [3] studied the phenotypic and genotypic variability of 15 important traits in 419 accessions of *G. hirsutum* L. (Upland cotton) grown in six different zones in 17 major cotton growing countries of the world.Using 299 polymorphic microsatellite markers, the studied resources were divided into two main groups. The first group (G1) was characterized by high yield, good fiber quality and late maturation. The second group (G 2) was characterized by low yields, fiber quality and precocity. During the study, the proportion of genotypes of the first group gradually changed from early and middle ripeness to late ripeness.The results of the research showed that favorable types of alleles have accumulated, creating important conditions for the selection of germplasm.

Khezir Hayat et al [9] evaluated numerous specimens from global collections around the world, namely the United States, Australia, Venezuela, India, Uzbekistan, Turkey and other countries. Analysis of variance showed very significant differences between genotypes for all traits based on pooled data. Correlation analysis showed a significant relationship between fiber characteristics such as fiber length, fiber strength and micronaire. It was concluded that some genotypes can be used as potential parents in breeding such as: AB-80 and BA440 - to increase the percentage of fiber; YB-230 and Flora for fiber length and Delcerro and Menderes for fiber strength.

A study by authors from Pakistan [13] was conducted to assess variations in genetic diversity, yield and quality of cotton fiber, as well as analyze associations between them. It was found that the phenotypic coefficient of variation was higher than the genotypic coefficient for all studied traits. Correlation analysis showed that the yield of raw cotton had a significant positive relationship with the height of the plant, the number of bolls, fiber yield, evenness index , and the reflection coefficient at the genotypic level. Genetically diverse genotypes (AA-802, IUB-13, FH-159, FH-458 and CIM-595) have been identified and can be used for further improvement.

The aim of the research conducted by Jabbar et al. [8] was to identify promising cotton genotypes and further improve them.The analysis of agromorphological, productive and qualitative components of fiber among 40 lines of cotton according to 10 traits was carried out, the variation of signs and the correlation between them were studied. Highly significant genetic variability was revealed for most traits. Statistical analysis of the studied traits revealed that some characteristics have a positive correlation, while others have a negative one. Thus, micronaire showed a significant positive relationship with fiber yield percentage (r=0.34) and box weight (r=0.24), as well as a very significant negative relationship with fiber strength (r= -0.59).Genotypes characterized by mean values of various traits can be used in breeding programs to select lines with desired traits.

Yang et al.[19] through field and laboratory observation assessed the genotypic and phenotypic characteristics of 92 cotton genotypes from Tajikistan and Kyrgyzstan. The germplasm of these samples differed in qualitative and quantitative characteristics. Using phenotypic identification data for cluster analysis, all material was divided into 6 groups according to genetic distance.It has been established that the studied resources have a rich genetic diversity and the index of diversity of quantitative traits is higher than qualitative ones. The clustering results are not necessarily related to the source and origin of the source material.

Iqbal et al [7] report that cotton production in Pakistan has been falling short of its potential for many years due to loss of genetic diversity and lack of empirical studies. In this regard, they assessed the genetic diversity of 16 components of yield and fiber quality of 19 local genotypes (*Gossypium hirsutum* L.).The average value of the yield of raw cotton fluctuated in the range of 106.8 - 35.5 g. The ZB-18026 genotype showed the maximum mean value, while the ZB-18032 genotype showed the minimum mean value for this particular trait. Boll weight showed the highest values of phenotypic PCV (68.7088%) and genotypic GCV (61.0473%) variance, while seed index and fiber strength showed low GCV and PCV values. Information related to the genetic variability of genotypes for various traits can be used for further genetic evaluations.

The presented chronological review of world publications of recent years consisted of an in-depth study of the genetic diversity of cotton, carried out by various research methods. Due to the importance of knowledge of the source material in solving urgent breeding problems, the main goal of this study was to further study cotton varieties of genetic collections according to previously unexplored traits and properties. It seemed important to establish their phenotypic variability, the correlation between traits for further improvement and enrichment of the diversity of the collection.

2. Material and Methods

From the collection of the National Gene Bank of Azerbaijan, the best 77 varieties of cotton belonging to different biological species were selected according to a number of studied traits. However, these samples have not previously been evaluated for such important traits as fading immunity, fiber yield, and a complex quality traits of fiber. Field experiments in the 2022 season were laid in two repetitions on the territory of the Apsheron experimental base of the named Institute in accordance with the generally accepted rules of agricultural technology for growing cotton plants. The assessment of resistance to verticillium wilt was carried out according to the classical method of F.V. Voitenok [17] during the period of maximum manifestation of the disease, determining the number and percentage of diseased and healthy plants. Among the wide variety of cotton varieties, there is a noticeable difference in the degree of resistance to the disease. Among the wide variety of studied cotton varieties available, there is a noticeable difference in the degree of resistance to the disease.The damage intensity was assessed on a five-point scale: 0 - immune, 1-10% - highly resistant, 11-25% - resistant, 26-50% - tolerant, 51-80% - susceptible, 81-100% - highly susceptible. Testing of the qualitative features of the fiber was carried out on the electronic system HVI (HighVolumeInstrument) in triplicate, in accordance with the unified international classification. The correlation between the studied traits was established according to the generally accepted Pearson formula [11]. Statistical processing of field and laboratory data and calculation of correlation coefficients between features were carried out according to the method of B.A. Dospekhova [4] using the Microsoft Excel 2010 software package.

3. Research Results

At the Institute of Genetic Resources of the Ministry of Education and Science, where various plants are collected, preserved and studied, the cotton collection includes about 1500 samples. Detailed information on cotton diversity contained in the genetic collection can be used in the selection of initial material as a basis for obtaining genotypes with improved traits.

From the genetic collection of cotton, 77 best economically valuable varieties were selected, which were not previously evaluated for some important traits and properties. In this regard, in this study, such additional traits as the percentage of fiber yield, fiber quality characteristics, and plant resistance to wilt were evaluated. The expediency of supplementing the characteristics with new data and determining the genetic discrepancy between genotypes, as well as establishing correlative relationships between paired traits, is obvious. Analysis of variance of average data revealed a very wide range of differences in all additional features of genotypes (table).

Fiber yield as an important productive feature is the need for effective study. Analysis of the averaged values of two repetitions revealed significant differences between all variety samples.In the studied samples, this feature varied from 26.9% to 40,2%. Genotype Delceriro k-7146 showed the minimum mean value, while genotype GAA-0948 showed the maximum value for this quantitative trait.

In this study, special attention was paid to assessing the fiber quality of collection varieties.The upper mean length (UpperHalfMeanLength, UHML) was of paramount importance, since increasing the length of the fiber by one millimeter of implementation has financial surcharges. A highly significant genetic difference between the studied samples for the trait under discussion was revealed. The GAA-0987 genotype showed the minimum upper mean length (18.2 mm), while the maximum value (31.0 mm) was noted for the AP-156 genotype.

The Fiber Uniformity Index (UI) is a quality component that ranges from low (77%) to 85% and above according to world standards. In this experiment, the studied trait, depending on the collection diversity, varied from 77.2% for the GAA-0948 genotype to 97.2% for the AP-193 genotype.

Specific breaking load (Strength, Str) reflects the strength of the fiber and determines its economic value. To meet international requirements, this feature must be at least 28 g/tex. The studied genotypes showed a wide range of changes in the specific breaking load from 20.5 g/tex (GAA-0948) to 31.7 g/tex (Ganja-1003).

Along with this, the study took into account an important quality indicator - micronaire (Mic), which is a measure of the fineness and maturity of the fiber. The micronaire value should be moderate, i.e. not less than 3.5 and not more than 4.9 unit. Deviations from these indicators can have a negative impact on the cost of the fiber. Our analysis revealed that the minimum indicator (4.2 unit.) is characterized by the RAM-461 genotype, and the maximum (5.6 unit.) by the AGN-09112 genotype, exceeding the established limit.

The results of our analyses showed that all the studied samples were characterized by a different set of added features included in the study. Therefore, depending on the degree of manifestation of traits, the studied genetic diversity of cotton was divided into three groups. The first group included genotypes that were distinguished by very high positive values of individual traits with an insufficient value of other traits.

Table 1. Indicators of the most important features of collection samples of cotton

Catalog number	Sample name	Fiber yield, %	Indicators of quality fiber components				Plant disease, %
			Upperaverage length, (UHML), mm	Uniformity index, (Uİ), %	Specific breaking load (str), g/tex	Micronair, (Mic) unit	
1	VestIndiya – 4173	39.0±0.22	28.2±0.12	89.0±0.81	27.6±0.27	4.9±0.13	0
2	GAA-0939	37.5±0.19	29.5±0.09	92.0±1.12	29.1±0.31	4.5±0.10	0
3	GAA-0983	37.9±0.28	28.7± 0.12	90.6±1.19	27.2±0.28	4.6±0.09	8.3
4	Ganja-202	39.4±0.35	28.6±0.19	90.4±1.14	28.5±0.23	4.8±0.14	14.3
5	GAA-0997	37,9±0.20	29.5±0.10	89.6±1.21	27.5±0.22	4.5±0.09	0
6	Karabakh-117	38.0±0.25	29.9±0.15	91,5±1.06	28.7±0.25	4.6±0.13	0
7	Ganja-118	38.1±0.25	29.0±0.17	91.1±1.19	27.5±0.24	5.1±0.16	0
8	GAA-09114	39.5±0.30	28.6±0.17	88.2±1.12	27.2±0.23	4.7±0.14	0
9	Alakbari	37.2±0.22	30.0±0.19	93.8±1.20	26.5±0.21	4.7±0.11	13,3
10	Karabakh-11	39.3±0.34	28.9±0.06	90.3±114	28.7±0.26	4.8±±0.09.	0
11	Barakat	38.0±0.22	30.5±0.13	94.3±1.17	31.7±0.27	4.5±0.11	0
12	AF-16	37.9±0.18	29.3±0.17	90.1±1.16	27.0±0.21	4.9±0.13	14.3
13	Zafar	38.9±0.28	29.6±0.17	92.9±1.13	28.7±0.30	4.7±0.07	0
14	Ganja-183	39.6±0.40	29.4±0.20	89.6±1.10	28.3±0.25	4.4±0.09	0
15	Ganja-200	38.3±0.30	31.1±0.17	96.6±1.21	27.6±0.23	4.5±0.11	0

The second group, on the contrary, consisted of genotypes with a negative manifestation of individual traits. The third group was represented by genotypes of the *G.hirsutum* L. species, characterized by high and optimal traits. Thus, a descriptive analysis of 15 varieties of the last group (table) showed that the genetic distance between cotton samples by quantitative trait - fiber yield - varied from 37.2 ± 0.22% (Alakbari) to 39.6 ± 0.40% (Ganja - 183). The average value with the inclusion of all samples of this group was 38.4±0.18%.

An assessment of the variability of the main quality parameters of the fiber, in particular the upper average length (UHML), revealed the VestIndiya - 4173 genotype with a minimum indicator (28.2±0.12 mm.) and the Ganja-200 genotype with a maximum indicator (31.1±0.17 mm.), where the average value of all genotypes was 29.4±0.15 mm. Despite the fact that the indices of the uniformity index for the GAA-09114 and Ganja-200 genotypes vary widely (88.2±1.12% and 96.6±1.21%, respectively), nevertheless, the average value for all genotypes remains high (91.3±1.14 %), exceeding the international standard.

The next quality attribute studied is the specific breaking load (Str), which serves as an indicator of the quality factor of the fiber.The analysis performed revealed highly significant variability.The highest indicator (31.7±0.27) was recorded in the Barakat genotype, while the lowest indicator (26.5±0.21 g/tex) was in the Alakbari genotype, with an average value for all genotypes equal to 28.2±0.22 g/tex. Information was also obtained regarding the fiber quality component - microneura (Mic), the value of which is completely dependent on the fineness and maturity of the fiber. The evaluated trait had obvious differences, ranging from the minimum (4.4±0.09 unit) to the maximum (5.1±0.16 unit) in the Ganja-183 and Ganja-118 genotypes, respectively. It should be noted that micronaires of all genotypes, with the exception of Ganja-118, meet the requirements of the international classification. In addition, we studied the resistance of cotton plants to the wilt disease, which is widespread in all cotton-growing countries of the world, including Azerbaijan, the causative agent of which is the fungus Verticilli umdahllae. The data in the table indicate that among the studied diversity in samples Ganja-202 and AF-16, the percentage of affected plants was 14.3. In samples GAA-0983 and GAA-0983, the incidence was 8.3% and 13.3%, respectively. The intensity of damage to the rest of the samples was equal to zero.

Correlation analysis of 15 cotton genotypes was used to determine the degree and direction of the relationship between the studied traits. According to the results, the ratio between the productive trait - fiber yield and the quality trait - upper mean length (UHML) was found to be negatively correlated with a coefficient of -0.32. Between the fiber yield and two quality attributes - the uniformity index (Uİ and the specific breaking load (Str)), the correlation coefficients were -0.30 and -0.19, respectively. However, between fiber output and microneur (Mic), the positive correlation coefficient was high (0.44*) and credible at the 5% significance level. At the same time, the relationship between paired qualitative traits was also determined. In particular, a significant positive relationship (0.48*) was noted between the upper average length (UHML) and the uniformity index (Uİ). Between the upper average length and the specific breaking load (Str), the positive relationship is very high (0.74**) and significant at the 1% level. However, between the upper average length and the microneur (Mic), the relationship is negative with a coefficient of -0.56*. And, finally, the direction of the relationship between the specific breaking load and microneur was negative and manifested to a weak (-0.28) degree.

4. Conclusion

The article presents information on the study of cotton samples of the genetic collection. The selected genotypes have not previously been evaluated for important traits such as fiber yield, fiber quality, and wilt resistance. After determining additional traits and properties, all genotypes were divided into 3 groups, differing in the severity of traits. Among them, a group was identified, including 15 genotypes with a complex of positive traits. The main part of the genotypes of this group was resistant to wilt disease. Correlation analysis revealed the direction and degree of connection between paired features. A detailed study of collection diversity can serve as a basis for identifying genotypes with improved qualitative and quantitative potential.

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