Variability of Fiber Gin Turn out in Cotton Hybrids of the Species *G. Hirsutum L.* in Different Growing Zones

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Keywords: Fiber Variability, Cotton Hybrids, Environmental Adaptation.

Abstract: In 2018-2020, the variability of fiber gin turnout was studied in four hybrid combinations of cotton F_2-F_4, obtained by crossing introgressive forms with high-gin turn outing varieties of foreign selection in the conditions of the Tashkent, Fergana and Kashkadarya regions. To analyze the variability of economically valuable traits, we used a graph similar to a box plot used in descriptive statistics. It was shown that in all years of testing, regardless of the hybrid combination, a greater range of variability in gin turn out appeared in the Kashkadarya region. Moreover, both right-sided and left-sided transgressions were observed.

1 INTRODUCTION

One of the most important areas of work in the selection of any crop, including cotton, is identifying the response of plants to the environment, to stressful condition; determining the level of plant responsiveness to biotic and abiotic factors. In the process of growth and development, plants constantly interact with the environment, resulting in the process of adaptability of the organism or adaptation.

The basis of adaptation is variability, a property of an organism that reflects the mechanisms of its interaction with the environment; it is the most important factor in evolution, ensuring the adaptability of species and populations to changing environmental conditions (Zharkova et al., 2013).

Filipchenko Yu.A. in his book "Variability and Methods for its Study" defines the concept of "variability" as "... the phenomenon of some difference even among closely related individuals ... and there are no one type of organism that would not be subject to the effect of this phenomenon" (Filipchenko, 2001).

According to V.F. Pivovarov, E.G. Dobrutskaya, the goal of selection is to create genotypes that have a desired rate of variability (Dobrutskaya, 1997).

The study of the population composition of varieties and the ontogenesis of plants, the observations of different morphobiotypes should be carried out against different environmental backgrounds (Sinskaya, 1963).

One of the objectives of the research was to study the variability of traits that determine the phenotype of cotton plants during selection in four hybrid combinations, F2-F4, in the conditions of the Tashkent, Fergana and Kashkadarya regions.

2 MATERIALS AND METHODS

The work was completed between 2018-2020, in NIISSAVH (Tashkent region, Salar village) and its branches in the Fergana (Kuva) and Kashkadarya (Kasbi) regions, within the framework of the project MV-A-KH-8-2018-205 "Creation of productive cotton varieties using the adaptive potential of hybrids and lines, obtained with the participation of introgressive forms in various soil and climatic conditions of Uzbekistan."

The experiments were repeated four times, and the arrangement of combinations was randomized.

To analyze the variability of economically valuable traits, we used a box plot, used in descriptive

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Egamberdieva, S., Juraev, S. and Kurbanov, U.
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DOI: 10.5220/0014270400004738

In *Proceedings of the 4th International Conference on Research of Agricultural and Food Technologies (I-CRAFT 2024)*, pages 395-397
ISBN: 978-989-758-773-3; ISSN: 3051-7710

statistics, concisely depicting a one-dimensional probability distribution (variance). In our experiments, we drew three boxes in one table - these are distributions obtained for one trait in one year from three different regions. The left box is the distribution of the trait in the Tashkent region, the middle box is the distribution of the trait in the Fergana region, and the far-right box is the distribution of the trait in the Kashkadarya region. The group sizes do not differ; hence, they are comparable (Juraev et al., 2023, Juraev et al., 2023, Juraev et al., 2022, Alimova et al., 2022, Juraev et al., 2023).

3 RESULTS AND DISCUSSION

In 2018-2020 Four hybrid combinations of cotton F2-F4 were studied, obtained by crossing introgressive lines adapted to local conditions with high-yielding varieties of foreign selection.

Figures 1-3 show the results of variability in fiber yield for three generations of the F2-F4 hybrid combination [(L-247 x S-484) x L-248]. It shows that the greatest variability of the trait occurs in the third generation of hybrids tested in the Fergana region: the range was 8.9%. In the second and fourth generations, the variability of the trait ranged from 2.6 to 5.6%. The smallest range of variability in fiber yield for this combination was observed in the Tashkent region from 2.6 to 3.2%. In the Kashkadarya region, the range of variability of the trait was from 2.6 to 5.2%. This combination is also characterized by high average fiber yields of 38.5-40.4%.

The hybrid combination [(Bukhara 6x L-h) x L-247) x (L-247 x S-6593)] had the greatest variability in fiber yield in the Kashkadarya region: in F2, F3 and F4, respectively 6.2, 5. 1 and 7.1% (Fig. 4 - 6). In the remaining two areas, the amplitude of the trait variability was significantly less, from 2.8 to 5.1%. Due to selections among this hybrid population, it was possible to increase the average fiber yield.

The average fiber yield of the hybrid combination [L-248 x (L-243 x S-2552)] was relatively low, ranging from 33.8 to 38.3. However, in different generations and in different regions there were forms with a fiber yield of 39 – 41.8%. The highest amplitude of variability of the trait, 8.8%, was observed in the Kashkadarya region in the third generation. In the remaining two regions, the variability of the trait ranged from 3.4 to 4.5% (Fig. 7-9).

For the hybrid combination L-248 x S-2016, with the exception of the fourth-generation experiment in the Kashkadarya region, where the variability in fiber yield was 10.7%, the range of variability in the experiments was relatively narrow - from 1.7 to 4.7%. The average fiber yield for this combination also varied between years (Fig. 10-12).

The results of a three-year trial showed significant differences in fiber yield both between hybrid combinations and between groups in the regions. Analysis of variance of hybrids showed that the share of the influence of the genotype on the variability of the trait in F2 was equal to 72%, in F3 - 41%, in F4 - 40.1%. The influence of the environment on the trait in F2 was 11.3%. In F3, the influence of the environment on the trait turned out to be unreliable, since the P-value for the environmental factor was greater than 0.05. The contribution of the environment to the manifestation of the trait in F4 was 12.6%. In F4, the hybrid combination F4 [(F8 L-247 x S-484) x L-248] was highlighted, which showed stability of the trait over the years, while its average fiber yield in different regions reached 39-40%.

4 CONCLUSIONS

To summarize, it can be noted that in all years of testing, regardless of the hybrid combination, the widest range of variability in fiber yield appeared in the Kashkadarya region. Moreover, both right-sided and left-sided transgressions were observed. Analysis of phenotypic variability in fiber yield in hybrids of different genetic origins showed that the magnitude of variation in the value of the trait largely depends on the contribution of the genotype.

As V.V. Syukov writes, molecular genetic studies in recent years confirm that phenotypic variability includes, in addition to paratypic and genotypic variability, also genotype-environment interactions, which are mainly epigenetic in nature (Syukov et al., 2010). A.H. Paterson et al (Paterson et al., 1991) found in tomatoes that different QTLs appear for the same trait under different environmental conditions. Similar results were obtained by C.W. Stuber et al (Stuber et al., 1992) on corn, M.C. Ungerer et al (Ungerer et al., 2003) on Arabidopsis, Zh. Jiang et al (Jiang et al., 2001) on soybeans, as well as A. Börner et al (Börner et al., 2002), Yu.V. Chesnokov and colleagues (Chesnokov et al., 2008, Chesnokov et al., 2012), V.V. Syukov et al. (Syukov et al., 2012) on wheat.

Our previous studies have shown that genotypic variability makes a fairly significant contribution to the formation of fiber yield, ranging from 42.9 to 60.7%. External conditions influenced the trait from

10 to 21%. The influence of the interaction of genotype-environment factors on fiber yield turned out to be insignificant.

Using genetically enriched breeding material in various ecological zones, we managed to create varieties with a wide reaction rate based on the expression of polygenes that are adequate to changes in a complex of environmental factors.

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