Using Genetic Statistical Methods in Creation of Cotton Plant Varieties in Uzbekistan

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Abstract: *The analysis of selective and genetic parameters of 5 cotton plant families and their 20 hybrid combinations, obtained by means of diallel crossing scheme under the conditions of Uzbekistan. The main consistencies ofgenetic determination of one-boll mass of raw cotton are determined by the methods of statistical genetics. Basing onthe study of hybrids, the genetic sources with the high general and specific combining ability of one-boll mass of rawcotton are allocated, basing on which TashDAU-100 cotton plant variety is created and transferred to the NationalMeasurement Assurance System.*

Keywords: line, hybrid, quantitative features, diallel crossing

1. Introduction

Studying the complex of interconnected features and finding the ways to accelerate stabilization of selective lines, created by means of distant hybridization, becomes of special urgency. The more reliable detection of the best genotypes ininitial hybrid population or selected line is urgent, which determines its further selective prospectivity at creation of the newvariety. This allows unite genotypes gradually – firstly, with minimal divergence and then more remote from each other. Thebest families united in the same cluster create genetic core of the future variety, which will have the best stable economically valuable features, when the negative interconnections between the features will be graded as much as possible.

According to I.S. Varuntsyan [2], the smaller the number of generations left, the smaller is its basis, the geneticdiversity, characteristic of the variety during its first years, is more and more limited. Lewis considers this the negative phenomenon, as the wide population diversity, the mixture of initial genotypes is a barrier against the unfavourable conditions, illnesses etc. The evaluation of the families left is not always correct. The loss of heterogeneity or decreasein the initial genetic diversity, as a consequence of the accepted variety preservation system, will restrict the limits of itsadjustment to the diversity of cultivation conditions.

Delay in quantitative genetics has lasted for a long time. The difficulties in studying the genetics of quantitativefeatures are explained by their complex genetic nature. Polygenes, controlling quantitative features, reveal not only additive effect, but also non-additive one, caused by interallelic and intergenic interactions. Their manifestation can change significantly under the influence of environmental conditions. All this complicates genetic analysis and makes it necessary to applyspecial genetic and statistical models, allowing estimating combined action of polygene system more accurate [6, 7, 8].

The development of mathematical genetics appeared to have many prospects for theory and practice of selection, mainly in the sphere of heterosis breeding, the theory of hybridization and selection, the development of estimationcriteria for genotypic population structure and selection efficiency. Much has not been included into selection practice,but the prospects of this aspect are obvious. Thus, F.Kh. Abdullayev [1] distinguished the main consistencies of geneticdetermination of a range of economically valuable features, such as grain productivity, the elements of yield structureand chemical composition, and adaptive properties by the methods of statistical genetics. The correlation connectionsbetween these features and properties are determined.

The aim of the paper is to create the phenotypically unimodal families, identical according to the approbated morpho-economic features, to study them and to develop the method of creating the promising cotton plant varieties, which are very unimodal and adjusted to environmental conditions, basing on the genetic and statistical methods.

2. Materials and Methods

The study was conducted in Cotton Breeding, Seed Production and Agro-Technologies Research Institute under the Ministry of Agriculture and Water Economy of the Republic of Uzbekistan.

5 families of L-93 line cotton plant of *G.hirsutum* L. species and their hybrids obtained by means of diallel crossing were used as a starting material for research. Diallel crossing was carried out by the first B. Griffing's method [3, 4].

The argotechnology, generally accepted at cotton plant growing in Tashkent oblast, was conducted. Seedingwas carried out three times according to the scheme of 60 x 30-1. The genetic and statistical analyses were carried outusing MS Excel computer program according to B.A. Dospekhov [5].

3. Results

In Table 1 the indices of one-boll mass of raw cotton at families and F_1 hybrids are shown. The data show thatone-boll mass of raw cotton at the studied families was of 5.85-6.38 g and did not differ much from the same indices atF_1hybrids (5.68-6.59 g). In the study, the families with the

indices of economically valuable features, morphologicallytypical for L-93, were used. As it is obvious from the data in Table 1, the indices of one-boll mass of raw cotton did nothave significant differences as between families and hybrid combinations, so as among hybrid combinations. In thisregard studying the dominancy indices of these features is of certain interest.

Table 1: The indices of raw cotton mass at families and F_1 hybrids

Families and hybrids	One-boll mass of raw cotton, g (X ± Sx)	hp
C-1	5.85 ± 0.06	
C-2	5.91 ± 0.06	
C-3	6.10 ± 0.08	
C-4	5.98 ± 0.11	
C-5	6.38 ± 0.10	
C-1 x C-2	5.89 ± 0.08	0.67
C-1 x C-3	6.24 ± 0.14	2.17
C-1 x C-4	5.85 ± 0.15	-1.17
C-1 x C-5	6.05 ± 0.02	-0.25
C-2 x C-1	5.68 ± 0.02	-6.67
C-2 x C-3	6.07 ± 0.07	0.43
C-2 x C-4	5.87 ± 0.15	-2.67
C-2 x C-5	5.93 ± 0.18	-0.92
C-3 x C-1	5.98 ± 0.07	0.90
C-3 x C-2	6.23 ± 0.13	2.5
C-3 x C-4	6.27 ± 0.02	3.92
C-3 x C-5	6.22 ± 0.06	-0.13
C-4 x C-1	6.05 ± 0.11	2.21
C-4 x C-2	6.13 ± 0.13	6.08
C-4 x C-3	6.21 ± 0.13	2.96
C-4 x C-5	6.18 ± 0.18	0.04
C-5 x C-1	6.33 ± 0.10	0.83
C-5 x C-2	6.20 ± 0.15	0.23
C-5 x C-3	6.20 ± 0.16	-0.25
C-5 x C-4	6.59 ± 0.13	1.98
HCP0,5	0.44	

It is obvious from the data presented in Table 1 that the negative value of dominancy indices, i.e. degradationof the average feature indices, was obtained in 7 cases. In 3 cases, negative hybrid vigour was obtained amounted to from1.2 to 6.7 in C-2 x C-1, C-1 x C-4, C-2 x C-4 combinations. At C-3 x C-1, C-5 x C-1, C-1 x C-2 families incomplete dominance of big-boll parent was noted, at C-4 x C-1, C-3 x C-2, C-4 x C-2, C-3 x C-1, C-4 xC-3, C-3 x C-4, C-5 x C-4 family hybrids, positive hybrid vigour was observed amounted to from 2.2 to 6.1. In direct and indirect crossing combinationsof C-3 x C-1, C-1 x C-3 and C-3 x C-4, C-4 x C-3 families positive hybrid vigour was observed. 13 combinations out ofthe studied 20 crossing combinations had incomplete dominance and positive hybrid vigour of the feature of one-boll massof raw cotton. At the usage of C-2 family as female parent the decreased indices were observed compared with parents inthe most cases. At the usage of this family as a male parent the domination of big-boll parent was noted.

We also evaluated combining ability of families on one-boll mass of raw cotton. The obtained results areshown in Figure 1.
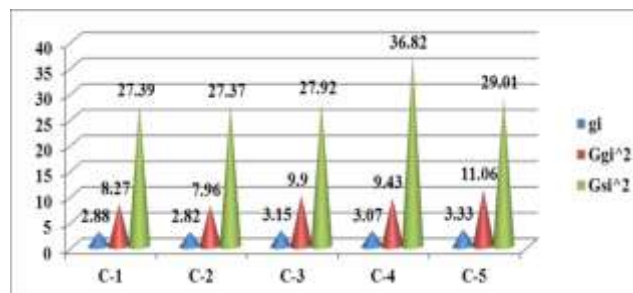
Figure 1: The evaluation of GCA effects and GCA and SCA variances on the feature of one-boll mass of raw cotton.

In the histogram presented in Figure 1 it is shown that the higher indices of the general combining ability wereobtained at C-3, C-4, C-5 families, while at the last family this index was the largest one. The indices of the generalcombining ability at families did not have significant differences and were of 2.82-2.88. The highest indices of GCAvariances were noted at C-3, C-4, C-5 families, with the highest value at C-5. The lowest value of GCA variances wasnoted at C-2 family.

At all families, SCA variances are higher than GCA variances, denoting the prevalent role at inheritance ofgene feature with dominant and epistatic effects. The highest values of SCA variances were noted at C-4, C-5 familieswith the highest value at C-4. The values of SCA variances at C-1, C-2, C-3 families did not have significant differences and were of 27.37-27.92.

Conclusions

1) In the most hybrid combinations incomplete dominance and positive hybrid vigour of the feature of oneboll mass of raw cotton were noted. At the usage of C-2 family as a female parent in the most cases, the decreased indices of one-boll mass of raw cotton were observed, and as a male parent, the dominance of big-boll parent was noted. Incombinations with C-5 family the positive result was observed, as in direct, as in indirect combinations.
2) The studied cotton plant families had various GCA and SCA according to one-boll mass of raw cotton,which allows differentiating them on the degree of combining ability manifestation.
3) Diallel analysis had shown that one-boll mass of raw cotton is controlled by genes with dominant and epistatic effects, when SCA variances dominated over GCA variances. Cotton plant families having high combining abilityon one-boll mass of raw cotton in the diallel crossing system were allocated.
4) The studied cotton plant families differ not only by GCA, but also have significantly different SCA. Thismeans that at selection these families can be used as in synthetic selection, as in heterosis breeding.
5) Basing on the study of hybrids, the genetic sources with the high general and specific combining ability ofone-boll mass of raw cotton are allocated, basing on which TashDAU-100 cotton plant variety is created and transferredto the National Measurement Assurance System.

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