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Studies on the Degree of Genetic Divergence for Different Quantitative Traits Between Paremntal Lines of Silkworm, *Bombyx mori* L., Hybrids

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A study was conducted to establish the degree of genetic divergence between different hybrid forms and rearing conditions through estimation of the minimum number of genes (allelic pairs) differentiating parents in terms of specific quantitative traits. It was established that the minimum gene number, differentiating parental lines in the inheritance of cocoon was 1, of cocoon shell weight - between 1 and 2, and of silk filament length- between 2 and 3. The variability in the specific genetic parameter could be explained by the reliability of the statistical-and-genetic method used and the expression of genes affecting the formation of each of the characters tested. Gene expression, in its turn, is conditioned both by the gene interaction within the genotype, and the different genotype response to environmental change. To go deep in the problem, experiments should be conducted under strictly controlled conditions, reducing the mathematical-and-genetic analysis to a physiological level, and hence to analyze the genetic nature of the specific quantitative character formation and its genetic control.

Key words : Silkworm, Hybrids, Genetic divergence, Quantitative traits

Introduction

So far, the scientific literature has not given any reliable theoretical and experimental means for estimating and identifying the exact number of genes that differentiate the parental lines of hybrids in terms of specific quantitative characters. Rokitzkii (1978) and Dragavtzev (1982) gave some formulae for measuring the degree of genetic divergence between hybrid forms through estimating the minimum number of genes differentiating their parents. In this aspect, Gershenson (1979) pointed out that the gene number, determined through these formulae, was relatively close to the actual number and could be used to accumulate some genetic information on qantitative character heritability.

The subject of the present study was to establish the degree of genetic divergence in the most important quantitative characters between parental lines of promising silkworm hybrids.

Material and Methods

To measure the degree of genetic divergence between silkworm hybrids by estimating the minimum number of genes, differentiating their parents in the most important quantitative traits, we used the formula of Castle and Wright (Rokitzkii, 1978):

$$n = \frac{D^2}{8\sigma^2 F_2 - \sigma^2 F_1}$$

where:

n-minimum number of genes (allelic pairs);
D^2-difference between the mean character values of P_1 and P_2;

σ^2-F_1 and F_2 variances.

The following characters were tested: cocoon weight, cocoon shell weight, silk filament length, and shell ratio. From each hybrid, 60 cocoons (30 female and 30 male individuals) were analyzed.

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Results and Discussion

Initially, we used in our studies all three formula known for measuring the degree of genetic divergence between hybrid forms, i.e.: of Castle and Wright, of Serebrovskii, and that of Burten (Rokitzkii, 1978). Later, we turned to use only the formula of Castle and Wright, which proved to be relatively more convenient, allowing no subjective determination of the recessive and dominant parents, and giving generally more precise and stable results.

Here, we are giving the results from measuring the degree of genetic divergence in different hybrids and rearing conditions (seasons of silkworm rearing). Actually, we made an attempt to illustrate the possibilities of using this approach in silkworm rearing, without taking upon ourselves the mechanism and structural organization of genetic material, nor treating the problem of the right number of genes that control the quantitative characters tested.

Table 1 shows some comparative numerical data about the minimum number of genes, differentiating the parental lines of 4 line hybrids, for the characters of cocoon weight, cocoon shell weight, silk filament length, and shell ratio, produced during three different seasons of silkworm rearing (spring, summer, and autumn). Some variability in the parameter, characterizing the minimum gene number both by traits and during the different seasons, was observed. In most of the cases, however, the coincidence was close enough to indicate that a relatively small number of genes (effective factors) (Mather, 1949) affected the formation of the quantitative characters tested. For example, the minimum number of genes affecting cocoon weight heritability was 1, that for cocoon shell weight and raw silk ratio varied between 1 and 2, and for silk filament length - between 2 and 3. The results obtained were in complete agreement with the results of our previous investigations on other line hybrids, tested under conditions of high air temperature and humidity (Petkov and Nguen Long, 1987).

In our opinion, the variation in the estimated minimum number of genes should not be ascribed only to some inaccuracy of the statistical-and-genetic method used. It could be suggested that the estimated genetic parameter showed the degree of genetic divergence in a specific environment. In other words, it informed only about the degree of genetic divergence expressed, but not about the real one (Rokitzkii, 1978).

In order to understand better the results obtained, we shall try to interpret in detail some peculiarities of the approach adopted to determine the degree of genetic divergence between silkworm crossing lines. As the tested characters are usually determined by many genes, it is inevitable to admit some simplifications and limitations in the statistical-and-genetic model used.

In this aspect, Rokitzkii (1978) showed that these simplifications and limitations could be reduced to the suggestion that either the effect of these genes was equal and they were *adominant*, or all genes, increasing some trait,

Table 1. Degrees of genetic divergence for different quantitative traits between parental lines of silkworm hybrids

Hybrids	Minimum number of genes							
	Cocoon weight		Cocoon shell weight		Shell ratio		Silk filament length	
	Number	Approx	Number	Approx	Number	Approx	Number	Approx
Spring								
H 1/18×H 2/1	0.78	1	0.97	1	1.04	2	1.73	2
H 2/1×H 1/18	0.59	1	0.67	1	0.98	1	1.89	2
B 2/21×B 1/18	0.34	1	1.08	2	0.39	1	2.37	3
B 1/18×B 2/21	0.52	1	1.34	2	0.44	1	2.87	3
Summer								
H 1/18×H 2/1	0.82	1	1.08	2	0.47	1	2.23	3
H 2/1×H 1/18	0.61	1	0.97	1	0.55	1	1.94	2
B 2/21×B 1/18	0.33	1	1.39	2	0.67	1	2.09	3
B 1/18×B 2/21	0.44	1	1.31	2	0.78	1	2.23	3
Autumn								
H 1/18×H 2/1	0.93	1	1.37	2	1.11	2	2.96	3
H 2/1×H 1/18	0.78	1	0.81	1	0.97	1	1.89	2
B 2/21×B 1/18	0.28	1	1.24	2	0.48	1	1.27	2
B 1/18×B 2/21	0.38	1	1.18	2	1.08	2	1.33	2

were found in an *adominant* parent, and the decreasing genes - in a recessive one. According to the same author, irrespective of these limitations, the forms used in all cases gave sufficient information about the degree of genetic divergence between the lines involved in the hybrid forms in terms of the specific quantitative trait. In our opinion, the variability in the specific genetic parameter could be explained both by the non-observance of the indicated conditions, and by the expression of genes (Lobashov, 1967). The gene expression, on its part, could be determined both by their interaction within the specific genotype, and by the different response to environmental factors (in our case, this was the season of silkworm rearing). Thus, gene expression proved to be the response of similar genotypes to environmental change.

Unlike the heritability analysis, which is based only on the comparison of parent variances (P1 and P2), F1 and F2, the analysis of the number of genes, affecting the character tested, is based both on the comparison of variances and the arithmetic means of the progenies obtained. In terms of variation statistics, operating with arithmetic means as a measure of general trends and variances as a measure of variation, this approach, in our opinion, is more correct and reliable.

We assumed the working hypothesis that the variation in the parameter characterizing the gene number, was due both to the impossibility of observing the limiting conditions and to the expression of genes affecting the trait. The relative notions obtained for the degree of genetic divergence between the different hybrids and rearing conditions for the most important quantitative silkworm traits, however, should not be taken as absolute as so far, there are no theoretical and experimental methods to determine how far the degree of genetic diversity is due to inclusion or exclusion of new genes, affecting the trait when environmental conditions change, and how far these are effects of gene expression.

The results of measuring the degree of genetic divergence of quantitative traits between different hybrid forms and rearing conditions showed that the minimum gene number differentiating their parental lines for the cocoon weight character was 1, for shell weight - between 1 and 2, and for silk filament length - between 2 and 3.The variability in the specific genetic parameter could be explained by the expression of genes, that affected the traits, this expression being conditioned both by gene interaction and by the different response of the separate genotypes to environmental conditions. To go deep into the nature of the problem, a special equipment is necessary to conduct the experiments under strictly controlled conditions, reducing the mathematical-and-genetic analysis to a physiological level, and from that position to analyze the genetic nature of the specific trait formation and its genetic control.

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