

Heritability Estimates in the Silkworm for Different Productive Characters with their Genetic and Phenotypic Correlations¹

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ABSTRACT

The relatively high heritability values, for most seric characters, suggest that genetic improvement can be achieved easily by selection. The positive and very high genetic correlation value between the fresh cocoon weight and dried cocoon weight, and the considerable genetic correlations between the dried cocoon weight and all seric characters both indicate that selection due to fresh cocoon weight leads inclusively to genetic improvement in seric characters.

INTRODUCTION

The mulberry silkworm *Bombyx mori* L. is of great economic value in many Asiatic and European countries and is supposed to be propagated in developing countries. Several genetic studies have been carried out for the improvement of its production in quantity and quality (1,2,3,4,5).

The present studies aimed to adopt the sib-analysis method (which has not been used before as far as we know) in estimating the heritabilities for different seric characters and their phenotypic and genetic correlations. The results expected from this system are the most reliable for such investigations. As no silkworm moths are available from tested cocoons for further generations, the half-sibs and full-sibs will be the nearest relatives to be reared under the same conditions for determining the genetic and non-genetic variances necessary for hereditary studies in the characters of their silk production.

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MATERIALS AND METHODS

Rearing procedure

This study was carried out at the Sericulture Department, Ministry of Agriculture, Dokki, Giza, A. R. Egypt, during the year 1969. The breeding room was air conditioned at 25°C and a relative humidity of 75%. The parental race in this study was the standard multivoltine breed in Pakistan.

This multivoltine Pakistanian race was imported in 1969 from Industries Corporation Sericulture, Rajshahi, East Pakistan. Eggs are small in size and pale-yellow coloured. Mature larvae are bluish white with normal markings. Cocoons are golden yellow in colour and spindle shaped.

The eggs of the parental race were hatched directly in the breeding room. As soon as the small larvae hatched they were provided with slices of mulberry leaves then transferred to the rearing tray. The breeding room and the equipments were previously cleaned and treated with disinfectants. The larvae were provided four times daily with cleaned mulberry leaves of Japanese variety. The larval stage continued for 27 days. After the complete formation of the cocoons which lasted from 8 to 10 days, they were numbered, weighed and put in the wooden boxes.

Experiments for the determination of adequate time for successful mating of one male moth to more than one female

It was necessary for the application of sib analysis method in the estimation of heritability value for different characters in the silkworm, to mate each male to at least three females. It was tried in this way to determine the duration of mating and resting to produce all fertilized eggs. Six experiments were carried out for this investigation.

In the first experiment, copulation was allowed to continue with each of the three females for five minutes only, without any rest time, but in this case the eggs obtained from the three female moths were unfertilized.

In the second experiment, the male was allowed to mate each female for ten minutes without any rest time after separation. In this case, the eggs deposited by the female moths were unfertilized except for a small number of those laid by the first one.

In the third experiment, copulation lasted for fifteen minutes without any rest time for the male between the successive matings. In this case, more than three quarters of the eggs obtained from the first female (167 eggs from 201) were fertilized, while all the others were unfertilized.

In the fourth experiment, copulation was allowed for thirty minutes with each female without any rest time for the male after separation. All the eggs obtained from the first female in this case were almost fertilized (334 eggs from 351) while the eggs of the other two females were not.

In the fifth experiment, the male mated each female for thirty minutes, with a resting period for thirty minutes between the mating procedures. In this experiment, the eggs deposited by the first and the third females (440 and 356 eggs, respectively) were fertilized, but those obtained from the second female were unfertilized.

In the sixth experiment, the fixed time for mating each female was thirty minutes, but the resting time was prolonged to one hour. The eggs deposited by the three females were all fertilized in this case. It is therefore concluded that a single male moth can fertilize the eggs of three females providing that the mating process lasts for thirty minutes and that the male rests for one hour between each two subsequent pairings.

According to the last result, 7 males (sires) were used, each for mating three females (dams). From each of the 21 females, 30 offspring individuals were used in the investigation except one which had 25 only. The heritabilities, genetic correlations and phenotypic correlations were estimated for several characters in the full-sibs and half-sibs.

Equations used in the statistical analyses

(1) Heritability

The heritability is defined as the ratio of additive genetic variance to phenotypic variance or the regression of the additive genetic value on the phenotypic value. It was calculated by the following formulae:

$$h_s^2 \text{ (from sire component of variance)} = \frac{4(\sigma_s^2)}{\sigma_s^2 + \sigma_d^2 + \sigma_e^2}$$

$$h_d^2 \text{ (from dam component of variance)} = \frac{4(\sigma_d^2)}{\sigma_s^2 + \sigma_d^2 + \sigma_e^2}$$

$$h_{s\&d}^2 \text{ (from both components)} = \frac{2(\sigma_s^2 + \sigma_d^2)}{\sigma_s^2 + \sigma_d^2 + \sigma_e^2}$$

$$= \frac{\sigma_s^2 + \sigma_d^2}{2}$$

Where h^2 = heritability
 σ_s^2 = sire components of variance
 σ_d^2 = dam components of variance
 σ_e^2 = component of variance between full sibs

Form of analysis of half-sib and full-sib families

Source of variance	d.f.	Mean squares	Expected mean squares
Between sires	$s - 1$	MS_s	$\sigma_e^2 + k \sigma_d^2 + dk \sigma_s^2$
Between dams (within sires)	$s(d - 1)$	MS_d	$\sigma_e^2 + k \sigma_d^2$
Between full-sibs	$sd(k - 1)$	MS_e	σ_e^2

Where s = number of sires
 d = number of dams per sire
 k = number of offspring per dam

(2) Genetic correlations

The estimation of genetic correlation rests on how a trait in a certain individual and another in its relative are related as compared to non-relatives, in a manner analogous to the estimation of heritabilities.

Instead of computing the components of variance of one character from an analysis of variance, the components of covariance of the two characters from an analysis of variance are computed. The analysis of covariance takes exactly the same form as the analysis of variance.

Thus the genetic correlation between two traits is calculated as:

$$r_{gg'} \text{ (from sire component of variance)} = \frac{\sigma_{ss'}}{\sqrt{\sigma_s^2} \sqrt{\sigma_{s'}^2}}$$

$$r_{gg'} \text{ (from dam component of variance)} = \frac{\sigma_{dd'}}{\sqrt{\sigma_d^2} \sqrt{\sigma_{d'}^2}}$$

where $\sigma_{ss'}$ = sire covariance component

$\sigma_{dd'}$ = dam covariance component

σ_s^2 = sire component of variance for a trait

$\sigma_{s'}^2$ = sire component of variance for another trait.

σ_d^2 = dam component of variance for a trait

$\sigma_{d'}^2$ = dam component of variance for another trait.

(3) Phenotypic correlations

This is determined from measurements of the two characters in a number of individuals of the population in the same way as the genetic correlation. It is calculated by the following formula:

$$r_{pp'} = \frac{\sigma_{ss'} + \sigma_{dd'} + \sigma_{ee'}}{\sqrt{\sigma_s^2 + \sigma_d^2 + \sigma_e^2} \sqrt{\sigma_{s'}^2 + \sigma_{d'}^2 + \sigma_{e'}^2}}$$

Where $r_{pp'}$ = phenotypic correlation between two characters

RESULTS AND DISCUSSION

Description of the breed

The different silk characters were estimated in 50 cocoons of the parental Pakistanian race when reared under the local lab conditions. The weight of a fresh cocoon ranged between 0.7621 and 1.1978 gram averaging 1.0334 ± 0.0127 gram. When dried, the cocoon weight ranged between 0.2249 and 0.4252 gram averaging 0.3390 ± 0.0065 gram. The maximal length of the cocoon averaged 3.15 ± 0.02 cm (range 2.75 – 3.45 cm) and the maximal width of the cocoon averaged 1.23 ± 0.01 cm (range 1.1 – 1.37 cm). The length of the silk filament reeled from the cocoon ranged between 210 and 400 meters averaging 300 ± 5.91 meters. The weight of silk filament ranged between 0.0602 and 0.0958 gram and averaged 0.0759 ± 0.0015 gram.

The seric resistance averaged 35 ± 1.34 decigrams ranging from 17 to 51 decigrams. Its elasticity averaged 47 ± 0.9798 millimeters/meter ranging from 32 to 56 millimeters/meter. The thickness of the filament averaged 2.24 ± 0.0347 deniers ranging from 1.8 to 2.8 deniers.

The mean number of eggs deposited by the Pakistanian female moths was 467 ± 8.46 and ranged between 389 and 574 eggs.

Heritability estimates

It was at first decided to estimate the heritability of the fresh cocoon weights by the parent off-spring regression. For this purpose, the weight of paternal and maternal

Table 1 Weights (in grams) of fresh cocoons of the parent moths used in the triple matings

Paternal cocoons		Maternal cocoons		Mean weight (mid-parents)
No.	Weight	No.	Weight	
A	1.0192	1	1.0374	1.0283
		2	0.9813	1.0003
		3	0.9943	1.0068
B	0.9867	4	1.0413	1.0140
		5	1.1693	1.0780
		6	1.0024	0.9946
C	0.9625	7	1.0024	0.9825
		8	1.0869	1.0247
		9	1.1843	1.0734
D	1.0027	10	1.1728	1.0878
		11	1.0036	1.0032
		12	1.0158	1.0093
E	0.8796	13	1.0029	0.9413
		14	1.0143	0.9469
		15	0.8735	0.8766
F	0.8731	16	1.0068	0.9399
		17	1.0174	0.9453
		18	1.0821	0.9776
G	1.0039	19	1.1659	1.0849
		20	0.8645	0.9342
		21	1.0436	1.0238

cocoons in the triple matings were recorded and their mean weights (mid-parents) were calculated (Table 1). The mean weights of fresh cocoons in the off-spring reared during the subsequent season (as shown in Table 2) were very much smaller than those of the parental cocoons due to change in the environmental and feeding conditions. The heritability estimated in this way was 0.1926. This heritability value is less if compared with that calculated by the sib analysis method shown later. The sib method was adopted in all the following estimations for two reasons:

- (1) In this method all individuals (progeny) live under the same conditions to minimize the environmental errors.
- (2) It is the only accurate method to estimate the heritability value of the silk characters where the parental cocoons are destroyed and cannot be reeled to get their threads to be compared with those of the off-spring.

The mean weights and seric measurements of the half-sibs are recorded in Table 2 and their analyses of variance components are recorded in Table 3. Table 4 contains the heritability estimates and both phenotypic and genetic correlations.

The heritability for the fresh cocoon weight was 0.41 when estimated from the sire component, and 0.547 from the dam component and its mean value was 0.479. For the dry cocoon weight, the heritability estimates were 0.61 from the sire component, 0.678 from the dam component and 0.644 from their mean value.

Table 2 Mean cocoon weights and seric characters in half-sibs

Parents	Cocoon weight (gm)		Silk filament					
	σ	φ	Fresh	Dried	Length (meters)	Weight (grams)	Resistance (decigrams)	Elasticity (mm/m)
A	1		0.7394	0.2322	262	0.0512	45	50
	2		0.7145	0.2230	254	0.0478	46	46
	3		0.6170	0.1983	238	0.0419	44	47
B	4		0.7016	0.2278	276	0.0552	38	49
	5		0.6490	0.2039	196	0.0364	30	44
	6		0.6661	0.2096	264	0.0479	36	47
C	7		0.6603	0.2087	254	0.0460	32	44
	8		0.5935	0.1882	213	0.0385	32	43
	9		0.6770	0.2199	259	0.0488	39	47
D	10		0.6793	0.2186	243	0.0474	47	48
	11		0.5971	0.1832	243	0.0395	36	45
	12		0.6716	0.2106	325	0.0511	48	45
E	13		0.5938	0.1850	219	0.0393	34	46
	14		0.6591	0.2151	273	0.0517	41	45
	15		0.5646	0.1839	253	0.0432	39	41
F	16		0.6196	0.1965	242	0.0534	26	41
	17		0.6613	0.2102	237	0.0490	32	45
	18		0.6708	0.2137	251	0.0491	38	51
G	19		0.5451	0.1645	227	0.0364	23	46
	20		0.5932	0.1826	224	0.0365	25	49
	21		0.5211	0.1567	217	0.0308	18	41

The heritability for length of silk filament and that for seric elasticity were both slightly negative when estimated from sire component (-0.093 and -0.061 , respectively). A negative value of heritability is of course unrealistic, but negative h_s^2 with such low magnitude could give an estimate of zero. However, the heritability, when based on dam component, was too high for silk length ($h_d^2 = 1.02$) and reasonable (0.386) for seric elasticity. The mean heritability estimation (h_{s+d}^2) was 0.414 and 0.162 for both traits respectively.

The heritability for silk weight was 0.338 when estimated from sire component and 0.845 from dam component and its mean value was 0.592 .

In all the previously mentioned traits it was noticed that the dam components had been more or less greater than the sire components indicating gross amounts of variance due to environment associated with the dams. This might be because σ_d^2 as estimated for such a model contains part of the dominance and additive by dominance genetic variation more than σ_s^2 . Also, the environment affecting this trait could have been more variable with the progeny of the different sires.

On the other hand, the seric resistance analysis shows that the between dams component was considerably lower than the between sires component, so there cannot be much nongenetic variance or variance due to common environment. However, $\sigma_s^2 51.02$ gives

Table 3 Analysis of variance components for the different characters and their heritability estimates.

Source of variance	D.F.	Weight of fresh cocoon		Weight of dried cocoon		Length of silk		Weight of silk		Seric resistance		Seric elasticity	
		Mean squares	Variance component	Mean squares	Variance component	Mean squares	Variance component	Mean squares	Variance component	Mean squares	Variance component	Mean squares	Variance component
Between sires	6	0.1667	0.0012	0.0231	0.00018	17628.83	-64.5	0.0021	0.000012	5214.67	51.02	142	-0.9
Between dams (within sires)	14	0.0562	0.0016	0.0070	0.0002	23391.57	714.69	0.0010	0.00004	643.64	19.48	222.8	5.67
Between fullsibs	604	0.0089	0.0089	0.0008	0.0008	2148	2148	0.0001	0.0001	64.17	64.17	54	54
Heritability estimates from:													
Sire component (h_s^2)		0.410		0.610		-0.093		0.338		1.515		-0.061	
Dam component (h_d^2)		0.547		0.678		1.02		0.845		0.579		0.386	
Sire and dam component ($h_{s&d}^2$)		0.479		0.644		0.414		0.592		1.047		0.162	

Table 4 Heritabilities and genetic and phenotypic correlations

$r_{pp'}$	$r_{gg'}$	x_1	x_2	x_3	x_4	x_5	x_6
Sire		<u>+0.410</u>	+1.01				
Dam	x_1	<u>+0.547</u>	+1.06				
Mid-parents		<u>+0.479</u>					
Sire			<u>+0.610</u>		+0.9343	+0.7505	
Dam	x_2		<u>+0.678</u>	+0.574	+0.9091	+0.4679	+0.727
Mid-parents		+0.3994	<u>+0.644</u>				
Sire				<u>-0.093</u>			
Dam	x_3			<u>+1.02</u>	+0.8463	+0.699	+0.455
Mid-parents			+0.3232	<u>+0.414</u>			
Sire					+0.338	+0.6883	
Dam	x_4				<u>+0.845</u>	+0.6859	+0.454
Mid-parents			+0.1190	+0.4049	<u>+0.592</u>		
Sire						+1.515	
Dam	x_5					<u>+0.579</u>	+0.6451
Mid-parents			+0.7309	+0.1826	+0.1603	<u>+1.047</u>	
Sire							<u>-0.061</u>
Dam	x_6						<u>+0.366</u>
Mid-parents			+0.1691	+0.0608	+0.1361	+0.3455	<u>+0.162</u>

N.B: x_1 = Fresh cocoon w.
 x_2 = Dried cocoon w.
 x_3 = Silk filament l.
 x_4 = Silk filament w.
 x_5 = Seric Resistance
 x_6 = Seric Elasticity.

Estimates on the diagonal are heritabilities (underlined).
 Estimates above the diagonal are genetic correlations.
 Estimates under the diagonal are phenotypic correlations.

$h_s^2 > 1$, which is not sensible (1.515) while $h_d^2 = 0.579$. Generally, this trait seems to be highly heritable as its heritability estimated from both components was 1.047.

From the heritability estimates reported here it can be concluded that genetic improvement in seric resistance of Pakistan 4 race can be achieved easily through selection. Increasing weight of cocoon and weight and length of silk filament by means of selection will be somewhat slower than for seric resistance, but selection may be of no use for genetic improvement in seric elasticity.

Phenotypic correlations

Phenotypic correlations between cocoon and silk characters were all positive as was expected. The estimate of 0.3994 for the correlation between weights of fresh and dried cocoons is considerable. Dried cocoon weight was highly correlated with seric resistance (0.7309), relatively low with length of silk filament (0.3232) but very low with both of seric elasticity (0.1691) and weight of silk filament (0.1190).

Length of silk filament was moderately correlated with weight of silk filament (0.4049), but slightly correlated with both of seric resistance (0.1826) and seric elasticity (0.0608)

The phenotypic correlations between weight of silk filament and both of seric resistance and seric elasticity were low as they were 0.1603 and 0.1361, respectively. The correlation between seric resistance and seric elasticity was 0.3455.

Genetic correlations

Genetic correlations between cocoon and silk characters were all positive and relatively high. The highest estimate was that between weights of fresh cocoons and dried cocoons as it was 1.01 when based on variance of sire component and 1.06 when based on variance of dam component.

Genetic correlations between some of the other characters are based on both of sire and dam component of variance such as that between weight of dried cocoons and weight of silk filament which was very high as its value was 0.9343 and 0.9091 when estimated by the two systems respectively. The genetic correlation between dried cocoon weight and seric resistance varied from 0.7505 (on sire component) to 0.4679 (on dam component). The genetic correlation between weight of silk filament and seric resistance was relatively high and equal when based on either sire component of variance (0.6883) or dam component of variance (0.6859).

The other genetic correlations were based only on dam component of variance. From these characters dried cocoon weight was more closely genetically correlated with seric elasticity than with length of silk filament as their values were 0.7270 and 0.5740, respectively. Weight of silk filament was highly genetically correlated with length of silk filament (0.8463) but slightly correlated with seric elasticity (0.4540). Seric resistance was relatively closely correlated with both of length of silk filament (0.6990) and seric elasticity (0.6451). The genetic correlation between length of silk filament and seric elasticity was relatively low (0.4550).

The estimates of phenotypic correlation in the present study indicate that a fair amount of improvement in silk quantity and quality after being reeled can be achieved by the early selection of cocoons according to their weights before being dried. Improving these characters genetically is dependent, however, on the genetic correlations between the characters.

The very high genetic correlation between fresh and dried cocoon weights (1.01 and 1.06) and the considerably high genetic correlations between dried cocoon weight and all of the silk characters (0.574 – 0.9343) indicate that a high proportion of genetic gain (from selection on fresh cocoon weight) may be carried on the heavier and better silk production. While it is preferred to select directly for the characteristic concerned, it would be impossible to keep moths alive for future generations after reeling their silk filament for test. The high genetic correlations among all the seric characters ensure that the selection applied in fresh cocoons will induce an improvement in all the characters leading to silk production of superior quantity and quality.

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LITERATURE CITED

1. Casan, M. 1966. The effect of the multiple matings on the prolificity of the silkworms and on their productivity. Agricole Statinua Centrale De Apicultura Sericultura, Bucuresti, Lucrari Stintifice 7(2):111-121.
2. Kotbi, F. A. 1962. Genetic studies in certain races of silkworm *Bombyx mori* L., M.Sc. Thesis, Faculty of Agriculture, Ain-Shams University, Cairo, Egypt.
3. Nagatomo, T. 1926. On the sex-linked inheritance of quantitative characters in the silkworm, *Bombyx mori* L. J. Sci. Agric. Soc., Tokyo, 281:155-180.
4. Shen, T. H. 1928. On the inheritance of some quantitative characters in *Bombyx mori* L. J. Coll. Agric. Univ. Tokyo, 10:36-66.
5. Tanaka, Y. 1953. Genetics of the silkworm *Bombyx mori* L. Advances of Genetics 5:239-317.

المكافئ الوراثي لبعض الصفات الانتاجية في دودة الحرير التوتية وقيم التلازم الوراثي والظاهر بينها

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المستخلص

استهدفت هذه الدراسة استخدام طريقة تحليل الاخوة في تقدير المكافئ الوراثي لصفات الحرير المختلفة الذي تنتجه ديدان القز التوتية ، وكذلك الارتباطين الظاهري والوراثي بين هذه الصفات إذ نظرا لعدم امكان الحصول على فراشات من الشرائق المختبرة لتربية أجيال تالية ، فان الاخوة الاشقاء وغير الاشقاء يكونون هم أقرب الأقارب لتربيتهم تحت نفس الظروف لتقدير الاختلافات الوراثية وغير الوراثية الضرورية لدراسة صفات الحرير الناتج .

وأجريت هذه الدراسة على أوزان الشرائق الطازجة والمحففة وكذلك على صفات خيوط حرير الشرنقة من حيث الطول والوزن والمتانة والمرونة ، وظهر منها ان قيم المكافئ الوراثي لمعظم خصائص الحرير التي تبسده مرتفعة تدل على أنه يمكن تحقيق التحسين الوراثي بسهولة عن طريق الانتخاب ، وتدل القيم الموجبة المرتفعة جدا في التلازم الوراثي بين وزن الشرنقة الطازجة ووزنها جافا ، وقيم التلازم الوراثي المعقولة بين وزن الشرنقة الجافة وكل صفات الحرير ، على أن الانتخاب على أساس وزن الشرنقة الطازجة يؤدي بصفة عامة الى التحسين الوراثي في خصائص الحرير المدروسة .