

Evaluation of Silk Yield Characters using Biparental Progenies of Silkworms (*Bombyx mori*)

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ABSTRACT. *The biparental progeny genetic design was used to produce full-sib F₁ hybrid families in order to evaluate their performance in shell weight, cocoon weight and cocoon shell percentage. For this purpose 18 pure lines were selected as parents to produce 9 F₁ hybrids.*

Heterosis was observed in 8 hybrids for shell weight and cocoon weight. The hybrid NR 212 x NZYB had the highest shell weight of 0.39 g and cocoon weight of 1.86 g while the hybrid Race 11 x Race 17 showed the highest mean value for cocoon shell percentage of 22.1%. Their performances were better than those of the currently recommended variety.

The narrow sense heritability calculated from mid parent/offspring regression was high for all 3 characters indicating that variability was due mainly to additive genes. Hence it should be possible to produce superior recombinant inbred lines from these crosses in the future.

INTRODUCTION

The first attempt to establish a silk industry in Sri Lanka was made in 1900. Under the five year plan of 1971-1976, another attempt was made but expected results were not achieved.

Since 1976 sericulture industry in Sri Lanka has come under a separate authority, The Silk and Allied Products Development Authority (SAPDA). At present SAPDA is engaged in promotional activities of this industry.

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The national silkworm breeding stock which is maintained at the Silkworm Breeding Centre, Nilambe is comprised of 46 purelines of both multivoltine and bivoltine races introduced from India, China, Japan and Italy.

Hybrids issued to farmers by SAPDA for commercial rearing do not comply to the technological and economical requirements of the industry. Some of these inferior characters are low cocoon weight (1.5 g), low shell percentage (18%) and low cocoon yield (26 kg) per box (per 20,000 eggs).

As a solution to these constrains SAPDA introduced several exotic Japanese and Korean races but they did not perform well due to unfavorable environment and diseases.

Two significant problems involved in the commercial aspects of sericulture are the breeding of silkworms of high productivity and prevention of silkworm diseases. It was observed that the large number of available races provided a considerable genetic base for the development of commercial varieties but it was not totally exploited.

The objective of this study is to select superior parents and use them in the BIP genetic design to produce hybrid combinations and to evaluate the performance of the hybrids. Although there are more than 15 economically important traits considered for selection, this study include 3 important characters only, namely shell weight, cocoon weight and silk percentage.

MATERIALS AND METHODS

Selection of pure lines

Eighteen pure races, comprising 9 Chinese and 9 Japanese were selected and crossed in the form of a biparental progeny design to produce 9 F_1 hybrid families (Table 1).

In addition to the above crosses, all the parental lines were selfed and their progenies reared together with the hybrids. Biparental mating consists of crossing n_1 number of males to n_1 number of females to produce n_1 number of full-sib families.

Table 1. Biparental crosses.

Cross	Parents	
	Japanese race	x Chinese race
1	A	B
2	6	5
3	10	1
4	12	7
5	16	15
6	11	17
7	NR 212	NZYB
8	NT	YBZC
9	H5T	NR - 12

The total variation of the biparental progeny can be subdivided into mean variation between fullsib families and mean variation within full-sib families (Mather, 1977).

Analysis of Variance

Source	DF	SS	MS	EMS
Between family	$n - 1$	$r(Y_i - \bar{Y}_{..})^2$	MS_B	$W + r\sigma^2_B$
Within family	$n(r - 1)$	$\sum_j (Y_{ij} - \bar{Y}_{i.})^2$	MS_W	W

Fisher (1918) has developed the following relationship with regards to the biparental progeny resulting from crossing inbred lines.

$$\begin{aligned}
 \text{Variance of true} \\
 \text{biparental progeny means } \sigma^2_B &= \text{Covariance of} \\
 &\text{full-sib families} \\
 &= 1/2D + 1/4H
 \end{aligned}$$

Within family variances, t_w^2 = E

The covariance of parent and offspring = Cov.(P.O.)
= $1/2D/V(P) = h^2_N$

The regression on offspring on parent = B_{OP}
= $Cova (P.O.)/V_{(P)}$

This relation is known as heritability (Lush, 1937).

$V_{(P)}$ = Total variance of the attribute in the parental generation.
D = Additive genetic variation
H = Dominance variation
r = Number of individuals per family
E = Non-heritable variance.

The most important function of the heritability in genetic study of a metric character is its predictive role expressing the reliability of the phenotypic value as a guide to breeding value (Falconer, 1960).

RESULTS

Shell weight, cocoon weight and cocoon shell percentage of full-sib families were analyzed. The narrow sense heritability of these characters were estimated through parent-offspring regression analysis.

Shell weight

Analysis of variance indicated significant difference between full-sib families (Table 2).

Table 3 gives the mean shell weight of parents and their corresponding offspring, comparison of parents for the trait (P_1 vs. P_2) and test for heterosis (F_1 vs. P_1). Significant parental differences were observed in all crosses except 3, 6 and 7. All hybrids except 9 showed marked improvement in shell weight over their better parents indicating heterosis. Hybrid of cross No. 7 (NR 212 x NZYB) gave the highest shell weight of 39.62 cg per cocoon.

Table 2. Analysis of variance.

SOURCE	DF	MS		
		Shell Weight	Cocoon Weight	Shell %
Between Full - Sib Families	8	290.00*	2271.82*	28.25*
Within Families	441	8.47	529.52	2.47

* Significant at Probability = 0.05

The percentage of improvement of hybrids over their better parents is shown in Table 4 for shell weight. Highest improvement is given by cross No. 7 and no improvement in crosses 2 and 9.

The narrow sense heritability presents the true breeding value of a trait. Narrow sense heritability of shell weight estimated through parent offspring regression analysis is given in Table 5. Shell weight shows the highest h^2_N of 86% compared to the other two characters. High heritability value indicates that the variability is due mainly to additive genes.

Cocoon weight

ANOVA of cocoon weight is given in Table 2. Significant differences between full-sib families were observed. Mean cocoon weights of parents and their offspring are given in Table 3. Significant parental differences were observed in all crosses except 5, 7 and 8. Heterosis was observed in all hybrids except 9.

Table 4 shows the relative improvement in cocoon weight of hybrids in comparison to their better parents. Cross No. 8 (NT x YBZC) shows the highest improvement (23.15%). Narrow sense heritability of cocoon

Table 3. Mean values of parents and hybrids.

Shell weight (in centigrams)									
	1	2	3	4	5	6	7	8	9
P ₁	30.52	35.42	27.34	25.36	28.64	33.18	32.68	29.56	36.36
P ₂	32.24	29.70	26.52	30.52	30.64	32.86	32.18	31.36	29.18
F ₁	35.22	37.20	32.38	34.50	34.34	39.00	39.62	38.14	35.74
P ₁ vs P ₂	*	*	ns	*	*	ns	ns	*	*
F ₁ vs P ₂	*	*	*	*	*	*	*	*	ns
better									
Cocoon weight (in centigrams)									
P ₁	139.6	172.4	146.7	142.5	154.2	164.2	162.9	139.9	164.9
P ₂	145.3	156.8	156.7	157.2	153.1	151.6	156.4	144.4	148.7
F ₁	165.9	185.9	173.2	176.2	174.3	178.2	186.9	176.8	170.3
P ₁ vs P ₂	ns	*	*	*	ns	*	ns	ns	*
F ₁ vs P ₂	*	*	*	*	*	*	*	*	ns
better									
Silk percentage									
P ₁	22.12	20.80	18.86	18.00	18.70	20.38	20.19	21.32	22.32
P ₂	22.48	19.17	17.16	19.55	20.28	21.93	20.79	22.52	19.78
F ₁	21.45	20.27	18.96	19.74	19.89	22.10	21.50	21.65	21.13
P ₁ vs P ₂	ns	*	*	*	*	*	*	*	*
F ₁ vs P ₂	ns	ns	ns	ns	ns	ns	ns	ns	ns
better									

* Significant at P = 0.05
 ns = not significant

Table 4. Relative improvement of hybrids.

Cross	Shell weight		
	P better	F1	% improvement
7	32.68	39.62	21.33
3	27.34	32.38	18.43
8	32.36	38.14	17.86
6	33.18	39.00	17.54
4	30.52	34.50	13.04
5	30.64	34.34	12.07
1	32.24	35.22	9.27
2	36.36	35.74	none
		Cocoon weight	
8	144.4	177.8	23.13
7	162.9	186.9	14.73
1	145.3	165.9	14.17
5	154.2	174.3	13.03
4	157.2	176.2	12.08
3	156.7	173.2	10.52
6	164.2	178.2	8.52
2	172.4	185.9	7.83
9	164.9	170.5	none

Table 5. Narrow sense heritability.
(from Parent - Offspring Regression Analysis).

Character	Heritability
Shell weight	0.86
Cocoon weight	0.58
Silk percentage	0.66

weight (Table 5) estimated through parent – offspring regression analysis was as high as 58%.

Cocoon shell percentage

The results of ANOVA of cocoon shell percentage (Table 2) indicate significant difference between full – sib families. Table 3 indicates significant parental differences but absence of heterosis.

The narrow sense heritability estimated through parent – offspring regression analysis was as high as 66% (Table 5) indicating that variation is mainly due to additive gene effects.

DISCUSSION

For two of the characters, shell weight and cocoon weight, the means of most hybrids were greater than the means of their better parents (Table 3) indicating heterosis.

As all selected parents are pure lines, they should possess homozygous alleles at each segregating locus. As shown in Table 3 even though some parents are similar in performances for shell weight (3, 6 and 7) and cocoon weight (15, 7 and 8), they have produced hybrids with heterosis. Such parents may possess dispersed dominant genes responsible for shell weight or cocoon weight. Therefore, heterosis was most probably due to dispersed dominant genes in the parents. Petkow *et. al.*, (1987) showed that dominance and epistatic effect have the highest share in inheritance of shell weight and cocoon weight. Ranatunga *et. al.*, (1990) analyzed shell weight, cocoon weight and cocoon shell percentage using diallel genetic design and suggested that heterosis was probably due to epistatic effect.

Among the parents, Race 6 and Race H5T showed highest shell weight. Race 6, Race 11 and H5T were the parents that had highest cocoon weight. Race YBZC, Race – A and Race B were the parents that had highest shell percentage (Table 6).

Table 6. Mean performance of parents.

Cross	Race	Shell wt. (cg)	Cocoon wt. (g)	Shell %
1	A	30.52	139.58	21.86
	B	32.24	145.34	22.18
2	6	35.42	172.60	20.52
	5	29.70	156.86	18.93
3	10	27.34	146.70	18.60
	1	26.52	156.86	16.90
4	12	25.38	142.48	17.80
	7	30.52	157.20	19.41
5	16	28.64	154.20	18.57
	15	30.64	153.12	20.01
6	11	33.18	164.12	20.21
	17	32.18	151.64	21.66
7	NR 212	32.86	163.18	20.13
	NZYB	32.18	156.40	20.57
8	NT	29.56	139.94	21.12
	YBZC	32.36	140.44	23.04
9	H5T	36.36	164.96	22.04
	NR - 12	29.21	148.70	19.64

The best F_1 hybrids for shell weight were Race 11x17 and Race NR 212 x Race NZYB. For cocoon weight highest scoring F_1 hybrids were Race 6 x Race 5, Race NR 212 x NZYB and Race 11 x Race 17.

Selection of any silkworm variety depends on silk yield (shell weight). The highest cocoon shell percentage was given by the F_1 , Race 11 x Race 17. The highest improvement of shell weight was by cross No. 7 (21.23% : Race NR 212 x Race NZYB) and highest cocoon weight improvement was by cross No. 8 (23.13% : Race NT x Race YBZC).

Heterosis was observed in shell weight and cocoon weight. Significant parental differences indicate that many genes are segregating between the parents. High heritability values indicate that most of the variations observed is due to additive genes. Significant parental differences were observed in silk percentage although no heterosis was observed indicating an absence of significant dominance as substantiated by estimate of narrow sense heritability of 66%. Hence, although heterosis was not observed in silk percentage, the large number of genes segregating gives a possibility of extracting many superior recombinant lines for silk percentage. In some crosses (3, 6 and 7 for shell weight and 1, 5, 7, 8 for cocoon weight) although no significant parental differences were observed, their F_1 hybrids showed significant heterosis indicating that the dominant genes were dispersed between the parents and thus caused heterosis.

From the results of the experiment, it is evident that superior recombinant inbred lines could be obtained from all three characters since many genes are shown to be segregating between the parents. Narrow sense heritability values indicate that most variation is due to additive genes, giving more evidence for the possibility of extracting superior recombinant inbred lines from all crosses.

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