

Estimation of Genetic Components of Variance in Biparental Progenies of Bivoltine Silkworm (*Bombyx mori* L.)

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Components of genetic variation were estimated for five metric traits using 24 biparental progenies (N. C. Design III) generated from F₂ generation of a commercial bivoltine silkworm hybrid, SH₆ × NB₄D₂. Variance due to additive ($\sigma^2 A$) and dominance ($\sigma^2 D$) gene effects was significant for single cocoon weight and shell weight. However, magnitude of former was greater than latter indicating preponderance of additive gene action in the inheritance of these two traits. Average degree of dominance was in the range of partial dominance for all the traits. High estimates of heritability (ns) indicated operation of genes with large additive effects, hence, scope exists for improvement of present populations through a few cycles of selection.

Key words: *Bombyx mori* L., Gene Action, Biparental mating, North Carolina Design III.

Introduction

Breeding strategies and selection procedures aimed at synthesis of new and high yielding genotypes, calls for a sound knowledge of nature and magnitude of various gene effects operative in the inheritance of yield and yield component traits. Several biometric designs are available which allow the estimation of various types of gene effects and allied genetic parameters. Biparental mating is one such efficient and powerful tool at the disposal of a breeder, which can be used (1) To break tight linkages and

hence unfavourable character associations. (2) For rapid generation of additive type of genetic variability. Since this mating system tends to convert repulsion phase linkages into coupling phase linkages, bias caused by repulsion phase linkages in the estimation of dominance variance is dissipated. Hence a more realistic estimation of components of genetic variance and allied genetic parameters is possible. Although biparental mating designs have been extensively used in plant improvement programmes, there are not many reports of such studies in *Bombyx mori* L. (Kamili *et al.*, 1999), Keeping this and the above mentioned advantages of biparental mating design in view, an attempt was made to evaluate some BIPs (biparental progenies) generated from F₂ generation of a commercial hybrid, SH₆ × NB₄D₂. In the present paper estimates of genetic components of variance, average degree of dominance and heritability (ns), following North Carolina Design III (Comstock and Robinson, 1948, 1952) are presented.

Materials and Methods

24 BIPs were developed in a bivoltine silkworm hybrid, SH₆ × NB₄D₂ by back crossing 12 F₂ male moths to each of the parental breeds *viz.*, SH₆ and NB₄D₂. (The male moths were utilized for 2nd mating after an hour's rest at 5°C). Twenty-four families, thus generated, were divided at random into 3 sets, each having eight families arising from four different male groups. The experimental materials so generated were evaluated in a completely randomized block design with two replications for each treatment. Each replication comprised 200 silkworms (after 3rd moult). Rearing was conducted during spring (April - May), 2004 following the recommendations made by Krishnaswami (1978) and Dar and Singh (1998). The

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data collected in respect of 5 metric traits *viz.*, single cocoon weight, shell weight, shell ratio (%), Effective rate of rearing (ERR%) and yield/10,000 larvae by weight were subjected to estimation of variance components using the method proposed by Comstock and Robinson (1948, 1952) as described by Singh and Chaudhary (1985). Average degree of dominance was calculated as:

$$\bar{d} = \frac{\sqrt{\sigma^2_{mp}}}{2\sigma^2_m}$$

Where \bar{d} = Average degree of dominance

σ^2_{mp} = Variance due to interaction of males and parents.

σ^2_m = Variance due to males

Standard errors of variance estimates were calculated by the method suggested by Moll *et al.* (1960).

Results and Discussion

Mean squares due to sets (Table 1) were significant for ERR (%) and yield/10,000 larvae indicating existence of sufficient variability between sets in the manifestation of

these traits. Mean squares due to parents in sets were significant for single cocoon weight and shell ratio (%), indicating substantial contribution of parents to the variation among biparental progenies. However, mean squares due to males in sets were significant and greater in magnitude than mean squares due to interaction of males and parents for all the five traits indicating significant contribution of males to the variation among progenies.

Estimates of components of variance (Table 2) revealed existence of significant variability due to males (σ^2_m) and due to interaction of males with parents (σ^2_{mp}) for single cocoon weight and shell weight. For rest of the traits both types of these variances were nonsignificant. Variance due to additive type of gene action (σ^2_A) was greater in magnitude than variance due to dominance deviation (σ^2_D) for all the traits indicating operation of additive gene action in the inheritance of these traits. Estimates of σ^2_e were significant for all the traits indicating significant contribution of environment in the variance of these traits. Predominance of additive gene action for ERR (%), single cocoon weight, single shell weight and shell ratio (%) has also been reported by Kamili *et al.* (2000). However, the same author in an earlier study (Kamili *et al.*, 1999) following triple test cross mating design reported greater role

Table 1. Analysis of variance for metric traits in silkworm *Bombyx mori* L.

Source of variation	d.f.	Mean Squares				
		Single cocoon weight	Shell weight	Shell ratio (%)	ERR (%)	Yield/10,000 larvae
Sets	2	22.750	11.090	2.47	16.4*	5.47*
Replication in sets	3	4.000	3.990	0.83	16.0*	16.0*
Parents in sets	3	393.417*	5.420	6.19*	7.72	0.78
Males in sets	9	387.194	22.520*	4.22*	17.71*	6.61*
Males × parents in sets	9	97.861*	14.530	1.97	12.09*	2.25
Error	21	9.142	9.143	1.50	4.76	1.33

*Significant at $p = 0.05$.

Table 2. Estimates of variance, average degree of dominance and heritability for 5 metric traits in silkworm *Bombyx mori* L.

Components of variance	Single cocoon weight	Single Shell weight	Shell ratio (%)	ERR (%)	ERR Yield/10,000 larvae by weight
σ^2_{mp}	44.36* ± 20.90	2.70* ± 0.47	0.24 ± 0.47	3.67 ± 2.67	0.46 ± 0.52
σ^2_m	94.51* ± 41.28	3.35* ± 0.46	0.68 ± 0.46	3.24 ± 1.92	1.32 ± 0.71
σ^2_A	378.05* ± 165.12	13.40* ± 1.84	2.72 ± 1.84	12.96 ± 7.68	5.28 ± 2.84
σ^2_D	88.72* ± 20.90	5.40* ± 0.47	0.48 ± 0.47	7.33 ± 2.67	0.92 ± 0.52
σ^2_e	9.14* ± 2.69	9.14* ± 0.44	1.50* ± 0.44	4.76* ± 1.40	1.33* ± 0.39
\bar{d}	0.48	0.63	0.42	0.75	0.42
$h^2(ns)$	0.79	0.48	0.58	0.52	0.70

*Significant at $p = 0.05$.

of dominance type of gene action in the inheritance of yield/10,000 larvae. This contradiction in results could be because of different genetic constitution of F₂ base population and the three tester parents utilized by these workers in their study.

Average degree of dominance (\bar{d}) was less than unity in all the traits indicating partial dominance. Estimates of heritability (h^2) were fairly high for all the traits indicating operation of genes with large additive effects. Thus, in the present set of materials, additive genetic variance accounted for most of genetic variability. Hence, there is scope for improvement of present populations through a few cycles of selection in early segregating generations.

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