

## Estimation of Gene Effects in Four Bivoltine Silkworm (*Bombyx mori* L.) Crosses

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Six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $BC_1$ ,  $BC_2$  and  $F_2$ ) of four bivoltine silkworm crosses (SKAU-R-1  $\times$  Yakwei, SKAU-R-6  $\times$  Yakwei,  $CSR_2 \times CSR_4$  and  $SH_6 \times NB_4D_2$ ) were evaluated in a completely randomized block design with 5 replications for each treatment. The generation mean 2 in respect of 3 metric traits (single cocoon weight, single shell weight, and shell ratio %), were subjected to Cavallis joint scaling test. Additive dominance model was found to be adequate in  $CSR_2 \times CSR_4$  and  $SH_6 \times NB_4D_2$  for single cocoon weight and shell weight and SKAU-R-6  $\times$  Yakwei for shell ratio (%). Whereas, in rest of the crosses epistasis was evident in the traits under investigation. Magnitude of additive gene effect (d) was greater than dominance (h) in  $SH_6 \times NB_4D_2$  and SKUA-R-6  $\times$  Yakwei for shell ratio (%) and in  $CSR_2 \times CSR_4$  for shell weight. Thus selection for these traits in early segregating generations of these crosses would be effective for obtaining considerable genetic gain.

**Key words:** *Bombyx mori* L., Bivoltine, Gene effects, Epistasis, Generation mean.

### Introduction

Sericulture, being a rural-based agro industry is suited for improving the social and economic condition of rural poor. India has emerged as the second largest producer of raw silk and contributes about nineteen percent of global silk production (Datta *et al.*, 2001). More than 90% of silk

produced in India is of multivoltine or multi  $\times$  bivoltine in origin, which due to inherent poor quality, can not compete in the international market. The demand for quality silk produced by genetically superior bivoltine breeds, is growing both at domestic and international markets. J&K state is the only traditional bivoltine belt in India, which because of salubrious climatic conditions for silkworm rearing and mulberry cultivation can produce quality bivoltine silk. The state has set a target of 1500 metric tones of cocoon production by 2010 (Anonymous, 1999). This target can be achieved by development and adoption of improved crop production and protection technologies. The major thrust areas should be development of new and high yielding mulberry and silkworm genotypes.

Among other reasons, lack of productive silkworm breeds has been identified as a major constraint in boosting cocoon production of the state (Trag *et al.*, 1992). Attempts to evolve new and more productive bivoltine breeds/hybrids, suited to agro-climatic conditions of Jammu & Kashmir state resulted in the production of a productive hybrid namely SKAU-HR-1 which was subsequently authorized for commercial exploitation in temperate area of Jammu and Kashmir state (Kamili, 1996). Generally the parental stocks of a particular hybrid have the tendency of losing their potential after some time due to continuous inbreeding, therefore, evolution of new and more productive breeds is essential to maintain and increase productivity level. A thorough knowledge of nature and magnitude of various gene effects operative in the inheritance of quantitative traits is a prerequisite for formulation of effective breeding strategies aimed at synthesis of superior genotypes.

Although several biometrical designs have been employed in silkworms to gather such information, in most of these designs epistasis is presumed to be absent. Since epistasis has been reported to play an important role in the inheritance of many metric traits in silkworm

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(Kamili *et al.*, 1998). The present investigation was, therefore, carried out to gather information about various components of genetic variance in four crosses with the ultimate object of initiation of new breeding programmes.

## Materials and Methods

Six generations *viz.*, P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> raised from 4 bivoltine silkworm hybrids (SKAU-R-1 × Yakwei, SKUA-R-6 × Yakwei, CSR<sub>2</sub> × CSR<sub>4</sub> and SH<sub>6</sub> × NB<sub>4</sub>D<sub>2</sub>) and their 7 parents were reared at the Division of Sericulture, Mirgund Kashmir during summer season (July - August) 2003, following the recommendations suggested by Dar and Singh (1998). The experiment was laid out in a completely randomized block design with 5 replications for each treatment. Each replication comprised 250 worms (after 3<sup>rd</sup> moult). Data in respect of 3 metric traits *viz.*, single cocoon weight, single shell weight and shell ratio (%) were collected on the basis of randomly selected cocoons. The sample size was 20 cocoons for non segregating generations (P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub>) and 40 cocoons for backcross generations (BC<sub>1</sub> and BC<sub>2</sub>) and 100 cocoons for F<sub>2</sub> generation.

The adequacy of additive-dominance (non-epistatic) model was tested by joint scaling test as proposed by Cavalli (1952). The test involves estimation of parameters m, d and h followed by a comparison of observed generation means with the expected values derived from estimates of these 3 parameters. The values of X<sup>2</sup> for (6 - 3) degrees of freedom were used to test adequacy of non-epistatic

model. The digenic interactions (i, j and l) were worked out following the method suggested by Hayman (1958).

## Results

The values of X<sup>2</sup> for (6 - 3) degrees of freedom (Table 1), exceeded table value at 0.01 probability level in crosses SKAU-R-1 × Yakwei and SKAU-R-6 × Yakwei for single cocoon weight and shell weight and in SKUA-R-1 × Yakwei for single cocoon weight and shell weight and in SKUA-R-1 × Yakwei for shell ratio (%). Significance of X<sup>2</sup>, hence, indicated the presence of non allelic interaction. However, X<sup>2</sup> test was non-significant in CSR<sub>2</sub> × CSR<sub>4</sub> and SH<sub>6</sub> × NB<sub>4</sub>D<sub>2</sub>, which indicated adequacy of additive dominance model. The gene effects (m), (d) and (h) were significant for shell ratio (%) in SH<sub>6</sub> × NB<sub>4</sub>D<sub>2</sub> and SKUA-R-6 × Yakwei and for shell weight in CSR<sub>2</sub> × CSR<sub>4</sub>. The (h) was significant for single cocoon weight and shell ratio (%) in CSR<sub>2</sub> × CSR<sub>4</sub>. Among interaction effects i (ad × ad) was significant for single shell weight in SKAU-R-1 × Yakwei and SKUA-R-6 × Yakwei; j (ad × dom) for single cocoon weight in SKUA-R-1 × Yakwei and l (dom × dom) for single shell weight in SKUA-R-6 × Yakwei.

## Discussion

Genetic variations observed between individuals in quantitatively inherited traits may be the result of additive or

**Table 1.** Values of joint scaling test, estimates of gene effects and type of epistasis for three metric traits in 4 silkworm crosses

Traits	Cross	Joint scaling test (X <sup>2</sup> )	Gene effects						Type of epistasis
			m	(d)	(h)	(i)	(j)	(l)	
Single cocoon weight	SKAU-R-1 × Yakwei	56.94**	180**	-1	22.5	10	92*	-25	Duplicate
	SKAU-R-6 × Yakwei	366.57**	186**	-1	20	6	-7	-8	Duplicate
	CSR <sub>2</sub> × CSR <sub>4</sub>	0.1509 <sup>NS</sup>	142.3**	0.0049	52.4*	-	-	-	-
	SH <sub>6</sub> × NB <sub>4</sub> D <sub>2</sub>	0.0108 <sup>NS</sup>	165.8**	-0.0059	0.0002	-	-	-	-
Single shell weight	SKAU-R-1 × Yakwei	718.00**	37**	-1	225.5*	183*	-3.5	-7	Duplicate
	SKAU-R-6 × Yakwei	28.00**	37**	-1	10.5*	-34	2.5	-112*	Duplicate
	CSR <sub>2</sub> × CSR <sub>4</sub>	1.539 <sup>NS</sup>	31.67**	1.13*	0.189*	-	-	-	-
	SH <sub>6</sub> × NB <sub>4</sub> D <sub>2</sub>	1.928 <sup>NS</sup>	29.72**	0.78	-0.344	-	-	-	-
Shell ratio (%)	SKAU-R-1 × Yakwei	24.23**	20.31**	-0.9	4.65	0.68	-2.495	0.99	Complimentary
	SKAU-R-6 × Yakwei	0.62 <sup>NS</sup>	18.74**	1.56*	0.96*	-	-	-	-
	CSR <sub>2</sub> × CSR <sub>4</sub>	1.799 <sup>NS</sup>	21.08**	-0.76	-2.292*	-	-	-	-
	SH <sub>6</sub> × NB <sub>4</sub> D <sub>2</sub>	3.48 <sup>NS</sup>	17.78**	0.186*	-	0.12*	-	-	-

\* and \*\* denote significance at p = 0.05 and p = 0.01, respectively.

NS denotes non-significant.

non-additive gene actions or both. Non-additive gene actions may comprise allelic interactions (dominance) and or/non allelic (epistatic) interactions. A thorough knowledge of all these components of genetic variations is a prerequisite for adoption of effective breeding and selection methodologies aimed at evolution of new and more productive breeds. Although several biometrical designs like diallel analysis and bi-parental cross analysis has widely been used for estimation of additive and dominance effects, they do not provide information about additive  $\times$  additive, additive  $\times$  dominance and dominance  $\times$  dominance components of non-allelic interactions which have been reported to play an important part in the manifestation of heterotic potential of some silkworm breeds (Kamili *et al.*, 1998). Keeping this in view 4 bivoltine silkworm (*Bombyx mori* L.) crosses between 7 genetically divergent breeds *viz.*, SKAU-R-1, SKUA-R-6, CSR<sub>2</sub>, CSR<sub>4</sub>, SH<sub>6</sub>, NB<sub>4</sub>D<sub>2</sub> and Yakwei were included in the present study to gather knowledge on the genetic architecture of 3 important metric traits. In the present study Cavallis joint scaling test indicated adequacy of additive-dominance model in CSR<sub>2</sub>  $\times$  CSR<sub>4</sub> and SH<sub>6</sub>  $\times$  NB<sub>4</sub>D<sub>2</sub> for single cocoon weight and shell weight and in SKUA-R-6  $\times$  Yakwei, CSR<sub>2</sub>  $\times$  CSR<sub>4</sub> and SH<sub>6</sub>  $\times$  NB<sub>4</sub>D<sub>2</sub> for shell ratio (%). Magnitude of additive gene effects (d) was greater than dominance (h) indicating preponderance of additive gene effects in the expression of these traits. Thus selection in early segregating generations would be effective for obtaining considerable genetic gain with the above mentioned crosses. However, dominance (h) gene effects were significant and greater in magnitude than corresponding additive (d) component for single cocoon weight and shell ratio (%) in CSR<sub>2</sub>  $\times$  CSR<sub>4</sub>, therefore, selection for these traits may be postponed till advanced generation. Regarding the classification of epistasis, which largely depends on the signs of h and l (similar signs of (h) and (l) indicate predominance of complementary epistasis while different signs indicate duplicate interaction), a duplicate type of gene interaction was evident in SKUA-R-1  $\times$  Yakwei and SKUA-R-6  $\times$  Yakwei for single cocoon weight and shell weight whereas, complimentary interaction prevailed for shell ratio in SKUA-R-1  $\times$  Yakwei. In silkworm breeding programmes, the presence of epistasis has either been ignored or assumed to be absent which does not seem plausible. Hence due importance needs to be given

to these components of genetic variance in the formulation of breeding programmes with the present set of experimental materials.

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