Genetic variation of some quantitative traits in ten exotic varieties of silkworm, *Bombyx mori* L.

Md. Kamrul Ahsan and S.M. Rahman
Department of Zoology, University of Rajshahi, Rajshahi-6205, Rajshahi.

Abstract: An investigation was conducted with ten exotic varieties of silkworm, *Bombyx mori* L. to estimate variability, heritability and genetic advance for nine quantitative characters. A wide range of variation was observed for the majority of the traits and a major portion of the total phenotypic variation was of genetic in nature. The maximum phenotypic and genotypic coefficient of variation was found in filament length (21.45, 21.44) and the minimum in hatching percentage (1.52, 1.44), respectively. A moderate to high heritability was recorded for these varieties. Filament length showed the highest heritability (99.98). A comparatively high heritability accompanied by a high genetic advance was also noted for majority of the traits. Substantial variability, high heritability and high genetic advance for filament length, weight of mature larvae, total number of eggs laid per female and effective rate of rearing by weight recorded in this study would afford scope for effective selection.

Key words: *Bombyx mori,* genetic variation, exotic varieties.

Introduction

Collection of varietal materials of mulberry silkworm, *Bombyx mori* L. and their evaluation is a pre-requisite for the improvement of the economic traits (Akanda *et al.,* 1998, Ahsan & Rahman, 2008). But very little attention has so far been given for the improvement of mulberry silkworm in Bangladesh. The detailed genetic analysis of quantitative characters of the available varieties of *B. mori* has not been investigated till to date although studies on the variation of yield and yield contribution characters are of great importance for the improvement of silk yield (Rahman & Khalequzzaman, 1993; Reza & Rahman, 1996, 2005). The progress and success in any breeding programme for evolving superior breeds depends upon the nature and magnitude of genetic variability in the available materials. If the variability in the population of largely in genetic nature with least environmental effect, the probability of isolating superior genotype is high. Since this variability is highly influenced by the environment, it becomes difficult to predict the contribution of genetic factors against environmental effects. With this back ground, the present investigation was undertaken to study the genetic variability among ten exotic stocks available in Bangladesh.

Materials and methods

Ten exotic varieties of silkworm namely, Dong - 34(M), Ziangsu - 12(J), RB - 001, RB - 112, Bivoltine - J, NB_7, NB_{18}, NB_4D_4, SK_1 and SK_2 selected from Bangladesh Sericulture Research and Training Institute, Rajshahi constituted the base material of this experiment. Standard rearing techniques recommended by Krishnaswami (1978) were followed. Disease free layings (dfls) from each breed were reared on rearing trays in a randomized block design with three replications. Nine quantitative characters such as total number of eggs laid per female (TEL), hatching percentage (HP), weight of mature larvae (LW), effective rate of rearing by number (ERRn), effective rate of rearing by weight (ERRw), cocoon weight (CW), shell weight (SW), filament length (FL) and estimated cocoon yield per 100 dfls (ECY) were collected from each replication for statistical analysis. Genotypic (δ^2g) and phenotypic (δ^2p) variations were estimated by the formula given by Burton & De Vane (1953) and the coefficient of variability was worked out as described by Burton (1952). Heritability in broad sense was estimated by the following formula given by Hanson *et al.* (1956).

Heritability (Broad sense) = δ^2g/ δ^2p x 100

The expected genetic advance was estimated by the following formula:

Genetic advance (GA) = δ^2g / δ^2p x k $\sqrt{\delta^2}$ p.

Where k has a value of 2.06 which is the expectation in 5% selection intensity from a large population (Lush, 1949; Miller *et al.,* 1958)

Results and Discussion

Analyses of variances of nine quantitative characters are shown in Table1. The genotype items showed highly significant results indicating pronounced racial diversity have been substantiated by the finding of Tayade 1987, Ahsan *et al.,* 2001; Reza & Rahman, 2005. Similar results on varietal differences with respect to larval and cocoon characters in *B. mori* have been reported by Sidhu *et al.* (1969), Ahsan *et al.* (1998) and to larval characters by Reza *et al.* (1993). The replication items revealed insignificant results showing homogeneity in different parts of the present investigation.

The results on overall range, mean with SE and genetic variability for different characters are shown in Table 2. Phenotypic variances (δ^2p) were generally greater than their corresponding genotype (δ^2g) or environmental (δ^2e) variances in all the cases. Closer δ^2p and δ^2g as well as higher δ^2g than δ^2e for all the characters indicated that the major part of the phenotypic variation was of genotypic in nature.

Estimates on phenotypic (CVp), genotypic (CVg) and environmental (CVe) co-efficient of variability, heritability (H$_b$), genetic advance (GA) and genetic advance as percentage of mean (GA%) have been presented in Table3. The maximum phenotypic and genotypic coefficient of variation was found in filament length and the minimum in hatching percentage. The range of phenotypic co-efficient of variation was from 1.52 - 21.45 and of genotypic was 1.44 - 21.44. Where as the highest environmental coefficient of variation was recorded in estimated cocoon yield / 100 dfls

(5.38) and lowest in shell weight (0.15). The genotypic coefficient of variation alone is not sufficient to determine the amount of variation which is heritable. The heritable portion of variation can be found from heritability estimates and genetic gain (Johnson *et al.,* 1955). In this study the highest heritability (H$_b$) was obtained for FL (99.89) followed by LW, TEL, FRRw, CW, HP, FRRn, SW and lowest in ECY (72.29). The genetic advance (GA) estimated for different characters ranged from 0.087 (SW) - 363.45 (FL). When genetic advance was expressed as percentage of respective means (GA%), highest score was noted in FL (44.15) followed by SW, LW, TEL, ERRw, CW, ECY, ERRn and lowest in HP(2.82).

In this results FL, LW, TEL and ERRw showed comparatively high coefficient of variability, heritability, as well as genetic advance and genetic advance as percentage of mean indicates that a wide range of genetic diversity existed which could be used in a breeding programme. It also indicated the importance of additive gene effects in these characters and phenotypic selection of these characters would be effective (Panse, 1957; Rahman & Rahman, 1990; Reza *et al.,* 1993).

A number of characters showed high heritability but low genetic advance. This might happen due to the intra or inter allelic interaction. In such situation recurrent selection may be adopted to these trails (Pershad *et al.,* 1986, Rahman & Rahman, 1990; Ahsan & Rahman 2008).

Table 1. Mean square of ANOVA for nine quantitative characters in *B. mori.*

	df	MS								
		TEL	HP	LW	ERRn	ERRw	CW	SW	FL	ECY
Variety	9	6943.63**	5.35**	1.47**	6.48**	182.24**	0.0422**	0.00656**	93521.05**	17.38**
Replication	2	14.09	0.02	0.0039	0.025	0.67	0.0002	0.00049	24.62	2.73
Error	8	18.64	0.19	0.0037	0.27	.097	0.00037	0.00035	34.56	1.97

** $p < 0.001$

Table 2. Range, Mean with SE and components of variance of different characters in *B. mori.*

Characters	Range	Mean	SE	δ^2p	δ^2g	δ^2e
TEL	445.17 - 70.18	518.35	3.53	2326.97	2308.33	18.64
HP	88.50 - 94.00	91.02	0.35	1.91	1.72	0.19
LW	3.25 - 5.00	4.16	0.05	0.4925	0.4888	0.0037
ERRn	64.00 - 69.51	66.25	0.42	2.34	2.07	0.27
ERRw	76.52 - 97.40	87.76	0.50	61.39	60.42	0.97
CW	1.14 - 1.46	1.33	0.0157	0.01431	0.01394	0.00037
SW	0.17 - 0.29	0.233	0.0153	0.00242	0.00207	0.00035
FL	605.17- 1000	823.28	4.8	31196.72	31162.16	34.56
ECY	19.28 - 29.58	26.08	1.15	7.11	5.14	1.97

Table 3. Phenotypic (CVP), genotypic (CVg) and environmental (CVe) coefficient of variation, heritability (Hb), genetic advance (GA) and genetic advance as percentage of means (GA%) of different characters in *B. mori.*

Characters	CVp	CVg	CVc	Hb	GA	GA%
TEL	9.31	9.27	0.83	99.20	98.58	19.02
HP	1.52	1.44	0.48	90.05	2.54	2.82
LW	16.87	16.81	1.46	99.25	1.43	34.49
ERRn	2.31	2.17	0.78	88.46	2.79	4.21
ERRw	8.93	8.85	1.12	98.42	15.89	18.10
CW	8.99	8.88	1.45	97.41	0.24	18.05
SW	21.11	19.53	0.15	85.54	0.087	37.20
FL	21.45	21.44	0.71	99.89	363.45	44.15
ECY	10.22	8.69	5.38	72.29	3.97	15.25

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