

Genetic variability, correlation, path analysis and construction of selection index in mulberry silkworm, *Bombyx mori* L. I. Genetic variability

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Abstract: The genotypic variability and heritability for nine quantitative characters in 65 varieties of silkworm, *B. mori* L. have been investigated. Variation among genotypes were highly significant ($p < 0.001$) for all the characters indicating the existence of a real difference among the genotypes which are suitable for breeding purposes. The highest heritability was obtained for shell weight followed by filament size (FS), filament length (FL), expected cocoon yield out of 100 dfls (ECY), surviving percentage of larvae (SPL), cocoon weight (CW), egg hatching percentage (EHP) and mature larval weight (MLW). Comparatively high heritability accompanied by a genetic advance was recorded for FL and total number of eggs laid per female (TEL) indicating the importance of additive gene effects of these characters, but shell weight, cocoon weight and filament size showed high heritability and low genetic advance indicating the involvement of non-additive gene systems in the inheritance of these characters. So selection on the basis of these characters, with relatively more emphasis upon filament length and total number of eggs laid per female to obtain high yielding varieties of *B. mori* is suggested.

Key words: Genetic variability, *Bombyx mori*.

Introduction

Selective breeding is aimed at improving the existing ones and developing new breeds and hybrids which is essentially a creative process and is dependent on the study of genetic parameters and genetic architecture forming a basis for most appropriate selection scheme. Consequently, success in any breeding programme for evolving superior breeds depends on the selection of parental material on the basis of their genetic variability, geographical distribution and per se performances and some physio-morphological characters is essential (Akanda *et al.*, 1998). To get idea of the genetic variability existing among the varieties with regard to the quantitative characters of economic importance it becomes necessary to apply appropriate method of biometrical analysis. The concept of multiple gene inheritance of quantitative traits is now one of the most important principles of genetics which require refined statistical method. Smith (1944) proposed polygenic concept of quantitative characters and Mather (1949) on the basis of this concept detailed Fisher's (Fisher *et al.*, 1932) statistical method to study genetic components of variance as well as environmental variance.

In silkworm quantitative character is jointly controlled by multiple genes and environmental factors (Reza & Rahman, 2005; Zhao *et al.*, 2007; Ahsan & Rahman, 2008). So the yield potential of *B. mori* needs to be improved through an effective breeding programme. But very diminutive concentration has so far been given for the improvement of the mulberry silkworm, *Bombyx mori* L. in Bangladesh (Reza & Rahman, 2005; Ahsan *et al.*, 2010).

Studies were therefore, undertaken to estimate the genetic variability, heritability and genetic advance for some important quantitative characters and correlations among them at phenotypic and genotypic levels of *B. mori*.

Materials and Methods

The material for the present investigation comprised of 65 multivoltine (indigenous, developed and exotic) and bivoltine (developed and exotic) varieties of mulberry silkworm *B. mori*. The names of the varieties are listed in Table-1.

The eggs of these varieties were brushed (3dfls for each genotype) in a randomized design with three replications each. The rearing was conducted in the rearing house No. 2 of the Bangladesh Sericulture Research and Training Institute, Rajshahi. Scientific technology of silkworm rearing was followed according to Krishnaswami (1978) and Rahman (1983). Data recorded for this study were: total number of eggs laid per female (TEL), egg hatching percentage (EHP), mature larval weight (MLW), surviving percentage of larvae (SPL), cocoon weight (CW), shell weight (SW), length of filament (FL), filament size (FS) and estimated cocoon yield out of 100 dfls (ECY). Genotypic (σ^2_g) and phenotypic (σ^2_p) 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).

Table-1. Varieties of *Bombyx mori* L. used in the experiment.

1. Nistari	14. BSR-3 (p)	27. BSR-95/10(P)	40. Bipul	53. Ziangu (P)
2. Nistari (P)	15. BSR-3 (m)	28. BSR-95/14(P)	41. BSRI-83/1	54. Dong 34(M)
3. Nistari (M)	16. BSR-10 (m)	29. BSR-95/22(P)	42. BSRI-83/2	55. Dong 34 (P)
4. Nistari L	17. Nistid white (P)	30. BSR-98/1(P)	43. BSRI-83/3	56. BV (M)
5. Nistari G	18. BSR-JB	31. BSR-98/2(P)	44. BSRI-85/1	57. BV (P)
6. ISK	19. BSR-IM(P)	32. BSR2000/1(GM)	45. BSRI-85/2	58. RB (M)
7. MBY- 011S (P)	20. BSR-(GL)	33. BSR-02/1(M)	46. BSRI-85/3	59. RB (P)
8. BN P	21. BSR-92/2(P)	34. BSR-02/2(P)	47. BSRI-J	60. RB-001 (M)
9. BN (M)	22. BSR-92/5(P)	35. BSR-02/3	48. Urboshi-1	61. RB-001 (P)
10. NN-7B (P)	23. BSR-92/7(P)	36. BSR-03/1	49. Urboshi-4	62. RB-111
11. NM-7B (M)	24. BSR-92/8(P)	37. BSR-03/2	50. BSRI-801	63. RB-112
12. BSR-1 white (p)	25. BSR-92/14(P)	38. O ₅	51. BSRI-802	64. RB-SB (M)
13. BSR- white (m)	26. BSR-92/16(P)	39. R ₁ S ₁	52. Ziangu 12-J	65. RB-SP (P)

Heritability (Broad sense) = $\sigma^2g / \sigma^2x \times 100$

The expected genetic advance was stimulated by the following formula:

$$\text{Genetic advance (GA)} = \sigma^2g / \sigma^2p \times k \sqrt{\delta^2 p}$$

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

An analysis of variance showed that the item, genotype was highly significant for all the characters studied indicating that the varieties possess a wide range of genetic diversity and these materials are suitable for breeding purposes (Table 2.). Varietal differences with respect to egg, larval and cocoon characters in *B. mori* have been reported by Ahsan *et al.* (2000). Similar results on varietal diversity have also been substantiated by the findings of Pershad *et al.* (1986), Govindan *et al.* (1987), Toyade (1987), Reza & Rahman (1996), Ahsan & Rahman (2008) and Ahsan *et al.* (2010). Results on overall range, mean with standard error and genetic variability for different characters have been presented in Table 3. Phenotypic variances (σ^2p) were generally greater than their corresponding genotypic (σ^2g) or environmental variances (σ^2e) in all the cases. Closer values of σ^2p and σ^2g as well as higher values of σ^2g than σ^2e for all the characters implied that the major portion of the phenotypic variation was of genotypic in nature.

Phenotypic (CV_p), genotypic (CV_g) and environmental (CV_e) co-efficient of variability, heritability (H), genetic advance (GA) and genetic advance as percentage of mean (GA%) were estimated and presented in Table 4. The

maximum phenotypic and genotypic co-efficient of variation was found in SW and the minimum in EHP whereas the highest environmental co-efficient of variation was recorded in FL and the lowest in SW. 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. In this study, SW, ECY, FL and TEL showed very high heritability together with high phenotypic (CV_p) and genotypic (CV_g) coefficient of variability. On the other hand, FS, SPL and CW showed very high heritability but moderate phenotypic and genotypic coefficient of variability together with low environmental coefficient of variability. Ahsan & Rahman, (2008) reported high heritability together with high phenotypic and genotypic coefficient of variability of total eggs laid by female. The result of Ahsan *et al.* (2010) is similar with the present findings who reported a high heritability coupled with high phenotypic and genotypic coefficient of variability for FL and ECY.

In the present experiment the highest heritability was obtained for SW followed by FS, FL, ECY, SPL, CW, EHP and MLW. But very low heritability for CW and for silk richness was reported by Nassirillaevev & Abbasov (1980). Similar low values of heritability were also noted by Tsocheva (1981) who investigated relationship between cocoon length versus diameter. Ozdzesska & Kremky (1987) also noticed a very high heritability value for hatching percentage and survival rate; however, they found a very low value for filament length, cocoon weight and shell weight.

Table 2. Analysis of variance for nine quantitative characters in *B. mori*.

Item (df)	F-value								
	TEL	EHP	MLW	SPL	CW	SW	FL	FS	ECY
Within Varieties (64/128)	223.56*	38.08*	16.47*	125.91*	96.51*	619.60*	157.72*	185.15*	132.41*
Within Replication (2/128)	1.32	0.07	0.13	0.52	0.39	1.63	0.69	2.06	0.02

* P<0.01

Table 3. Range, mean with S. E. and component of variance of different characters of *Bombyx mori*.

Characters	Range	Mean \pm S E	σ^2_p	σ^2_g	σ^2_e
TEL	309.30 - 699.37	477.81 \pm 8.470	8093.890	7986.24	107.650
EHP	80.13-97.87	91.03 \pm 0.980	19.130	17.700	1.430
MLW	2.16-3.96	2.99 \pm 0.140	0.180	0.150	0.030
SPL	60.29-99.94	84.22 \pm 1.140	83.620	81.660	1.960
CW	0.9000-1.6200	1.28 \pm 0.020	0.031	0.030	0.001
SW	0.1042-0.2960	0.17 \pm 0.002	0.002	0.002	0.000
FL	347.30-792.70	577.89 \pm 12.770	13027.700	12783.01	244.690
FS	1.44-2.88	2.20 \pm 0.030	0.080	0.080	0.000
ECY	19.99-46.05	32.69 \pm 0.820	44.650	43.650	1.000

 σ^2_p : Phenotypic variance; σ^2_g : Genotypic variance; σ^2_e : Environmental variance.**Table 4.** Phenotypic (CVp), genotypic (CVg), environmental (CVe), coefficient of variation, heritability (H), genetic advance (GA) and genetic advance as percentage of mean (GA%) of different characters of *Bombyx mori*.

Characters	CVp	CVg	CVe	H	GA	GA%
TEL	18.83	18.70	4.75	98.67	182.87	38.27
EHP	4.81	4.62	1.25	92.51	8.34	9.16
MLW	14.00	12.82	0.98	83.75	0.72	24.16
SPL	10.86	10.73	1.53	97.65	18.40	21.84
CW	13.76	13.55	0.27	96.95	0.35	27.48
SW	24.66	24.60	0.07	99.51	0.08	50.57
FL	19.75	19.56	6.50	98.12	230.71	39.92
FS	12.87	12.77	0.24	98.40	0.58	26.09
ECY	20.44	20.21	1.75	97.77	13.46	41.17

Filament length and TEL expressed the highest genetic advance together with high heritability. It indicated the importance of additive gene effects of these characters (Rahman, 1984; Reza *et al.*, 1993; Ahsan *et al.*, 2010). SW, CW and FS exhibited high heritability and low genetic advance, suggesting limited scope for manipulation of these characters. These could be due to non-additive gene action which includes dominance and epistasis (Ahsan & Rahman, 2008). In such situations progeny testing and a recurrent selection might be helpful to improve these traits (Rahman, 1984; Rao, 1997; Ahsan *et al.*, 2000; Ahsan & Rahman, 2010). Here SPL and ECY showed high heritability and moderate genetic advance. Sen *et al.* (1995) had also shown high heritability and moderate genetic advance for MLW and CW in multivoltine silkworms. Reza *et al.* (1993) and Reza & Rahman

(1996) found a non-additive component of genetic variation as an important feature of some larval and cocoon characters in *B. mori*. Govindan *et al.* (1987) also found a non-additive component of genetic variation as an important feature of some larval and cocoon characters in *B. mori*. Kantaratanakul *et al.* (1987) reported in favour of additivity with respect to filament length.

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