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GENETIC VARIABILITY, HERITABILITY AND CORRELATION ANALYSIS FOR SOME CHARACTERS IN HYBRIDS OF THE MULBERRY SILKWORM, *BOMBYX MORI* L.

Md. Kamrul Ahsan*, Sowdagar Mahfuzar Rahman and Md. Tajimul Haque[1]

Department of Zoology, University of Rajshahi, Rjshahi 6205, Bangladesh
[1]Former Senior Scientific Officer, Bangladesh Sericulture Research and Training Institute, Rajshahi 6100, Bangladesh; *Corresponding author: email: md_kahsan@yahoo.com

Abstract: Genetic variability, heritability and correlation analysis for some important economic characters in 35 hybrids of the silkworm, *Bombyx mori* L. have been investigated. Higher heritability values were recorded for effective rate of rearing by number (ERRn), followed by estimated cocoon yield per 100 dfls (ECY), weight of mature larvae (WML), filament length (FL) and effective rate rearing by weight (ERRw). Furthermore, characters such as FL, ERRn, ERRw and ECY showed higher genetic advance coupled with higher heritability values, indicating the importance of additive gene effect of these characters. The genotypic correlations were higher than the phenotypic correlations for all the characters under study. These low phenotypic correlations could be due to a modifying effect of environment of the association of characters at genotypic level. Most of the characters showed positive significant correlation to each other except ERRn and ERRw pair at phenotypic level. Therefore, proper attention should be given to these characters, especially WML, FL and ECY, in selection programmes for genetic gain in *B. mori.*

Key words: Genetic variability, heritability, correlation, economic characters, *B. mori.*

mvivsk: cq©ÎkwU ksKiRvZ †ikgKxU, *Bombyx mori* e¨envi K‡i wKQ ¸i“ZcY© ˆewk‡ó¨i †KŠwjZwËK e¨eavb, ‡nwiU¨vwewjwU Ges mnmsme wbY©‡qi Rb¨ GB M‡elYwUi cwiKíbv Kiv n‡qwQj| chv©qµwgK fv‡e msL¨vq KvhKi cjcvj‡bi nvi, cwZ 100 wW‡g †KvKb Drcv`‡bi cwigvb, cY©v½ jvfvi IRb, mZvi ˆ`N¨ Ges IR‡b KvhKi cjcvj‡bi nvi ˆewkó¨¸wji Rb¨ D"P †nwiU¨vwewjwU ZvwjKvf³ Kiv n‡q‡Q| AwaKš mZvi ˆ`N¨, msL¨vq KvhKi cjcvj‡bi nvi, IR‡b KvhKi cjcvj‡bi nvi, cwZ 100 wW‡g †KvKb Drcv`‡bi cwigvb ˆewkó¨mgn D"P †RwbwUK G¨WfvÝ c`k©‡bi mv‡_ mv‡_ D"P †nwiU¨vwewjwU cKvk K‡i‡Q, A_©vr G mg¯ ˆewk‡ó¨i †¶‡Î GwWwUf wR‡bi cfve ¸i“ZcY| GB M‡elYvi Aaxb mg¯ ˆewk‡ó¨i Rb¨ †d‡bvUvBwc‡Ki ZjbvqK †R‡bvUvBwc‡Ki mnmsme †ekx| wbg †d‡bvUvBwcK mnmsme G mg¯ ksKiRv‡Z D³ ˆewk‡ó¨i Dci cwi‡e‡ki cwigZ cfv‡ei Kvi‡Y n‡Z cv‡i| †d‡bvUvBwc‡Ki †¶‡Î msL¨vq KvhKi cjcvj‡bi nvi Ges IR‡b KvhKi cjcvj‡bi nvi Qvov G M‡elYvi Ab¨vb¨ ˆewkó¨ abvZ¥K ZvrchcY mnmsme c`kb K‡i| AZGe GB mg¯ ˆewkó¨, we‡kl K‡i cY©v½ jvfvi IRb, mZvi ˆ`N¨ Ges cwZ 100 wW‡g †KvKb Drcv`‡bi cwigvb ˆewkó¨¸wji w`‡K †igkKx‡Ui *B. mori* †KŠwjZwËK DbœwZ‡Z wbe©vPb †cwMÖ‡gi mgq we‡kl `wó w`‡Z n‡e|

Introduction

An understanding of the nature and magnitude of gene effects controlling complex characters of an organism are very important in adopting appropriate breeding procedures. Fisher (1918) was credited with defining the genetic variability in terms of gene effect and further partitioning it into additive, dominance and epistatic components. Several statistical models had also been developed to analyze the inheritance of polygenic characters (Fisher *et al.* 1932; Weight 1935; Mather 1949; Robinson *et al.* 1949; Comstock and Robinson 1952). In *Bombyx mori* L. quantitative characters, such as cocoon weight, shell weight, shell ratio and filament length are simultaneously controlled by multiple genes and environmental factors (Reza and Rahman 2005; Zhao *et al.* 2007; Ahsan and Rahman 2008). Estimation of correlation and heritability in the genetic studies of quantitative characters is of special significance for selection of *B. mori* (Singh *et al.* 1994). Extensive research has been carried out in different countries on the genetic analysis in *B. mori*, but very little information is available on the inheritance of the quantitative characters in respect to the silkworm races and hybrids reared in Bangladesh (Reza and Rahman 2005). Here we report the genetic variability, heritability and genetic advance for some important quantitative characters in a large number of hybrids of *B. mori*, along with correlations among the characters at both phenotypic and genotypic levels.

Materials and Methods

The materials for this experiment were produced from 18 bi- and multivoltine varieties of *B. mori,* the parental stocks of which were obtained from the Germplasm Bank maintained at the Bangladesh Sericulture Research and Training Institute (BSRTI), Rajshahi. The following crossing schedules were made to produce 35 F_1 hybrids:

1. BSR-3(M)×HTHRB-3	2. BSRTI-1×HTHRB-3	3. BSRTI-3×HTHRB-3	4. BSRTI-4×HTHRB-3
5. BSRTI-5×HTHRB-3	6. BSR-3(M)×FT-B	7. BSRTI-1×FT-B	8. BSRTI-3×FT-B
9. BSRTI-4×FT-B	10. BSRTI-5×FT-B	11.HTHRB-3×BSR-3(M)	12. HTHRB-3×BSRTI-1
13. HTHRB-3×BSRTI-3	14. HTHRB-3×BSRTI-4	15. HTHRB-3×BSRTI-5	16. FT-B×BSR-3(M)
17. FT-B×BSRTI-1	18. FT-B×BSRTI-3	19. FT-B×BSRTI-4	20. FT-B×BSRTI-5
21. 95/10×CCY-1	22. 95/10×CCY-3	23. 95/10×CCY-4	24. 95/14×CCY-1
25. 95/14×CCY-2	26. 95/22×CCY-1	27. CCY-1×CCY-3	28 CCY-1×Ziangsu-P
29. BV-M×CCY-2	30. CCY-2×Dong-P	31. S98×CCY-3	32. S98×CCY-4
33. BV-M×S98	34. S98×Dong-P	35. S98×Ziangsu-P	

1. BSR-3(M)×HTHRB-3	2. BSRTI-1×HTHRB-3	3. BSRTI-3×HTHRB-3	4. BSRTI-4×HTHRB-3
5. BSRTI-5×HTHRB-3	6. BSR-3(M)×FT-B	7. BSRTI-1×FT-B	8. BSRTI-3×FT-B
9. BSRTI-4×FT-B	10. BSRTI-5×FT-B	11.HTHRB-3×BSR-3(M)	12. HTHRB-3×BSRTI-1
13. HTHRB-3×BSRTI-3	14. HTHRB-3×BSRTI-4	15. HTHRB-3×BSRTI-5	16. FT-B×BSR-3(M)
17. FT-B×BSRTI-1	18. FT-B×BSRTI-3	19. FT-B×BSRTI-4	20. FT-B×BSRTI-5
21. 95/10×CCY-1	22. 95/10×CCY-3	23. 95/10×CCY-4	24. 95/14×CCY-1
25. 95/14×CCY-2	26. 95/22×CCY-1	27. CCY-1×CCY-3	28 CCY-1×Ziangsu-P
29. BV-M×CCY-2	30. CCY-2×Dong-P	31. S_{98}×CCY-3	32. S_{98}×CCY-4
33. BV-M×S_{98}	34. S_{98}×Dong-P	35. S_{98}×Ziangsu-P	

Eggs from disease-free layings (dfls) of the F_1 hybrids for each genotype were brushed in a randomized design with three replicates each. Scientific technology of silkworm rearing (Krishnaswami 1978, Rahman 1983) was maintained in the rearing house No. 2 of the BSRTI, Rajshahi. Economic characters recorded for this study were: weight of mature larvae (WML), effective rate of rearing by number (ERRn), effective rate rearing by weight (ERRw), filament length (FL) and estimated cocoon yield per 100 dfls (ECY). Data were analyzed successively for estimated genetic variability, heritability and genetic advance according to the formulae described by Lush (1949), Burton (1952), Burton and De Vane (1953), Johnson *et al.* (1955) and Hanson *et al.* (1956). The phenotypic and genotypic correlations were calculated in the usual way.

Results and Discussion

Results on overall range, mean with standard error and genetic variability for different characters have been presented in Table 1. The major part of the total variation in the present study was contributed by the genotypic components in all the characters. The item variety on the ANOVA was highly significant for all the characters indicating that the varieties possess a wide range of genetic diversities and these materials are suitable for breeding purposes. Varietal differences with respect to egg, larval and cocoon characters in *B. mori* have been reported by Ahsan *et al.* (2000). Similar results on varietals diversity have also been substantiated by the findings of Reza and Rahman (1996) and Ahsan and Rahman (2008).

Estimates of phenotypic (CVp), genotypic (CVg) and environmental (CVe) co-efficient of variation, heritability and genetic advance for all the characters have been presented in the Table 2. FL and ECY showed very high heritability together with high CVp and CVg variability values. On the other hand, WML and ERRn showed very high heritability but low CVp and CVg variability values together with CVe variability. Mirhosseini *et al.* (2005) estimated higher heritability of cocoon weight and cocoon shell weight than that of cocoon shell ratio. Singh *et al.* (1994) also showed maximum heritability in single shell weight (80.20%) followed by pupal weight with high heritability.

The estimates of heritability and genetic advance give the heritable portion of variation. Heritability estimate along with genetic gain is more useful than the heritability value alone in predicting the resultant effect for selecting the best individuals (Johnson *et al.* 1955). In the present investigation FL, ERRn, ERRw and ECY expressed the highest genetic advance together with higher heritability which indicated the importance of additive gene effects of these characters (Panse 1957; Rahman 1984). It also suggested a wide range of genetic diversity which could be used in breeding programmes and phenotypic selections of these characters effectively. Rao (1997) reported that the characters such as single shell weight (in bivoltine) and single cocoon weight, single shell weight and filament length (in multivoltine) varieties showed higher values for heritability and genetic advance.

Higher heritability does not always give higher genetic advance as was indicated by Johnson *et al.* (1955). Higher heritability but relatively lower genetic advance was observed for WML, which suggested limited scope for manipulation of this character. These could be due to non-additive gene action which includes dominance and epistasis (Liang and Walter 1968). In such situations, progeny testing and recurrent selection might be helpful to improve these traits (Rahman 1984; Rao 1997; Ahsan *et al.* 2000; Ahsan and Rahman 2008). Sen *et al.* (1995) demonstrated high heritability and moderate genetic advance for larval weight and single cocoon weight in multivoltine silkworms. Reza and Rahman (1996) found a non-additive component of genetic variation as an important feature of some larval and cocoon characters in *B. mori.*

Estimated phenotypic (r_p) and genotypic (r_g) correlations between all pairs of characters are shown in Table 3. In general, r_g values were greater in magnitude than r_p ones. These low r_p values could be due to a modifying effect of environments of the association of characters at genotypic level (Rahman 1984). Similar results were also reported by Ahsan and Rahman (2000).

Most of the characters under study showed positive significant correlation to each other except ERRn and ERRw at phenotypic level. Shamachary *et al.* (1980) found significant positive correlations of MLW with cocoon weight and shell weight in *B. mori*. Mistri and Jayaswal (1992) found high significant positive correlation between shell weight and cocoon weight and shell weight and pupal weight in both sexes in *B. mori.* Singh *et al.* (1994) reported the same results between shell weight and fecundity. Chatterjee and Pradeep (2003) investigated the relationship between yield potential and molecular markers in silkworm. Genetic parameters and character association of the present study are suggestive of the inherent association of the characters to each other, especially WML, FL and ECY, and thus implying prime importance to include them in selection programmes for genetic gain in *B. mori.*

Table 1. Preliminary statistics and components of variance of different characters in the experimental hybrids of *B. mori*.

Characters	Range	Mean ± SE	MS	δ^2p	δ^2g	δ^2e
WML	29-45.5	35.86 ± 0.41	37.33***	12.61	12.36	0.26
ERRn	37.72-98.87	76.78 ± 0.71	802.86***	268.13	267.37	0.77
ERRw	15.89-147.41	123.67 ± 7.94	955.23***	381.43	286.90	94.53
FL	328-1044	633.64 ± 27.92	95859.36***	32732.74	31563.31	1169.44
ECY	13.29-44.68	30.47 ± 0.85	241.45***	81.20	80.13	1.07

WML= weight of mature larvae, ERRn= effective rate of rearing by number, ERRw= effective rate of rearing by weight, FL= filament length, ECY= estimated cocoon yield per 100 dfls; ***= P<0.001; δ^2p= phenotypic variance; δ^2g= genotypic variance; δ^2e= environmental variance.

Table 2. Phenotypic (CVp), genotypic (CVg) and environmental (CVe) coefficient of variation, heritability (Hb), genetic advance (GA) and genetic advance as percentage of the mean (GA%) values for different characters of *B. mori* hybrids.

Characters	CVp	CVg	CVe	Hb	GA	GA%
WML	0.73	0.72	0.103	97.97	7.17	1.47
ERRn	3.35	3.34	0.18	99.71	33.64	6.87
ERRw	3.99	3.46	1.99	75.22	30.26	6.18
FL	36.97	36.30	6.99	96.43	359.38	73.44
ECY	29.57	29.38	3.40	98.68	18.32	60.12

WML= weight of mature larvae, ERRn= effective rate of rearing by number, ERRw= effective rate of rearing by weight, FL= filament length, ECY= estimated cocoon yield per 100 dfls.

Table 3. Phenotypic (r_p) and genotypic (r_g) correlation coefficients between all pairs of characters of *B. mori* hybrids.

Variables		WML	ERRn	ERRw	FL
ERRn	r_p	0.423*			
	r_g	0.431*			
ERRw	r_p	0.469**	0.291ns		
	r_g	0.549***	0.341*		
FL	r_p	0.55***	0.688***	0.418*	
	r_g	0.565***	0.702***	0.508**	
ECY	r_p	0.612***	0.947***	0.438**	0.779***
	r_g	0.622***	0.954***	0.513**	0.803***

WML= weight of mature larvae, ERRn= effective rate of rearing by number, ERRw= effective rate of rearing by weight, FL= filament length, ECY= estimated cocoon yield per 100 dfls; *= P<0.05; **= P<0.01; ***= P<0.001; ns= not significant.

Conclusion

Genetic variability, heritability and correlation analyses for important economic characters such as WML, ERRn, ERRw, FL and ECY in 35 hybrids *B. mori* L. revealed that most of the characters showed positive significant correlation to each other except ERRn and ERRw at phenotypic level. Therefore, proper attention should be given to these characters, especially WML, FL and ECY, in selection programmes for genetic gain in the mulberry silkworm.

References

Ahsan MK, Rahman SM. 2008. Genetic variability and correlation analysis in hybrids of mulberry silkworm,*Bombyx mori* L. for egg characters Univ. j. zool. Rajshahi Univ. 27,13-16.

Ahsan MK, Rahman SM. 2000. Correlation and path coefficient analysis of some yield contributing characters in hybrids of mulberry silkworm, *Bombyx mori* L. J. Asiat.Soc. Bangladesh, Sci. 26(2), 197-202.

Ahsan MK, Rahman SM, Ali IA. 2000. Variability of some quantitative traits in the hybrids of silkworm, *Bombyx mori* L. Univ. j. zool. Rajshahi Univ. 19, 20-24.

Burton GW. 1952. Quantitative inheritance in grass. Proc. 6th Inter. Grassland Cong. 1, 277-283.

Burton GW, De Vane EH. 1953. Estimating heritability in tall fescue (*Fescuta arundinacae*) from replicated clonal meteriasa. Agron. J. 45, 579-604.

Chatterjee SN, Pradeep AR. 2003. Molecular markers (RAPD) associated with growth, yield, and origin of the silkworm, *Bombyx mori* L. in India Russian Journal of Genetics. 39(12), 1365-1377.

Comstock RE, Robinson HF. 1952. Estimates of average dominance of genes, "Heterosis". Iowa State College Press, 495-516.

Fisher RA. 1918. The correlation between relatives on the supposition of Mendelian inheritance. Trans. Roy. Soc., Edinb. 52, 399-433.

Fisher RA, Immer FR, Tedin O. 1932. The genetic interpretation of statistics of the 3rd degree in the study of quantitative inheritance. Genetics. 17, 107-124.

Hanson CH, Robinson HF, Comstock RE. 1956. Biometrical studies of yield in segregation populations of Korean lespedeza. Agron. J. 48, 268-272.

Johnson HW, Robinson HF, Comstock RE. 1955. Estimates of genetic and environmental variability in soyabean. Agron. J. 47, 314-318.

Krishnaswami S. 1978. New Technology of silkworm rearing. Central Silk Board, India. 23pp.

Kumaresan P, Sinha RK, Urs SR. 2007. An analysis of genetic variation and divergence in Indian tropical polyvoltine silkworm, *Bombyx mori* L. genotypes Caspian J. Env. Sci. 5(1), 11-17.

Liang GHL, Walter TL. 1968. Heritability estimates and gene effects for agronomic traits in grain sorghum. Crop Sci. 8(1), 77-80.

Lush JL. 1949. Heritability of quantitative characters in farm animals. Heriditas (suppl.). 35, 256-261.

Mather K. 1949. Biometrical genetics. Dover publication, New York.

Mirhosseini SZ, Ghanipoor M, Shadparvar A, Etebari K. 2005. Selection indices for cocoon traits in six commercial silkworm, (*Bombyx mori*) lines. The Philippine agricultural Scientist. 88(3), 328-336.

Mistri PK, Jayaswal KP. 1992. Studies on phenotypic correlations between some economic traits of silkworm, *Bombyx mori* L. Bull. Seric. Res. 3, 26-29.

Panse VG. 1957. Genetics of quantitative characters in relation of plant breeding. Indian J. Genet. 17, 318-324.

Rahman SM. 1983. Technology of mulberry silkworm rearing suitable for the climatic condition in Bangladesh. Reshom 1,71-79.

Rahman SM. 1984. Studies on the genetic improvement of eri silkworm, *Philosamia ricini*. Boisd of Bangladesh. Ph.D thesis, Department of Zoology, Rajshahi University. 419pp.

Rao PRT. 1997. Genetic architecture and gene action in *Bombyx mori* L. Ph.D thesis , Department of Zoology, University of North Bengal, Darjeeling-734430, India. 191pp.

Reza AMS, Rahman SM. 1996. The genetic variability, heritability and genetic advance in silkworm, *Bombyx mori* L. Bangladesh J. Agri. 21, 1-6.

Reza AMS, Rahman SM. 2005. Genetic parameters of some yield and yield contributing traits in silkworm, *Bombyx mori* L. Univ. j. zool. Rajshahi Univ. 24, 55-58.

Robinson HF, Comstock RE, Harvey PH. 1949.Estimates of heritability and the degree of dominance in corn. Agron. J. 41, 353-359.

Sen SK, Das SK, Rao PRT, Ghosh B, Das NK, Chattopadhyay S, Roy GS, Sinha SS. 1995. Studies on some important genetic parameters in silkworm, *Bombyx mori* L. Indian J. Genet. 55(3), 238-242.

Shamachary M, Samson V, Krishnaswami S. 1980. Some useful correlation studies of silkworm and its products such as cocoon, pupa, shell and egg weight. Indian J. Seric. 19, 4-8.

Singh T, Chandrashekharaiah, Samwo MV. 1994. Selection strategies in relation to correlation and heritability in the silkworm, *Bombyx mori* L. Bull. Seric. Res. 5, 37-41.

Weight S. 1935. The analysis of variance and correlation relatives with respect to deviations from an optimum. J. Genet. 30, 243-256.

Zhao Y, Chen K, He S. 2007. Key principles for breeding spring-and-autumn using silkworm varieties: from our experience of breeding 873×874. Caspian J. Env. Sci. 5(1), 57-61.

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