

STUDIES ON SOME IMPORTANT GENETIC PARAMETERS IN SILKWORM (*BOMBYX MORI* L.)

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ABSTRACT

A study on genetic variability was made with 5 x 5 diallel of genetically divergent multivoltine lines to determine the importance of quantitative traits of mulberry silkworm, *Bombyx mori* L. Data were collected from rearings made during four commercial seasons of West Bengal. The study of phenotypic and genotypic variation, coefficient of variation, heritability and genetic advance for 10 quantitative traits indicated additive and nonadditive effects of genes which facilitates selection for the amelioration of breeds.

Key words: Genotypic and phenotypic variation, heritability, genetic advance,
Bombyx mori L.

Studies on genotypic and phenotypic variability, heritability and genetic advance play an important role in planning the selection scheme for the improvement of economically important traits in plants and animals as well. Extensive review, on the agreement between estimated and realised genetic parameters has been made on various animals, which showed difference between the realised and estimated genetic parameters. Further, accuracy of selection index can be improved by considering the realised heritability estimate and depending on the selection response, the traits can also be adjusted [1, 2]. Heritability estimates have been worked out on the hoarding of sugar syrup in honey bee using cumulative selection differential and a considerable gain has been achieved [3]. In tasar silkworm, *Antheraea mylitta* D. genotypic and phenotypic variability and correlations, heritability (broad and narrow sense) genetic advance, environmental effects etc., have been reported earlier [4-6]. In mulberry silkworm, *Bombyx mori* L., some authors [7-9] have estimated a few of the above parameters sporadically. Narasimharaju et al. [10] worked extensively on genetic variability in different types of hybrids only.

The present study, has been undertaken to understand the nature and extent of phenotypic and genotypic variability, heritability (broad sense) and genetic advance of

10 quantitative traits in 5 multivoltine silkworm breeds and their possible hybrids for adopting a suitable selection criterion for further improvement through breeding.

MATERIALS AND METHODS

The genetic divergence of multivoltine silkworm parental stock of this institute was measured by using Mahalanobis' D^2 statistics [11]. The breeds were grouped into 5 clusters. Five multivoltine breeds, Nistari, Raj, CB5, G and B, one from each cluster, were selected and crossed in 5 x 5 diallel. Rearings were conducted during two favourable (Falgooni and Agrahayani) and two unfavourable (Jaistha and Bhaduri) commercial rearing seasons of West Bengal as per the standard schedule. Data were collected on 10 quantitative traits of economic importance (Table 1).

The phenotypic and genotypic variance and coefficient of variation were calculated following Burton and De Vane [12]. Heritability in broad sense was estimated as per the formula given by Lush [13] and Allard [14], ($h^2 = \sigma_g^2 / \sigma_p^2$). The genetic advance (percentage of mean) was worked out using the method of [15].

RESULTS AND DISCUSSION

The mean, range, standard error, CD and SD for different traits are presented in Table 1. Analysis of variance (ANOVA) revealed that the pure breeds or hybrids were significant for all traits ($P \geq 0.01$). The maximum range was found in shell weight, followed

Table 1. Phenotypic variability of ten traits in silkworm

Trait	Range	Mean	SE	CD, 5%	S.D.
Fecundity (No.)	367.0 - 472.7	420.6	5.76	33.4	28.8
Hatching (%)	90.3 - 96.5	93.8	0.31	3.0	1.6
Larval period (days)	21.0 - 22.2	21.4	0.06	0.2	0.3
Weight of 10 mature larvae (g)	20.2 - 31.7	27.4	0.53	1.1	2.7
Survival (%)	78.0 - 93.4	87.1	0.87	5.0	4.3
Yield / 10,000 larvae (kg)	8.0 - 12.1	10.3	0.20	0.7	1.0
Single-cocoon wt. (g)	0.9 - 1.4	1.2	0.03	0.1	0.1
Single-shell wt. (g)	0.1 - 0.2	0.2	0.00	0.0	0.0
Cocoon-shell ratio	13.2 - 15.9	15.0	0.12	0.5	0.7
Filament length (m)	412.5 - 691.2	573.1	15.61	55.3	78.1

by filament length and cocoon weight, and minimum for larval period and hatching percentage. Phenotypic and genotypic variabilities, heritability and genetic advance of different traits are presented in Table 2.

Table 2. Estimates of phenotypic and genotypic variability, heritability and genetic advance in silkworm

Trait	Variance		PCV	GCV	Heritability (%)	G.A. (%)
	phenotypic	genotypic				
Fecundity	4030	2881	15.1	12.8	71.5	22.2
Hatching	14.5	5.4	4.1	2.5	37.2	3.1
Larval period	0.4	0.4	3.0	2.9	88.9	5.6
Weight of larvae	30.0	28.9	20.0	19.6	96.3	39.6
Survival	90.8	65.1	11.0	9.3	71.7	16.2
Yield/10,000 larvae	4.2	3.7	19.9	18.7	88.0	36.2
Single-cocoon wt.	0.08	0.17	23.4	22.9	95.5	46.1
Single-shell wt.	0.00	0.00	30.2	29.5	95.9	59.6
Cocoon-shell ratio	2.1	1.8	9.6	8.9	86.2	17.1
Filament length	26971	23824	28.7	26.9	88.3	52.1

The difference between phenotypic and genotypic variances was highest for hatching percentage, depicting maximum environmental influence. Minimum differences were observed in most of the economic traits except survival and fecundity, indicating less environmental effect. The phenotypic and genotypic coefficients of variations (PCV, GCV) were lowest in larval period and highest in single-shell weight, followed by filament length and single-cocoon weight. The PCV was higher than GCV for all the traits. The difference between them was less for hatching percentage and larval duration.

The heritability expresses the proportion of the total variance that is attributable to the average effect of genes and determines the degree of resemblance between relatives [15]. With the exception of hatching percentage, broad sense heritability was high for all the traits and ranged from 71.5% (fecundity) to 96.2% (larval period) (Table 2). Therefore, the reliability of selection through phenotypic values of these traits is high. Heritability alone is not enough to describe the additive and nonadditive gene action for selection criterion. For this, estimation of genetic advance, in addition to heritability, is important. The observed genetic advance (GA) was high for shell weight (59.6%), filament length (52.1%), cocoon weight (46.1%), larval period (39.6%) and E.R.R. wt. (36.1%). For other traits GA was low in the range of 3.1% (hatching %) and 22.2% (fecundity).

It can be concluded from the above observations that mature larval wt., E.R.R. wt., cocoon wt., shell wt. and filament length, for which heritability as well as GA were high, are the traits governed by additive gene action, suggesting high selection value for these traits which can be improved through mass selection [16]. The other traits, except hatching percentage, have high heritability but low in genetic advance indicating prevalence of nonadditive gene actions. As such, progeny/family testing is to be practised for the improvement of these traits.

REFERENCES

1. A. K. Sheridan. 1988. Agreement between estimated and realised genetic parameters. *Animal Breed. Abstr.*, **58**: 877-889.
2. H. W. Johnson, H. F. Robinson and R. E. Comstock. 1955. Estimates of genetic and environmental variability in soyabean. *Agron. J.*, **47**: 314-418.
3. Anita M. Collins. 1986. Quantitative genetics. *In: Bee Genetics and Breeding* (eds. Thomas E. Rinderer). Academic Press, Inc., New York.
4. S. K. Sen, A. K. Sengupta and M. S. Jolly. 1976. Studies on genetic variability, correlation and path coefficient analysis, discriminate function in *A. mylitta* D. *Indian J. Seric.*, **15**: 9-14.
5. A. A. Siddiqui, A. K. Sengupta and K. Sengupta. 1985. Variability and correlation studies of shell weight and their contributing traits in *A. mylitta* D. *Sericologia*, **25**: 45-50.
6. A. A. Siddiqui, A. K. Sengupta, Ajit Kumar and K. Sengupta. 1988. Genotypic and phenotypic variability of some quantitative characters in *Antheraea mylitta* D. *Sericologia*, **28**: 187-192.
7. T. Gamo and T. Hirabayashi. 1983. Genetic analysis of growth rate, pupation rate and some quantitative characters by diallel cross in the silkworm, *Bombyx mori* L. *Japan J. Breed.*, **33**: 191-194.
8. S. B. Satenahalli, R. Govindan and J. V. Goud. 1990. Studies on gene action for some quantitative traits in silkworm, *Bombyx mori* L. *Entomon*, **15**: 227-230.
9. A. Sarkar, N. K. Das and B. C. Das. 1991. A diallel cross analysis of the cocoon weight in the silkworm, *Bombyx mori* L. *Sericologia*, **31**: 301-306.

10. R. Narasimharaju, R. Govindan, J. Asoka and S. G. Rayar. 1990. Genetic variability for quantitative traits in silkworm, *Bombyx mori* L. *Entomon*, **15**: 197–201.
11. G. Subba Rao, S. K. Das and N. K. Das. 1991. Genetic divergence among 15 multivoltine genetic stocks of silkworm, *Bombyx mori* L. *Indian J. Seric.*, **30**: 72–74.
12. G. W. Burton and E. M. De Vane. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478–481.
13. J. L. Lush. 1949. *Animal Breeding Plans* (3rd edn.). The Collegiate Press, Iowa, U.S.A.
14. R. W. Allard. 1960. *Principles of Plant Breeding*. John Wiley and Sons, New York, U.S.A.: 485.
15. D. S. Falconer. 1981. *Introduction to Quantitative Genetics* (2nd edn.). Longman, London: 281.
16. V. G. Panse. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet.*, **17**: 318–328.