Indian J. Genet., 72(1): 97-99 (2012)

Short Communication

Genetic variability and heritability of a few quantitative characters in *Antheraea assamensis* helfer - an indigenous Indian silkworm

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(Received: November 2011; Revised: January 2012; Accepted: February 2012)

The estimation of heritability of important economic traits is regarded as one of the quickest means to get an insight into the depth of gene environment interactions. The genetic mechanism involved in the expression of various traits in *Bombyx mori* pure races and hybrids were studied through heritability studies by several workers [1-4]. The genotypic and phenotypic variability have been studied in some quantitative traits in tasar silkworms [5, 6]. Systematic breeding efforts on muga silkworm, *Antheraea assamensis* Helfer have so far been neglected. For starting any improvement breeding work, information about the genetic variability in the population is a prerequisite. Hence, an attempt was made to estimate genetic variability, heritability, genetic advance and correlation of a few traits in the available germplasm of muga silkworm.

Eight biotypes of muga silkworm namely, Aa-SD, Aa-Blue, Aa-MM, Aa-GA, Aa-TM, Aa-IM, Aa-KA and Aa-SM were collected from the germplasm bank of the Central Muga Eri Research and Training Institute, Lahdoigarh, Jorhat (India) for the present study. The experimental materials were arranged in a randomised block design with four replications each. Each replication was represented by the eggs laid by individual gravid mother moths. Disease free layings (dfl) were prepared in the grainage of the Institute and incubated in the BOD at 25±1^{o}C. The eggs hatched after 8 to 9 days of oviposition. A few tender twigs of 'som' *Persea bombycina* were placed on the newly hatched larvae and after 3-4 hours of feeding in indoor, the twigs with the worms were shifted in outdoor on the foliages of Som. The rearing was conducted on the foliages of Som in outdoor under nylon net cover till maturity by following standard rearing technology in the experimental field of the Central Muga Eri Research and Training Institute, Lahdoigarh, Jorhat (India). The matured larvae were picked up and put in the bundle of dry twigs kept in cocooning bags for spinning inside the cocooning room. It completed the pupation inside the cocoon within 5-7 days in summer and 12-15 days in winter. Cocoons were harvested after full pupation. The important yield contributing characters *viz.,* fecundity, hatching percentage, number of cocoons per dfl, effective rate of rearing (ERR %), average cocoon weight, single cocoon shell weight, single cocoon filament length were recorded. The experimental data were collected between November, 2010 and June, 2011. The heritability (broad sense) and correlation of the yield contributing parameters were worked by following the method of Singh and Chowdhary [7] and Falconer [8].

The analysis of variance revealed significant differences among the biotypes in all the important economic characters studied. The existence of genetic variability in the economic characters indicated the scope for improvement of the population for these characters.

The components of genetic variation such as variances of genotype and phenotype together with their coefficient of variation, heritability (h^2 in broad sense)

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Online management by indianjournals.com

and genetic advancement are presented in Table 1. The single cocoon shell weight in the female showed highest Phenotypic Coefficient of Variation (PCV)% (19.252%) and Genotypic Coefficient of Variation (GCV)% (20.795%) and high estimated heritability (86%) followed by cocoon shell weight of the male with PCV% (13.669%), GCV% (15.890%) and heritability (67%) and fecundity with PCV% (10.282%), GCV% (10.695%) and highest heritability (92%). The GCV was near to PCV for most of the characters, indicating a highly significant effect of genotype on phenotypic expression with very little effect of environment. In the present study, heritability of the different characters ranged from 0.63 (number of cocoons per dfl) to 0.93 (male cocoon weight). High heritability estimates indicated the presence of large number of fixable additive factors and hence these characters may be improved by selection

The effectiveness of selection depends upon genetic advance along with heritability of the character to be improved. In the present study, high heritability along with medium to high genetic advance and high GCV attributable to the predominance of additive gene action was noticed for fecundity, female cocoon shell weight, male cocoon weight, male cocoon shell weight and filament length which indicates that selection based on these characters will be highly effective which is in conformity with the observations made in *Bombyx mori L.* [3, 9]. High heritability along with low genetic advance which is due to non-additive gene action (dominance and epistasis) for female cocoon weight and ERR was recorded in the present study. These indicated that selection for these characters will be less effective. However in such cases, progeny testing and recurrent selection would be helpful to improve these characters [10]. High heritability and moderate genetic advance was demonstrated for larval weight and single cocoon weight in multivoltine silkworms [11].

It is observed that genotypic correlations (r_g) are generally higher than the phenotypic correlations (r_p) values in most of the characters (Table 2). The low values of r_p could be attributed to the modifying effect of environments in the association of characters at the genotypic level. Fecundity showed significant positive correlation with number of cocoons per dfl and female cocoon weight while negative correlation with ERR which indicated that simultaneous selection of fecundity and cocoon weight would be effective for improvement of cocoon yield. Hatching percentage exhibited significant positive correlation with number of cocoons per dfl. Significant positive correlations were observed between the characters, number of cocoons per dfl and ERR. Female and male cocoon weights were found to have significant positive correlation with shell weight and filament length. Cocoon shell weight of both sexes showed significant positive correlation with filament length. Thus for improvement of filament length, cocoon weight and shell weight should be simultaneously selected.

It is concluded from the present study that for improvement of the muga silkworm *Antheraea assamensis* Helfer, simple phenotypic selection based on the characters fecundity, female cocoon shell weight, male cocoon shell weight and filament length will be highly effective. Progeny testing and recurrent selection will be an effective means to improve cocoon weight and ERR.

Table 1. Components of genetic variability in respect of 9 characters in muga silkworm*, A. assamensis*

Parameters	Genotypic variance	Phenotypic variance	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (Broad sense)	Genetic advance as % of mean
Fecundity	250.71	271.27	9.314	9.688	0.92	17.32
Hatching %	18.77	29.2	6.184	7.713	0.64	8.01
Cocoons per dfl	45.09	71.58	7.143	9.00	0.63	9.57
E.R.R. %	32.69	42.51	7.243	8.259	0.77	10.60
Female Cocoon weight	0.105	0.115	4.635	4.851	0.91	8.19
Female shell weight	0.012	0.014	19.218	20.758	0.86	31.38
Male Cocoon weight	0.093	0.10	6.946	7.203	0.93	11.40
Male Cocoon shell weight	0.0037	0.005	19.218	20.758	0.74	20.78
Filament length	1788.95	2650.87	12.331	15.018	0.67	17.34

Table 2. Genotypic and phenotypic co-relation of the different traits in Muga silkworm

Characters		Hatching%	No. of cocoon/ dfl	ERR%	Female cocoon weight	Female shell weight	Male cocoon weight	Male shell weight	Filament length
Fecundity	r_p	-0.07	0.75*	-0.78*	0.78*	0.07	0.37	0.54	0.40
	r_g	0.39	0.845**	-0.89**	0.837**	0.08	0.40	0.66	0.54
Hatching%	r_p		0.74*	0.24	0.23	0.24	0.50	0.26	0.38
	r_g		0.85**	0.25	0.29	0.39	0.61	0.27	0.56
No. of cocoon/dfl	r_p			0.77*	-0.16	-0.072	0.33	0.29	0.27
	r_g			0.75*	-0.15	-0.004	0.42	0.40	0.43
ERR%	r_p				-0.38	-0.42	-0.65	-0.71	-0.64
	r_g				-0.42	-0.48	-0.76*	-0.89**	-0.92**
Female cocoon weight	r_p					0.78*	0.363	-0.24	0.32
	r_g					0.74*	0.374	0.25	0.37
Female shell weight	r_p						0.675	-0.75*	0.77*
	r_g						0.757*	0.83*	0.84**
Male cocoon weight	r_p							0.82*	0.832*
	r_g							0.84**	0.905**
Male shell weight	r_p								0.765*
	r_g								0.842**

r_p : phenotypic; *Significant at 1% level; r_g : genotypic; **Significant at 5% level

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