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ESTIMATES OF GENETIC VARIABILITY FOR COMMERCIAL QUANTITATIVE TRAITS AND SELECTION INDICES IN BIVOLTINE RACES OF MULBERRY SILKWORM (*BOMBYX MORI* L.)

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ABSTRACT

Genetic variability for economically important quantitative traits and selection indices of 46 bivoltine races of mulberry silkworm (*Bombyx mori* L.) were estimated. High values of heritability along with genotypic and phenotypic coefficient of variations for filament length, single-shell weight and single- cocoon weight showed that the above characters are under genetic control. The correlations between single-cocoon weight and single shell weight as well as single-shell weight and shell ratio were highly significant. The selection index programme based on discriminant function analysis resulted into five clusters of 10 genotypes with lower index values for utilisation in hybridization and breeding programmes.

Key words: Genetic variability, quantitative traits, selection index, mulberry silkworm.

Silkworm (*Bombyx mori* L.) an economically important sericegenous insect is considered to be a good and convenient model system for genetical studies in the field of genetics and molecular biology [1, 2]. Studies on the quantitative traits of economic value and estimation of their genetic values are of great importance in silkworm for planning a purposeful breeding programme for improving yield potential as well as silk fibre quality. In silkworms, the characters, effective rate of rearing (%), single cocoon weight, single shell weight, shell ratio (%), and filament length are of economic significance. Using the line x tester [3] and diallel analyses [4], combining ability studies in silkworm races have been carried out but much remains to be done for improving and stabilizing production by developing new high yielding stable silkworm breeds and hybrids for tropical, subtropical and temperate sericultural zones. The theory of selection indices is helpful for combining various attributes in such a fashion that selection on the basis of resulting index gives the best possible economic gain at the genetic level [5, 6]. A large number of selection indices have been worked out in different agricultural crops but such studies are lacking in mulberry silkworm.

Hence the present investigation has been undertaken to study the genetic variability of quantitative traits and the selection indices of the silkworm genotypes for quantitative and qualitative improvement of silk yield.

MATERIALS AND METHODS

Forty six bivoltine mulberry silkworm races collected from different regions were used. These races were maintained in the Germplasm Bank of the Regional Sericultural Research Station, Kalimpong, West Bengal. The experiment was conducted in completely randomized block design (three replications of 200 worms each) and observations were recorded on quantitative traits of commercial value, such as, effective rate of rearing (%), single-cocoon weight (g), single-shell weight (g), shell ratio (%), and filament length (m). The standard rearing techniques of Krishnaswami [7] was followed. The effective rate of rearing was calculated by using the following formula:

$$\text{Effective rate of rearing (\%)} = \frac{\text{No. of good cocoons harvested}}{\text{No. of worms}} \times 100$$

On seventh day after spinning, the cocoons were harvested from each replication and divided into two parts. From one part, 50 cocoons were randomly selected for the analysis of filament length, and from the other part 100 cocoons were randomly used for sex separation. After sex separation, cocoon assessment was done with 25 male and 25 female cocoons in a Sortorious Interphase Balance (German Model: Type YDI 50Z) to determine average single-cocoon weight, single-shell weight and shell ratio. The data were subjected to analysis of variance, estimation of genotypic and phenotypic variance, and coefficients of variation (GCV, PCV). Heritability was analysed as per Singh and Chaudhary [8]. The correlation coefficients (Pearson's correlation coefficient) between the traits and selection indices of genotypes were computed in IBM PC/AT computer using the packages [9, 10] developed by International Maize and Wheat Improvement Centre (CIMMYT). The selection index programme was used to values of indices Z by the following formula:

$$\text{Index} = [(Yj-Mj)^2 * Ij] + [(Yi-Mi)^2 * Ii + \ldots + [(Yn-Mn)^2 * In]^{1/2}$$

where Yj . . . n—variable in Z units, Mj . . . n—selection objective, and Ij . . . n—selection intensity for traits j, i, . . . n.

$$Z = \frac{Yj - \bar{Y}}{S}$$

where Yj—value for the entry of j, $\bar{Y}$—mean of all entries, and S—standard deviation from the group mean.

RESULTS AND DISCUSSIONS

The analysis of variance (Table 1) showed highly significant difference for all the five commercial characters under study. Further, coefficients of variations (CV) for all these characters (Table 2) were in the range of 5.83–8.45, which confirms the reliability of the experiment as advocated by Gomez and Gomez [11]. The mean, range, phenotypic and genotypic variances, GCV and PCV for quantitative traits together with their heritability values are presented in Table 3. Filament length showed higher PCV and GCV and maximum heritability, followed by single-shell weight and single-cocoon weight. The genetic correlation studies (Table 4) revealed highly significant positive correlation coefficients between single-cocoon weight and shell weight (r = 0.55), as well as shell weight and shell ratio (r = 0.70). Very low nonsignificant correlation was observed between filament length and other traits except shell ratio. The effective rate of rearing showed significant negative correlation to single-cocoon weight, single-shell weight and shell ratio. This suggests that increase in the effective rate of rearing may decrease silk output.

For assigning the selection intensities, it is essential to consider the relative heritability of variables and correlation between them [12–14]. Since filament

Table 1. ANOVA for five commercial traits of bivoltine silkworm

Source	d.f.	Effective rate of rearing			Single-cocoon weight			Single-shell weight			Shell ratio			Filament length		
		S.S.	M.S.	F	S.S.	M.S.	F	S.S.	M.S.	F	S.S.	M.S.	F	S.S.	M.S.	F
Genotypes	45	4595.5	102.1	2.67**	3.95	0.09	7.12**	0.267	0.06	7.19**	235.9	5.24	2.05**	1817975.5	40399.5	13.5**
Experimental error	92	3512.7	38.2		1.13	0.01		0.076	0.001		234.7	2.55		275282.0	2992.2	
Total	137	8108.1			5.09			0.344			470.6			2093257.5		

**Significant at 1% level.

Table 2 Mean performances of 46 bivoltine mulberry silkworm races

Genotype	Effective rate of rearing (%)	Single-cocoon wt. (g)	Single-shell wt (g)	Shell ratio (%)	Filament length (m)
KPG-A	85.0	1.76	0.37	21.4	975.7
KPG-B	88.7	2.10	0.46	21.9	1158.7
KPG-SL	92.7	2.12	0.41	19.7	905.3
A	94.3	2.09	0.40	19.1	1073.0
B	84.3	2.12	0.43	20.2	1070.0
C	91.3	1.93	0.35	18.3	887.0
D	94.7	1.97	0.35	17.9	1007.3
P 49	94.0	1.72	0.31	17.2	780.3
P 327	93.3	1.78	0.29	16.0	914.0
P 316	95.0	1.89	0.32	17.2	926.7
BR3R122	95.7	1.84	0.36	19.0	994.0
AR3R1-21	96.3	1.80	0.35	19.4	936.0
AR3R1-17	93.7	1.74	0.31	17.9	785.3
CHANGNANG	95.3	1.71	0.29	17.1	858.3
TOKAI	84.7	2.00	0.45	22.6	945.7
P 5	86.3	2.02	0.38	19.0	945.7
HOWLAK-J	86.7	2.03	0.35	17.1	917.0
C 108	92.3	2.03	0.36	18.1	972.3
NB4D2	94.0	2.05	0.39	19.5	960.7
J 122	90.0	1.80	0.31	18.6	1043.7
JAM-21	83.3	2.13	0.40	18.8	864.3
YS-3	85.0	1.95	0.37	19.0	944.3
NB-18	86.0	2.26	0.46	20.4	1084.0
K.S. (O)	83.7	2.02	0.38	19.1	891.0
SHEKAI	89.0	1.73	0.35	20.3	1324.7
P 8	90.7	2.14	0.41	19.3	803.7
P 7	89.7	2.11	0.39	18.6	995.0
NB3C1	83.7	1.90	0.35	18.5	945.3
ZEBRA-SL	87.3	2.03	0.39	18.2	911.3
SH-6	87.3	1.73	0.32	19.2	1087.3
AZERBAIJAN	88.0	1.90	0.37	19.6	950.7
9 x 10 (C)	63.0	2.19	0.41	18.7	887.0
B. WHITE	86.3	2.03	0.39	19.2	1039.0
JAM-2	93.3	2.28	0.40	17.8	990.0

(Contd.)

Table 2. (contd.)

Genotype	Effective rate of rearing (%)	Single-cocoon wt. (g)	Single-shell wt (g)	Shell ratio (%)	Filament length (m)
J2C3	82.7	2.84	0.32	17.6	995.0
JD-6	90.7	1.65	0.30	18.6	1100.0
S 164	91.3	1.77	0.35	19.7	802.3
OKUSA	88.3	2.17	0.42	19.3	762.7
SF-19	95.7	1.96	0.39	19.8	1014.3
J 112	92.7	1.80	0.34	18.4	969.3
SHEKAI-2	88.7	2.06	0.36	17.7	838.3
SF-17	94.0	2.16	0.38	17.9	831.7
N124C124	93.0	1.78	0.28	15.7	815.7
K.S. (CONS)	82.0	2.04	0.40	19.7	795.0
N 134	93.0	1.63	0.31	19.2	876.7
BL-1	80.0	2.00	0.38	19.3	699.7
S.E ± M	4.4	0.08	0.02	1.1	38.7
CD (P = 0.05)	8.7	0.16	0.04	2.2	76.8
CV	6.9	5.68	7.79	8.5	5.8

length showed higher heritability and positive correlation with shell ratio and also has major contribution in silk fibre yield [12], it is desired to put greater selection pressure for this trait. Cocoon characters like single-cocoon weight and single-shell weight showed higher heritability and higher correlation between each other and therefore these traits should be

Table 3. Mean, variability and heritability of economically important quantitative traits in mulberry silkworm

Character	Range	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (in broad sense)
Effective rate of rearing (%)	63.0–96.3	130.8	92.6	12.8	10.8	0.71
Single-cocoon weight (g)	1.63–2.84	0.10	0.08	15.9	14.9	0.87
Single-shell weight (g)	0.28–0.46	0.01	0.01	21.9	20.5	0.87
Shell ratio (%)	15.7–22.6	7.15	4.61	14.1	11.3	0.64
Filament Length (m)	699.7–1324.7	42643..6	39651.4	22.0	21.2	0.93

Table 4. Simple correlation coefficient matrix (r) of variables in mulberry silkworm

Characters	Effective rate of rearing	Single cocoon weight	Single shell weight	Shell ratio
Single-cocoon weight	-0.37^{*}			
Single-shell weight	-0.37^{*}	0.55^{**}		
Shell ratio	-0.25^{*}	0.06^{NS}	0.69^{**}	
Filament length	0.06^{NS}	0.01^{NS}	0.14^{NS}	0.35^{*}

*,**Significant at 5% and 1% levels, respectively.

NS—nonsignificant

given higher weightage in selection programmes. Since shell ratio has low heritability but shows positive correlations with single-shell weight and filament length, lower weightage should be given to these traits. Though the effective rate of rearing did not show positive correlation with any of the characters, its relative importance can not be ignored in view of the economic value in cocoon production [12]. Since our aim is to enhance quality as well as quantity in silk production, it is desirable to obtain breeding values for various economic parameters and manipulate them simultaneously through discriminant function analysis by applying the standard selection parameters (Table 5) for all the commercial traits in selection index programme which resulted into five clusters of 10 genotypes having good yielding capacity with higher quality of silk fibre (Table 6). These genotypes, viz. KPG-B, NB-18k, A, B, JAM-2, TOKAI, SF-19, KPG-SL, NB4D2 and P 7, showed relatively low index values (11.3–16.5) in comparison to the remaining 36 genotypes. The index variable represents the Euclidean distance of the set of the variables to the objective desired by the selector [10]. The lower the value of the index, the closer the genotype is likely to be objective to the defined, hence superior.

Table 5. Discription of standard selection parameters applied for variables in selection index programme of mulberry silkworm

Variable	Target	Intensity	Desired target
Effective rate of rearing	3.0	5.0	106.7
Single-cocoon weight	3.0	10.0	2.6
Single-shell weight	3.0	10.0	0.5
Shell ratio	3.0	5.0	22.8
Filament length	3.0	10.0	1289.1

On the basis of Euclidean distances [10] of the variables with respect to the desired objective, five clusters were made. Cluster I had only one genotype (KPG-B) with the lowest index value of 11.3, Cluster II also consisted of one genotype (NB-18) with index value of 12.1. Both these clusters were very close to the selection objective. Further, cluster III

Table 6. Selection indices of selected silkworm races in different clusters and mean performance of five quantitative characteristics

Cluster	Genotype	Index	Quantitative characters				
			effective rate of rearing	single-cocoon weight	single-shell weight	shell ratio	filament length
I	KPG-B	11.3	88.7	2.10	0.46	21.9	1158.7
II	NB-18	12.1	86.0	2.26	0.46	20.3	1084.0
III	A	14.4	94.3	2.09	0.40	19.1	1073.0
	B	14.4	84.3	2.12	0.43	20.2	1070.0
IV	JAM-2	15.4	93.3	2.28	0.40	17.8	990.0
	TOKAI	15.9	84.7	2.00	0.45	22.6	945.7
	SF-19	16.0	99.7	1.96	0.39	19.8	1014.3
V	KPG-SL	16.2	92.7	2.12	0.41	19.7	905.3
	NB4D2	16.3	94.0	2.05	0.39	19.5	960.7
	P 7	16.5	89.7	2.11	0.39	18.6	995.0

included two genotypes (A and B), evolved at the Regional Sericultural Research Station, Pampore (J&K), having similar index values (14.4). The genotypes of these three clusters were evolved in the local temperate conditions, hence it is obvious from their rearing performances that these genotypes are well acclimatized to the temperate conditions and may be reared successfully in the temperate sericultural zones of the country. Cluster IV contained three genotype, i.e. JAM-2, TOKAI and SF-19 with index values ranging from 15.4–16.0 and Cluster V also with three genotypes (KPG-SL, NB4D2 and P 7) showed index range of 16.2–16.5. The genotypes of clusters III to V may be used as good combiners in hybridization. Further, genotypes like TOKAI and KPG-SL showed sex-limited attributes. They may be utilized as male counterparts in commercial (F_1) grainages in tropical zone to minimise the requirement of seed cocoons.

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