

## Estimation of Genetic Parameters for Some Quantitative Traits in Mulberry Silkworm

<sup>1</sup>E. Talebi and <sup>2</sup>G. Subramanya

<sup>1</sup>Faculty of agriculture, Islamic Azad University, Darab Branch, Darab, Fars, Iran

<sup>2</sup>DOS in Sericulture Science, University of Mysore, Manasagangotri, Mysore, India

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**Abstract:** The objective of the present study is to estimate genetic parameters in two bivoltine races; C<sub>108</sub> and NB<sub>4</sub>D<sub>2</sub> and two multivoltine races; Pure Mysore and Nistari. Data were collected during pre-monsoon, monsoon and post-monsoon 2009 by analysing thirteen quantitative traits. Genetic parameters were estimated by varcomp procedure using type 1 method with SAS software. All traits displayed high broad sense heritability (above 50 %) except hatching percentage (17.93 %). Phenotypic correlation estimates between mentioned traits ranged from -0.927 to 0.993.

**Key words:** *Bombyx mori* • Heritability • Phenotypic correlation

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### INTRODUCTION

A great diversity of mulberry silkworm *Bombyx mori* L. exists globally through which several silkworm breeds are evolved by selection or cross breeding. Quantitative genetics help in the studies of the inheritance of polygenic traits among related individuals. In animal population subject to artificial selection, genetic parameters are required to be estimated to formulate breeding plans. Animal and plant breeders need to be able to predict the outcome of artificial selection on traits of economic interest, traits which are undoubtedly affected by many loci and alleles. Statistical analysis is a crucial tool for analyzing genome data and genetic parameters, which are now becoming increasingly available for a variety of species and for giving precise explanations regarding genetic variation in quantitative traits occurring among species, populations, families and individuals. Availability of diverse genetic stock, gives ample choice for the breeder in selection of initial parents of his desire. Heritability is one of the most useful parameters in animal breeding and it is important to know the size of the heritability when planning a breeding program as well as when predicting the response to selection or individuals breeding values [1].

Improving cocoon and silk filament characters is the most important breeding goal. Mirhosseini *et al.* [2] with use of REML procedure found that cocoon weight and shell weight had higher heritability, while the heritability of shell percentage was lower. The highest heritability of cocoon weight and shell weight was observed in 101433

strain (0.73). Heritability of shell percentage in Koming1 was higher than that of the other varieties (0.61). Talebi Esfandarani *et al.* [3] using parental full-sib method demonstrated moderate heritability in respect to cocoon weight, shell weight, pupal weight and shell ratio. Malik *et al.* [4] revealed that the heritability for fecundity, larval weight, yield by weight, yield by number, cocoon weight, shell weight, shell percentage and filament length had ranged from 0.487 to 0.682.

It is important to know if and how much the improvement in one trait will cause simultaneous changes in other traits. The selection of one character is found to result in correlated changes on other economic characters. Heritability ( $h^2$ ) estimates of shell weight is medium to high (0.2-0.7) and has positive genetic correlation with some traits such as cocoon weight, shell percentage, larval weight, filament length, raw silk percentage and egg weight [5-7, 1]. Mirhosseini *et al.* [2] found that among the cocoon traits studied, the best conclusion was observed between cocoon weight and shell weight (0.54-0.95) with 101433 strain showing the highest correlation coefficient. Negative correlation between cocoon weight and cocoon shell percentage was obtained in 107, Koming1 and Y and a positive correlation in the 110, 101433 and Xinhong1 strains. The highest correlation between the above traits belonged to the variety Xinhong1 (0.22). In the studied varieties (except 107), a relatively high positive genetic correlation was observed between shell weight and shell percentage. The highest correlation in the said traits belonged to the variety Koming1 (0.68).

The main objective of this study is to estimate genetic parameters including broad sense heritabilities and phenotypic correlations among thirteen quantitative traits for four silkworm (*Bombyx mori*) races

### MATERIALS AND METHODS

Four silkworm genotypes included two bivoltine; NB<sub>4</sub>D<sub>2</sub> and C<sub>108</sub> and two multivoltine; Nistari and Pure Mysore reared during 2009 in the germplasm bank of the Department of Sericulture Science, University of Mysore, Mysore, India. The rearing was conducted in three seasons viz. pre-monsoon, monsoon and post-monsoon following the method suggested by Krishnaswami [8]. The characteristic features of the four races are shown in Table (1).

Three replicates of three hundred larvae per each season were maintained. Ten fifth instar larvae from each replicate were randomly picked up a day before spinning and their weight were recorded. The larvae were separately left on mountages for spinning and cocoons were harvested. The data pertaining to thirteen metric traits viz., fecundity, hatching percentage, larval weight, larval duration, cocoon yeild/10000 larvae by number, cocoon yeild/10000 larvae by weight, cocoon weight, shell weight, shell ratio, filament length, pupation rate, denier and renditta were recorded following standard procedure. Genetic parameters were estimated based on type 1 model using varcomp procedure with SAS version 9. Heritability estimates were calculated by the following formulae suggested by Al-Jibouri *et al.* [9].

$$\text{Heritability (Broad sense)} = H^2 = \sigma_g^2 / \sigma_p^2$$

where,

$\sigma_g^2$  = genotypic variation

$\sigma_p^2$  = phenotypic variation

Simple correlation coefficients between pairs of characteristics were calculated using the formula:

$$r_{xy} = \frac{\sum [(x-\bar{x})(y-\bar{y})]}{\sqrt{[\sum (x-\bar{x})^2 \sum (y-\bar{y})^2]}}$$

where

$r_{xy}$  = Simple correlation coefficient between characters x and y.

### RESULTS AND DISCUSSION

The mean value ( $\pm$  standard error) of four parental races for thirteen quantitative traits are presented in Table (2). From the table it is evident that the two bivoltine races are superior for productivity traits where as multivoltine are superior for viability traits. The broad sense heritability estimates were calculated for thirteen traits (Table 3). Heritability estimates for fecundity, hatching percentage, larval weight, larval duration, cocoon yeild/10000 larvae by number, cocoon yeild/10000 larvae by weight, cocoon weight, shell weight, shell ratio, filament length, pupation rate, denier and renditta, ranged from 17.93 to 98.44 %. However, the heritability estimates in four races were low for hatching percentage (17.93 %) that it indicated the role of high environmental influence on this trait. The larval duration, cocoon yeild/10000 larvae by number and denier had moderate heritability (67.58, 58.32 and 66.13 %, respectively). The fecundity, larval weight, cocoon yeild/10000 larvae by weight, cocoon weight, shell weight, shell ratio, filament length, pupation rate and renditta showed high heritability.

It is evident that heritability estimates were different in the four races among the thirteen quantitative traits. In the bivoltine race, C<sub>108</sub>, the higher values of broad sense heritability (> 80 %) were seen for the all traits except larval weight, cocoon weight and shell ratio and the heritability estimates for NB<sub>4</sub>D<sub>2</sub> revealed above 80 % for the all traits except fecundity and shell ratio. In the two multivoltine races, the heritability estimates for all thirteen traits in Pure Mysore computed above 80 % and the heritability for Nistari estimated less than 80 % for fecundity, hatching percentage, cocoon yeild/10000 larvae by number, cocoon yeild/10000 larvae by weight, shell ratio, pupation rate, denier and renditta. Falconer [10] stated that high heritability may arise due to the action of additive genes. Talebi and Subramanya [10] reported that the three traits namely cocoon weight, shell weight and filament length indicated GCA/SCA ratio above one thereby demonstrating the additive type of gene action for the inheritance of these traits. Murthy and Subramanya [11] estimated that heritability (broad sense) for cocoon weight, shell weight, shell ratio and filament length ranged from 70-86, 70-81, 81-83, 61-73 percent

Table 1: Characteristic features of four races of silkworm *Bombyx mori*

Races	Voltinism	Larval pattern	Cocoon colour	Cocoon shape
C <sub>108</sub>	Bivoltine	Plain	White	Oval
NB <sub>4</sub> D <sub>2</sub>	Bivoltine	Plain	White	Dumb-bell
Pure Mysore	Multivoltine	Plain	Green	Spindle
Nistari	Multivoltine	Marked	Golden yellow	Oval

Table 2: Mean value±SE of thirteen quantitative traits in four races of silkworm *Bombyx mori*

Races	Season	Fecundity	Hatching %	Larval duration(h)	Larval weight(gm)	Yield by no.	Yield by kg	Cocoon weight(gm)
C <sub>108</sub>	monsoon	506.33±2.60	95.69±0.02	595.00±1.15	3.90±0.05	8880.30±31.30	15.64±0.08	1.75±0.00
	Post -monsoon	491.33±2.40	95.06±0.29	603.33±0.88	3.85±0.24	8650.00±30.60	14.85±0.03	1.70±0.01
	pre-monsoon	473.33±1.76	94.15±0.02	552.00±1.53	3.79± 0.55	8121.00±1.73	14.79±0.08	1.74±0.01
NB <sub>4</sub> D <sub>2</sub>	monsoon	535.7±11.20	96.83±0.04	621.00±0.58	4.27±0.07	9042.30±3.71	16.72±0.06	1.80±0.00
	Post -monsoon	512.00±2.08	94.73±0.06	604.00±1.15	4.19±0.03	8236.70±3.18	15.87±0.05	1.75±0.01
	pre-monsoon	492.67±1.20	95.68±0.03	598.00±1.15	4.06±0.16	8638.70±1.76	14.70±0.03	1.75±0.00
Pure Mysore	monsoon	465.33±1.20	96.72±0.05	622.67±1.86	2.07±0.02	9795.70±0.33	10.75±0.06	1.03±0.00
	Post -monsoon	460.67±0.88	96.69±0.03	622.67±0.88	2.06±0.05	9675.00±12.50	10.89±0.02	0.91±0.00
	pre-monsoon	472.33±0.88	95.33±0.02	619.33±0.88	1.72±0.09	9561.00±3.79	10.24±0.02	0.88±0.00
Nistari	monsoon	409.33±3.84	94.11±0.93	517.00±0.58	3.03±0.14	9512.00±57.80	13.18±0.10	1.23±0.00
	Post -monsoon	405.67±3.76	94.47±0.30	547.00±8.50	2.97±0.23	9368.00±54.90	12.51±0.26	1.14±0.02
	pre-monsoon	396.33±2.73	93.28±0.16	511.00±1.15	2.82±0.14	9322.70±53.40	12.72±0.12	1.07±0.01

Cont.

Races	Season	Shell weight(gm)	Shell ratio	Filament length(m)	Pupation rate	Denier	Renditta
C <sub>108</sub>	monsoon	0.34±0.00	19.49±0.05	982.33±4.06	85.73±0.06	2.68±0.02	8.32±0.03
	Post -monsoon	0.32±0.00	18.56±0.21	938.67±9.84	85.10±0.08	2.47±0.05	8.45±0.02
	pre-monsoon	0.34±0.00	19.40±0.26	877.70±17.00	82.61±0.11	2.25±0.01	7.88±0.04
NB <sub>4</sub> D <sub>2</sub>	monsoon	0.38±0.00	20.91±0.41	1024.30±2.91	87.54±0.17	2.56±0.01	7.86±0.03
	Post -monsoon	0.36±0.00	20.68±0.15	1006.30±2.60	82.89±0.03	2.45±0.01	8.28±0.02
	pre-monsoon	0.35±0.00	20.04±0.05	982.67±3.53	80.73±0.06	2.69±0.03	8.91±0.04
Pure Mysore	monsoon	0.14±0.00	13.31±0.06	425.00±1.53	95.94±0.01	1.89±0.02	11.13±0.03
	Post -monsoon	0.12±0.00	12.60±0.06	391.00±2.89	94.71±0.07	1.66±0.01	11.29±0.04
	pre-monsoon	0.10±0.00	11.74±0.14	390.67±2.03	93.64±0.01	1.76±0.03	12.84±0.06
Nistari	monsoon	0.19±0.00	15.04±0.28	457.00±3.46	97.18±0.29	1.71±0.01	13.54±0.36
	Post -monsoon	0.16±0.00	13.81±0.38	428.00±2.31	96.21±0.12	1.86±0.01	12.95±0.15
	pre-monsoon	0.13±0.00	12.48±0.73	422.00±4.04	95.93±0.06	1.77±0.06	13.55±0.23

Yield by no.= Cocoon yeild/10000 larvae by number, Yield by kg = Cocoon yeild/10000 larvae by weight

Table 3: Broad sense heritability for thirteen quantitative traits in four races of silkworm *Bombyx mori*

Races	Fecundity	Hatching%	Larval duration	Larval weight	Yield by no.	Yield by kg	Cocoon weight	Shell weight	Shell ratio	Filament length	Pupation rate	Denier	Renditta
C <sub>108</sub>	0.945	0.870	0.994	0.289	0.988	0.941	0.662	0.886	0.661	0.868	0.992	0.949	0.969
NB <sub>4</sub> D <sub>2</sub>	0.762	0.994	0.979	0.973	0.999	0.993	0.861	0.986	0.417	0.939	0.997	0.939	0.988
Pure Mysore	0.918	0.995	0.289	0.997	0.988	0.967	0.998	0.993	0.955	0.963	0.996	0.902	0.993
Nistari	0.475	0.038	0.824	0.929	0.421	0.485	0.953	0.953	0.649	0.909	0.793	0.507	0.195
Total	0.768	0.179	0.676	0.981	0.583	0.881	0.971	0.963	0.861	0.984	0.887	0.661	0.832

Table 4: Correlation coefficients for thirteen quantitative traits in four races of silkworm *Bombyx mori*

Characters	Fertility	Hatching%	Larval duration	Larval weight	Yield by no.	Yield by kg	Cocoon weight	Shell weight	Shell ratio	Filament length	Pupation rate	Denier
Hatching%	0.572 ***											
Larval duration	0.760 ***	0.801 ***										
Larval weight	0.533 ***	-0.104	-0.046									
Yield by no	-0.497 ***	0.269	0.020	-0.828 ***								
Yield by kg	0.581 ***	-0.058	-0.019	0.981 ***	-0.783 ***							
Cocoon weight	0.675 ***	0.017	0.113	0.966 ***	-0.858 ***	0.953 ***						
Shell weight	0.731 ***	0.091	0.188	0.955 ***	-0.842 ***	0.948 ***	0.993 ***					
Shell ratio	0.726 ***	0.117	0.194	0.945 ***	-0.825 ***	0.933 ***	0.981 ***	0.992 ***				
Filament length	0.787 ***	0.131	0.281	0.924 ***	-0.837 ***	0.920 ***	0.979 ***	0.986 ***	0.972 ***			
Pupation rate	-0.739 ***	-0.76	-0.303	-0.802 ***	0.906 ***	-0.759 ***	-0.891 ***	-0.898 ***	-0.883 ***	-0.927 ***		
Denier	0.775 ***	0.206	0.337 *	0.866 ***	-0.737 ***	0.849 ***	0.930 ***	0.934 ***	0.920 ***	0.963 ***	-0.880 ***	
Renditta	-0.865 ***	-0.347 *	-0.481 ***	-0.763 ***	0.769 ***	-0.769 ***	-0.878 ***	-0.898 ***	-0.892 ***	-0.922 ***	0.896 ***	-0.881 ***

Yield by no.= Cocoon yeild/10000 larvae by number, Yield by kg = Cocoon yeild/10000 larvae by weight, \* = significant at 0.05%, \*\*\* = significant at 0.001%.

respectively. Maghbool *et al.* [12] reported high broad sense heritability (above 80 %) for larval duration, larval weight, cocoon weight, shell weight, shell ratio, cocoon yeild/10000 larvae by number, cocoon yeild/10000 larvae by weight, pupation rate, filament length, denier, raw silk recovery, fecundity and hatching.

The data in table 4 depicted correlations of thirteen traits under study. Correlations between traits are a measurement of the degree of common factors causing the variation in each of the two traits. Phenotypic correlation estimates between mentioned traits ranged from -0.927 to 0.993. The cocoon yeild/10000 larvae by number exhibited significant negative correlation with fecundity and larval weight. As well as, pupation rate depicted significant negative correlation with all traits except renditta and cocoon yeild/10000 larvae by number. The renditta showed significant negative correlation with all traits except pupation rate. The races with high amount of cocoon yeild/10000 larvae by number, pupation rate and renditta have high resistance to environmental effect like disease, temperature, humidity etc. Generally, best races with high production have low resistance to environmental effect, then correlation between cocoon yeild/10000 larvae by number, pupation rate and renditta with another traits should be negative. Umashankara and Subramanya [13] have demonstrated correlation for five cocoon productivity traits in selected indian silkworm races for cocoon weight, shell weight, pupal weight and shell ratio. From their findings it is evident that there is higher significant genotypic correlation between shell weight and cocoon weight, pupal weight and shell ratio. In a relevant findings, genotypic and phenotypic correlation estimated between cocoon weight, shell weight, pupal weight and shell ratio ranged from -0.446 to 0.982 [3].

As regards to the traits larval weight and cocoon weight, it is evident that there is high heritability and high significant correlation between them thereby suggesting that breeders can select larval weight and cocoon weight as important breeding parameters to improve the silk yield in *Bombyx mori* L.

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