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Genetic Variability and Relationship among Cocoon Traits in Japanese Lines of Silkworm *Bombyx mori,* L

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ABSTRACT

Genetic parameters and economic values of some important traits in three Japanese commercial silkworm varieties (107, 101433 and 153) were analyzed and selection indices for these traits were constructed. Individual recordings on cocoon weight, shell weight and shell ratio were carried out in eight generations. Heritability and correlation coefficients were estimated by REML method. Heritability of cocoon weight and cocoon shell weight were higher than heritability of cocoon shell ratio. Genetic correlation between cocoon weight and cocoon shell weight for 107, 101433 and 153 lines were 0.921, 0.911 and 0.915, respectively. Genetic correlation between cocoon weight and cocoon shell percentage for 107, 101433 and 153 lines were -0.229, 0.374 and 0.088, respectively. Genetic correlation between cocoon shell weight and cocoon shell percentage for 107, 101433 and 153 lines were 0.699, 0.830 and 0.800, respectively. The highest heritability for cocoon weight belonged to 101433 (0.468) lines. Also the lowest heritability for cocoon weight belonged to 153 (0.400) line. The highest and lowest heritability for cocoon shell weight belonged to 101433 (0.503) and 107 (0.292) lines, respectively. Meanwhile the highest and lowest heritability for cocoon shell percentage belonged to 101433 (0.259) and 153 (0.172) lines, respectively. With respect to the results of this study it is concluded that separate breeding strategy must be designed in the varieties and different selection index constructed. Also economic characters have high heritability showing that individual index selection can be performed efficiently to improve important traits in a few generations.

Key words: Silkworm, Cocoon, Genetic Correlation, Heritability, Line

INTRODUCTION

In sericulture numerous traits are considered important. Productive traits namely economic traits included cocoon weight, cocoon shell weight, and cocoon shell percentage. These traits have important role in silk production, since silk as final product of sericulture prepare from cocoon shell in silk factories. Annually it is rearing silkworm larvae and producing silk. If there are weak productive characteristic in commercial lines, silk production will decrease and produce expensively. The aim of silkworm breeding is to improve economic traits in order to increase the profit of silk producers and other sections of sericulture industry. The importance of these traits in various parts of this industry is different. The reproductive traits are considered important for egg producers while cocoon producers are interested in improved production potential, cocoon shell percentage and disease resistance (Singh *et al.* 1998).

Because the economic importance of different traits is not similar, hence the main emphasis should be focused on the traits which have more value in economic efficiency of production system. The use of selection index for genetic and economic improvement of traits in the shortest time will have the highest improvement (Harris, 1970). The selection index method was used for the first time by Hazel in 1943 for animal breeding (Hazel, 1943). There are approximately 2000 different races and breeds of *Bombyx mori* used in silk production (Reddy, 1986). Twenty one characters of this species are recognized as contributing in silk yield quantitatively or qualitatively (Chatterjee *et al.* 1990). Kumar *et al.* (1995) have reported the genetic variability for economically important quantitative traits and selection indices of 46 bivoltine races of *Bombyx mori*. 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 characters are under genetic control.

Nagaraja *et al*. (1996) have reported that high heritability was shown by fecundity, maximum larval weight, cocoon yield by weight, cocoon yield by number, effective rate of rearing, and rates of adult emergence and pupation in *Samia cynthia ricini*. It appears, therefore, that selection for these traits should be effective in improving them.

Rangaiah *et al*. (1995) have showed that the expected genetic advance was high for cocoon weight and maximum larval weight while it was lowest for larval duration. It is thus best to base a selection programme on traits like cocoon weight and maximum larval weight since heritability and genetic advance are coupled to give maximum selection response.

A lot of researchers have studied the heritability of these characteristics in mulberry silkworm (Satenahalli *et al.* 1990, Bhargava *et al.* 1993, Kumar *et al.* 1995, Rangaiah *et al.* 1995, Ksham *et al.* 1995, Nagaraja *et al.* 1996). But a few studies had been done on determining the better selection indices based on important characteristics. The selection index method which incorporates genetic, phenotypic and economic parameters has been widely used for determining the selection emphasis in livestock breeding (Harris and Newman, 1992). Advanced methods of animal genetic evaluation simultaneously incorporate selection index theory with the statistical estimation of and allowance for non genetic effects on animal performance (Henderson, 1974). Amer and Hofer (1994) were considered the effects of uncertain parameters on the expected response and the distribution of responses from index selection. Kumaresan *et al.* (2000) have performed the selection index program for quantitative traits of 56 multivoltine silkworm races which resulted into three clusters of ten genotypes with lower index values for utilization in hybridization. In another study (Kumar *et al*. 1995) selection indices of 46 bivoltine races of silkworm were determined.

This experiment was conducted for estimating of heritability, genetic correlation, environment correlation and phenotype correlations of three traits including cocoon weight, cocoon shell weight, and cocoon shell percentage in three commercial lines including 107, 101433 and 153 (Xihang1) on the basis of eight successive generation's data.

MATERIALS AND METHODS

The present investigation has been performed on 3 commercial Japanese silkworm varieties which were reared in Iran's Silkworm Research Center including 153, 107 and 101433. These varieties are high productive and combining abilities (GCA and SCA) especially based on reproductive characters. These varieties isolated during a long-term silkworm breeding program at Iran's Silkworm Research Center. Today these varieties supply the most silkworm-egg of Iran as commercially. Silkworm rearing technique included single batch rearing system (ESCAP, 1993). Feeding and other conditions of larval rearing were conducted following the standard procedure (ESCAP, 1993). All three lines were reared at two rearing seasons including spring and autumn. Experiment was conducted during four successive years and eight rearing season. In each rearing season, all studied lines were reared in 24 families and was prepared cocoon records individually. Data was obtained from 8 rearing periods or generations (4 spring rearing seasons and 4 autumn rearing seasons) as well as base population (80 male and 80 female cocoons in each line) were used.

In each line and generation, 24 families were reared so that 30 male and 30 female full sib cocoons were individually recorded for cocoon traits per family.

In order to estimate genetic and environmental parameters of cocoon weight, shell weight and shell percentage, three-trait selection indices, selection index programme was performed in each generation for selecting top cocoons. Assuming that genetic and environmental interactions are negligible, the environmental variances are simply the differences between phenotypic and genetic components. Covariances between traits, partitioned in a similar manner into genetic, environmental and phenotypic components. Also, heritability is the proportion of phenotypic variation in a population that is attributable to genetic variation among individuals. Phenotypic variation among individuals may be due to genetic and/or environmental factors. Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. Genetic correlation refers to the proportion of variance that two traits share due to genetic causes. Outside the theoretical boundary case of traits with zero heritability, the genetic correlation of traits is independent of their heritability: i.e., two traits can have a very high (or low) genetic correlation even when the heritability of each is low and vice versa.

Totally, the size of data used for estimating genetic parameters was 8800 records per line for each trait. Variance and covariance components were estimated with the method of restricted maximum likelihood (REML) through derivative free algorithm based on full sib data in a 3 traits animal model and then genetic, environmental and phenotypic correlations and also heritability of traits were derived. restricted (or residual) maximum likelihood (REML) approach is a particular form of maximum likelihood estimation which does not use the full set of observations available, but instead uses a likelihood function calculated from a transformed set so that nuisance parameters have no effect. It is used as a method for fitting linear mixed models. In contrast to conventional maximum likelihood estimation, REML can produce unbiased estimates of variance and covariance parameters. To meet this end, DXMUX program of DFREML software was used. The mixed model for estimating variance and covariance components was as follows:

$$y_{ijkl} = \mu_i + G_j + S_k + u_1 + e_{ijkl}$$

where y_{ijkl} is individual record for trait i, μ_i is the mean effect for trait i, G_j is effect for generation (year-season) j, S_k is effect for sex k (male and female), u_l is additive genetic value (random effect) for animal l and e_{ijkl} is residual effect. In this model μ_i, G_j, and S_k were considered as fixed effects.

RESULTS AND DISCUSSION

In Tables and Figures 2, 3 and 4, genetic correlations, environmental correlations and phenotypic correlations among cocoon weight, cocoon shell weight and cocoon shell percentage are shown, respectively. Genetic correlation, environment correlation and phenotype correlations of cocoon weight- ,cocoon shell weight for 107 line were 0.921, 0.478 and 0.729, for 101433 were 0.911, 0.676 and 0.794 and for 153 line were 0.915, 0.625 and 0.753. Genetic correlation, environment correlation and phenotype correlations of cocoon weight- cocoon shell percentage for 107 line were -0.229, -0.208 and -0.205, for 101433 were 0.374, -0.119 and -0.067 and for 153 line were 0.088, -0.193 and -0.112, respectively. Genetic correlation, environment correlation and phenotype correlations of cocoon shell weight- cocoon shell percentage for 107 line were 0.699, 0.517 and 0.592, for 101433 were 0.830, 0.420 and 0.631 and for 153 line were 0.800, 0.375 and 0.610 respectively. In Table and Figure 1, the heritability of traits are shown. The highest heritability for cocoon weight was 101433 (0.468) lines. Also the lowest heritability for cocoon weight was 153 (0.400) line. The highest and lowest heritability for cocoon shell weight was 101433 (0.503) and 107 (0.292) lines, respectively. Meanwhile the highest and lowest heritability for cocoon shell percentage belonged to 101433 (0.259) and 153 (0.172) lines respectively.

Heritability of cocoon weight was higher than cocoon shell weight in 107 and 153 lines, while it was lower in 101433 line. Cocoon shell percentage had lower heritability in all the lines, which is expected to show lower genetic gain in the selection programs. From obtained heritabilities, it is concluded that cocoon weight and cocoon shell weight are more under control of additive effects, while cocoon shell percentage is mostly controlled by non-additive effects and non-genetic effects. Environmental and phenotypic correlations among traits had the same trend as additive genetic correlations.

Due to higher negative genetic correlation between cocoon weight and shell percentage in the line 107, it is expected that by restricting of genetic gain for cocoon weight, the emphasis on shell percentage is more increased. The expected genetic improvement of cocoon weight in 101433 was higher due to higher heritability and genetic correlation with shell weight. Accordingly, the higher expected improvement of shell weight in 101433 is due to its higher heritability and correlation with cocoon weight. Kumar *et al.* (1995) have showed that the correlations between single cocoon weight and single shell weight as well as single shell weight and shell percentage were highly significant. Sofi *et al.* (1999) and Jayaswal *et al.* (2000) have revealed high genetic correlation between cocoon characters. Ksham *et al.* (1995) have reported that high positive genetic and phenotypic correlations (0.75 and 0.95, resp.) were found between cocoon yield and cocoon weight. The same was also true between single shell weight and filament length (0.66 to 0.70), and single shell weight and denier (0.78 to 0.85). The results indicated a good scope for selecting using filament length and denier for the improvement of cocoon yield.

Ksham *et al.* (1995) have reported that the heritability for quantitative traits was comparatively higher and ranged from 48 to 64% with little tendency for the standard error to increase with the estimate, while the range of heritability for fitness traits was much lower (18-25%). The data supported the classical hypothesis that the fitness traits would exhibit lower heritabilities compared to the traits in other categories. Bhargava *et al.* (1993) have reported that heritability was very high (71.4-86.7%) for larval duration, single-shell weight, filament length, larval weight and single-cocoon weight. Moderate heritability (<70%) was observed for cocoon yield (65.3%) and shell ratio (69.8%), indicating that these 2 characters were influenced by the environment. Singh *et al.* (1998) and Malik *et al.* (1999) have reported similar results. Ashoka and Govindan (1990) have showed high heritability as well as genetic gain for cocoon weight and shell weight indicating additive gene action and moderate to high heritability and low genetic gain for shell percentage, implying that this may be predominantly under control of non additive gene action. Rangaiah *et al*. (1995) indicated high heritability for shell percentage and shell weight while moderate along with high genetic advance for cocoon weight.

As a result, it is expected that restricting the genetic improvement of cocoon weight in line 101433 causes considerable reduction of shell weight gain. Since, the shell weight is the most important economic trait, hence the improvement of reduction in this trait will bring about great economic losses. Results of a study (Famula, 1992) demonstrated that linear programming is a more effective method to limit correlated response than restricted selection index, but response to selection in the unrestricted traits is greater with restricted selection index than with linear programming. Leiri *et al*. (2004) have suggested that BLUP selection should always be preferred to restricted BLUP selection because of the smaller risk of selection and this choice is especially important for the situation where the genetic parameters act as limiting factors for the achievement of intended genetic gains. As a result, in line 101433 the breeding strategy could be concentrated on cocoon weight and shell weight.

CONCLUSIONS

With respect to the results of this study it is concluded that there are different correlation and heritabilities between commercial silkworm lines. Thus the separate breeding strategy must be designed in the varieties and different selection index constructed. Also economic characters have high heritability showing that individual index selection can be performed efficiently to improve important traits in a few generations. One of the reasons possibly is that all the varieties are reared in a standard condition and environmental factors have insignificant effects on phenotypic variation of the traits. Today silkworm lines are selected based on more genetics characteristics e.g. general combining ability and special combining ability. These parameters and also increasing×increasing effects produce a high heterosis. Furthermore there have been reports regarding to this concept previously and there must be more attention toward these genetic resources. Finally obtained results showed cocoon weight and cocoon shell weight having high heritability and cocoon shell percentage have lower heritability. These results emphasis additive gene effects on cocoon weight and cocoon shell weight traits. But cocoon shell percentage controlled by non-additive gene effects.

Additive genetic effects consist of the effects of two or more alleles of different loci combined in such a way that the sum of their effects in unison is equal to the sum of their effects individually. Such phenomena are only possible when the alleles involved do not interact with one another in such a way that would modify, hinder, or amplify the effects of any one gene involved. An additive genetic effect is a form of quantitative inheritance as the effects of the combined genes can be simply added together. Additive genetic effects are different from cumulative gene action because in the last, the effects of the genes combined create an action of increased intensity (http://en.wikipedia.org/wiki/Additive_genetic_effects).

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Table 1. Heritability of cocoon weight, shell weight and shell percentage in the studied varieties.

Trait	107	101433	153
cocoon weight	0.434	0.468	0.400
shell weight	0.292	0.503	0.397
shell percentage	0.215	0.259	0.172

Table 2. Additive genetic correlations among cocoon weight, shell weight and shell percentage in the studied varieties.

Correlation between	107	101433	153
Cocoon weight & shell weight	0.921	0.911	0.915
Cocoon weight & shell percentage	-0.229	0.374	0.088
Shell weight & shell percentage	0.699	0.830	0.800

Table 3. Environmental correlations among cocoon weight, shell weight and shell percentage in the studied varieties.

Correlation between	107	101433	153
Cocoon weight & shell weight	0.478	0.676	0.625
Cocoon weight & shell percentage	-0.208	-0.119	-0.193
Shell weight & shell percentage	0.517	0.420	0.375

Table 4. Phenotypic correlations among cocoon weight, shell weight and shell percentage in the studied varieties.

Correlation between	**107**	**101433**	**153**
Cocoon weight & shell weight	0.729	0.794	0.753
Cocoon weight & shell percentage	-0.205	-0.067	-0.112
Shell weight & shell percentage	0.592	0.631	0.610

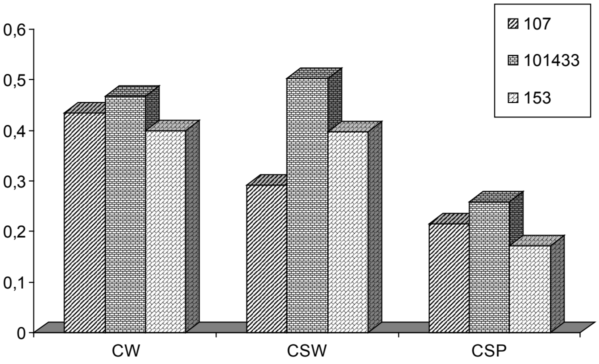

Fig. 1. Heritability of cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP).

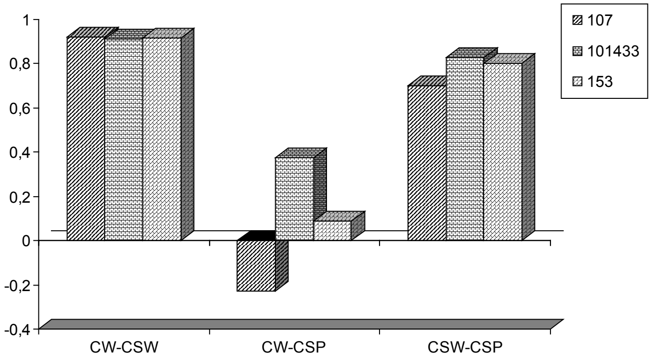

Fig. 2. Genetic correlation between cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP).

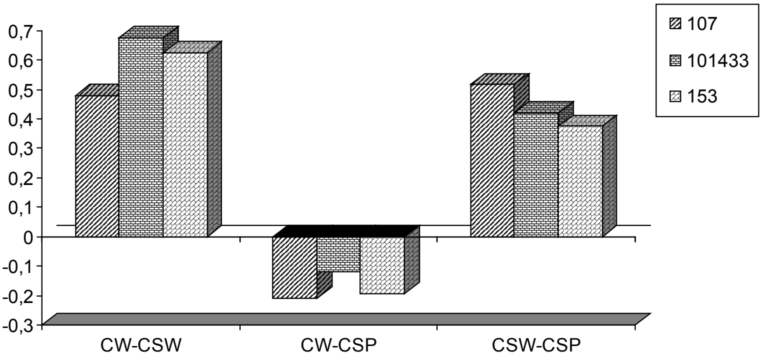

Fig. 3. Environmental correlation between cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP).

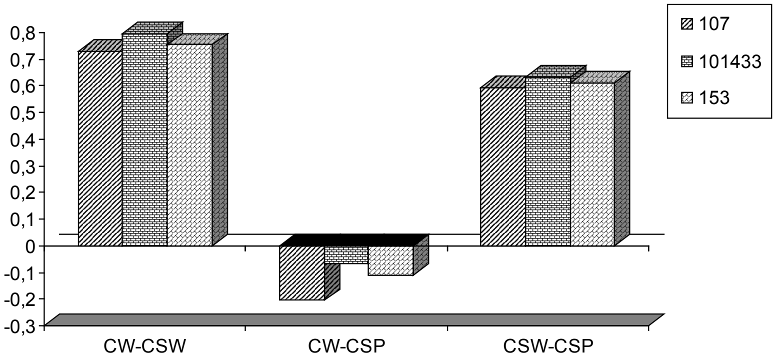

Fig. 4. Phenotypic correlation between cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP).

REFERENCES

Amer, P. R., Hofer, A., 1994, Optimum bias in selection index parameters estimated with uncertainty. *Journal of Animal Breeding and Genetics,* 111: 89-101.

Ashoka, J., Govindan, R., 1990. Genetic estimates for quantitative traits in bivoltine silkworm, *Bombyx mori* L. *Mysore Journal of Agricultural Science,* 24: 371-374.

Bhargava, S. K., Thiagarajan, V., Ramesh Babu, M., Nagaraj, B., 1993, Heritability of quantitative characters in silkworm (*Bombyx mori* L.). *Indian Journal of Agricultural Science,* 63: 358-362.

Bhatia, V. K., Paul, A. K., 1996, Empirical comparison of different selection strategies for genetic improvement. *Indian Journal of Animal Science*, 66: 1026-1032.

Chatterjee, S. N., Nagaraj, C. S., Giridhar, K., 1990*, An approach to silkworm breeding. In:* workshop on biometrical genetics proceedings (Ed. By R. K. Datta), Central Sericultural Research and Training Institute, Mysore, 11-16 pp.

Economic and Social Commission for Asia and the Pacific (*ESCAP*), 1993, Principles and techniques of silkworm breeding. New York, United Nations. 114.

Famula, T. R., 1992, A comparison of restricted selection index and linear programming in sire selection. *Theoretical and Applied Genetics*, 84: 384-389.

Harris, P. L., 1970, Breeding for efficiency in livestock production: Defining the economic objectives. *Journal of Animal Science*, 30: 860-865.

Harris, D. L., Newman, S., 1992, How does genetic evaluation become economic improvement? In Proceeding of Symposium on Application of Expected Progeny Differences to Livestock Improvement. 84th Annual Meeting. American Society of Animal Science. Pittsburgh, Pennsylvania. August 9-11. pp 125-132.

Hazel, L. N., 1943, The genetic basis for constructing selection indices. *Genetics,* 2: 476-490.

Henderson, C. H., 1974, General flexibility of linear model techniques for sire evaluation. *Journal of Dairy Science*, 57: 963-972.

Jayaswal, K. P., Masilamani, S., Lakshmanan, V., Sindagi, S. S., Datta, R. K., 2000, Genetic variation, correlation and path analysis in mulberry silkworm, *Bombyx mori* L. *Sericologia,* 40: 211-223.

Ksham, G., Kumar, S. N., Nair, S., Datta, R. K., 1995, Heritability, genetic and phenotypic correlation studies on fitness and quantitative traits of bivoltine silkworm *Bombyx mori* L. *Indian Journal of Sericulture,* 34: 22-27.

Kumar, P., Bhutia, R., Ahsan, M. M., 1995, Estimates of genetic variability for commercial quantitative traits and selection indices in bivoltine races of mulberry silkworm (*Bombyx mori* L.). *Indian Journal of Genetics and Plant Breeding*, 55: 109-116.

Kumaresan, P., Sinha, R. K., Sahni, N. K., Sekar, S., 2000, Genetic variability and selection indices for economic quantitative traits of multivoltine mulberry silkworm, *Bombyx mori* L. genotypes. *Sericologia*, 40: 595-605.

Leiri, S., Nomura, T., Hirooka, H., Satoh, M., 2004, A comparison of restricted selection procedures to control genetic gains. *Journal of Animal Breeding and Genetics,* 121: 90-100.

Malik, G. N., Masoodi, M. A., Kamili, A. S., Aijaz, M., 1999, Estimation of direct selection parameters in a diallel set of bivoltine silkworm, *Bombyx mori* L. *Entomonology,* 24: 253-257.

Nagaraja, M., Govindan, R., Narayanaswamy, T. K., 1996, Genetic viability for quantitative traits in eri silkworm *Samia cynthia ricini* Boisduval. *Insect Environment*, 2: 108-109.

Perez-Enciso, M., Toro, M., 1992, Classical and mixed model analysis of an index selection experiment for fecundity in *Drosophila melanogaster*. *Journal of Animal Science,* 70: 2673-2681.

Rangaiah, S., Govindan, R., Devaiah, M. C., Narayanaswamy, T. K., 1995, Genetic studies for some quantitative traits among multivoltine races of silkworm, *Bombyx mori* L. *Mysore Journal of Agricultural Science*, 29: 248-251.

Reddy, G. S., 1986, *Genetics and breeding of silkworm, Bombyx mori L. In:* Lectures on Sericulture (Ed. Boraiah G.), Suramaya Publishers, Bangalore, India, 70-80 pp.

Satenahalli, S. B., Govindan, R., Goud, J. V., Magadum, S. B., 1990, Genetic parameters and correlation coefficient analysis in silkworm *Bombyx mori* L. *Mysore Journal of Agricultural Science*, 24: 491-495.

Shadparvar, A., 1997, Determination of optimum breeding goal for Holstein dairy cows in Iran. [PhD dissertation]. College of Agriculture, Tarbiat Modarres University. Tehran, Iran. 198p.

Singh, T., Chandrasekharaiah, S., Samson, M. V., 1998, Correlation and heritability analysis in the silkworm, *Bombyx mori* L. *Sericologia*, 38: 1-13.

Sofi, A. M., Masoodi, M. A., Kamili, A. S., 1999, Estimation of heritability and correlation of some quantitative traits in line × tester analysis in silkworm, *Bombyx mori* L. *Mysore Journal of Agricultural Science*, 33: 289-296.

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