

*Full Length Research Paper*

# Estimation of genetic parameters in three commercial silk-worm lines of Iran

S. Darmand<sup>1</sup>, A. Lavvaf<sup>1\*</sup>, A. R. Seidavi<sup>2</sup>, N. Eila<sup>1</sup>, S. Nematollahian<sup>3</sup> and T. Farahvash<sup>4</sup>

<sup>1</sup>Department of Animal Science, Karaj Branch, Islamic Azad University, Karaj, Iran.

<sup>2</sup>Department of Animal Science, Rasht Branch, Islamic Azad University, Rasht, Iran.

<sup>3</sup>Iran Silkworm Research Center (ISRC), Rasht, Iran.

<sup>4</sup>Department of Animal Science, Shabestar Branch, Islamic Azad University, Shabestar, Iran.

Accepted 26 August, 2011

In order to estimate genetic parameters of the cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP) of three industrial lines of silk-worm (number 31, 103 and 107), data were collected from three successive generations. (Co)variance components were as follows: additive genetic variation ( $\delta^2_a$ ) and environmental variation ( $\delta^2_e$ ) of traits and additive genetic covariance ( $cov_{a1, 2}$ ) and environmental covariance ( $cov_{e1, 2}$ ). Heritability of traits was estimated with maximum likelihood procedure (REML) by using algorithms (DFREML) based on a three trait animal model. Data were from half-sibs and the heritability and genetic, phenotypic and environmental correlation were estimated between traits. The highest heritability for CW was estimated in lines 31 and 107 (0.58 and 0.58, respectively) and the lowest heritability for CW was in line number 103 (0.28). The highest and lowest heritability for CSW was in lines 107 and 103 (0.70 and 0.01, respectively). Also, the highest heritability for CWP was in line 31 (0.48) and the lowest value was in line 103 (0.077). The highest  $\delta^2_g$  for CSP was estimated in line 103 (0.004) and lowest  $\delta^2_g$  was estimated in line 107 (0.001). The highest and lowest  $\delta^2_a$  for CW were estimated in lines 103 and 31 (0.0004 and 0.00003, respectively). The  $\delta^2_g$  for CW was high in line 31 (0.604) but low in line 103 (0.257). The highest and lowest  $\delta^2_e$  for CW were in lines 103 and 107 (0.02 and 0.01, respectively). Furthermore, the highest  $\delta^2_e$  for CSW was estimated in line 103 (0.0013) but minimum  $\delta^2_e$  was in line 107 (0.0007). Maximum  $cov_{a1, 2}$  for CW-CSW was estimated in line 103 (0.00087) and minimum value was estimated in line 31 (0.00012). A high  $cov_{e1, 2}$  for CW- CSP was estimated in line 103 (0.093) but it was low in line 31 (0.00026). The highest  $cov_{g1, 2}$  for CSW-CSP was in line 103 (0.002) but it was low in line 31 (0.00079).

**Key words:** Cocoon, correlation, heritability, genetic (Co) variance.

## INTRODUCTION

In domestic animal breeding programs, there are different selection criteria (Ghanipour, 2002). In practical condition, it is very important to increase the mean value of many traits at the same time, but it is known that different traits may be correlated (positively or negatively) or have no relation and these traits will have different values. Consequently, estimating heritability and correlation between economical traits would be of a great significance (Ghanipour et al., 2008, Seidavi, 2010a, b).

In some studies, high heritability values were reported

for cocoon weight, cocoon shell weight and cocoon shell percentage (Petkov, 1997; Seidavi et al., 2009), also it was mentioned that these traits have great importance and would answer better to selection due to their  $h^2$  values. Heritability values estimated for cocoon shell weight is moderate to high (0.2 to 0.7) and has positive genetic correlation with other traits such as cocoon weight, cocoon shell percentage, larval weight, string length, pure silk percentage and egg weight (Singh et al., 1998).

The results of another study showed that fitness traits have lower heritability and there is positive environmental and genetic correlation between cocoon production and weight of each cocoon (0.75 and 0.95, respectively).

\*Corresponding author. E-mail: [aynmkind@yahoo.com](mailto:aynmkind@yahoo.com).

Evaluating genetic parameters for about 17 different traits showed that fertility, larval weight, cocoon weight, cocoon count, effective breeding rate and butterfly rate had high heritability values (Ghanipoor et al., 2008; Seidavi, 2010c, 2011). Since there is very little information about genetic parameters of Iranian silk-worm lines, it is difficult to recognize the superior lines and breed them. Consequently, this research was conducted in order to collect records from these lines and data were analyzed to estimate genetic parameters for the first time. This could help to identify performance of each line correctly and to clarify the differences between these lines.

**MATERIALS AND METHODS**

The data were collected from silk-worms which were kept in Iran Silkworm Research Center (ISRC), Pasikhan, Rasht. Iran. Data consisted of individual records from cocoon weight (CW), cocoon shell weight (CSW) and cocoon shell percentage (CSP) with the number of animals, father, mother, generation, family and the sex of animals. In this study, data consisted of three generation in three years (2001, 2002 and 2003) from three industrial line of silk-worm (31, 103 and 107). In order to estimate genetic parameters, records from 8 family × 3 generation × 3 line × 3 trait × 2 sex × 25 individual (n = 10800 records) were used. The base population was made by random sampling and recording from the whole individuals at first year. Then, sex of chrysalis was identified. (Co) variance components were estimated by maximum likelihood procedure (REML) (Meyer, 1997) using algorithm (DFREML) (Meyer, 1997) and three trait animal model (Henderson mixed model). In order to estimate heritability and phenotypic, genotypic and environmental correlations, data from half-sibs were analyzed by DXMUX software and POWELL procedure of DFREML (31). Covariation between traits was estimated by using the model as follows:

Cov<sub>1,2</sub> = correlation coefficient of 1 and 2 × standard deviation of 1 × standard deviation of 2. The model used to estimate genetic parameters was as follows:

$$Y_{ijklm} = \mu + L_i + S_j + M_k + A_l + e_{ijklm}$$

Where, L<sub>i</sub> is the effect of line (i=1, 2, 3); S<sub>j</sub> is the effect of year, generation, breeding period or year- season (j=1, 2, 3); M<sub>k</sub> is the effect of sex (k=1, 2) and A<sub>l</sub> is the additive genetic effect. The matrix form of the listed model is as follows, though it is not necessary to repeat the model in the matrix notation:

$$Y = Xb + Zg + e$$

Where Y is an n×1 vector of observations (CW, CSW and CSP); X is an n×f matrix of fixed effects related to observations (generation, sex, lines); b is an f×1 matrix of fixed effects; Z is an n×s matrix of random effects related to observations; g is an s×1 matrix of random effects; e is an n×1 matrix of residual. Mixed model equations for estimating random effects are as follows:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & X'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} b \\ g \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

In the next step, after estimating (Co)variance components of population for each line, BLUP (Meyer, 1997) was used to evaluate individual additive genetic value by DFRML software. Data used were information from individual, full-sib and other relatives, which

made more accurate estimations. The amount of genetic progress was calculated after estimating mean additive genetic value of each generation and each line, by using equation as follows:

$$\Delta G_{n \square 1 \square n} = \bar{G}_{n \square 1} - \bar{G}_n$$

Where  $\Delta G_{n \square 1 \square n}$  is the additive genetic progress of traits per generation;  $\bar{G}_{n \square 1}$  is the average additive genetic value in generation number (n+1) and  $\bar{G}_n$  is the average additive genetic value in generation number (n). Additive genetic progress of traits in generation number (n) was calculated as follows:

$$\Delta G_{n,0} = \bar{G}_n - \bar{G}_0$$

Where,  $\Delta G_{n,0}$  is the additive genetic progress of traits per generation in comparison to base population in both groups;  $\bar{G}_n$  is the average additive genetic value in generation number (n) and  $\bar{G}_0$  is the average additive genetic value in generation number (0).

The additive genetic trend of CW, CSW and CSP in lines was calculated by the regression of additive genetic value per generation. The model was as follows:

$$a_{ij} = bS_i + e_{ij}$$

Where a<sub>ij</sub> is the individual additive genetic value; b is the coefficient of regression of additive genetic value per generation; S<sub>i</sub> is the i<sup>th</sup> generation and e<sub>ij</sub> is the residuals.

In order to calculate genetic and phenotypic trend and average changes in breeding value (for each line and for all three line) and for generation in all lines, records were collected and analyzed by means procedure in SAS software. Information about amount of observation, mean values, standard deviations and minimum and maximum values of each trait was calculated per line and per generation and for different sexes. In order to determine changes of breeding value, the statistical model was used as follows:

$$Y_{ij} = \mu + S_i + e_{ij}$$

Where Y<sub>ij</sub> is the individual record or phenotype; μ is the mean value; S<sub>i</sub> is the effect of the breeding period or year or generation - season (i : 1, 2, 3); e<sub>ij</sub> is the residual.

**RESULTS AND DISCUSSION**

Summary of results are shown in Tables 1 to 6. The genetic variance and additive and environmental deviation are shown in Table 1. The highest heritability for CW was in lines 31 and 107 (0.575 and 0.578, respectively) and it was 0.282 in line 103. Highest and lowest heritability for CSW were in lines 107 and 103, respectively (0.7 and 0.01, respectively). Also, the highest heritability for CSP was in line 31 (0.48) but it was about 0.0768 in line 103.

Maximum δ<sup>2</sup><sub>g</sub> for CW was estimated in line 31 (0.48) and the minimum was in line 107 (0.0007). The amount of δ<sup>2</sup><sub>g</sub> for CW was intermediate in line 103 than line 107 (0.0038 to 0.0007). Highest and lowest δ<sup>2</sup><sub>g</sub> for CSW was

**Table 1.**  $\delta_g^2$ ,  $\delta_e^2$  and  $h^2$  estimated for traits in the three lines.

Lines	Parameter	CW	CSW	CSP
31	$\delta_g^2$	0.00115411	0.00002608	0.60460900
	$\delta_e^2$	0.01888759	0.00116570	2.73823700
	$h^2$	0.05758571	0.06000000	0.48008810
103	$\delta_g^2$	0.00385683	0.00040727	0.25770000
	$\delta_e^2$	0.0204924	0.00132340	3.09621940
	$h^2$	0.02820606	0.011071381	0.07683547
107	$\delta_g^2$	0.00071182	0.00014354	0.43206890
	$\delta_e^2$	0.01158650	0.00070496	1.85198500
	$h^2$	0.05787968	0.70000000	0.18916700

**Table 2.**  $cov_{g1,2}$  and  $cov_{e1,2}$  estimated for traits in the three lines.

Line	Parameter	CW-CSW	CW-CSP	CSW-CSP
31	$cov_{g1,2}$	0.00012144	0.00026415	0.00079421
	$cov_{e1,2}$	0.00328457	0.02274174	0.01129949
103	$cov_{g1,2}$	0.00087731	0.09315262	0.00204893
	$cov_{e1,2}$	0.00364535	0.02518907	0.01280240
107	$cov_{g1,2}$	0.00022375	0.00175372	0.00157508
	$cov_{e1,2}$	0.00200058	0.01464855	0.00722656

in lines 103 and 31, respectively (0.004 and 0.000026, respectively).  $\delta_g^2$  for CSP was maximum in line 31 (0.604) but it was minimum in line 103 (0.257).

The highest and lowest  $\delta_e^2$  for CW was in lines 103 and 107, respectively (0.02 and 0.01, respectively). Also, the most  $\delta_e^2$  for CSW was estimated in line 103 (0.0013) but the least  $\delta_e^2$  was in line 107 (0.0007). In Table 2, the estimations of additive and environmental covariance between traits for the three lines are shown. The highest  $cov_{g1,2}$  for CW- CSW was 0.00087 in line 103 and it was smaller in line 31 (0.00012). Maximum  $cov_{g1,2}$  for CW- CSP was 0.093 in line 103 and the minimum amount was in line 31 (0.00026). Maximum  $cov_{g1,2}$  for CSW- CSP was found in line 103 (0.002) but it was lowest in line 31 (0.00079).

The highest amount of  $cov_{e1,2}$  for CW-CSW was estimated in line 103 (0.0036) and the least measure was in line 107 (0.002). Also, it was 0.025 for CW- CSP in line 103 and 0.014 in line 107. Maximum  $cov_{e1,2}$  for CSW- CSP was in line 103 (0.012) and minimum amount was in line 107 (0.007). Table 3 shows the phenotypic trend for traits in the three lines. All lines had negative and decreasing trend for CW, CSW and CSP. CW had the lowest value (-0.1 g). Otherwise, it was -0.02 g for CSW. T value for CW and CSW was significant ( $P < 0.01$ ).

The phenotypic trend estimated for all traits in line 31 was negative and declining. The estimated measure for CSW (-0.18 g) was the lowest but it was the highest for

CW (-0.04 g). T value for CW and CSW in line 31 was significant ( $P < 0.01$ ).

The phenotypic trend in line 103 for CW, CSW and CSP showed reducing trend and it was for CW lower than other traits (-0.01). Phenotypic trend of CSW (-0.03) was higher than other traits in line 103. T- value of CW and CSW in line 103 was significant ( $P < 0.01$ ). Phenotypic trend in line 107 for CW (-0.09) and CSW (-0.01) showed decelerating trend and it was lower for CW. Otherwise, It was additive and positive for CSW. T-value of CW and CSP was significant in line 107 ( $P < 0.01$ ). Table 4 shows the estimates of genetic trend of traits in the three lines. The results indicate that genetic trend in all lines was additive and positive for CSW (0.001047) but negative and decreasing for CW (-0.0002) and CSP (-0.0069). Also, it was negative and reduced for CW (-0.00006) and positive and additive for CSW (0.003) and CWP (0.004) in line 31. Genetic trend of CW (-0.001) and CSW (-0.0002) was reduced. It was additive for CSP (0.002) in line 103. In spite of reducing genetic trend of CSW (-0.0001) and CSP (-0.0271) it was additive for CW (0.0006) in line 107. Table 5 summarizes variation of change in breeding value of different generations in the three lines. F-value showed no difference between traits. Table 6 shows comparison between different breeding values of different generations in the three lines. There was no significant difference between CW, CSP and CPW in generations of line 31, but it was true in line 103

**Table 3.** Phenotypic trend of traits.

Line	Parameter	CW (g)	CSW (g)	CSP
31	Estimated value	-0.173	-0.041	-0.188
	Standard error	0.008	0.001	0.0872
	T- value	-20.453 **	-29.804 **	-2.159 ns
103	Estimated value	-0.131	-0.030	-0.076
	Standard error	0.009	0.001	0.097
	T- value	-14.329 **	-18.230 **	-0.788 ns
107	Estimated value	-0.091	-0.016	150.0
	Standard error	0.006	0.001	0.081
	T- Value	-13.181 **	-15.039 **	1.834 ns
Total	Estimated value	-0.132	-0.029	-0.039
	Standard error	0.005	0.001	0.053
	T- value	-25.189 **	-27.251 **	-0.743 ns

\*\* P&lt;0.01.

**Table 4.** Genetic trend of traits.

Line	Parameter	BV of CW (g)	BV of CSW (g)	BV of CSP
31	Estimated value	-0.00006	0.0030	0.0040
	Standard error	0.0003	0.0107	0.0107
	T- value	-0.1730	0.3370	0.3810
103	Estimated value	-0.0010	-0.0002	0.0020
	Standard error	0.0006	0.0002	0.0040
	T- value	-1.8100	-1.2900	0.5260
107	Estimated value	0.0006	-0.0001	-0.0271
	Standard error	0.0001	0.0001	0.0072
	T- value	3.2160	-1.6060	-3.7560
Total	Estimated value	-0.0002	0.0010	-0.0069
	Standard error	0.0002	0.0035	0.0044
	T- value	-0.7980	0.2980	-1.5460

\*\* P&lt;0.01.

only for CSW and CSP. Also, CW were different in generations 1 and 2, there is significant difference between generations 1 and 2 with 3. CSW of all generations were the same in line 107 and CW were similar in generations 1 and 2 but it differed with generation 3.

High  $cov_{g1, 2}$  indicates that traits were influenced by more common genes. Li (1992) reported that selection of parents based on CW, significantly affected the reproductive and resistance in offspring. Also, it is likely because there was no significant negative correlation between these parameters. He suggested that lines could be selected base on CW separately and same selection

intension should not be used for all the lines.

There were intensively negative values for cytoplasm and additive maternal effects. Consequently, if CW increases, it could reduce CSW. If CW increases, likely CSP decreases but as there is positive relation between direct effects of CW and CSP, it seems that crossing between lines could produce crosses with higher CW and CSP. On the other hand, there is a high and positive significance between direct and maternal effects of CW and CSP, and then these traits could be improved by crossbreeding.

Mirhoseini et al. (2005) reported that heritability of CW

**Table 5.** Results of ANOVA of changes in mean breeding value of different generations in the three lines.

Trait S.V.	BV of CW		BV of CSW			BV of CWP		
	Error	Total	Model	Error	Total	Model	Error	Total
S.S.	0.534	0.536	0.174	105.547	105.722	1.137	171.621	172.758
M.S.	0.0001	-	0.021	0.029	-	0.142	0.048	-
F value	-	-	0.740	-	-	2.950	-	-
R <sup>2</sup>	0.005			0.001			0.006	
C.V.	3618.989			-7058.852			9999.990	
B.V.	0.0003			-0.002			0.002	

  

	Gene.	Lin.xGene.	Lin.	Gener.	Lin.xGene.	Lin.	Gener.	Lin.xGene.
S.S.	0.0005	0.0016	0.0550	0.0303	0.0896	0.2441	0.1202	0.7733
M.S.	0.0002	0.0004	0.0275	0.0151	0.0224	0.1220	0.0601	0.1933
F value	1.790	2.790	0.930	0.510	0.760	2.540	1.250	4.010

Gene., generation; lin, line.

**Table 6.** Comparison of change in breeding value in different generations separated by different lines.

Line	Generation	BV of CW (g)	BV of CSW (g)	BV of CWP
31	1	0.00055 <sup>a</sup>	-0.00052 <sup>b</sup>	-0.00052 <sup>b</sup>
	2	0.00023 <sup>b</sup>	-0.02260 <sup>c</sup>	-0.02260 <sup>c</sup>
	3	0.00042 <sup>a</sup>	0.00199 <sup>a</sup>	0.00290 <sup>a</sup>
103	1	0.00164 <sup>a</sup>	0.00079 <sup>a</sup>	0.10400 <sup>b</sup>
	2	0.00143 <sup>a</sup>	0.00067 <sup>a</sup>	0.12400 <sup>a</sup>
	3	-0.00062 <sup>b</sup>	0.00020 <sup>b</sup>	0.01460 <sup>c</sup>
107	1	-0.00134 <sup>c</sup>	-0.00130 <sup>a</sup>	0.01960 <sup>a</sup>
	2	0.00078 <sup>a</sup>	0.00055 <sup>a</sup>	0.01770 <sup>a</sup>
	3	-0.00012 <sup>b</sup>	-0.00051 <sup>a</sup>	-0.03460 <sup>b</sup>

<sup>a,b,c</sup> P<0.05.

and CSW was 1 percent of CSP. Singh et al. (1998) indicated that CSP had maximum heritability (80.20). Bahargava et al. (1995) suggested that traits such as CSW (in 2 generations) and CW, CSW and fiber length (in multi generations) had high heritability and genetic progress. The percentage of blue spot eggs, non hatched eggs and dead eggs had high heritability and low genetic progress. Other authors suggested that there is limited chance to improve these traits (Rahman, 1984; Govindan et al., 1991; Ahsan and Rahman, 1997; Ahsan and Rahman, 2000).

Sekharappa et al. (1999) estimated high heritability and moderate genetic progress for larval weight and CW in multi generation breeds. Rahman (1984) and Ramesh et al. (2001) indicated that there is no additive factor affecting genetic variation which significantly affects some larval and cocoon traits. Generally,  $r_g$  was higher than  $r_p$ . This is likely because of the changing effect of the environment of each trait (Rahman, 1984).

Ahsan and Rahman (1997, 2000) have already reported similar results in domestic silk-worm. Total egg per female, had non-significant genetic and phenotypic correlation with most traits except un-fertilized egg percentage. Percentage of un-fertilized eggs and blue spot eggs had significant (+ or -) correlation. Chatterjee et al. (1993) reported positive correlation between weight of mature domestic silk-worm larva, CW and CSW. Doira et al. (1992) showed that there was positive correlation between CSW and CW and also between CSW and weight of Chrysalis of both sexes. Singh et al. (1998) reported similar results for CSW and fertility. Seidavi et al. (2007) indicated estimating the economical coefficients and genetic parameters of reproductive and resistance traits and quantitative characteristics of cocoon based on the breeding system in breeding institutes of Iran; is of great importance. It makes selecting parental lines in order to produce commercial eggs more profit.

Other researcher showed that CW and CSW, and also

CW and CSP were highly correlated (Singh et al., 1994). Some articles separately indicated high genetic correlation between cocoon traits (Singh et al., 1998). Albeit high genetic and phenotypic correlation (75 and 95%, respectively) was reported between total cocoon production and individual cocoon weight (Singh et al., 1998); they also reported similar results for CW and fiber length (66 and 70%, respectively) and CSW and denier (78 and 85%, respectively). They suggested selection based on fiber length and denier would increase cocoon production. Also, they found that in spite of low heritability of fitness, viability and reproductive traits (18 to 25%), those traits had high heritability values (48 to 64%) (Singh et al., 1994, 1998).

Other research indicated that larva period, CSW, fiber length, larval weight and CW had high heritability. Also, traits such as cocoon production and CSP had high heritability (65 and 70%, respectively) which indicates lower environmental effects on these traits. It was in agreement with other researchers (Beckwitt and Arcidiacono, 1994, Beckwitt et al., 1998, Bhargava et al., 1993, 1994, 1995).

Characteristics such as cocoon weight, weight of 10000 larvae, total cocoon production in Japanese line were highly affected by additive genetic, consequently, genetically breeding programs could be done with high genetic progress. It appears that there is negative additive correlation between productive traits and resistance, which slows genetic progress in silk-worm lines. Non-additive genetic variation has very low effect on live larva count and cocoon production, but it affects live chrysalis count and CSW. CW was significantly affected by non-additive genetic variation.

High positive correlation between two important economic traits (CW and CSW) showed that selection based on CW, would increase CSW, although there is low  $r_g$  between CW and CSP. CW and CSP are genetically correlated with CSW; selecting CW would increase them. CSW is a significant economic trait and it is difficult to record. As there is high genetic correlation between CSW and CW, selecting CW would increase CSW. Results show that CW and CSW had high heritability and genetic progress, although CSP had lower heritability. It should be mentioned that high heritability never makes high genetic progress in all cases (Singh et al., 1994).

Reports indicated in spite of this fact that additive genetic had effect on this trait; it had high heritability and low genetic progress which indicates the effects of non-additive genetic genes on this trait (such as dominance and epistatic). In these situations, repeated selection and offspring test would be helpful for genetic progress. When trait has a moderate or high heritability, then it has low genetic progress. More non-additive genetic effects, consequently influence these traits and they would respond better to reverse selection and crossbreeding.

Since the amount of the response to selection per

generation is followed by selection intensification, heritability and genetic correlation and genetic progress of traits influenced by heritability, then genetic progress could be considered as an index for breeding programs and selection in lines.

Despite cocoon characteristics are influenced by both additive genetic and non-additive genetic effects, resistance traits are not affected by non-additive genetic effects, which indicate that additive effects genetically control traits. Consequently, it is expected that selecting Japanese lines based on better resistance, would improve this trait in crosses. Despite the high resistance in Chinese lines, they have low genetic variation, so selection could not be a good way to improve these traits. It seems that Japanese and Chinese lines have significant different genetic potential of resistance. Year and production season have major effect on variation of CW and CSP, although they have lower effect on CSW. Results show that economic traits in silkworm are influenced by interaction between genetic  $\times$  environment interaction; it would be difficult to estimate lines correctly (Mu et al., 1995). It is known that when environmental conditions change, this would affect epistatic and dominant genes, level and expression of them and average values of traits differs between breeds and lines (Mu et al., 1995).

Researcher reported fertility had maximum genetic and phenotypic variation and environmental effects mostly affected fertility and CSW. Length of larva period and silk percentage is rarely influenced by the environment. CSW, CSP and maximum larval weight had the highest heritability and fertility and CW had moderate heritability and length of larva period had low heritability (Ghanipour et al., 2001).

Not only is that genetic linkage is made by polytrophic traits, but also linkage between genes on a chromosome could make a temporary correlation. Results of regression analyses indicated that selection for higher egg production was correlated with chrysalis's weight but it should be considered that because of the slow genetic progress of egg production, chrysalis should not be very heavy. In higher weights, the correlation between chrysalis weight and egg production decreases. Also, chrysalis and larva weight, survival percentage and fiber length were highly correlated. Reports show that laying had positive correlation with CW and CSW and negative correlation with CSP and resistance. Ability of producing silk is a very important and complicated trait which has negative correlation with fiber length but positive correlation with fiber luxury. These traits are affected by factors such as temperature, moisture, light and weather (Ghanipour et al., 2001).

## Conclusion

Considering the results of this paper, it is recommended

that economic coefficients, genetic parameters and quantitative characteristics of cocoon should be estimated for different commercial lines and different breeding institutes in Iran. This will offer better opportunity to the selection of parental lines in order to produce egg.

## ACKNOWLEDGEMENT

This manuscript was obtained from the MSc thesis of S. Darmand at Islamic Azad University, Karaj Branch, Karaj, Iran.

## REFERENCES

- Ahsan MK, Rahman SM (1997). Correlation and path coefficient analysis in indigenous varieties of silkworm, *B. mori* L. J. Zool. Rajshahi. Univ., 16: 35-38.
- Ahsan MK, Rahman SM (2000). Correlation and pathcoefficient analysis of some yield contributing characters in hybrids of mulberry silkworm, *Bombyx mori* L. J. Asiat. Soc. Bangladesh. Sci., 26(2): 197-202.
- Beckwith R, Arcidiacono S (1994). Sequence conservation in the C-terminal region of spider silk proteins Spidroin from *Nephila claipeis* *Tetragnathidae*. *Araneus bicentarius Araneidae*. J. Biol. Chem., 269: 6661-6663.
- Beckwith R, Arcidiacono S, Stote R (1998). Evolution of repetitive proteins: spider silks from *Nephila claipeis* *Tetragnathidae* and *Araneus bicentarius Araneidae*. Insect. Biochem. Mol., 28(3): 121-130.
- Bhargava SK, Rajalakshmi E, Thiagarajan V (1994). An evaluation index for silk yield contributing traits in *Bombyx mori* L. Indian. Textile. J., 105: 83-84.
- Bhargava SK, Thairarayan V, Ramesh Babu M, Nagaraja B (1993). Combining ability and genetic analysis of quantitative traits in silkworm *Bombyx mori* L. J. Genet. Breed. 46: 330-327.
- Bhargava SK, Venugopal A, Choudhuri CC, Ahsan MM (1995). Productivity in bivoltine breeds. Indian Textile J., 105(6): 112-114.
- Chatterjee SN, Ramamohana Rao P, RavindraSingh RK, Datta A (1993). Genetic variability in mulberry silkworm *Bombyx mori* L. breeds with low silk yield. Indian J. Seric., 32: 69-86.
- Doira H, Fujii H, Kawaguchi Y, Kihara H, Banno Y (1992). Genetic Stocks and Mutations of *Bombyx mori*, Institute of Genetic Resources, Kyushu. University. Japan.
- Ghanipoor M (2002). Determination selection index for three industrial lines of Iranian silkworm. Msc. Theses. University of Ghilan. Iran. Persian. p. 143.
- Ghanipoor M, Mirhoseini SZ, Seidavi AR, Shadparvar AA, Bizhannia AR (2001). Estimation of genetic parameters for economical traits of six industrial lines of silkworm. Agric. Sci., Res. 2 (1): 31- 38.
- Ghanipoor M, Nematollahian S, Seidavi AR, Mirhoseini SZ, Mavvajpour M, Bizhannia AR (2008). Evaluation of genetic parameters and crossbreeding effects of economic traits on silkworm pure lines in the crisscrossing system. Res. J. Univ. Isfahan Sci., 35(6): 137-144.
- Govindan R, Salanahali SB, Goad V, Guiaiaja MK, Magadam SB (1991). Graphic analysis of gene action for some larval and cocoon traits in silkworm. Mysore Agric. Sci., 24: 474-481.
- Li W (1992). Genetic path network among quantitative characters in silkworm. Sericologia, 32: 543-548.
- Meyer K (1997). DFREML: program to estimate variance components by restricted maximum likelihood using a derivative-free algorithm. User Notes. Ver., p. 3.0.
- Mirhoseini SZ, Ghanipoor M, Shadparvar A, Etebari K (2005). Selection indices for cocoon traits in six commercial silkworm, *Bombyx mori* lines. Philippine Agric Sci., 88(3): 328-336.
- Mu ZM, Liu QX, Liu XL, Li WG, Sun ZY (1995). Genetic research of vitality and cocoon quality traits of silkworm. J. Shandong Agric. Univ., 26(2): 157-163.
- Petkov N (1997). Study on heterosis, depression and degrees of domination in interline hybrids of silkworm moth, *Bombyx mori* L. I. Technological traits of cocoons. Zhivotnovdni-Nauki. 34(1-2): 76-80.
- Rahman SM (1984). Studies on the genetic improvement of eri silkworm, *Philosamia ricini*. Boisd of Bangladesh. Ph.D Thesis, Department Zoology, Rajshahi Univ., p. 419.
- Ramesh Babu M, Chandrashekharaiah H, Lakshmi L, Prasad J (2001). Silkworm (*Bombyx mori* L.) genetic stocks—anevolutionary analysis. Bull. Ind. Acad. Seri., 5: 9-17.
- SAS (1997). SAS/STAT User Guide for personal computers, Cary, NC: SAS institute.
- Seidavi A, Mirhoseini SZ, Bizhannia AR, Ghanipoor M (2007). Evaluation of the effect of selection of some cocoon quantitative traits in Dodeman folk (3P) and correlation between these traits with reproductive parameters and F<sub>1</sub> silkworm resistance to disease. J. Biol. Iran., 20(3): 262-268.
- Seidavi AR (2010a). Estimation of genetics parameters and selection effect on genetic and phenotype trends in silkworm commercial pure lines. Asian J. Anim. Vet. Adv., 5(1): 1-12.
- Seidavi AR (2010b). Investigation on effect of individual selection based on cocoon weight on additive genetic value and selection index value in six commercial silkworm pure lines. World J. Zool. 5(1): 7-14.
- Seidavi AR (2010c). Relationship between Season and Efficiency of Individual Selection in Six Peanut and Oval Lines of Silkworm. Int. J. Eng. Technol., 2(2): 211-214.
- Seidavi AR (2011). Analysis of combining ability for some parameters in Iranian lines of silkworm *Bombyx mori* L. (Lepidoptera: Bombycidae). Annals Biol. Res., 2(2): 158-163.
- Seidavi AR, Mirhoseini SZ, Mavvajpour M, Ghanipoor M, Bizhannia AR, Qotbi A, Chamani M (2009). Additive genetic variations and selection index changes of economic traits of the silkworm commercial pure lines against parent selection pressure. American-Eurasian J. Agric. Environ. Sci., 6(4): 460-465.
- Sekharappa BM, Radhakrishna PG, Keshavareddy KS, Dandin SB (1999). Breeding of bivoltine silkworm races with better survival and high silk content for tropics-Karnataka. Sericologia, 39: 205-210.
- Singh T, Chandrasekharaiah A, Samson MV (1998). Correlation and heritability analysis in the silkworm, *Bombyx mori*. Sericologia, 38: 1-13.
- Singh T, Chandrasekharaiah MV, Samwo S (1994). Selection strategies in relation to correlation and heritability in the silkworm, *Bombyx mori* L. Bull. Seric. Res., 5: 37-41.