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Estimation of Genetic Parameters and Selection Effect on Genetic and Phenotype Trends in Silkworm Commercial Pure Lines

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Abstract: This study was conducted to analyze genetic parameters in six commercial Iranian silkworm pure lines including Japanese origin pure lines of 31, 103 and 107 and Chinese origin ones of 32, 104 and 110. All stages of rearing, recording and collecting data were performed over four rearing periods. Quantitative traits of Cocoon Weight (CW), Cocoon Shell Weight (CSW) and Cocoon Shell Percentage (CSP) were evaluated in this study. Covariance components of the characters are estimated by means of REML method. It is estimated heritability, phonotypical, environmental and genetical correlations using DFREML software package. From obtained results, genetic parameters including heritability and genetic correlation for economical trait were different significantly; hence it must be applied appropriate breeding strategies in each pure line. Cocoon weight and CSW heritability was higher than CSP one. Additive genetic correlation between CW-CSW, CSW-CSP and CW-CSP was high, medium and low, respectively. From obtained results, response to selection for cocoon weight and cocoon shell weight are higher than cocoon shell percentage since latest trait had lower heritability. Therefore, it is expected correlated traits improve using selection based on cocoon shell weight. Furthermore, genetic trend of traits were negative and significant at non-selected populations. Phenotype trend of traits also were negative and significant at selected and non-selected populations which is cleared environmental conditions decline at improvement generations.

Key words: Heritability, genetic correlation, silkworm, genetic trend, cocoon

INTRODUCTION

Researchers are noticed to genetic parameters of live organisms from previous years. Liu *et al*. (1995) trait fluorine-resistance heritability in the silkworm and they found the controller alleles realized dominance relative to trait this mainly by genes effects are controlled as additive. They also found dominance effect and realized the impact of parent material, but they were not identified the other genes and interactions. Finally, heritability this trait on the fluoride sensitivity and persistence, were calculated 86.08 and 78.40% respectively. Bhargava *et al*. (1993) also studied heritability of seventeen traits in the silkworm. Based on their results, heritability for larval duration, cocoon shell weight, cocoon weight, fiber length and weight of 10000 matured larva were high amounts (71.40-86.70%) and for two other traits were average amounts. They stated heritability of these two traits were 65.30 for cocoon production and 69.80% for percentage of cocoon shell. These findings indicate that two recent traits are affected by environmental conditions. Already Rayar *et al*. (1989) studied structure of genetic diversity for 18 economical traits in 13 one-way and 16 three-way silkworm varieties. They demonstrated heritability of larva weight, larval duration, cocoon shell weight and length of fiber is high. They also report cocoon fiber length have the most improvement under selection process. Phenotypic variation coefficients of all traits were higher than variance genotype coefficients. These findings indicated that the effect of environmental factors is negligible. Also, Lin *et al.* (1994) were studied heritability and other genetic characteristics for cocoon weight loss during degumming process in silkworm.

Kshama *et al.* (1995) also were reviewed heritability and genotype and environment correlations in three competence-related traits including fertility, persistence and rate of growth and four quantitative traits including cocoon weight, cocoon shell weight, length and diameter of the fiber in two strains NB7 NB4D2 and their crosses. They reported the amount of heritability were higher in quantitative traits and they were between 48-64%, while the competence-related characteristics have less heritability and were about 25-18%. Thus these results confirm the classic hypothesis that the competence traits have less h heritability than other traits. They also estimated both genotype and environment correlations. Based on their results, there are genotype and environment positive correlations between cocoon production and cocoon single weight. They reported similar results for cocoon weight and fiber length, cocoon weight and denier yarn. They demonstrated selection based on the length and fiber denier result to good improvement for cocoon production. Nagaraja *et al.* (1996a) studied genetic parameters of 17 different traits. Their results indicate heritability are high for fertility, the maximum larval weight, cocoon weight and number of produced cocoon, effective rearing rate, pupation rate and moth emergence rate. These findings and Seidavi *et al.* (2008b) report demonstrated selection have high efficiency in these cases. Also, many researches were conducted in order to investigation on silkworm genetic and breeding (Govindan *et al.*, 1991; Jayswal *et al.*, 2000; Islam *et al.*, 2005; Kamrul and Rahman, 2008).

Kumar *et al.* (1995) calculated genetic characteristics of quantitative traits in 46 bivoltine varieties. They emphasize that fiber length, cocoon weight and cocoon shell weight have high heritability and controlled under gene factors largely. Meanwhile, the correlation between cocoon weight and cocoon shell weight and also between cocoon shell weight and cocoon shell percentage were very significant.

Silkworm egg production process includes three stages i.e., 3P (pure line), 2P (ancestors) and P (parents). All breeding programs and selection must apply in 3P generation and silkworm pure lines are reared under limited size and high pressure selective breeding pressure.

There is little information about genetic parameters of Iranian commercial pure lines. Therefore, this experiment was conducted for study and estimation of genetic parameters (co-variance components of additive and environmental genetic, heritability, additive genetic correlation, genetic improvement and genetic trend) for characteristics of cocoon weight, cocoon shell weight and percentage of cocoon shell. Also, it is estimated the effect of individual selection based on cocoon weight on phenotypic and genetic trends in six Iranian commercial silkworm pure lines.

MATERIALS AND METHODS

This study was conducted at Islamic Azad University, Rasht Branch during 2009 using six silkworm varieties data that they are conserved as Iran commercial pure lines. Three pure lines have Japanese origin (31, 103 and 107) and three pure lines have Chinese origin (32, 104 and 110) and all these six pure lines reproduced and preserved in Iran Silkworm Research Center. All rearing stages including larval rearing, feeding, cocoon production, silkworm egg preparation and conservation, hatching and related ancillary activities such as pebrin microscopic experiment, investigation on fetal development, recording and collecting data was conducted in the Iran Silkworm Research Center under standard conditions. Studied quantitative characteristics included cocoon weight (g), cocoon shell weight (g) and cocoon shell percentage (%). Recorded characteristics of cocoon weight and cocoon shell weight were performed using a precision digital balance.

Data are recorded during four consecutive generations or rearing duration. First, it was established base population for each pure line from 3P (pure lime) populations. Each pure line was contained two groups as selected and random groups. For each pure line, it is selected in selected group 40 male and 40 female cocoons which had superior amounts of the cocoon weight in their populations in each sex. These selected individuals recorded based on three individual trait included cocoon weight, cocoon shell weight and cocoon shell percentage and then mated together randomly. Furthermore, in each pure line, a randomized or control group was constructed using 40 male and 40 female cocoons which they are assigned randomly without any selection and they had cocoon weight equal to population average. These randomized individuals also recorded for three individual trait included cocoon weight, cocoon shell weight and cocoon shell percentage and then mated together randomly. Therefore, there were 40 silkworm egg batches in each pure line for each selected and randomized groups. Totally, there were 960 records in base population for each trait (cocoon weight, cocoon shell weight and cocoon shell percentage). Rearing and silkworm egg production in future generations for selected and control groups were followed in separate paths.

At the first generation or 3P population from 40 batches in each group and pure line, it is hatched 8 silkworm egg batches which had superior hatchability and fecundities. Consequently, each group in each pure line was contained eight full-sib families. In the end of the rearing duration and cocoon production and after determining of the individuals' sexuality, in order to pedigree construction 25 male and 25 female cocoons recoded in the each family based on cocoon weight, cocoon shell weight and cocoon shell percentage. Totally first generation data included 4800 records for each trait and included 800 records for each pure line. Finally, 40 male and 40 female cocoons selected randomly among the eight families from each pure line and group and mated randomly for silkworm egg construction of next generation.

Stages of rearing and producing raw data in second (2P) and third (P) generations were conducted as same as the first generation. Totally data files include 15360 records for each of the three studied traits (2560 records in each pure line). It should be noted that individual selection was applied only in the base population and all mates were conducted in next generations as randomly.

Estimation of genetic parameters, heritability, genetic correlation, environmental correlation and phenotypic correlation were conducted based on randomized data. However, genotype and phenotypic trends were estimated based on total data included both selected and randomized groups.

Additive and environmental covariance components (residual effects) were estimated for three studied characteristics using Restricted Maximum Likelihood (REML) by means of Derivative-Free REML (DFREML) based on animal model (three- traits in Henderson mixed equations, using full-sib records (Meyer, 1997). Environmental and phenotypic characteristics were estimated. It was estimated heritability, genetic correlation, environmental correlation and phenotypic correlation between traits. It were used the DXMUX program, POWELL Procedure and DFREML software version 3.1 with convergence 10^{-8}.

Phenotypic trend of cocoon weight, cocoon shell weight and cocoon shell percentage in each pure line is calculated in each selected and randomized group separately using the following statistical model:

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

where, a_{ij} in above equation is individual phenotypic value, b is regression of phenotypic value to generation (trait phenotypic trend), S_i is ith generation and e_{ij} is the residual effects.

Additive genetic trend of cocoon weight, cocoon shell weight and cocoon shell percentage in each pure line is calculated in each selected and randomized group separately using the following statistical model:

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

where, a_{ij} in above equation is individual additive genetic value, b is regression of additive genetic value to generation (trait genetic trend), S_i is ith generation and e_{ij} is the residual effects. The DFREML and SAS statistical software were used for estimation of genetic and phenotypic trends their significant using DNMRT method (Duncan, 1951; SAS, 1997).

RESULTS

Table 1 shows trait heritability. Heritability limits of cocoon weight were between 0.408 (pure line 31) and 0.473 (pure line 103) and for cocoon shell weight were between 0.348 (pure line 107) and 0.486 (pure lines 103 and 104) and for percentage of cocoon shell were between 0.099 (pure line 32) and 0.402 (pure line 31), respectively. From obtained results, heritability of cocoon shell percentage was less than the two other traits. Totally heritability of three traits including cocoon weight, cocoon shell weight and cocoon shell percentage were 0.496, 0.499 and 0.313, respectively.

Table 2 shows genetic correlation coefficients between cocoon traits. There are high correlations between cocoon weight and cocoon shell weight. These findings indicate that these two traits affected by common major genes and environmental factors. This

Table 1: Heritability (± Standard error) of cocoon weight, cocoon shell weight and cocoon shell percentage in studied pure lines

Pure line	Cocoon weight	Cocoon shell weight	Cocoon shell percentage
31	0.408±0.042	0.463±0.043	0.402±0.040
103	0.473±0.044	0.486±0.047	0.157±0.047
107	0.434±0.048	0.348±0.052	0.325±0.076
32	0.450±0.042	0.402±0.044	0.099±0.035
104	0.461±0.040	0.486±0.041	0.357±0.067
110	0.426±0.043	0.433±0.044	0.154±0.046
All pure lines	0.496±0.015	0.499±0.016	0.313±0.023

Table 2: Genetic correlation between cocoon weight, cocoon shell weight and cocoon shell percentage in studied pure lines

Pure line	Cocoon shell weightand cocoon shell percentage	Cocoon weight and cocoon shell percentage	Cocoon weight and cocoon shell weight
31	0.622	-0.074	0.702
103	0.391	0.030	0.923
107	0.452	-0.369	0.772
32	0.268	-0.120	0.910
104	0.640	0.100	0.836
110	0.503	0.177	0.935

Table 3: Environmental correlation between cocoon weight, cocoon shell weight and cocoon shell percentage in studied pure lines

Pure line	Cocoon weight and cocoon shell weight	Cocoon weight and cocoon shell percentage	Cocoon shell weight and cocoon shell percentage
31	0.687	-0.235	0.521
103	0.699	-0.171	0.559
107	0.713	-0.021	0.641
32	0.541	-0.289	0.622
104	0.678	-0.138	0.606
110	0.654	-0.216	0.585
All pure lines	0.666	-0.196	0.577

phenomenon is explained easily because of cocoon shell weight is constituted a part of cocoon weight. Additive genetic correlation between these two traits were between 0.702 (Pure line 31) and 0.935 (Pure line 110). Genetic correlation coefficient between these two traits was 0.831 in all pure lines. From obtained results, there are low genetic correlations between cocoon weight and cocoon shell percentage (-0.369 in pure line 107 and 0.177 in pure line 110) that showed it is difficult improve these two traits simultaneously via breeding programs. This coefficient was negative in pure lines of 31, 107 and 32 and was 00.039 in the total pure lines.

Each of these two traits shared in one of sectors of sericulture industry, since cocoon weight is effective and importance for silkworm rearers (farmers), but cocoon shell percentage is effective and importance for silk factories. Considering the results, if it is definite economic efficiency function for each section separately, the average increscent in each of these characteristics solely can be decreased efficiency of reciprocal economic sector largely. But it must be pointed that the all components of a industrial system have some interactions with each other and it should be definite economic efficiency function based on considering the total profit and subsidiary components (egg production, cocoon, silk fiber and silk textile) at national level. Furthermore, any system planning for trait genetic improvement must be applied based on the relative economic values.

From obtained results, it was achieved positive and moderate additive genetic correlation between cocoon weight and cocoon shell percentage between 0.268 in pure line 32 and 0.640 in pure line 104, which was 0.514 in all pure lines. Since, the most important economic trait in silkworm is cocoon shell weight and this trait also possessing a high correlation with cocoon weight and cocoon shell percentage, with regard to its high heritability and response to selection, it is necessary to emphasize breeding programs must be concentrated on the this trait.

Table 3 shows environmental correlation coefficients between cocoon traits. From obtained results, it was achieved positive and moderate environmental correlation between cocoon shell weight and cocoon shell percentage between 0.521 in pure line 31 and 0.641 in pure line 107, which was 0.577 in all pure lines.

Table 4 shows phenotype correlation coefficients between cocoon traits. From obtained results, it was achieved positive and moderate phenotype correlation between cocoon shell weight and cocoon shell percentage between 0.488 in pure line 103 and 0.617 in pure line 104, which was 0.546 in all pure lines.

Table 5 shows genetic trend (genetic value regression to generation) for pure lines separately. Genetic trend of cocoon weight, cocoon shell weight and selection index in non-selected group were negative only in pure line 31 (-0.016 g, -0.0003 g and -527 Rials per generation, respectively). The highest genetic trend of cocoon weight, cocoon shell weight and selection index belonged to pure line 32 (0.041 g/generation), pure line 107 (0.013 g/generations) and pure line 107 (2961 rials/generation), respectively. Genetic trend of

Table 4: Phenotype correlation between cocoon weight, cocoon shell weight and cocoon shell percentage in studied pure lines

Pure line	Cocoon weight and cocoon shell weight	Cocoon weight and cocoon shell percentage	Cocoon shell weight and cocoon shell percentage
31	0.692	-0.170	0.564
103	0.796	-0.106	0.488
107	0.730	-0.151	0.564
32	0.676	-0.231	0.524
104	0.747	-0.043	0.617
110	0.764	-0.109	0.542
All pure lines	0.742	-0.131	0.546

Table 5: Genetic trend (breeding value regression to generation) of cocoon weight, cocoon shell weight, cocoon shell percentage and selection index in studied pure lines*

	Cocoon weight (g/generation)		Cocoon shell weight (g/generation)		Cocoon shell percentage (percentage/generation)		Selection index (rials/moth/year/generation)	
Pure line	Non-Selected group	Selected group	Non-Selected group	Selected group	Non-Selected group	Selected group	Non-Selected group	Selected group
31	-0.016^{sl}	-0.033^{sl}	-0.003^{sl}	-0.013^{sl}	0.024^{ns}	-0.395^{sl}	-527^{sl}	-3308^{sl}
103	0.010^{sl}	-0.039^{sl}	0.004^{sl}	-0.008^{sl}	0.131^{sl}	0.059^{sl}	990^{sl}	-1252^{sl}
107	0.031^{sl}	0.027^{sl}	0.013^{sl}	0.011^{sl}	0.309^{sl}	0.238^{sl}	2961^{sl}	2493^{sl}
32	0.041^{sl}	0.018^{sl}	0.006^{sl}	0.001^{ns}	-0.209^{sl}	-0.160^{sl}	465^{sl}	-270^{ns}
104	0.010^{sl}	-0.003^{ns}	0.006^{sl}	0.005^{sl}	0.222^{sl}	0.293^{sl}	1559^{sl}	1553^{sl}
110	0.023^{sl}	-0.002^{ns}	0.005^{sl}	0.002^{sl}	-0.060^{sl}	0.087^{sl}	721^{sl}	544^{sl}

* s5: Significant at 0.05 level; sl: Significant at 0.01 level; ns: Non significant

Table 6: Genetic trend (breeding value regression to generation) of cocoon weight, cocoon shell weight, cocoon shell percentage and selection index in all pure lines*

Group	Cocoon weight (g/generation)	Cocoon shell weight (g/generation)	Cocoon shell percentage (percentage/generation)	Selection index (rials/moth/year/generation)
Non-Selected	0.016^{sl}	0.005^{sl}	0.071^{sl}	1030^{sl}
Selected	0.005^{sl}	0.0001^{ns}	0.017^{ns}	-37^{ns}

* s5: Significant at 0.05 level; sl: Significant at 0.01 level; ns: Non significant

cocoon shell percentage in pure line 31 was not significant and these trends were negative in pure lines of 32 (-0.209 percentage/generation) and 110 (-0.060 percentage/generation). The genetic trends of cocoon shell percentage had the highest amount in pure line 107 (0.309 percentage/generation) significantly ($p<0.05$). It is concluded that if low production pure lines mated randomly, due to higher resistance and lower mortality, have high genetic stability and maintenance their genetic potential largely. But since high production pure lines have non-stability genetic structure, it is necessary to applied appropriate selection and breeding programs to keep their production high level.

In selected group, genetic trend of cocoon weight in pure lines 104 and 110 were not significant and were negative in pure lines 31 and 103 (-0.033 and -0.039 g/generation, respectively) and were at the highest level in pure line 107 (0.027 g/generation) significantly ($p<0.01$). Genetic trend of cocoon shell weight was not significant in pure line 32. This trends were negative in pure lines 31 and 103 (-0.013 and -0.008 g/generation, respectively) negative and was at the highest level in 107 pure line 107 (0.011 g/generation). Trend of selection index was not significant in the pure line 32. This trends were negative in pure lines 31 and 103 (-3308 and -1252 rial/generation) and was at the highest level in pure line 107 (2493 rials/generation) significantly ($p<0.01$). Genetic trend of the cocoon shell percentage were negative in pure lines 31 and 32 (-0.395 and -0.160 percentage/generation, respectively) and was at the highest level in pure line 104 (0.293 percentage/generation).

Table 6 is presented genetic trend (genetic value regression to generation) for all pure lines. Genetic trend of total pure lines (Table 6) indicates that the genetic trends were significant and positive in non-selected population for cocoon weight (0.016 g/generation),

Table 7: Phenotype trend (phenotype value regression to generation) of cocoon weight, cocoon shell weight, cocoon shell percentage and selection index in studied pure lines*

	Cocoon weight (g/generation)		Cocoon shell weight (g/generation)		Cocoon shell percentage (percentage/generation)	
Pure line	Non-Selected group	Selected group	Non-Selected group	Selected group	Non-Selected group	Selected group
31						
103	-0.096^{sl}	-0.136^{sl}	-0.026^{sl}	-0.043^{sl}	-0.347^{sl}	-0.884^{sl}
107	0.071^{sl}	-0.143^{sl}	-0.019^{sl}	-0.037^{sl}	-0.234^{sl}	-0.339^{sl}
32	-0.049^{sl}	-0.072^{sl}	-0.011^{sl}	-0.016^{sl}	-0.069^{ns}	-0.058^{ns}
104	-0.036^{sl}	-0.083^{sl}	-0.017^{sl}	-0.027^{sl}	-0.659^{sl}	-0.567^{sl}
110	-0.067^{sl}	-0.106^{sl}	-0.017^{sl}	-0.024^{sl}	-0.163^{s5}	-0.074^{ns}
	-0.049^{sl}	-0.105^{sl}	-0.016^{sl}	-0.026^{sl}	-0.456^{sl}	-0.306^{sl}

* s5: Significant at 0.05 level; sl: Significant at 0.01 level; ns: Non significant

Table 8: Phenotype trend (phenotype value regression to generation) of cocoon weight, cocoon shell weight, cocoon shell percentage and selection index in all pure lines*

Group	Cocoon weight (g/generation)	Cocoon shell weight (g/generation)	Cocoon shell percentage (percentage/generation)
Non-Selected	-0.061^{sl}	-0.018^{sl}	-0.314^{sl}
Selected	-0.108^{sl}	-0.029^{sl}	-0.379^{sl}

* s5: Significant at 0.05 level; sl: Significant at 0.01 level; ns: Non significant

cocoon shell weight (0.005 g/generation), cocoon shell percentage (0.071 percentage/generation) and selection index (1030 rials/generation) ($p<0.01$); whereas this trend was negative in selected populations for cocoon weight (-0.005 g/generation) ($p<0.01$). Also, these trends were not significant in selected populations for cocoon shell weight, cocoon shell percentage and selection index.

Table 7 shows phenotypic trend (phenotypic value regression to generation) for pure lines separately. Phenotypic trend of the cocoon weight, cocoon shell weight and cocoon shell percentage in selected and non-selected groups were negative and significant ($p<0.01$) and this trend was not significant only in pure lines of 107 and 104 for cocoon shell percentage (Table 7). Phenotypic trend of the cocoon weight and cocoon shell weight in selected group were less than non-selected group. Only phenotypic trend of cocoon shell percentage in pure lines of 32 and 110 in selected group were higher than non-selected group. In non-selected group, phenotypic trend of the cocoon weight, cocoon shell weight and cocoon shell percentage were at the highest level in pure line 32 (-0.036 g/generation), 107 (-0.011 g/generation) and 103 (-0.234 percentage/generation) respectively. Also, phenotypic trend of the cocoon weight, cocoon shell weight and cocoon shell percentage in non-selected group were at the lowest level in pure line 31 (-0.096 g/generation), 31 (-0.026 g/generation) and 32 (-0.659 percentage/generation) respectively. In selected group, phenotypic trend of the cocoon weight, cocoon shell weight and cocoon shell percentage were at the highest level in pure line 107 (-0.072 g/generation), 107 (-0.016 g/generation) and 110 (-0.306 percentage/generation) respectively. Also, phenotypic trend of the cocoon weight, cocoon shell weight and cocoon shell percentage in selected group were at the lowest level in pure line 103 (-0.143 g/generation), 31 (-0.043 g/generation) and 31 (-0.884 percentage/generation), respectively.

Table 8 shows phenotypic trend (phenotypic value regression to generation) for all pure lines. From Table 8 it is showed that phenotypic trend of cocoon weight, cocoon shell weight and cocoon shell percentage in non-selected population (-0.061, -0.018 g/generation and -0.314 percentage/generation, respectively) are higher than selected population (-0.108, -0.029 g/generation and -0.379 percentage/generation), respectively ($p<0.01$).

DISCUSSION

Ghanipoor *et al.* (2007) also were demonstrated lower heritability for cocoon shell percentage. Heritability of cocoon weight in pure lines of 107 and 32 were higher than compare with the cocoon shell weight.

Lower heritability for cocoon shell percentage means cocoon shell has low genetic diversity and affected under environmental conditions largely. Therefore improvement progress in the breeding programs for this trait especially under individual selection will be difficult. Ghanipoor *et al.* (2006b) studied based on the characteristics of the 10000 records belonged some silkworm pure lines during nine generations and showed that additive genetic variance for cocoon weight in pure lines of 107, 153 and 154 are higher than other pure lines. Also additive genetic variance for cocoon shell weight in pure lines of 110, 101433 and Y were higher than other pure lines. Meanwhile they reported environmental variance for the cocoon shell percentage was higher than other cocoon traits. Mirhosseini *et al.* (2004) were estimated cocoon weight heritability between 0.374-0.500, cocoon shell weight heritability between 0.366-0.752 and cocoon shell percentage heritability between 0.192-0.337. Mirhosseini *et al.* (2005b) estimated the genetic parameters of economic characteristics for native breeds of silkworm. They are believed there is high heritability for most economic characteristics.

Previously, Ghanipoor *et al.* (2007) found that the selection based on index in pure lines have significant effect on improvement the cocoon weight and cocoon shell percentage in silkworm hybrids. Also, Ghanipoor *et al.* (2007) showed heritability of cocoon shell percentage is lower than cocoon weight and cocoon shell weight. Ghanipoor *et al.* (2005) in another study showed heritability of laying traits in pure line are between 0.08-0.27, heritability percentage of fertility are between 0.03-0.26 and heritability of hatching percentage are between 0.03-0.16. Mirhosseini *et al.* (2004) estimated high heritability for cocoon weight and cocoon shell weight. They were estimated low heritability for cocoon shell percentage. They realized that the high genetic correlation between cocoon shell weight with two other traits, it is expected by selecting of individual based on cocoon shell weight can improve on correlated characteristics e.g. cocoon weight and cocoon shell percentage. Mirhosseini *et al.* (2007c) investigated on the effect of sexuality characteristics on cocoon trait feasibilities and they concluded heritability of cocoon weight, cocoon shell weight and cocoon shell percentage in males were higher than female sex. Thus it cans accelerate genetic gain in males using high selection pressure. Mirhosseini *et al.* (2005b) and Mavvajpoor *et al.* (2006) showed that economic characteristics of native silkworm have high heritability and it is possible their improvement based on appropriate planning in long-term. Mu *et al.* (1995) analyzed the eight traits in two Chinese and three Japanese varieties and realized pupation rate, cocoon shell weight, cocoon weight, cocoon shell percentage, cocoon production and weight of 10000 larva controlled by some genes with additive and dominant effects. But they did not fount any epistatic effect on these traits. They also expressed cocoon shell weight, cocoon shell percentage and cocoon weight of 10000 larva controlled mainly by the relative dominance genes, but other characteristics inherited mainly as dominant. These researchers were also subject to the specific heritability of cocoon shell weight, cocoon shell percentage and cocoon weight of 10000 larva are more than other characteristics. Similar reports published by Chatterjee *et al.* (1993).

Seidavi *et al.* (2008a) studied effect of phenotypic selection for parents based on cocoon weight on the reproductive characteristics and reminded that there are positive genetic correlation between productive and reproductive characteristics in the Chinese pure lines and individual selection cause improvement of reproductive characteristics. Mirhosseini *et al*. (2002) showed that the some trait response against direct selection is caused to high heritability. Also, there are high genetic correlations between some characteristics of pure line and selection for each one of these characteristics can improve the expected correlated trait. Ghanipoor *et al*. (2006c) in another study were found that in some pure lines due to negative genetic correlations are likely to reduce reproductive potential against increscent of selection pressure for cocoon traits. Grekov (1989) stated there is a positive correlation between the weight of cocoon shell weight and cocoon weight (+0.659) and thus selection should be applied based on cocoon shell weight, but it must also be considered the cocoon weight and fiber length simultaneously. Petkov (1989) also studied genetic properties of some new silkworm varieties and found correlation between cocoon shell weight and cocoon shell percentage is 0.528-0.653. He suggested pure line selection applied based on cocoon shell weight, but it be considered cocoon weight and fiber length. Rangaiah *et al*. (1995) studied fertility, larval growth, larvae weight, cocoon weight, shell cocoon weight and cocoon shell percentage in 18 silkworm varieties. They calculated phenotypic and genotype correlations between six traits. They emphasized that genotypes correlation are higher than phenotypic correlations in all cases. Cocoon weight, cocoon shell weight and cocoon shell percentage had positive correlations with fertility and they are therefore proposed breeding programs must be emphasized on these trait selection.

Obtained results regarding additive genetic correlation between these traits is accordance with results of Nagaraja *et al*. (1996b), Mirhosseini *et al*. (2004, 2007a, b). Mirhosseini *et al*. (2002) in another study also reported genetic correlation between cocoon weight and cocoon shell weight are 0.709-0.989, the genetic correlation between cocoon weight and cocoon shell percentage is -0.124-0.564 and additive genetic correlation between cocoon shell weight and cocoon shell percentage is 0.270-0.835 in studied pure lines.

Generally, genetic trend of traits in non-selected groups were higher than selected groups. It is due to genetic tangible decline of the traits under non-breeding programs in the successive generations. At this group also it is found low production pure line (107) had higher genetic stability than high production pure lines (31 and 103). Mirhosseini *et al*. (2005a) studied the genetic trend of biological and quantitative characteristics of silkworm populations under high selection pressure and found genetic improvement will decline and decrease in successive generations due to loss of genetic diversity. Mirhosseini *et al*. (2008) obtained a positive genetic trend for the genotype value (genetic competency) during the 8 generations.

Present results have significance outputs and also provided experiment aim and goals. Based on obtained results, we can use these results and suggestions for future silkworm breeding programs and performance improvement of silkworm pure lines.

Finally, obtained results about phenotypic and genotype trends in pure lines had similar results. Ghanipoor *et al*. (2006a) also reviewed phenotypic trend of the production traits in silkworm under genetic selection condition and demonstrated phenotypic trend and improvement of economical traits are different in pure lines and affected by various factors like heritability. Also, differences between studied genotypes and other genotypes in other studies are possible reason where results differ from previous studies.

CONCLUSION

As conclusions it should be expressed the genetic parameters such as heritability and genetic correlation between economic traits are different in silkworm pure lines. Thus, it must be selected appropriate strategy for each pure line. Response to selection for cocoon weight and cocoon shell weight were high, since these two traits have higher heritability than cocoon shell percentage. Genetic correlation between weight cocoon- cocoon shell weight, cocoon shell weight-cocoon shell percentage and cocoon weight - cocoon shell percentage were high, moderate and low, respectively. So, using the selection cocoon shell weight can improve the correlated traits. The genetic trends of traits in the non-selected populations were negative and significant which indicates there is a kind of un-wanted breeding program. Finally, phenotypic trend of traits were negative in selected and non-selected populations which cleared environmental conditions will decline at successive generations.

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