

## Additive Genetic Variations and Selection Index Changes of Economic Traits of the Silkworm Commercial Pure Lines Against Parent Selection Pressure

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**Abstract:** This experiment was conducted in order to investigation on additive genetic changes and selection index changes of silkworm economic traits including cocoon weight, cocoon shell weight and cocoon shell percentage under individual selection pressure based on cocoon weight. Individual selection of parents were applied in selected group for one generation in all studied pure lines. No selection performed in non-selected group. Silkworms were reared at four successive generations without further selection. Population covariance components are calculated and additive genetic values and economic genetic improvement (selection index change) of individuals were predicted using Best Linear Unbiased Prediction. Response to selection for cocoon weight and correlated trait like cocoon shell weight in the first generation for pure lines 103 and 104 was higher than other pure lines. Additive genetic changes of the cocoon shell percentage were negative in the selected group of pure lines 31 and 32. Obtained results indicated that the genetic changes in total generations were negative for cocoon weight, cocoon shell weight and the selection index. Negative changes are due to loss resulting failure to selection performing and reduce the frequency of high productive genes.

**Key words:** Gain • Improvement • Genetic • *Bombyx mori* • index

### INTRODUCTION

Sericulture have huge role in rural economy in many countries. Silkworm varieties are the most important items for development of silk industry. They are the key factor determining quality of silkworm eggs. Meanwhile, they directly influence the initiative of silkworm raisers and the quality of cocoon and silk [1]. Hence silkworm breeding and genetics have critical role in performance improvement of *Bombyx mori*.

Mirhosseini *et al.* [2] studied effects of selection by means of selection index based on cocoon traits on genetic changes of reproductive traits. They showed selection based on cocoon weight have the highest positive effect on the laying traits, while the rate of genetic changes was small for hatchability.

Ashoka and Govindan [3] determined genetic properties including phenotypic and genetic variance, covariance, heritability and genetic gains for nineteen

economic traits. They demonstrated genotype covariance constitute major component of the phenotypic covariance for all studied traits. They had also expressed there are high heritability and genetic improvement for the larva number, cocoon weight, cocoon number, cocoon shell weight, fiber length and fiber weight, which indicates there is additive gene effects. Thus basen on their findings we can improve offspring performance using phenotype selection. Larval period, pupation period and cocoon shell percentage had moderate heritabilities and low genetic gains showed that these traits control by non-additive gene effects and hence hybridization and continual selection gives better results for these traits improvement.

Narasimaraju *et al.* [4] also studied genetic properties of eighteen traits in silkworm and found genetic changes of studied traits are between 8.62-48.66% and the larval weight, cocoon shell weight, fiber length, fiber weight fiber denier have genetic changes above 20%.

Satenahalli *et al.* [5] also showed cocoon shell weight, fiber length and larval weight have high heritability and genetic gains. They also concluded that there are positive correlation between pupa weight, cocoon weight, cocoon shell weight, the maximum larval weight, fiber length, pupation period, fiber diameter, fecundity, and hatchability.

At the present time, there is little information about the effect of individual selection based on the cocoon weight on additive genetic and selection index changes of economic trait silkworm. Therefore, this experiment was conducted in order to investigation on additive genetic changes and selection index changes of silkworm economic traits including cocoon weight, cocoon shell weight and cocoon shell percentage under individual selection pressure based on cocoon weight. This experiment will study selection efficiency for additive genetic gains and selection index improvement in economic traits.

## **MATERIALS AND METHODS**

This study was conducted using six silkworm varieties 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 (parent parent parent) 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 that 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, 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 that 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, 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 recorded 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.

Additive genetic and environmental covariance (residual effects) components were estimated for triple traits 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) [6]. It were used the DXMUX program, POWELL Procedure and DFREML software version 3.1 with convergence  $10^{-8}$ .

Population covariance components are calculated and additive genetic values of individuals were predicted using Best Linear Unbiased Prediction (BLUP) by means of DFREML software. The information of person, her (his) family and other their relatives are used to increment of prediction accuracy. The genetic value mean of

individuals were estimated in each generation and group of pure lines, and then it was estimated additive genetic improvement in one generation (generation n+1) using the following equation:

$$\Delta G_{(n+1),n} = \bar{G}_{n+1} - \bar{G}_n$$

**Which:**

$\Delta G_{(n+1),n}$  = additive genetic improvement of trait in one generation,  $\bar{G}_{n+1}$  = additive genetic value mean in generation n+1, and  $\bar{G}_n$  = additive genetic value mean in generation n.

Additive genetic improvement of total traits was estimated in generation n using the following equation:

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

**Which:**

$\Delta G_{n,0}$  = additive genetic improvement of total traits in one generation in compare with non-selected groups,  $\bar{G}_n$  = additive genetic value mean in generation n, and  $\bar{G}_0$  = additive genetic value mean in generation 0.

Additive genetic improvement of traits was estimated in selected group in compare with non-selected group after one selection generation using the following equation:

$$\Delta G_{s,c} = \bar{G}_{s0} - \bar{G}_{c0}$$

**Which:**

$\Delta G_{s,c}$  = additive genetic improvement of trait in selected group during generation 0 in compare with non-selected groups,  $\bar{G}_{s,0}$  = additive genetic value mean in selected group during generation 0, and  $\bar{G}_{c,0}$  = additive genetic value mean in non-selected group during generation 0.

It was necessary to calculate the true genetic improvement in first to third generations of the selected group, all individuals records in selected groups at all generations be corrected for selection effect (It must be subtracted from the correction factor). Correction factor was  $\Delta G_{s,c}$  or  $\Delta F_{s,c}$  which were equal based on theory.

Economic genetic improvement (selection index change) in one generation (generation n+1) was estimated using the following equation:

$$\Delta I_{(n+1),n} = \bar{I}_{n+1} - \bar{I}_n$$

**Which:**

$\Delta I_{(n+1),n}$  = economic genetic improvement in one generation,  $\bar{I}_{n+1}$  = economic genetic value mean in generation n+1, and  $\bar{I}_n$  = economic genetic value mean in generation n.

Genetic generation of economic improvement in all n using the following relationship was estimated:

Total economic genetic improvement in generation n was estimated using the following equation:

$$\Delta I_{n,0} = \bar{I}_n - \bar{I}_0$$

**Which:**

$\Delta I_{n,0}$  = total economic genetic improvement in selected group during one generation in compare with non-selected groups,  $\bar{I}_n$  = economic genetic value mean in generation n, and  $\bar{I}_0$  = economic genetic value mean in generation 0.

Economic genetic improvement was estimated in selected group in compare with non-selected group after one selection generation using the following equation:

$$\Delta I_{s,c} = \bar{I}_{s0} - \bar{I}_{c0}$$

**Which:**

$\Delta I_{s,c}$  = economic genetic improvement in selected group during generation 0 in compare with non-selected groups,  $\bar{I}_{s0}$  = economic genetic value mean in selected group during generation 0, and  $\bar{I}_{c0}$  = economic genetic value mean in non-selected group during generation 0.

General Linear Model (GLM) was used for data analysis and SAS 6.12 software was used for statistical analysis and their significant using DNMRT method [7, 8].

**RESULTS AND DISCUSSION**

In Tables 1, 2, and 3 are present the rate of additive genetic changes of cocoon weight, cocoon shell weight and cocoon shell percentage in pure lines during the four generations based on selected and non-selected groups. In Table 4 also is showing the rate of selection index changes during four generations. Meanwhile, In Table 5 is present the rate of genetic changes and selection index changes of total traits. The mean of genetic value and selection index in non-selected group at the first generation were consider as base (zero) and the rate of changes were measured in comparison with these values. The response to selection for cocoon weight and correlated trait like cocoon shell weight in the first generation for pure lines 103 and 104 was higher than other pure lines. The response to individual selection has direct relationship with trait heritability [1]. Selection intensity at the present study was similar for all pure lines. The obtained results shows the response to selection are high in pure lines 103 and 104 which these pure lines have high heritabilities for cocoon weight and cocoon shell weight.

Table 1: Additive genetic changes in studied pure lines for cocoon weight (gr) at four successive generations (n) in selected and non-selected groups\*

Pure Line	Generation 1		Generation 2		Generation 3		Generation 4	
	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected
31	0	0.166	0.120	-0.006	-0.013	-0.018	-0.065	-0.058
103	0	0.175	0.057	-0.075	0.052	0.044	-0.053	-0.124
107	0	0.134	0.031	-0.073	-0.018	-0.020	0.087	0.112
32	0	0.154	0.018	-0.069	0.075	0.126	0.010	-0.072
104	0	0.203	0.063	-0.054	0.013	-0.010	-0.013	0.023
110	0	0.169	0.091	-0.030	-0.077	-0.112	0.116	0.128

\*Additive genetic changes in first generation= $g_{selected}-g_{non-selected}$

\*Additive genetic changes in other generations= $g_{n+1}-g_n$

Table 2: Additive genetic changes in studied pure lines for cocoon shell weight (gr) at four successive generations (n) in selected and non-selected groups\*

Pure Line	Generation 1		Generation 2		Generation 3		Generation 4	
	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected
31	0	0.0388	0.0312	-0.0012	-0.0121	-0.0096	-0.0053	-0.0214
103	0	0.0423	0.0167	-0.0217	0.0112	0.0086	-0.0088	-0.0233
107	0	0.0212	0.0135	-0.0014	-0.0037	0.0028	0.0304	0.0240
32	0	0.0326	-0.0038	-0.0189	0.0171	0.0283	-0.0034	-0.0232
104	0	0.0453	0.0077	-0.0219	0.0091	0.0088	0.0013	0.0092
110	0	0.0368	0.0246	-0.0094	-0.0192	-0.0227	0.0265	0.0328

\*Additive genetic changes in first generation= $g_{selected}-g_{non-selected}$

\*Additive genetic changes in other generations= $g_{n+1}-g_n$

Table 3: Additive genetic changes in studied pure lines for cocoon shell percentage (%) at four successive generations (n) in selected and non-selected groups\*

Pure Line	Generation 1		Generation 2		Generation 3		Generation 4	
	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected
31	0	0.028	0.168	0.004	-0.406	-0.275	0.449	-0.661
103	0	0.014	0.164	-0.196	0.039	-0.67	0.222	0.272
107	0	-0.315	0.336	0.690	0.022	0.408	0.618	-0.100
32	0	-0.148	-0.381	-0.167	-0.112	-0.034	-0.259	-0.299
104	0	-0.017	-0.297	-0.400	0.345	0.561	0.258	0.230
110	0	-0.038	0.216	-0.180	-0.177	0.020	-0.021	0.250

\*Additive genetic changes in first generation= $g_{selected}-g_{non-selected}$

\*Additive genetic changes in other generations= $g_{n+1}-g_n$

Table 4: Selection index changes in studied pure lines (Rials/moth/year) at four successive generations (n) in selected and non-selected groups\*

Pure Line	Generation 1		Generation 2		Generation 3		Generation 4	
	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected
31	0	6742	5791	-211	-3119	-2361	236	-5394
103	0	7311	3294	-4237	2036	1304	-940	-3317
107	0	2861	3188	1515	-582	1524	6816	3877
32	0	5225	-1629	-3684	2638	4788	-1252	-4753
104	0	7752	576	-4776	2452	2948	894	2173
110	0	6232	4778	-2091	-3759	-3866	4500	6284

\*Selection index changes in first generation= $I_{selected}-I_{non-selected}$

\*Selection index changes in other generations= $I_{n+1}-I_n$

Table 5: Total additive genetic and selection index changes (four generations) in studied pure lines in selected and non-selected groups\*

Pure Line	Cocoon weight (gr)		Cocoon shell weight (gr)		Cocoon shell percentage (%)		Selection index (Rials/moth/year)	
	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected	Non-Selected	Selected
31	0.042	-0.082	0.0138	-0.0323	0.211	-0.936	2908	-7966
103	0.057	-0.155	0.0191	-0.0365	0.425	0.008	4389	-6250
107	0.100	0.018	0.0402	0.0254	0.975	0.999	9421	6916
32	0.103	-0.015	0.0098	-0.0138	-0.752	-0.500	-244	-3649
104	0.064	-0.040	0.0182	-0.0039	0.306	0.390	3921	345
110	0.130	-0.014	0.0319	0.0006	0.018	0.090	5519	327

Gholami *et al.* [9] showed the cocoon shell weight has the highest genetic improvement and cocoon shell percentage has the lowest genetic improvement. The low response to selection in pure line 107 was due to low heritability of cocoon weight in this pure line. Mirhosseini *et al.* [10] also showed there is low genetic gain in pure line 107. In addition, due to low correlation between the cocoon weight and cocoon shell weight, there is low correlated response of cocoon shell weight for this pure line (0.0212 g). Correlated response to selection of cocoon shell percentage was positive for pure lines 31 and 103 and negative for other pure lines in the first generation.

Ghanipoor *et al.* [11] limited cocoon weight trait for the selection index and showed genetic improvement of cocoon shell percentage will increase. Improvement amount of selection index in the first generation according to cocoon weight and cocoon shell weight were high in pure lines 103 and 104 and low in pure line 107. Similar reports regarding genetic silkworm published by Nagaraju and Goldsmith [12].

Ghanipoor *et al.* [13] showed that selection by index have the high efficiency for genetic improvement for cocoon weight and cocoon shell percentage. Genetic changes in the second generation for cocoon weight, cocoon shell percentage and selection index were negative in the selected group, and positive in the non-selected group. Their result indicated that high selection pressure in populations result to loss of their genetic structure quickly, if it did not controlled their mates. Change averages of the selection index in the second generation were positive for pure line 107 since response to selection was low for cocoon weight and cocoon shell weight in the previous generation. Obtained result about genetic changes in third and fourth generations does not reveal certain trends. Mirhosseini *et al.* [14] also studied the effect of genetic selection by the index on economic genetic growth and showed different but positive responses.

Total additive genetic and selection index changes at four generations in studied pure lines in selected and non-selected groups is shown in Table 5. These results indicated that the genetic changes in total generations were negative for cocoon weight, cocoon shell weight and the selection index. Negative changes are due to loss resulting failure to selection performing and reduce the frequency of high productive genes. One of possible reasons of negative changes is random drift of gene due to small population size; while the populations without any selection programs indicate positive change and

trends. It is possible non-selected populations affected by the kind of non-known or uninformed selection due to selection of big cocoons. This reason can be justify a positive improvement in genetic improvement of cocoon weight and cocoon shell weight. Similar reports regarding genetic silkworm published by Kumaresan *et al.* [15].

Additive genetic changes of the cocoon shell percentage were negative in the selected group of pure lines 31 and 32. Gholami *et al.* [9] estimated genetic improvement of cocoon traits under selection pressure by selection index during five generations. According to their findings, genetic improvement of cocoon weight were between 0.176-0.427 gr, genetic improvement of cocoon shell weight were between 0.049-0.132 gr and genetic improvement of cocoon shell percentage were between 0.88-2.25%. These changes correlated with trait heritabilities and confirmed our results.

Ghanipoor *et al.* [16] studied six different selection strategies including two types of normal indices, two types of limited indices and two types of basic indices for genetic improvement of the silkworm economic traits. They have suggested that the selection indices have huge role for genetic improvement of traits. Mirhosseini *et al.* [17] also evaluated genetic improvement of the cocoon weight, cocoon shell weight and cocoon shell percentage. They demonstrated index programs have high efficiency for improvement of cocoon shell percentage, while phenotypic selection programs have better efficiency for some other pure lines for improvement of cocoon shell percentage. Ghanipoor *et al.* [11] showed if there were limited input, genetic improvement of cocoon weight would be high. However, while if there were non-limited input, genetic improvement of cocoon shell weight and cocoon shell percentage would be high. Our results correlated with these reports and confirmed their results.

As conclusion, responses to selection were high in pure lines 103 and 104 that these pure lines have high heritabilities for cocoon weight and cocoon shell weight. Hence, it is suggest selection programs apply in these pure lines for their performance improvement and rural economic development.

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