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Performance and Cocoon Color Segregation Manifested in Hybrids Between Native Races and Two Commercial Lines of Silkworm in Five Successive Generations

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Abstract: Five Iranian native silkworm races including Baghdad, Khorasan Orange, Guilan Orange, Khorasan Pink, Khorasan Lemon and two commercial lines of 107 and 110 were selected and reared using 12 families per each variety during the three years 2003-2005 included five generations in two seasons spring and autumn. In each family, 30 male cocoons and 30 female cocoons were individually recorded for cocoon weight, shell weight and shell ratio. The highest average of cocoon weight in the hybrids belonged to 107×Baghdad and Baghdad×107 ($P<0.05$). The highest average of cocoon shell weight belonged to Baghdad×107 and Guilan orange×107 ($P<0.05$). Also the highest average of shell ratio belonged to Khorasan orange×107 and Guilan orange×107 ($P<0.05$). Totally means of traits in native races with 107 were higher than native races with 110 ($P<0.05$). The obtained results manifested that the colored cocoons trait dominated over the character white cocoons in F1. The segregation obtained in the F2 generation was as 3 parts colored and one part white cocoons. The segregation obtained in first back-cross (BC1) was as 1 part colored and 1 part white cocoons. The cocoon color in F2 and BC1 had significant differences ($P<0.05$). From obtained data it is suggested that the responsible genes for the cocoon color in these varieties are presented as multi alleles in the silkworm population of the Iranian native races.

Key words: Native % *Bombyx mori* L. % Cocoon Color % Hybrids % Segregation

INTRODUCTION

Native silkworm races have the low performance and could not be commercially employed. Indigenous strains are valuable genetic resources. They have been affected by natural selection in the successive generations and adapted to indigenous diseases and environmental conditions. Genetic and phenotypic characterization of locally available native silkworm populations provides essential information to make rational decisions for the improvement and development of effective breeding programs (5). Also among economic characters of silkworm, pupation rate, single cocoon weight, cocoon shell weight and cocoon shell percentage are the main factors affecting the high yielding of cocoon [1].

It is a well known fact that there are a lot of genes and multi-alleles responsible for the cocoon color segregation [2]. The main cocoon color are yellow, golden yellow, pink, flesh, green and colorless or white. According to Lim *et al*. [3], the yellow and pinkish colors are due to carotinoids, carotenes and xanthophylls from the mulberry leaves. These colors are secreted from the middle silk gland and pigmented in sericine. The green color originates from the flavonoids and is secreted from the middle and posterior silk gland both. Taking into account that the carotinoids and xanthophyll have different biochemical structure compared to the flavonoids, it could be supposed that different genes are responsible for the yellow and for the green colors [2].

Kovalev and Sheveleva [4] reported that the silkworm larvae having yellow haemolimph could spin yellow as well as white cocoons, however the larvae with colorless haemolimph were able to spin white cocoons only. According to lim *et al*. [3], who cited some Japanese authors the known genes, responsible for yellow colored cocoons are C-golden yellow, Cd-light yellow, Ci-inner layer yellow, dy-dilute yellow, Y-yellow blood, Ya-mandarin yellow blood, Yc-yellow cocoon, Yf-yellow

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fluorescent and Yr-yellow brown. Tazima [2] reported that the gene Y was responsible for the yellow blooded larvae and yellow cocoon and was located on the second chromosome, 25.6 locus. The genes I and Is are known as yellow inhibitors which completely suppress Y and are responsible for the white cocoon. Lea [5] reported the genes responsible for the green cocoon are Ga, Gb and Gc.

Iranian silkworm native races have valuable potential and genes [6]. To date, there is not any study about colored cocoon production and genetics potential in Iranian native races. Hence, the present study was undertaken to acquire new races of silkworm, which can be high performance of productivity under future conditions. Simultaneous application of commercial lines and natives races is very useful in breeding programs [6]. On the other hand, it is important quality of segregation of cocoon color trait. This study was aimed to evaluate the cocoon color segregation manifested in hybrids between Iranian native and two commercial silkworm (*Bombyx mori* L.) races.

MATERIALS AND METHODS

The experiment has been undertaken during the period of 2003-2005 at the Iran Silkworm Research Center (ISRC). Five native silkworm races were used with colored cocoons included Khorasan orange, Khorasan lemon, Khorasan pink, Guilan orange and Baghdad (faint yellow color) and two commercial lines 107 and 110 with white cocoons. The line 107 was originated from the Japanese hybrid which breed during 10 generations in ISRC and had been introduced as a commercial line 107 from 2000. The origin of the line 110 was South Korean hybrid which breed during 9 generations in ISRC and had been introduced as a commercial line 110 from 1998.

All races were uni-bivoltine and were selected and reared for five generations in spring and autumn. In each family, 30 male cocoons and 30 female cocoons were individually recorded for cocoon weight (g), cocoon shell weight (g) and cocoon shell ratio (%). The data included approximately 40790 records on cocoon characteristics.

In the mating program, native races crossed with lines of 107 and 110. The F1, F2 and BC1 generations obtained using inbreeding and appropriate crosses. In each generation, various families for each race and hybrid have been reared under standard conditions until end of larval duration. The obtained cocoons were harvested separately, cleaned from the floss and divided according to their color, namely colored and white cocoons respectively. The group of the white cocoons included only white color without any nuances. The cocoons of each family were counted and was calculated the percentage of colored and white cocoons towards the sum of whole cocoons.

Then the correlation between the phenotypic segregation of the cocoon color and the theoretically expected one has been expressed by the criterion-chi-square and the data significance is tested based to fisher test. Collected data were subjected to statistical analysis of variance test to find out the low significant differences between each set of treated groups. For all analyses of variance, it is used Duncan’s Multiple Range Test using SPSS software.

RESULTS AND DISCUSSION

The obtained results showed highly significant variability for cocoon character means. Crosses of Baghdad, Guilan orange and Khorasan orange races with line 107 had better productive performance than other crosses (Figs. 1-3). Therefore selection based on above characters will be highly effective for performance improvement. Also it can conclude that some native races have promising future and could play important role in Iran’s sericulture industry.

Comparative means of economical traits are shown in Figs. 1-3. The highest average of cocoon weight (since up to down) in the hybrids belonged to 107×Baghdad, Baghdad×107, Khorasan lemone×107, 110×Baghdad and Khorasan pink×107. In the shell weight, the highest average (since up to down) in the hybrids belonged to Baghdad×107, Guilan orange×107, Khorasan lemone×107, 107×Baghdad and Khorasan pink×107, respectively. The highest average of shell ratio (since up to down) in the hybrids belonged to Khorasan orange×107, Guilan orange×107, Baghdad×107 and Khorasan pink×107. Totally means of traits in hybrids native silkworm races with 107 were upper than hybrids native silkworm races with 110, respectively.

Mirhosseini *et al*. [7] reported that the highest average of cocoon weight, shell weight, shell ratio, fecundity, fertility and hatchability belonged to Guilan (1.722 gr), Khorasan pink (0.318 gr), Khorasan pink (19.41 %), Khorasan orange (511.98), Khorasan Orange (92.01 %) and Guilan (87.86 %), respectively. Mean analysis of the studied characters showed that Khorasan lemon group had low production and reproduction potential and improvement of its performance takes much time.

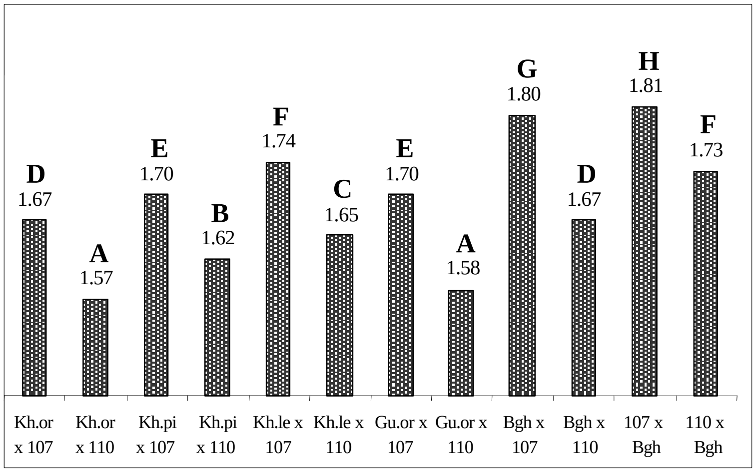

Fig. 1: Cocoon weight trait in different crosses at successive generations (g); Duncan test: Alpha = 0.05

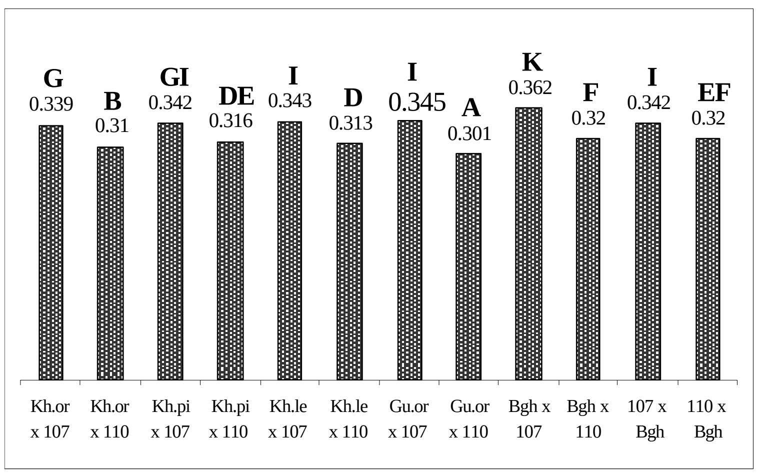

Fig. 2: Cocoon shell weight trait in different crosses at successive generations (g); Duncan test: Alpha = 0.05

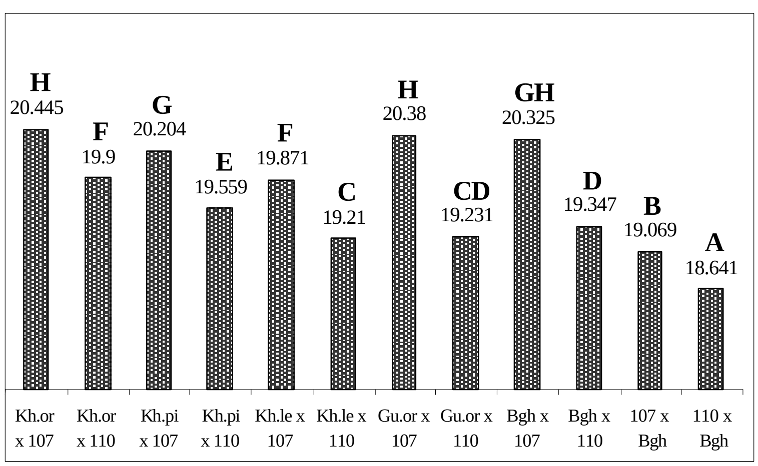

Fig. 3: Cocoon shell ratio trait in different crosses at successive generations (%); Duncan test: Alpha = 0.05

Table 1: Segregation of the cocoon color character in the crosses between Iranian native races and commercial lines of 107 and 110

Crosses	Number of family	Number of produced cocoons	Cocoon color in offspring: Colored		Cocoon color in offspring: White		Theoretically expected segregation	P^2 chi square	Significance
			Number	%	Number	%			
Guilan orange×107 (F1)	11	2509	2509	100.00	0	0.00	1	-	-
Guilan orange×107 (F2)	9	1688	421	24.94	1267	75.06	3:1	0.955	ns
Guilan orange×107(BC1)	9	1871	901	48.15	970	51.85	1:1	0.111	ns
Guilan orange×110 (F1)	11	1680	1680	100.00	0	0.00	1	-	-
Guilan orange×110 (F2)	9	1745	453	25.96	1292	74.04	3:1	0.354	ns
Guilan orange×110 (BC1)	9	1976	944	47.77	1032	52.27	1:1	0.048	ns
Khorasan orange×107 (F1)	14	3203	3203	100.00	0	0.00	1	-	-
Khorasan orange×107 (F2)	9	1865	492	26.38	1373	73.62	3:1	0.169	ns
Khorasan orange×107 (BC1)	9	2027	1004	49.53	1023	50.47	1:1	0.673	ns
Khorasan orange×110 (F1)	14	3045	3045	100.00	0	0.00	1	-	-
Khorasan orange×110 (F2)	9	1966	510	25.82	1456	74.18	3:1	0.398	ns
Khorasan orange×110 (BC1)	9	2006	992	49.45	1014	50.55	1:1	0.623	ns
Khorasan pink×107 (F1)	14	3105	3105	100.00	0	0.00	1	-	-
Khorasan pink×107 (F2)	9	1762	447	25.37	1315	74.63	3:1	0.721	ns
Khorasan pink×107 (BC1)	9	1841	940	51.06	901	48.94	1:1	0.363	ns
Khorasan pink×110 (F1)	14	3045	3045	100.00	0	0.00	1	-	-
Khorasan pink×110 (F2)	9	1777	471	26.51	1306	73.49	3:1	0.143	ns
Khorasan pink×110 (BC1)	9	1744	867	49.71	877	50.29	1:1	0.811	ns
Khorasan lemone×107 (F1)	14	3321	3321	100.00	0	0.00	1	-	-
Khorasan lemone×107 (F2)	9	1750	429	24.51	1321	75.49	3:1	0.636	ns
Khorasan lemone×107 (BC1)	9	1897	973	51.29	924	49.71	1:1	0.261	ns
Khorasan lemone×110 (F1)	14	3045	3045	100.00	0	0.00	1	-	-
Khorasan lemone×110 (F2)	9	1599	437	27.33	1162	72.67	3:1	0.031	ns
Khorasan lemone×110 (BC1)	9	1807	862	47.70	945	52.30	1:1	0.051	ns
Baghdad×107 (F1)	14	2334	2334	100.00	0	0.00	1	-	-
Baghdad×107 (F2)	9	3641	488	26.61	1346	75.49	3:1	0.112	ns
Baghdad×107 (BC1)	9	1861	968	51.19	893	49.81	1:1	0.082	ns
Baghdad ×110 (F1)	14	2526	2526	100.00	0	0.00	1	-	-
Baghdad ×110 (F2)	9	1738	418	24.05	1320	75.95	3:1	0.361	ns
Baghdad ×110 (BC1)	9	1798	892	49.61	906	51.39	1:1	0.741	ns
107× Baghdad (F1)	14	1289	1289	100.00	0	0.00	1	-	-
107× Baghdad (F2)	9	1897	436	22.98	1461	77.02	3:1	0.043	ns
107× Baghdad (BC1)	9	1583	771	48.70	812	51.30	1:1	0.303	ns
110 × Baghdad (F1)	14	3045	3045	100.00	0	0.00	1	-	-
110 × Baghdad (F2)	9	1923	497	25.84	1426	74.16	3:1	0.392	ns
110 × Baghdad (BC1)	9	1930	924	47.88	1006	52.12	1:1	0.062	ns

Table 1 represented the segregation of the cocoon color characters in the crosses between Iranian native races with commercial 107 and 110 lines. In all of the families the results of chi square test showed no significant and different between the theoretically expected and the really obtained phenotypic segregation of the cocoon color. On the other word, there are significant differences in our obtained results. Phenotypic ratios in the F2 generation revealed 3:1 for colored: white cocoons and in the first backcross (BC1), the ratio was 1:1 for colored vs. white cocoons and then the ratio was equal with theoretically expected. The different intensity of the yellow pigments of the cocoons allows us for supposing that each native race contained in its genome several multi alleles of the genes responsible [8-11]. Of course it is possible one independent gene to have multi allelic [12,13]. The new color obtained in F2 could be explained by the different interactions between the dominant alleles with the recessive one in the heterozygote. Also the crossing over occurring between the multi alleles could be also probably involved in this process compared to homozygote. BC generation showed less color diversity since the homozygote recessive parent the segregation.

Tezenov *et al*. [14] pointed out that all the cocoons in F1 were colored. From the obtained results, it can be concluded that the colored cocoon character dominated over the white cocoon character in F1. In F2, there appears a segregation ratio, namely 3 parts colored and 1 part white cocoons. The groups of the colored cocoons in F2 and BC1 crosses had different color, namely in Khorasan orange×107, Khorasan orange×110, Guilan orange×107 and Guilan orange×110 hybrids had orange, light orange, pink, light pink, faint yellow, lemon, light lemon and white cocoons. In Khorasan pink×107 and Khorasan pink×110 hybrids had orange, yellow, pink, light pink, faint yellow and white cocoons. In Khorasan lemone×107 and Khorasan lemone×110 hybrids were lemon, light lemon, faint yellow and white cocoons and in Baghdad crosses had faint yellow and white cocoons. In the backcrosses (BC1) whit the white cocoon races, 1 part colored and one part white cocoons observed. Tezenov *et al*. [14] agreed with the obtained results of crosses between Super 1× Hessa 2 with Bonde 517 manifested that the colored cocoons trait dominated over the character white cocoons in F1. In the F2 generation the segregation was 3 parts colored and one part white cocoons. In BC1 with the homozygote recessive parent the segregation obtained was 1 part colored and 1 part white cocoons. The colored cocoons in F2 and F3 had different nuances.

Raju and Krishnamurthy [15] reported from their crossing experiment with the multi voltine race pure Mysore having green cocoon with cocoon bivoltine hybrid NB4D2 × NB7 that in F1, all the cocoons were green and in F2 the segregation in the cocoon color was green, pale yellow, dull white and white. Different nuances in the cocoon color were detected also in this experiment.

Based on the obtained data, it could be supposed that one or several genes probably responsible for the cocoon color are presented as multi alleles in different native races [16-19]. Therefore it could propose further investigation should be made in order to detect the exact genes responsible for the cocoon color in the native races.

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