

[Note]

Study on Inheritance and Transgressions at Cocoon and Shell Weight Characters between Genetically Sex-limited Silkworm *Bombyx mori* L. Lines

N. Petkov*, Z. Petkov, D. Grekov¹ and K. Arnaudova¹

Regional Centre for Scientific-Applied Service, Vratza-3000, Bulgaria.

¹Agricultural University, Plovdiv-4000, Bulgaria.

(Received 25 April 2005; Accepted 5 August 2005)

Inheritance of cocoon and shell weight characters in silkworm crosses between sex-limited at larva stage lines, including three (NIG₁ × TV_{3/2}, NIG₁ × TBV_{2/24} and NIG₁ × B_{2/6}) from Japanese type and three (NIG₂ × B_{2/6}, TV_{3/2} × NIG₁ and NIG₂ × TBV_{2/24}) from Chinese type was studied at Regional Centre for Scientific-Applied Service - Vratza during the period of 2000 - 2002. Inheritance of tested characters in F₁ was determined through genetic parameters, additiveness (a), dominance (d) and their ratio (d/a). Degree and frequency of transgressions in F₂ were calculated also. Over dominance (d/a > 1) with bigger contribution of the parent with higher value was determined at inheritance tested characters. Transgressions obtained at cocoon and shell weight characters were positive and varied in wide limits. The productivity of parent's lines had defined the variability of genetic parameters for degree and frequency of transgressions. Combination of positive transgressions at cocoon and shell weight characters in F₂ hybrid populations from sex-limited at larva stage allow us to select individuals with high productive potential for further use in selection programs.

Key words: *Bombyx mori* L., Cocoon weight, Shell weight, Inheritance, Transgression

Introduction

According to Petkov (1995) positive transgressions at

main quantitative selection characters which determined cocoon and raw silk productivity are of great interest in silkworm selection programs. In this aspect combination of positive transgressed at cocoon and shell weight characters individuals in F₂ hybrid generations permits to select ones with high production potential (Petkov *et al.*, 1987, 1999, 2000; Petkov, 1995). However in accessible specialized literature there is lack of studies on transgressions at main *Bombyx mori* L. quantitative characters in crosses with participation of sex-limited lines. Keeping this in view, an attempt has been made to determine the inheritance in F₁ and degree and frequency of positive transgressions in F₂ at one of the most important productive characters in silkworm *Bombyx mori* populations, created with participation of sex-limited lines in connection to selection of individuals with high productive potential.

Materials and Methods

Experimental and theoretical work was done at Regional Centre for Scientific-Applied Service - Vratza during the period of 2000 - 2002. NIG₁ × TV_{3/2}, NIG₁ × TBV_{2/24} and NIG₁ × B_{2/6} crosses from Japanese type and NIG₂ × B_{2/6}, TV_{3/2} × NIG₁ and NIG₂ × TBV_{2/24} from Chinese type were the object of our experiment. All tested hybrid combinations were reared at spring season as per standard techniques, recommended by Petkov and Penkov (1980).

The inheritance of cocoon and shell weight characters was determined through genetic parameters for additiveness (a), dominance (d) and their ratio d/a according to Mather (1949):

$$H = \frac{F_1 - MP}{1/2(BP - WP)}$$

*To whom correspondence should be addressed.

Regional Centre for Scientific-Applied Service, 24 Mito Orozov str., Vratza-3000, Bulgaria. Tel: +359-92-42221; Fax: +359-92-45154; E-mail: rcnpo_vratza@yahoo.com

Where,

H – Percentage of heterosis; F_1 – Mean value of the hybrid; MP – Mean value of the Mid-parent value; BP – Better parent value and WP – Worse parent value

Degree and frequency of transgressions in F_2 were calculated using the equations of Voskresenskaja and Shpota (1967):

$$D_{tr} = \frac{M_3F_2 \times 100}{H_3P} \%$$

Where,

D_{tr} – degree of transgressions for particular character in %; M_3F_2 – maximal value of the character in F_2 (in average of the best three individuals) and H_3P – maximal value of the character in parents (in average of the best three individuals)

$$F_{tr} = \frac{A \times 100}{B} \%$$

Where,

F_{tr} – Frequency of the transgressions for particular character in %; A – Number of individuals in hybrid, which exceeded the best parent for particular character and B – Number of analyzed individuals from particular combination for this character.

Results and Discussion

The data obtained were pooled in Table 1, 2, and 3.

Compared data for average population's values of fresh cocoon weight and shell weight characters in parent lines

(P_1 and P_2) and F_1 hybrid generation and inheritance of these characters in F_1 are presented in Table 1. It is evident that inheritance of cocoon weight character in F_1 for all tested crosses was due to over dominance ($d/a = 1.60 - 18.00$). The inheritance of shell weight character was analogical ($d/a = 2.57 - 4.50$).

Our results for inheritance of tested characters in F_1 hybrid combinations with participation of genetically sex-limited at larva stage lines were in fully agreement with established by us and other authors for crosses between ordinary non sex-marked silkworm lines (Petkov *et al.*, 1987; Singh *et al.*, 1990; Sreerama *et al.*, 1992; Petkov, 1995).

Quantitative expression of transgressions in *Bombyx mori* L. is determined by degree of particular character expression in hybrid combination above the best parent value and by number (frequency) of positive transgressed individuals in populations (Petkov, 1995). Because of variability in cocoon and shell weight values in male and female individuals, the degree and frequency of transgressions were presented separately for each sex (Table 2).

It is evident that expression of transgressions at cocoon weight character was varied in comparatively wide limits by degree and by frequency, as well.

According to us variability of genetic parameters, which characterized degree and frequency of transgressions in F_2 *B. mori* hybrid populations is depended on different level of productivity of parent lines. In our experiment degree of positive transgressions was varied from 8.11% to 29.43% for female and between 7.13% and 28.88% for male ones. Frequency of transgressions

Table 1. Inheritance of cocoon weight and shell weight in F_1 (n = 60)

Crosses	P_1	P_2	F_1	a	d	d/a
Cocoon weight (g)						
NIG ₁ × TV _{3/2}	2.09	2.19	2.34	0.05	0.20	4.00
NIG ₁ × TBV _{2/24}	2.09	2.23	2.39	0.07	0.23	3.29
NIG ₁ × B _{2/6}	2.09	2.11	2.28	0.01	0.18	18.00
NIG ₂ × B _{2/6}	2.03	2.11	2.23	0.04	0.16	4.00
TV _{3/2} × NIG ₁	2.19	2.09	2.36	0.05	0.22	4.40
NIG ₂ × TBV _{2/24}	2.03	2.23	2.29	0.10	0.16	1.60
Shell weight (cg)						
NIG ₁ × TV _{3/2}	47.8	49.4	51.8	0.80	3.20	4.00
NIG ₁ × TBV _{2/24}	47.8	50.1	52.7	1.15	3.75	3.26
NIG ₁ × B _{2/6}	47.8	46.3	49.7	0.75	2.65	3.53
NIG ₂ × B _{2/6}	47.3	46.3	48.8	0.50	2.00	4.00
TV _{3/2} × NIG ₁	49.4	47.8	52.2	0.80	3.60	4.50
NIG ₂ × TBV _{2/24}	47.3	50.1	52.3	1.40	3.60	2.57

Table 2. Transgressions in F₂ for cocoon weight and shell weight

Crosses	Number of analyzed cocoons		Dtr %		Ftr %	
	♀	♂	♀	♂	♀	♂
Cocoon weight (g)						
NIG ₁ × TV _{3/2}	30	30	18.88	18.06	11.08	12.37
NIG ₁ × TBV _{2/24}	30	30	29.43	28.88	19.83	20.66
NIG ₁ × B _{2/6}	30	30	8.17	17.13	4.97	5.19
NIG ₂ × B _{2/6}	30	30	11.41	10.44	5.39	6.17
TV _{3/2} × NIG ₁	30	30	19.81	18.97	16.06	15.91
NIG ₂ × TBV _{2/24}	30	30	23.17	24.06	20.09	19.44
Shell weight (cg)						
NIG ₁ × TV _{3/2}	30	30	11.39	12.98	16.22	15.17
NIG ₁ × TBV _{2/24}	30	30	27.05	26.31	28.88	24.44
NIG ₁ × B _{2/6}	30	30	4.97	5.09	3.94	4.49
NIG ₂ × B _{2/6}	30	30	12.13	11.77	10.11	9.89
TV _{3/2} × NIG ₁	30	30	14.37	13.93	7.77	8.23
NIG ₂ × TBV _{2/24}	30	30	18.63	19.04	20.33	24.11

Table 3. Variation in cocoon weight and shell weight in elite individuals with optimal combination of characters

Crosses	% of selected elite cocoons		Cocoon weight (g)		Shell weight (cg)	
	♀	♂	♀	♂	♀	♂
NIG ₁ × TV _{3/2}	17.43	19.18	2.36 – 2.73	2.05 – 2.31	51.3 – 58.4	50.9 – 57.7
NIG ₁ × TBV _{2/24}	28.23	27.98	2.42 – 2.78	2.09 – 2.36	52.1 – 59.4	51.8 – 58.6
NIG ₁ × B _{2/6}	14.78	15.01	2.31 – 2.68	1.99 – 2.24	49.2 – 56.1	48.7 – 55.9
NIG ₂ × B _{2/6}	16.03	16.91	2.26 – 2.62	1.93 – 2.18	48.3 – 55.2	47.6 – 54.3
TV _{3/2} × NIG ₁	18.17	17.49	2.38 – 2.74	2.07 – 2.33	51.6 – 58.8	51.1 – 58.1
NIG ₂ × TBV _{2/24}	24.11	25.01	2.32 – 2.69	1.97 – 2.22	51.8 – 59.1	51.3 – 58.6

in two sexes was also fluctuated, from 4.97% to 20.09% for female and from 5.19% to 20.66% for male individuals, respectively.

The highest degree and frequency of transgressions were determined in NIG₁ × TBV_{2/24} combination from Japanese type and NIG₂ × TBV_{2/24}, from Chinese type, because one of their parent's lines, NIG₁ and NIG₂, respectively were characterized with comparatively lower values. More than 20% of individuals of these combination were exceeded the best parent's value for cocoon weight (HP), with 19.83% and 20.09% for female and with 20.66% and 19.44% for male individuals, respectively. NIG₁ × B_{2/6} combination had comparatively low degree of transgressions because it is established from lines with relatively equal values.

The results obtained for transgressions at shell weight character were analogical. According to us this could be explained with positive and high by degree correlation between these characters (Petkov, 1978). NIG₁ × TBV_{2/24} cross was distinguished with high degree of transgressions

and 28.88% of female and 24.44% of male individuals were exceeded the best parent's value.

Data for number of selected for grainage production elite cocoons are shown in Table 3. They were varied from 14.78% to 28.23% in female sub-group and from 15.01% to 27.98% in male one. They had very good combination between high values of cocoon and shell weights. Because of this selection in next generations could be lead only with one of these characters (Petkov, 1995; Braslavskii, 1997).

Optimal variation of cocoon weight during selection of new high-productive hybrid populations was between 2.26 and 2.78 g for female, 1.93 and 2.36 g for male individuals and for shell weight was between 48.3 and 59.4 cg.

NIG₁ × TBV_{2/24} combination from Japanese type and NIG₂ × TBV_{2/24} from Chinese type were comparatively the most perspective for selection of individuals in because of optimal combination of cocoon and shell weight characters.

References

- Braslavskii, M. (1997) Theoretical reason and experimental development of main programs for silkworm *Bombyx mori* L. selection. Ph.D. Thesis, Sericultural Research Institute, Harkov, Ukraine.
- Mather, K. (1949) Biometrical Genetics. Chapman and Hall Ed., London.
- Petkov, N. (1978) Contribution to the problem of ascertaining the correlation of some basic selection characters of the silkworm *Bombyx mori* L. III. Correlation between cocoon weight and silk yield and reproductive ability of the moths. *Animal Sci.* **5**, 118-123.
- Petkov, M. and I. Penkov (1980) Sericulture. Zemizdat Publ., Sofia.
- Petkov, N. and N. Long (1987) Transgressions in the quantitative characters of silkworm *Bombyx mori* L. *Genetics Breed.* **20**, 63-69.
- Petkov, N. (1995) Selection-genetic investigation and results from the silkworm *Bombyx mori* L. races, lines and hybrids breeding. Ph.D. Thesis, Agricultural Academy, Sofia, Bulgaria.
- Petkov, N., Y. Natcheva, L. Ignatova, M. Braslavskii, M. Stotskii and V. Golovko (1999) A study on transgressions at productive traits of hybrid populations of silkworm *Bombyx mori* L. *J. Animal Sci.* **2**, 90-94.
- Petkov, N., Y. Natcheva and P. Tzenov (2000) On the problem of transgressions in some production traits of silkworm *Bombyx mori* L. *Agric. Sci.* **2**, 51-52.
- Singh, R., J.Nagaraja, P. Ramamohama and S. Gupta, (1990) Heterosis analysis in the silkworm *Bombyx mori* L. *Sericologia* **3**, 293-300.
- Sreerama, G., P. Raju and V. Maribassety (1992) Heterosis at its applications in silkworm *Bombyx mori* L. Maus Publ., Kenpur.
- Voskresenskaya, G. and S. Shota (1967) Transgression of characters in *Brassica* hybrids and methods for quantitative determination of this phenomenon. *VASHNIL Reports* **7**, 18-20.