

ANALYSES OF GENE EFFECTS ON SOME COCOON CHARACTERS IN SILKWORM MORIL

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ABSTRACT

1. Estimates of genetic variance and covariance for individual characters showed that cocoon weight was controlled by both gene direct effect and maternal effect; Cocoon shell weight was controlled by gene direct effect mainly; Cocoon shell ratio was mainly due to maternal effect and sex x -linked effect.

2. Estimates of genetic covariance components of each pair of characters indicated that there were high significant positive relationships among most of genetic effects except maternal additive effect in cocoon weight and cocoon shell weight. There was a high positive relationship in direct effect between cocoon weight and cocoon shell ratio, but in cytoplasm effect and maternal effect were high negative relationships between them. Also there were high positive relationships in direct effect and maternal dominance between cocoon shell weight and cocoon shell ratio.

3. Predictions of gene effects pointed out that sex-chromosome effects ($\sum_{i=1}^8 L_{ii}$) on cocoon weight and cocoon shell weight both were lar-

ger positive values, that means cocoon weight and cocoon shell weight of females are generally higher than those of males in Silkworm. Standardized dominance directions of direct effects on cocoon weight and cocoon shell weight were high positive values, but standardized dominance direction of maternal effects on both of them were high negative values, it showed the two characters had larger heterosis in F_1 generation and depressed in F_2 generation. Sex-chromosome effect ($\sum_{i=1}^8 L_{ii}$) on cocoon shell ratio was high negative value, explaining that females usually have lower cocoon shell ratio than males. Standardized dominance directions of direct effect and maternal effect on cocoon shell ratio were not significant, predicting that the heterosis of cocoon shell ratio in F_1 generation is not obvious comparing to cocoon weight and cocoon shell weight.

Keywords, Silkworm, Cocoon characters, Genetical Analysis.

In previous paper (Jun Zhu, Jia long duan, 1994, published on JOURNAL OF BIO MATHS) Genetic Models and Analysis Methods For Sex-linked and Maternal Effects has been given. By the Models and Methods analyses of gene effects on cocoon characters in this paper was carried out and the results were as followings.

MATERIALS AND METHODS

Eight silkworm races (1. min hui, 2. 72 qiou, 3. shu 4, 4. shu 12, 5. da zao, 6. dong 34, 7. zhe 1, 8. hua 10,) were used to produce an incomplete diallel cross. Cocoon weights, cocoon shell weights and cocoon shell ratios of parents, F_1 generations and F_2 generations from the incomplete diallel cross were analysed according to genetic models for analyzing sex-linked and maternal effects proposed by JUN ZHU and JIA LONG DUAN.

All kinds of variance and covariance components of different characters were estimated by MINQUE (0/1) (JUN ZHU, 1992), basing on estimates of genetic covariances of each pair of characters genetic relative

coefficients were estimated late. Gene effect values of individual character were predicted by AUP method (JUN ZHU, 1993). After predicting dominance effects, standard dominance directions of direct effects (Δ_d) and standard dominance directions of maternal effects (Δ_{dm}) (JUN ZHU, 1993) were calculated further. Estimates and its S.E. of all genetic parameters were obtained by Jackknife's Method (JUN ZHU, 1992, 1993). Generation average of each genotype was taken as Jackknife's repeating sample unit. T test was used to do statistical testing for genetic parameters.

RESULTS AND DISCUSSES

Estimates of genetic variance and covariance of individual characters

Table 1. Estimates and Its Standard Errors of variance components of Cocoon Characters

Parameter	cocoon weight	cocoon shell weight	cocoon shell ratio
	Estimate \pm S.E.	Estimate \pm S.E.	Estimate \pm S.E.
$2 \sigma_A^2$	970.35** \pm 138.48	31.34** \pm 4.52	3.84** \pm 0.72
σ_D^2	1253.93** \pm 231.32	60.59** \pm 11.76	0.96** \pm 0.24
σ_L^2	259.60** \pm 20.36	1.48** \pm 0.28	2.24** \pm 0.23
$4 \sigma_{Am}^2$	1822.69** \pm 300.76	0.00 \pm 0.00	8.63** \pm 2.14
σ_{Dm}^2	232.89** \pm 46.33	10.94** \pm 2.22	0.99** \pm 0.20
$2 \sigma_{A.Am}$	-711.68** \pm 129.67	0.00 \pm 0.00	-2.76** \pm 0.87
$0.5 \sigma_{D.Dm}$	-168.54** \pm 37.41	-7.75** \pm 1.81	-0.18** \pm 0.05
σ_e^2	226.56** \pm 113.41	4.90** \pm 1.05	0.88** \pm 0.15

As table showed,

Cocoon weight was controlled by both direct effects and maternal effects, also the direct dominance effect was higher than direct additive, Maternal additive was larger than maternal dominance, cocoon shell weight was mainly affected by direct effects, direct dominance was larger than

direct additive. Cocoon shell ratio was first controlled by maternal additive, followed by direct additive. Cytoplasmic effects to the three characters were all significant, but variance components were still lower. Generally there was a negative relationship between direct effect and maternal effect. Variance value of total remainder effect was small, showing beside genetic effects analysed, the interferes from other effects and its errors could be thought less.

Estimates of genetic covariance components for each pair of characters

Table 2. Estimates of Relative Coefficients of Genetic Components to Cocoon Characters and Its Standard Errors

Parameter	cocoon weight & cocoon shell weight	cocoon weight & cocoon shell ratio	cocoon shell weight & cocoon shell ratio
	Estimate ±S.E.	Estimate ±S.E.	Estimate ±S.E.
r _A	0.54** ±0.06	-0.13 ±0.07	0.09 ±0.07
r _D	0.54** ±0.06	0.17** ±0.06	0.33** ±0.06
r _L	0.43** ±0.07	-0.72** ±0.05	-0.37** ±0.06
r _{Am}	0.00 ±0.00	-0.26** ±0.08	0.00 ±0.00
r _{Dm}	0.39** ±0.06	-0.04 ±0.07	0.18** ±0.07
r _{A/Am}	0.00 ±0.00	-0.05 ±0.03	0.00 ±0.00
r _{D/Dm}	0.22** ±0.06	0.02 ±0.05	0.16** ±0.05
r _e	0.46** ±0.07	-0.20** ±0.08	0.27 ±0.07

Table 2 indicated that there was a positive relationship high significantly between cocoon weight and cocoon shell weight in most of genetic effects except maternal additive. Therefore, if cocoon weight is increased in hybrid combination or breed, it can lead to cocoon shell weight increasing too. For cytoplasmic effects and maternal additive effects on cocoon weight and cocoon shell ratio there were high negative relationships

between them respectively, so, as cocoon weight of breed increases, it would lead to cocoon shell ratio decreasing. But due to there was a high significant positive relationship between direct effects of cocoon weight and cocoon shell ratio, expecting to develop a good hybrid combination with both high cocoon weight and high cocoon shell ratio. Also, there was a high significant positive relative between both direct effects and maternal dominances of cocoon shell weight and cocoon shell ratio, meaning that both cocoon shell weight and cocoon shell ratio could be improved in one hybrid combination at the same time.

Predictions of gene effect values

Table 3. Predicting Values of Genetic Effects on Cocoon Characters

genetic effects	i=1	i=2	i=3	i=4	i=5	i=6	i=7	i=8
cocoon weight								
A _i	4.06	9.13	26.03**	20.34**	-19.60**	-10.39	-20.25	-9.37
D _{ii}	-45.76	-12.85	-77.54	-56.69	-31.12	-77.18**	-81.90**	-57.46**
Li ₁	0.19	20.01**	21.98**	22.71**	18.49**	4.92	2.23	20.97*
Li ₂	-9.41	-13.73**	-8.35	-6.25	-13.14**	-25.78**	-27.77**	-7.10
A _{mi}	-10.40	-14.79*	-41.35**	-39.04	10.54	28.44**	41.32**	16.16
D _{mii}	2.23	21.16**	15.93	.87	29.85*	47.68**	55.77**	25.73*
cocoon shell weight								
A _i	3.53	0.99	3.15	1.57	-4.93*	-1.71	-2.61	0.01
D _{ii}	-15.20	1.02	-17.06	-8.16	-3.16	-14.41**	-12.74**	-17.58**
Li ₁	1.31*	0.63	1.52*	0.33	0.66	0.46	0.06	0.05
Li ₂	0.15	-0.93	0.73	-0.87	-0.25	-0.92	-0.99*	-2.04*
A _{mi}	—	—	—	—	—	—	—	—
D _{mii}	2.34	5.59**	4.03	4.33	2.13	13.99**	9.26*	9.03**
cocoon shell ratio								
A _i	1.38**	-0.87	-0.27	-1.42**	-1.44**	0.55	1.67*	0.38
D _{ii}	-0.91	1.64	-2.09	0.46	0.83	-0.46	0.62	-0.96
Li ₁	-1.30	-1.79**	-0.67	-1.73**	-1.93**	-1.00	-1.72**	-0.93
Li ₂	0.22	1.25**	2.70**	0.76	1.20*	1.67**	1.75**	1.52**
A _{mi}	-0.56	2.16**	0.02	1.37**	-0.92	0.01	-2.12*	0.03
D _{mii}	0.25	0.02	-0.01	0.29	-2.03*	1.89*	-1.40	-0.29

As to cocoon weight p_3 and p_4 parents had high significant positive additive effects and female sex-linked effects; p_6 and p_7 parents had high significant positive maternal additive dominance and female sex-linked effects. Therefore, F_1 female cocoon weight should be higher than others if p_6 and p_7 were used as female parents and p_3 and p_4 were used as male parents to cross for F_1 hybrid. Sex-chromosome effects ($\sum_{i=1}^8 L_{ii}$) to cocoon weight gave a higher positive value, this would explain why females have larger cocoon weight than males usually. Standardized dominance direction of direct effect to cocoon weight was a high significant positive value ($\Delta_0 = 6.19^{**} \pm 1.04$), however, standardized dominance direction of maternal effect to cocoon weight was a high significant negative value ($\Delta_m = -10.08^{**} \pm 1.71$) that could let us to know cocoon weight in F_1 generation will have a powerful heterosis, and depress in F_2 generation.

p_2 , p_6 , p_7 and p_8 parent's cocoon shell weights have high significant maternal additive. So, it would be considered that F_1 generations from these varieties taken as female parents produce higher amounts of cocoon shell weight. From the view of point that $\sum_{i=1}^8 L_{ii}$ to cocoon shell weight was a quite large positive value, female cocoon shell weight usually are higher than male's. Standardized dominance direction of direct effect to cocoon shell weight was a high significant positive value ($\Delta_0 = 5.38^{**} \pm 1.05$), but standardized dominance direction of maternal effect to cocoon shell weight was a high significant negative value ($\Delta_m = -9.10^{**} \pm 1.45$), it showed that cocoon shell weight in F_1 generation also existed a quite large heterosis, and depressed in F_2 generation.

Standardized dominance directions of direct effect and maternal effect to cocoon shell ratio both were not significant ($\Delta_0 = 1.17 \pm 1.45$ $\Delta_m = 0.48 \pm 1.37$), indicating the heterosis of cocoon shell ratio in F_1 generation

was not very obvious. The cocoon shell ratio of female usually appeared lower than that of male because of $\sum_{i=1}^8 L_{ii}$ to cocoon shell ratio being a high negative value. p_4 parent had high significant negative additive and positive maternal additive to cocoon shell ratio, on the contrary, p_7 parent had high significant positive additive and negative maternal additive to cocoon shell ratio. So, it would be hopeful that the F_1 generation produced with p_4 as female and p_7 as male produced higher cocoon shell ratio.

In practice female cocoon weights and cocoon shell weights of F_1 hybrids or races are higher than male's, male cocoon shell ratios are higher than female's generally. Much statistical data has showed that the heterosis of cocoon weight and cocoon shell weight both are among 10-30% and the heterosis of cocoon shell ratio is among 1-4% in F_1 generation.

Also, a higher heterosis will come from any kinds of F_1 generations and get down quickly in F_2 generations, see table 4.

Table 4. Heterosis in F_1 and F_2 generations (%)

characters Generations	Cocoon weight	Cocoon shell weight	Cocoon shell ratio	
F_1	13.42	20.11	6.28	Duan Jia long 1990
	15.67	18.51	1.98	Xia Jian-guo 1981
	21.74	30.53	6.96	Yang Ming-guan 1982
F_2	7.55	7.55	0.76	Duan Jia long 1990

All conclusions in this paper not only correspond to data above but also offer better models and methods for analysing gene effects to silkworm quantitative characters.

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