

Combining Ability of Diallel Crosses of Bivoltine Silkworm, *Bombyx mori* L.

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General and specific combining ability effects of six bivoltine breeds of silkworm (*Bombyx mori* L.) were evaluated for six quantitative characters through diallel method wherein parents, F₁s and reciprocals are involved. The breeds APS₁₁ and APS₂ were found to be the best general combiners for most of the traits studied. The high estimates of specific combining ability (sca) variance (σ^2_s) compared to general combining ability (gca) variance (σ^2_g) indicated the predominant role of non-additive gene action in the control of all the characters. Positive sca effects for majority of the traits were expressed by the combinations APS₁₃ × APS₆, APS₁₃ × APS₂, APS₁₁ × APS₆ and APS₅ × APS₂ out of 15 crosses. Among the 15 reciprocal crosses studied, the combination APS₈ × APS₁₃ showed positive reciprocal effects for all the six traits. With both the parents APS₅ and APS₂ being good general combiners the hybrid APS₅ × APS₂ showing high sca effects is recommended for commercial use.

Key words: Silkworm, *Bombyx mori* L., Combining ability, Diallel cross, Quantitative traits, Dominance, Non-additive gene action, Additive gene action

Introduction

Commercial exploitation of mulberry silkworm, *Bombyx mori* L. for increased production of quality silk warrants continuous development of superior bivoltine breeds and hybrids. Improvement of cocoon yield and silk technological traits are the main objectives in silkworm breeding programmes. Since silkworm is the only exceptional crop

where hybrids are used compulsorily (Yokoyama, 1957), creation of variability through gene recombination and utilization of desired variability through appropriate selection is important to amalgamate the desired characters present in different genotypes into a single breed/hybrid contributing to increased qualitative silk production. However, the *per se* performance of parental breeds is not always be the good indicator of the combining ability and its analysis therefore helps the breeders to understand the nature of gene action and to identify prospective parents/hybrids. Although extensive studies are reported on the combining ability studies in mulberry silkworm (Ravindra Singh *et al.*, 2003) to identify promising bivoltine F₁ hybrids following Line × Tester (Kempthorne, 1957) method, only a few works (He *et al.*, 1989; Moon and Han 1994; Bhargava *et al.*, 1995; Malik *et al.*, 1999) are reported following diallel method to measure general and specific combining ability of parental inbred lines, their crosses and to develop effective crosses. The present study is made to analyze the combining ability of newly developed bivoltine diallel crosses and to identify the best general combiners for cocoon yield and its important contributory traits.

Materials and Methods

Six newly synthesized bivoltine inbred lines of silkworm, *Bombyx mori* L. at Andhra Pradesh State Sericulture Research and Development Institute, Hindupur, India comprising APS₅, APS₁₁, APS₁₃ (oval shape cocoons), APS₂, APS₆ and APS₈ (peanut shape cocoons) are selected for the study are crossed in 6 × 6 diallel pattern to obtain 30 F₁s including reciprocal crosses. All the 30 F₁s along with six parents are reared in randomized block design and as per the standard method (Krishnaswami, 1978) with 3 replications each during February – March, 2002 under controlled conditions of temperature of 27 – 28°C with relative humidity of 80 – 85% during 1st, 2nd

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and 3th instars and temperature of 24 – 25°C with relative humidity of 70 – 75% during 4th and 5th instars. 300 individuals each per replication are retained after 3rd moult. Matured silkworms are mounted on collapsible plastic mountages and cocoons are harvested on 7th day after mounting. Data on cocoon yield by weight per 10,000 larvae (kg), pupation rate (%), single cocoon weight (g), single cocoon shell weight (cg), cocoon shell ratio (%) and filament length (m) is drawn and subjected to combining ability analysis using Griffing's (1956) approach. The materials involved in the analysis included parents (n), n(n – 1)/2 F₁s and reciprocals (method-1). Out of the two models considered by Griffing (1956) for analysis of combining ability, Eisenhart's model I (fixed effect) was considered compared to model II (random effect). The type of genetic control and inheritance for the above traits is also noted from the predictability ratio (Baker, 1978) between the estimates of general combining ability variance (σ^2_g) and specific combining ability variance (σ^2_s) was calculated as $2\sigma^2_g/(2\sigma^2_g + \sigma^2_s)$.

Results and Discussion

Analysis of variance for combining ability

Highly significant ($P < 0.01$) differences are observed for general combining ability (gca), specific combining ability (sca) and reciprocal differences for all the 6 characters studied (Table 1) except for the trait pupation rate indicating the role of additive and non-additive gene action for the traits studied. Predominant role of non-additive gene action in the control and inheritance of all the six traits is evidenced from the high estimates of sca variance (σ^2_s).

General combining ability effects

The prime motive of this investigation is the identification

of qualitatively and quantitatively superior breeds and their utilization as parents for hybridization programme. The combining ability effects for the six traits are presented in Table 2. The line APS₁₁ is found to be the best general combiner with high positive gca effects for five traits *viz.*, cocoon yield by weight per 10,000 larvae, single cocoon weight, single cocoon shell weight, cocoon shell ratio besides positive gca effects for filament length followed by APS₂ for 5 characters and the crosses involving these lines are expected to produce promising hybrids with improved performance for their respective traits. Further, the predictability ratio is less than unity for all the characters suggesting the preponderance of non-additive gene action. These results are in conformity with Bhargava *et al.* (1992) who observed high sca effects compared to gca effects for cocoon yield by weight per 10,000 larvae (-0.021), single cocoon weight (0.37) and single cocoon shell weight (0.089).

Specific combining ability effects

The sca effects of hybrids revealed the importance of both additive and non-additive gene action for the six characters studied. Among the 15 F₁ hybrids analyzed, the cross, APS₁₃ × APS₆ recorded positive sca effects for all the traits under study followed by APS₁₃ × APS₂ for 5 characters excluding pupation rate that is negative. The parental breeds in these two combinations are poor combiners indicating non-additive gene interaction.

However, additive gene action is evident with highly significant ($P < 0.01$) sca effects for cocoon yield by weight per 10,000 larvae in APS₅ × APS₂ and positive sca effects for the trait pupation rate in APS₁₃ × APS₁₁ and APS₂ × APS₈ wherein one of the parents in each combination *viz.*, APS₅, APS₁₁ and APS₂ respectively is a good combiner. Further, additive gene action is also evident in the combinations APS₁₁ × APS₂, APS₁₁ × APS₈, APS₁₃ × APS₂ for the traits cocoon weight, cocoon shell weight

Table 1. Analysis of variance of combining ability and estimates of variance components for quantitative traits in *Bombyx mori* L.

Source of variation	d.f.	Cocoon yield by weight per 10,000 larvae	Pupation rate	Single cocoon weight	Single shell weight	Cocoon shell ratio	Filament length
GCA	5	9.5075**	3.0854	0.1031**	0.0093**	4.5227**	16973.76**
SCA	15	4.1986**	3.48361**	0.0447**	0.0055**	3.9140**	5854.22**
Reciprocal differences	15	1.9719**	6.2372**	0.0225**	0.0027**	1.9549**	10481.59**
Error	70	0.0812	1.4706	0.0007	0.0000	0.0507	755.88
gca variance		0.4535	-0.0278	0.0050	0.0003	0.0611	942.001
sca variance		2.3908	1.1689	0.0256	0.0032	2.2432	2960.33
Predictability Ratio		0.1897	-0.0238	0.1949	0.1064	0.0272	0.31821

*, ** Significant at $P < 0.05$ and $P < 0.01$ respectively.

Table 2. Estimates of combining ability effects for quantitative traits in *Bombyx mori* L.

Parents/Hybrids	Cocoon yield by weight per 10,000 larvae	Pupation rate	Single cocoon weight	Single shell weight	Cocoon shell ratio	Filament length
General Combining ability effects						
APS13	-1.682	0.690*	-0.168	-0.044	-0.433	-56.820
APS5	0.159*	-0.260	0.089**	0.018**	-0.023	47.741**
APS11	0.506**	-0.682	0.064**	0.035**	1.144*	4.241
APS2	0.220**	0.318	0.040**	0.010**	0.029	-26.148
APS8	0.890**	-0.327	0.011	0.000	-0.103	29.491**
APS6	-0.094	0.262	-0.035	-0.018	-0.614	1.491
C.D (gi) 0.05	0.150	0.637	0.013	0.003	0.118	14.450
Specific Combining ability effects						
APS13 × APS5	-2.076	1.324	-0.251	-0.089	-2.288	-34.546
APS13 × APS11	-2.240	2.296**	-0.247	-0.082	-1.709	-26.713
APS13 × APS2	0.846**	-1.020	0.130**	0.033**	0.389**	80.509**
APS13 × APS8	1.177**	-1.243	0.096**	0.033**	0.741**	-10.963
APS13 × APS6	2.110**	0.419	0.265**	0.082**	1.500**	74.037**
APS5 × APS11	0.135	-0.204	0.110**	-0.009	-0.519	12.398
APS5 × APS2	1.688**	0.180	0.102**	0.052**	1.576**	-28.046
APS5 × APS8	-0.498	-1.176	0.180**	-0.018	0.828**	16.981
APS5 × APS6	0.219	-1.115	0.120**	0.032**	0.520**	18.315
APS11 × APS2	1.057**	-1.898	0.014	0.031**	1.457**	-5.380
APS11 × APS8	-0.629	-0.220	-0.001	0.018**	1.022**	7.315
APS11 × APS6	1.071**	0.709	0.111	0.054**	1.612**	47.815
APS2 × APS8	-1.376	1.713	-0.052	-0.018	-1.088	83.87**
APS2 × APS6	-0.259	-0.676	-0.019	-0.071	-0.570	-25.630
APS8 × APS6	-0.745	1.402	-0.077	-0.039	-1.764	-14.602
CD (Sij) at 0.05	0.341	1.453	0.305	0.007	0.270	32.950
Reciprocal effects						
APS5 × APS13	-0.150	-0.150	-0.065	-0.008	0.288	22.000
APS11 × APS13	-0.333	0.300	-0.069	-0.002	-0.438	-36.333
APS2 × APS13	0.033	-0.383	-0.061	-0.025	-0.668	98.833
APS8 × APS13	0.433*	2.250*	0.097**	0.031**	0.572**	100.000**
APS6 × APS13	0.683**	1.000	-0.050	-0.006	0.263	77.667**
APS11 × APS5	0.350	-0.483	0.019	0.003	-0.055	20.333
APS2 × APS5	0.450*	0.367	0.033	0.007	-0.012	126.833**
APS8 × APS5	1.600**	3.867*	-0.007	-0.011	-0.472	74.500**
APS6 × APS5	-1.367	2.017*	-0.166	-0.029	0.303	-109.500
APS2 × APS11	-0.233	-0.133	-0.064	-0.024	-0.447	41.667*
APS8 × APS11	-1.050	0.833	-0.053	-0.013	-0.007	3.667
APS6 × APS11	-0.333	-2.500	-0.085	-0.035	-0.748	-103.167
APS8 × APS2	-1.283	1.500	-0.202	-0.103	-3.293	55.500**
APS6 × APS2	1.650**	-3.067	0.108**	0.037**	0.985*	-8.667
APS6 × APS8	-1.900	1.567	-0.220	-0.057	-0.807	37.667
CD (Rij) at 0.05	0.402	1.710	0.036	0.008	0.318	38.970

*, ** Significant at P < 0.05 and P < 0.01 respectively.

and cocoon shell ratio and $APS_{13} \times APS_2$, $APS_{11} \times APS_6$, $APS_2 \times APS_8$ for the trait filament length which recorded highly significant positive sca. These observations confirm the role of both additive and non-additive gene action expression of single cocoon weight, single cocoon shell weight and cocoon shell ratio. Our observations on additive and non-additive gene action are fully in agreement with Rajalakshmi *et al.*, (1997) for single cocoon weight (0.183 in $CNR_{16} \times NB_4D_2$) and single cocoon shell weight (2.853 in $CNR_{16} \times NB_4D_2$ and with Chauhan *et al.*, (2000) for cocoon yield and yield contributing characters including filament length. However, the deviation in results from the operation of non-additive gene action observed by Rajalakshmi *et al.*, (1997) and Sudhakar Rao *et al.*, (2001) for filament length (87.208 in $CNR_{16} \times NB_4D_2$ and 79.399 in $BL_{67} \times B_{71}$) are attributed to the variations in the genetic makeup of new genotypes involved.

Reciprocal effects

The combination $APS_8 \times APS_{13}$ recorded highly significant ($P < 0.01$) to significant ($P < 0.05$) positive reciprocal effects for all the traits followed by $APS_2 \times APS_5$ for 5 characters excluding cocoon shell ratio. This supports the positive role of cytoplasmic inheritance.

The operation of additive \times dominance interaction in the hybrids showing significant sca involving good \times poor general combiners is well established as in case of the hybrid $APS_{11} \times APS_6$ wherein APS_{11} is a good combiner while APS_6 a poor combiner. Contribution of at least one good general combiner in the hybrid combination is expected to yield transgressive segregants in the later generation, which on exploitation may yield lines with increased merit. As has been observed (Simmonds, 1979) that the sca effects representing dominance and epistatic components of variance are not fixable in nature compared to significant gca effects related to additive \times additive interaction representing fixable component of variation (Griffing, 1956), the lines with positive gca could be used in future breeding programmes for improvement of respective traits. But crosses showing high sca effects involving parents with good gca could be exploited to produce promising hybrids with increased merit in the yield contributing characters. Accordingly, the combination $APS_5 \times APS_2$ with significant positive sca is adjudicated as a promising bivoltine hybrid wherein both the parents are good general combiners for the majority of the traits studied and is recommended for commercial use.

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