



Original Article

Genetic Analysis of Silk Technological Characters of Bivoltine Silkworm (*Bombyx mori* L.)

Hothur Lakshmi*, Modumudi Ramesh Babu#, Chandrashekharaiyah+, Ajay Kumar Goel+, Atul Kumar Saha* and Bharat Bhushan Bindroo*

* Central Sericultural Research and Training Institute, Central Silk Board, Berhampore (West Bengal)

+ Andhra Pradesh State Sericulture Research and Development Institute, Hindupur

Regional Eri Research Station, Central Silk Board, Shadnagar (Andhra Pradesh)

@ Andhra Pradesh State Sericulture Research and Development Institute, Hindupur

E-mail: lakshmicruti@gmail.com

ABSTRACT

Mulberry silkworm is the only exceptional crop where hybrids are used compulsorily for commercial exploitation. Increased production of quality silk warrants continuous development of superior silkworm breeds and hybrids in general and bivoltine is no exception. Selection of suitable parents, information on genotype x environment interaction and optimum expression of gene action of economic traits determine the crop success. In the present study, an attempt 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 contributory traits. Ten newly synthesized bivoltine inbred lines of silkworm, *Bombyx mori* L at Andhra Pradesh State Sericulture Research and Development Institute, Hindupur, India comprising of HTO₁, HTO₂, HTO₃, HTO₄, HTO₅ (oval shape cocoons), HTP₁, HTP₂, HTP₃, HTP₄ and HTP₅ (peanut shape cocoons) were crossed in 10 x 10 diallel pattern including direct, reciprocal, and foundation crosses and the data recorded for nine economic traits was analysed. The sca effects of hybrids revealed the importance of both additive and non-additive gene action for the nine traits studied. Among the 25 F₁ hybrids analyzed, the cross, HTO₅ x HTP₅ recorded significant (P<0.05) (survival rate) to highly significant (P<0.01) positive sca effects (eight traits) followed by HTO₅ x HTP₂ recorded highly significant (P<0.01) sca effects for seven traits. The combination HTO₅ x HTP₅ with highly significant positive sca is adjudicated as a promising bivoltine hybrid and is recommended for commercial use under high temperature (36±1°C) and low humidity (50%±5%) conditions.

Key words: Silkworm, breeds, hybrids, combining ability, sca, gca,

INTRODUCTION

Mulberry silkworm, *Bombyx mori* L by virtue of its economic importance has been continuously subjected for exploitation of quantitative and qualitative economic traits through various breeding methods. Since mulberry silkworm is the only exceptional crop where hybrids are used compulsorily [29] for commercial exploitation. Increased production of quality silk warrants continuous development of superior silkworm breeds and hybrids in general and bivoltine is no exception. Further, the objective of silkworm breeding is not only to synthesize new genotypes but also to identify sustainable silkworm hybrids for commercial use by the farmers [11]. As the *per se* performance of parental breeds alone is not always be the good reflection of the combining ability and its analysis therefore helps the breeders to understand the nature of gene action to identify prospective parents/hybrids [15]. Selection of suitable parents, information on genotype x environment interaction and optimum expression of gene action of economic traits determine the crop success [4]. Critical assessment of the variability present in the breeding materials is one of the pre-requisites for paving the way of combining most of the desirable traits present in different genotypes into a single combination. Different methods are in vogue for assessment of combining ability [22] of which Line x Tester method [8] involving both polyvoltine and bivoltine is widely being used by many silkworm breeders where as the diallel method involving bivoltine breeds is sparsely used [25,2,12,19,20,11]. Many attempts were made to identify promising F₁ hybrids through combining ability studies between polyvoltine x polyvoltine [10,17,3,24,21,22]; polyvoltine x bivoltine [5,28]; bivoltine x bivoltine [26,13,23,14,19,20,27,7,11] and bivoltine x univoltine silkworm breed [16]. In the present study an attempt 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 contributory traits following the method advocated by Griffing [6].

MATERIALS AND METHODS

Ten newly synthesized bivoltine inbred lines of silkworm, *Bombyx mori* L at Andhra Pradesh State Sericulture Research and Development Institute, Hindupur, India comprising of HTO₁, HTO₂, HTO₃, HTO₄, HTO₅ (oval shape cocoons), HTP₁, HTP₂, HTP₃, HTP₄ and HTP₅ (peanut shape cocoons) constituted the experimental materials. All the lines are crossed in 10 x 10 diallel pattern to obtain 90 F1s including direct, reciprocal, and foundation crosses. All these crosses including the 10 inbred lines were reared in randomized block design following the recommended rearing technique [9] each with 3 replications of 300 larvae retained after III moult under conditions of temperature of 36±1°C and humidity of 50%±5%. The data pertaining to nine economic traits *viz.*, fecundity, hatching percentage, survival rate, cocoon yield per 10000 larvae by weight, cocoon weight, cocoon shell weight, cocoon shell ratio, filament length and raw silk recovery were recorded and analyzed for combining ability by adapting Griffing [6], Model-I. The type of genetic control and inheritance for the above traits is also noted from the predictability ratio [1] between the estimates of general combining ability variance (σ^2_g) and specific combining ability variance (σ^2_s).

RESULTS AND DISCUSSION

The prime objective of the investigation is to identify qualitatively and quantitatively superior breeds and their utilization as parents for hybridization programme and the most promising hybrid with economic merit. Accordingly, the study is carried out by evaluating the gca and sca aspects that resulted in the identification of superior bivoltine hybrid for commercial exploitation under high temperature and low humidity conditions.

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 nine traits except for survival rate for gca (Table 1) indicating the role of additive and non-additive gene action. Predominant role of non-additive gene action in the control and inheritance of all the nine traits is evidenced from the high estimates of sca variance (σ^2_s).

TABLE 1. ANOVA FOR COMBINING ABILITY FOR NINE TRAITS OF ECONOMIC IMPORTANCE

Source of variation	Df	Mean sum of squares								
		Fecundity	Hatching	Yield / 10,000 larvae	Survival rate	Cocoon weight	Shell weight	Shell ratio	FL	RSR
gca	9	1480.528**	19.3069**	2.26265**	7.71059NS	0.0228**	0.00164**	0.84498**	16743.7**	1.08888**
sca	45	1807.001**	8.89728**	3.55389**	17.75969**	0.0318**	0.00183**	1.57855**	9335.22**	1.09158**
Reciprocal	45	1494.011**	11.5484**	3.79419**	39.63307**	0.0303**	0.00183**	2.38030**	10601.8**	0.91907**
Error	198	374.4531	1.37525	0.41394	5.20434	0.00242	0.00013	0.18972	1326.532	0.15758
gca variance		55.303	0.08966	0.0924	0.1253	0.00102	0.00008	0.03276	770.85	0.04656
sca variance		1432.54	7.5220	3.13995	12.555	0.02932	0.00170	1.38884	8008.69	0.93339
Predictability Ratio		0.03861	0.0119	0.0294	0.00998	0.03478	0.04705	0.02359	0.09625	0.04988

FL= Filament length; RSR = Raw silk recovery ; gca = general combining ability; sca = specific combining ability; df = degree of freedom; ** Significant ($p < 0.01$)

General Combining Ability effects

The general combining ability effects for the nine traits are presented in Table 2. The inbred line HTO₅ is found to be the best general combiner recording positive gca effects for seven traits *viz.*, fecundity, hatching percentage, cocoon yield per 10000 larvae by weight, cocoon weight, cocoon shell weight, filament length and raw silk recovery followed by HTP₅ for four traits *viz.*, fecundity, cocoon weight, shell weight and filament length. The crosses involving these lines are expected to produce hybrids with improved performance for respective economic traits. Further, the

predictability ratio is less than unity (high sca effects compared to gca effects) for all the traits suggesting the preponderance of non-additive gene action which is inconformity with the observations drawn by Bhargava *et al.* [2] and Ramesh Babu *et al.* [20].

TABLE 2. GCA EFFECTS

Breed	Fecundity	Hatching	Yield / 10,000 larvae	Survival rate	Cocoon weight	Shell weight	Shell ratio	FL	RSR
HTO ₁	-0.197	0.225	-0.049	-0.207	0.005	0.006*	0.287*	1.023	-0.051
HTO ₂	7.603	-0.096	0.363*	0.935	-0.006	0.002	0.193*	2.827	0.039
HTO ₃	3.587	-0.963	-0.081	0.048	-0.037	-0.013	-0.316	-26.030	-0.422
HTO ₄	1.787	0.859*	-0.490	-1.357	-0.024	-0.005	0.018	-31.111	-0.157
HTO ₅	12.87*	1.855*	0.288*	0.393	0.054*	0.011*	0.017	46.789*	0.376*
HTP ₁	-2.663	0.372	-0.076	-0.028	0.008	0.001	-0.003	-7.951	-0.141
HTP ₂	-10.697	-1.538	-0.514	-0.300	-0.040	-0.014	-0.356	27.803*	-0.154
HTP ₃	1.370	0.292	-0.060	0.262	-0.024	-0.001	0.184*	-12.134	0.098
HTP ₄	16.897*	0.009	0.520*	0.553	0.008	0.001	0.013	2.414	0.248*
HTP ₅	13.237*	-0.153	0.099	-0.299	0.055*	0.012*	-0.004	51.977*	0.164
\bar{g} at 0.05	8.0949	0.4906	0.2691	2.8806	0.0206	0.0047	0.1822	15.236	0.1661
\bar{g} at 0.01	10.656	0.646	0.354	3.792	0.027	0.062	0.240	20.057	0.219

FL= Filament length; RSR = Raw silk recovery; * Significant ($p < 0.5$)

Specific Combining Ability effects

The sca effects of hybrids as presented in Table 3 revealed the importance of both additive and non-additive gene action for the nine traits studied. Among the 25 F₁ hybrids analyzed, the cross, HTO₅ x HTP₅ recorded significant ($P < 0.05$) (survival rate) to highly significant ($P < 0.01$) positive sca effects (eight traits) followed by HTO₅ x HTP₂ recording significant ($P < 0.05$) sca effects for the trait survival rate, highly significant ($P < 0.01$) sca effects for seven traits *viz.*, fecundity, hatching percentage, cocoon yield per 10000 larvae by weight, cocoon weight, cocoon shell weight, filament length and raw silk recovery and positive sca effects for cocoon shell ratio. At least one parental breed in these combinations *i.e.*, HTO₅ is good general combiner indicating the role of additive gene action. In the combination, HTO₁ x HTP₃ that recorded highly significant sca effects for the traits fecundity, hatching percentage, cocoon yield per 10000 larvae by weight, cocoon weight, filament length and raw silk recovery, both the parents are poor combiners indicating non-additive gene action. The combinations, HTO₁ x HTP₁ and HTO₃ x HTP₃ and HTO₄ x HTP₁ recorded positive sca for all the nine traits under study also suggest the operation of non-additive gene action as both parents are poor combiners. These observations confirm the role of both additive and non-additive gene action in the expression of cocoon yield per 10000 larvae by weight, cocoon weight, shell weight, shell ratio, filament length and raw silk recovery as observed by Rajalakshmi *et al.*, [18] for single cocoon weight; Chauhan *et al.*, [4] for cocoon yield and yield contributing characters including filament length and Ramesh Babu *et al.*, [20] for the traits cocoon weight, shell weight, shell ratio and filament length. Although, non-additive gene action was observed in certain new hybrid combinations for the trait filament length as observed by Sudhakara Rao *et al.* [27], the highly significant ($P < 0.01$) positive gca effects observed for the combination HTO₅ x HTP₅ indicate the additive gene action and corroborate with the observations of [5], [26] & [23]. Non-additive gene action was found to be in operation for the trait raw silk recovery as evidenced from greater sca compared to gca as observed by Bhargava *et al.*[2]. The variations in the type of gene action in different hybrid combinations evaluated may be attributed to their varied genetic make-up.

Reciprocal Effects

The reciprocal effects of twenty five combinations are presented in Table 4. The combination HTP₅ x HTO₅ recorded highly significant ($P < 0.01$) to significant ($P < 0.05$) positive reciprocal effects for all the nine traits except for the trait survival rate that recorded non-significant positive effects. HTP₅ x HTO₄ recorded highly significant ($P < 0.01$) reciprocal effects for the traits fecundity, hatching percentage, cocoon yield per 10000 larvae, cocoon weight, shell weight, shell ratio, filament length and raw silk ratio and significant (0.05) effects for the trait survival rate followed by HTP₂ x HTO₅. This supports the positive role of cytoplasmic inheritance.

TABLE 3. SCA EFFECTS OF F1s

Hybrid combination	Fecundity	Hatching	Yield /10,000 larvae	Survival rate	Cocoonweight	Shell weight	Cocoonshe ll ratio	FL	RSR
HTO ₁ x HTP ₁	15.813	2.640**	1.007**	3.751*	-0.006	0.003	0.109	49.641*	0.261
HTO ₁ x HTP ₂	-10.987	0.733	1.771**	2.472	0.128**	0.007	-1.150	29.505	0.924**
HTO ₁ x HTP ₃	38.447**	3.236**	2.686**	2.085	0.268**	0.051	-0.381	120.406**	0.956**
HTO ₁ x HTP ₄	1.213	-0.547	-1.447	-5.364	0.01	0.019**	0.977**	-3.462	0.406
HTO ₁ x HTP ₅	16.08	-0.035	0.306	-0.612	-0.007	-0.011	-0.594	-116.887	-0.028
HTO ₂ x HTP ₁	-6.487	-0.127	-0.387	2.941*	-0.055	-0.044	-1.322	-142.674	-0.746
HTO ₂ x HTP ₂	-12.62	0.666	-0.635	-3.237	-0.007	-0.022	-1.151	-21.794	0.151
HTO ₂ x HTP ₃	-15.02	1.620*	1.601**	1.668	0.210**	0.050**	-0.626	125.949**	1.266**
HTO ₂ x HTP ₄	-2.087	1.186	-0.199	1.127	0.051	0.020**	0.507	11.995	0.882**
HTO ₂ x HTP ₅	-8.72	-0.952	0.152	-2.571	0.109**	0.002	-1.146	16.529	-0.984
HTO ₃ x HTP ₁	8.197	0.961	-0.418	-7.579	0.110**	0.012	-0.075	37.706	0.416
HTO ₃ x HTP ₂	-26.937	-0.379	-2.015	1.092	-0.160	-0.058	-1.500	-64.671	-0.588
HTO ₃ x HTP ₃	18.163	2.408**	0.572	1.68	0.057	0.016*	0.297	12.004	0.627**
HTO ₃ x HTP ₄	26.930*	-0.825	0.434	-3.244	0.201**	0.005	-1.985	-31.735	0.177
HTO ₃ x HTP ₅	-45.870	-1.314	-0.748	-2.134	-0.032	-0.003	0.211	-31.668	0.527*
HTO ₄ x HTP ₁	-9.337	-0.727	1.869**	3.729*	0.161**	0.047**	0.616**	161.537**	1.517**
HTO ₄ x HTP ₂	-31.803	0.333	0.424	-3.753	0.144**	0.034**	0.237	-55.762	0.631**
HTO ₄ x HTP ₃	51.463**	2.620**	0.578	3.260*	-0.036	-0.021	-0.666	-35.863	0.512*
HTO ₄ x HTP ₄	-3.27	2.220**	-0.11	-3.639	0.077*	0.006	-0.454	-40.33	0.162
HTO ₄ x HTP ₅	-9.237	2.598**	0.237	-6.262	0.144**	0.020**	-0.498	3.463	0.112
HTO ₅ x HTP ₁	-29.087	2.193**	-0.387	-3.799	0.015	-0.002	-0.296	15.85	0.767**
HTO ₅ x HTP ₂	39.280**	4.053**	3.019**	3.581*	0.239**	0.056**	0.251	143.304**	1.064**
HTO ₅ x HTP ₃	-47.620	-1.544	-0.654	-5.157	-0.001	-0.024	-1.072	-99.289	0.046
HTO ₅ x HTP ₄	21.147	2.306**	-0.777	2.536	-0.105	-0.032	-0.717	-15.978	-0.338
HTO ₅ x HTP ₅	57.513**	2.768**	2.614**	3.130*	0.141**	0.051**	1.039**	145.459**	1.162**
S.E (sij) @ 0.05	24.434	1.481	0.812	2.88	0.062	0.0142	0.549	45.989	0.501
S.E (sij) @ 0.01	32.166	1.949	1.069	3.79	0.082	0.0188	0.724	60.542	0.659

FL= Filament length; RSR = Raw silk recovery; * Significant (p< 0.05); ** Significant (p< 0.01)

TABLE 4. SCA EFFECTS OF RECIPROCAL

Hybrid combination	Fecundity	Hatching	Yield /10,000 larvae	Survival rate	Cocoonweight	Shell weight	Cocoonshe ll ratio	FL	RSR
HTP ₁ x HTO ₁	18.167	0.333	-0.07	-2.100	0.119*	0.033**	0.405	51.013*	0.700*
HTP ₁ x HTO ₂	41.667*	0.083	1.946**	-0.367	0.241**	0.057**	-0.171	71.456**	-0.250
HTP ₁ x HTO ₃	-39.507	-2.733	-3.336	-11.42	-0.085	-0.036	-0.992	-70.001	0.150
HTP ₁ x HTO ₄	28.667*	2.600**	0.791	-1.162	0.115**	0.013	-0.680	32.250	-0.217
HTP ₁ x HTO ₅	-11.333	0.083	-1.941	-9.750	0.018	-0.024	-1.538	46.420	-0.033
HTP ₂ x HTO ₁	-22.333	0.483	-1.690	-1.850	-0.088	-0.034	-0.087	-48.000	0.350
HTP ₂ x HTO ₂	-3.500	-3.867	-1.334	-5.517	0.035	-0.018	-1.502	-29.766	-0.167
HTP ₂ x HTO ₃	-15.167	2.817**	1.217	-1.825	0.162**	0.020*	-0.759	34.771	0.167
HTP ₂ x HTO ₄	11.500	4.817**	-2.044	-9.808	0.009	-0.023	-1.387	-20.175	-0.517
HTP ₂ x HTO ₅	7.667	1.100	-0.003	0.708	0.013	-0.005	-0.405	7.898	0.517
HTP ₃ x HTO ₁	2.167	0.650	-0.554	-0.125	-0.014	-0.017	-0.689	51.764*	0.100
HTP ₃ x HTO ₂	-48.833	-2.750	0.206	-0.750	0.063	-0.013	-0.438	25.417	0.533
HTP ₃ x HTO ₃	-12.667	-2.167	1.483**	0.025	0.228**	0.044*	-0.323	127.269**	0.667
HTP ₃ x HTO ₄	-33.500	0.267	2.551**	0.150	0.372**	0.071**	-0.452	231.167**	0.083
HTP ₃ x HTO ₅	3.500	0.900	-0.875	-5.617	0.095*	-0.043	-3.496	13.747	-1.08
HTP ₄ x HTO ₁	-26.000	-4.850	-0.673	-5.433	0.072*	-0.005	-1.187	-69.250	-0.633
HTP ₄ x HTO ₂	33.167*	3.967**	0.736	-0.600	0.119*	0.013	-0.775	117.489**	0.033
HTP ₄ x HTO ₃	-51.500	-5.017	-1.174	-3.908	-0.005	-0.037	-1.876	44.923	-0.400
HTP ₄ x HTO ₄	-25.167	-1.617	-0.728	-9.708	0.213**	0.017*	-1.511	2.749	-0.250
HTP ₄ x HTO ₅	-33.667	-0.800	2.408**	-1.833	0.331**	0.080**	0.641*	209.500**	1.150**
HTP ₅ x HTO ₁	-79.000	-2.800	-2.659	-2.933	-0.17	-0.052	-0.865	-13.382	-0.050
HTP ₅ x HTO ₂	-33.333	-4.967	-1.884	-6.850	-0.059	-0.038	-1.331	-145.392	0.183
HTP ₅ x HTO ₃	-17.500	-3.733	-1.978	-7.500	-0.047	-0.050	-2.247	-45.165	-0.08
HTP ₅ x HTO ₄	-49.333	-0.467	-2.652	-14.03	0.055	-0.027	-1.971	-108.063	-1.117
HTP ₅ x HTO ₅	-26.833	-0.600	0.303	0.458	0.084*	0.005	-0.697	26.833	0.133
S.E (rij) at 0.05	26.983	1.635	0.897	3.181	0.068	0.016	0.607	50.788	0.554
S.E (rij) at 0.01	35.521	2.152	1.181	4.188	0.090	0.021	0.799	66.857	0.729

FL= Filament length; RSR = Raw silk recovery; * Significant (p< 0.05); ** Significant (p< 0.01)

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