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# **Research Article**

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# Analysis of Stability parameters in the bivoltine breeds of silkworm Bombyx mori L

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**Abstract:** Genotype-environment (G-E) interaction and stability parameters were analyzed for ten each of oval and dumbbell silkworm bivoltine genotypes reared during three different seasons of the year. Quantitative economic traits *viz.*, fecundity, cocoon yield / 10000 larvae by number, cocoon yield / 10000 larvae by weight, cocoon weight, shell weight, cocoon shell percentage, filament length, denier, raw silk percentage, renditta, neatness and boil-off loss were evaluated. The mean sum of squares (MS) for the breeds and environments was highly significant in both oval and dumbbell breeds in respect of all the traits except for renditta clearly indicating substantial variation among the breeds and seasons. However, the G-E interaction was found to be non-significant for all the traits among oval breeds, while among the dumb-bells, only four traits, namely, yield by number, yield by weight, filament length and neatness showed significant G-E interaction. Two stability parameters, *viz.*, regression coefficient (bi) and deviation from regression (s<sup>2</sup>di) were analyzed in both oval and dumb-bell breeds, which showed significant differences for most of the traits. Based on values of the two stability parameters for the 12 economic traits and cumulative ranking, CSR2, JPN8 (oval) and CSR16 (dumb-bell) were found to be stable genotypes, while, S5 (oval) and BBE267 (dumb-bell) were the least stable. **Keywords:** silkworm breeds, G-E interaction and stability analysis

## INTRODUCTION

The success of sericulture industry depends upon several factors of which the impact of the environmental factors such as biotic and abiotic factors is of vital importance. Among the abiotic factors, temperature plays major role on the growth and productivity of silkworm, a poikilothermic insect [1]. It is also known that, late age silkworms prefer relatively lower temperature than the young age ones and fluctuation of temperature during different larval stages was found to be more favorable for growth and development of larvae than constant temperature. As per available literature, quality cocoons production is possible if the temperature is within the range of 22 to 27°C and above these levels makes cocoon quality poorer [2].

The main objective of silkworm rearing is to produce qualitatively and quantitatively superior cocoons, which in turn have a direct bearing on the raw silk production. He and Oshiki[3] used survival rate of silkworm as a main characteristic for evaluating thermo-tolerance. The climatic conditions prevailing in the tropics are most unpredictable. In order to introduce bivoltine races in a tropical country, like India, it is necessary to have stability in cocoon crop under high environment. In fact, temperature Genotype environment interactions are of major importance to the silkworm breeders while developing new breeds. The concept of genotype environment interactions has been well documented in both plants and animal species [4].

Development of bivoltine silkworm genotypes, which can adopt to wide range of diversified environments, is the ultimate goal of any breeders involved in breeding programme. Genotype environment interactions are extremely important in evaluation of genotypes as they reduce the genotypic-stability values under diverse environments [5]. A genotype is considered to be adaptive / stable one with high mean yield and low degree of fluctuation in yielding ability in diverse environments [6].

Therefore, the present study was carried out to evaluate genotype environment interaction to understand the extent of adoptability/stability in performance under varying environmental conditions in respect of quantitative traits and to identify stable genotypes under varied environments.

#### MATERIALS AND METHODS

Twenty bivoltine genotypes, *viz.*, CSR2, CSR3, CSR12, CSR17, CSR27, JPN7, JPN8, S5, BBE226, BBI276 (oval) and CSR4, CSR6, CSR16, CSR26, S1, S9, D13, 5HT, BBE247, BBE267 (dumb-bell) with known genetic background were drawn from germplasm bank of CSR&TI, Mysore and CSGRC, Hosur and were reared in three replications during three different seasons of the year, *viz.*, summer, rainy and winter by following standard rearing method. The data on 12 quantitative traits such as fecundity, yield/10000 larvae by number, yield/10000 larvae by weight, cocoon weight, shell weight, cocoon shell ratio, filament length, filament size, raw silk percentage, renditta, neatness and boil-off loss traits were recorded and evaluated.

Genotype-environment interactions as well as stability analysis were carried out by following the standard model of Eberhart and Russel [7]. The data on the 12 pre- and post-cocoon traits was subjected to environment-wise analysis of variance and combined analysis of variance (mean sum of squares) for the oval and dumb-bell parental breeds. The stability analysis of the quantitative traits was measured for two stability parameters, namely, regression coefficient (bi) and deviation from regression ( $s^2$ di). A genotype with unit regression coefficient (bi=1) and the deviation from regression not significantly different from zero (s<sup>2</sup>di=0) is considered to be a stable genotype. Eberhart and Russel (1966) proposed formula used in stability analysis for emphasizing both linear (bi) and non-linear (s<sup>2</sup>di) component of genotype-environment interaction and judging the stability of a genotype is as under.

 $y_{ij} = \alpha_{i+} \beta_i e_{j+} \delta_{ij}$ 

where,

 $y_{ij}$  =Performance of *i*-th genotype at the *j*-th environment,

 $a_i$  = Mean of *i*-th genotype over all the environments,

 $e_j$  = Mean of all genotypes at the *j*-th environment minus the grand mean,

 $\beta_i$  = Regression coefficient of *i*-th genotype to environment change,

 $\delta_{ij}$  = Deviation from regression of the *i*-th genotype in the *j*-th environment.

In addition to the above, the Windostat Statistical software package (version 7.0) developed by INDOSTAT, Hyderabad is utilized for computing stability analysis and analysis of variance parameters.

#### RESULTS

Pooled analysis of variance ANOVA mean data of three replications during different seasons showed highly significant differences among the genotypes for all the economic traits studied (Tables 1 & 2) indicating the presence of genetic variability among the genotypes. The genotype environment interaction was further partitioned into linear and non-linear (pooled deviation) components. The genotype environment (linear) interaction was highly significant for all the parameters, when tested against pooled deviation, which revealed that there are genetic differences among genotypes for their regression on the environmental index. Estimation of environmental index for all the traits showed that rainy and winter seasons were most favorable for realizing yield potential of genotypes while it was not as much of during summer environment. Thus, performance of the genotype environment interaction varied from season to season.

With regard to oval breeds, the mean sum of squares for the genotypes and environment was highly significant for all the traits except for shell percentage and renditta clearly indicating substantial variation among the genotypes and seasons. However, the genotype environment interaction was found to be nonsignificant for all the traits, while the linear portion of the GxE was significant for fecundity, yield by number and boil-off loss traits (Table 1). In case of dumbbell genotypes, the mean sum of squares for the genotypes and environments were highly significant for all the traits, except in case of renditta. The GxE interaction was significant for only four traits *i.e.*, yield by number, yield by weight, filament length and neatness, while linear regression of GxE was significant for the above four traits and also in shell weight (Table 2).

The mean values for economic traits, regression coefficient (bi) and deviation from regression (s<sup>2</sup>di) for oval and dumb-bell genotypes in respect of different environment are as presented in Tables 3 and 4, respectively. Among the oval genotypes, the stability parameters were non-significant for fecundity, filament length, denier and raw silk percentage, while the remaining traits showed significant differences. The 'bi' values were significant for CSR2, JPN8 and S5 breeds for yield by weight, CSR17, CSR27 and JPN8 for cocoon weight, CSR3 for shell percentage and renditta, JPN7 for boil-off loss parameters. The 's<sup>2</sup>di' values were significant in CSR27 for yield by number, BE226 for yield by weight, JPN7 for cocoon weight, S5 for shell weight, CSR27, JPN7 and S5 for shell percentage, JPN7 and S5 for renditta and BBE226 for boil-off loss traits (Table 3).

In case of dumb-bell parental genotypes, the stability parameters were found to be significant for all the 12 traits in one or the other genotype. The 'bi' values were significant in BBE247 for fecundity, D13 for yield by number, CSR16 and D13 for yield by weight, BBE267 for shell weight, CSR6 and D13 for filament length, CSR26 and BBE247 for denier, S1 for raw silk percentage, S9 for neatness and CSR6 for boil-off loss traits. The 's<sup>2</sup>di' values were significant in BBE247 for gield by number, BBE267 for yield by number, BBE247 for yield by number, BBE247 for yield by weight and denier, BBE267 for cocoon weight, shell weight, shell percentage and renditta (Table 4).

The oval parental genotypes were ranked based on the values of two stability parameters for the 12 economic traits. The cumulative ranks for the 12 traits clearly indicates that among the ten oval genotypes, CSR2 and JPN8 with the cumulative ranks of 136 are the most stable genotypes, while S5 with the rank of 164 appears to be the less stable genotype (Table 5). Similarly, ranking of dumb-bell parental genotypes based on the values of two stability parameters for the 12 economic traits is presented in Table 6. It is clearly evident that, CSR16 is the most stable genotype with a cumulative rank value of 89, while BBE267 is the least stable one.

DF Fecundity Yield by Yield by Shell Filament Filament Raw silk Source of variation Cocoon Cocoon number weight Weight Weight shell Length size Percentage (Denier) Ratio 9 609.9\*\*\* 180828.7\* 4.049\* 0.033\* 0.004\* 40088.0\* 0.897\*\* Genotypes 1.663 0.336\* \*\* \*\* \*\* \*\* \*\* \*\* 0.049 2 8912.9\*\*\* 641574.4\* 4.278\* 0.044\* 0.002\* 0.479 12963.0\* 2.928\*\*\* Environments \*\* \*\* \*\* \*\* Gen. x Env. 165.9 43692.5 0.058 0.003 0.000 2141.2 0.039 0.259 18 0.917 Env. + (Gen. x 20 1040.6\*\*\* 103480.7\* 0.480\* 0.007 0.000\* 0.873 3223.3 0.040 0.526\* Env.) Environments 17825.8\*\* 0.087\* 0.004\* 0.958 25926.0\* 0.099 5.856\*\*\* 1283149.0 8.556\* 1 \*\*\* \*\* (Linear) \*\* \*\* Gen. x Emv. 9 264.1\* 65090.7\* 0.043 0.003 0.000 0.961 2121.8 0.043 0.333 (Linear) 10 0.003\* 0.000\* 1944.5\*\* 0.168\*\*\* **Pooled Deviation** 61.0 20084.6\*\* 0.087\* 0.786\* 0.031 \*\* \* \* \* Pooled Error 54 43.1 0.001 0.0000.224 0.013 4746.8 0.031 648.1 0.033 29 Total 906.9 127485.2 1.588 0.015 0.001 1.118 14664.1 0.132 0.641

#### Table 1: Analysis of variance (ANOVA) of mean values of yield parameters in oval breeds

#### Table 2: Analysis of variance (ANOVA) of mean values of yield parameters in dumb-bell breeds

Source of variation	DF	Fecundity	Yield (No.)	Yield (Weight)	Cocoon Weight	Shell Weight	Cocoon shell Ratio	Filament <b>Length</b>	Filament size (Denier)	Raw silk Percentage
Genotypes	9	852.0***	81615.2* **	1.108** *	0.013*	0.003* **	5.121** *	10457.8* **	0.343* **	2.596***
Environments	2	7508.0** *	495365.0 ***	13.416* **	0.211* **	0.006* **	2.181*	69119.6* **	0.710* **	7.847***
Gen. x Env.	18	103.0	19329.2*	0.379*	0.003	0.000	0.481	1282.4*	0.019	0.176
Env. + (Gen. x Env.)	20	843.5***	66932.8* **	1.683** *	0.024* *	0.001* **	0.651	8066.1** *	0.088* *	0.943***
Environments (Linear	1	15016.0* **	990730.1 ***	26.833* **	0.422* **	0.011* **	4.362*	138239.2 ***	1.420* **	15.693** *
Gen. x Emv. (Linear)	9	101.9	31007.5*	0.642**	0.002	0.000*	0.385	2071.1*	0.024	0.254
Pooled Deviation	10	93.7***	6885.8** *	0.105*	0.003* **	0.000* **	0.520** *	444.2	0.013	0.089
Pooled Error	54	21.5	942.4	0.044	0.001	0.000	0.101	585.5	0.007	0.246
Total	29	846.1	71489.4	1.505	0.020	0.001	2.038	8808.3	0.167	1.456

Parameter $\rightarrow$	F	ecund	ity	Yie	ld by n	umber	Yiel	d by we	ight	Co	coon we	ight
Genotype ↓	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s <sup>2</sup> di	Mean	bi	s <sup>2</sup> di
CSR2	561	0.82	-100.9	9275	1.31	-10522.7	16.1	1.22*	-0.12	1.912	1.93	-0.002
CSR3	550	0.77	-127.0	9326	0.47	4427.5	16.1	1.16	-0.1	1.862	0.66	0.002
CSR12	545	1.25	-113.3	9147	1.42	-11023.9	16.0	1.05	-0.11	1.856	1.09	0.000
CSR17	537	1.04	-30.04	9172	2.00	24248.4	16.0	1.31	-0.1	1.855	1.77*	-0.003
CSR27	536	1.32	-1.703	9163	2.19	46840.8*	14.8	1.10	-0.09	1.821	0.28*	-0.003
JPN8	530	0.71	22.92	9153	1.04	39716.1	16.0	0.53*	-0.12	1.715	0.28*	-0.003
JPN7	537	1.33	-104.7	9193	0.34	-7119.9	16.0	0.91	-0.11	1.854	1.07	0.014*
S5	524	0.63	-136.5	9192	0.15	177.94	16.0	0.85*	-0.12	1.837	0.83	-0.002
BBE226	521	1.67	-135.1	8740	0.42	-12187.5	14.2	0.89	0.36*	1.613	0.87	-0.002
BBI276	514	0.46	-76.84	8642	0.67	-10745.3	12.7	0.98	0.01	1.627	1.22	-0.002
Mean	536			9103			15.4			1.795		

Table 3: Mean values of different seasons of	n Stability parameters analysis fo	r oval genotypes
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Parameter→	S	hell we	ight	Coc	coon she	ll ratio	Fi	lament l	ength		Denier	
Genotype ↓	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di
												-
CSR2	0.452	1.15	-0.0002	23.70	2.94	0.190	1075	1.72	4465.1	2.81	-0.95	0.009
					-							-
CSR3	0.440	1.12	-0.0002	23.65	3.1*	-0.260	1036.	1.74	4622.1	2.87	-1.02	0.020
					-							-
CSR12	0.434	1.52	-0.0002	23.62	1.001	-0.198	1074	2.21	-2159.9	2.79	0.598	0.030
CSR17	0.438	1.52	-0.0001	23.61	0.004	-0.170	1053	1.85	1813.9	2.80	2.45	0.090
					-							-
CSR27	0.455	1.27	-0.0002	25.01	0.595	0.960*	1029	1.23	-2093.4	2.80	1.02	0.007
					-							-
JPN8	0.395	0.65	-0.0002	23.01	1.145	-0.080	1203	0.94	-1980.6	2.11	1.28	0.030
												-
JPN7	0.437	1.90	-0.0002	23.65	5.380	1.820**	1000	0.31	-1613.2	2.26	0.94	0.030
												-
S5	0.431	-0.8	0.0008*	23.50	7.080	3.060***	1108	-0.63	-1372.8	2.67	1.78	0.020
BBE226	0.376	0.95	-0.0001	22.34	0.014	-0.220	864	0.26	-2107.0	3.06	5.61	0.000
											-	
BBI276	0.366	0.80	-0.0002	22.49	0.430	0.130	804	0.38	-2173.4	3.04	1.704	0.040
Mean	0.422			23.46			1025			2.72		

Parameter→	F	Raw silk	%		Renditta			Neatnes	SS	Boil-off loss			
Genotype ↓	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	
CSR2	19.3	-0.07	-0.17	5.24	2.8	0.00	92.4	1.64	-0.06	23.00	1.25	0.265	
CSR3	19.0	0.96	0.16	5.34	-3.11*	-0.01	92.0	1.39	-0.103	23.67	1.53	-0.130	
CSR12	19.2	1.08	-0.13	5.31	-1.0	-0.01	91.8	0.28	0.39*	23.00	2.05	0.205	
CSR17	19.2	1.60	-0.19	5.24	0.1	-0.01	91.8	0.18	0.40*	23.00	1.61	-0.123	
CSR27													
	19.0	0.53	-0.18	5.22	-0.7	0.02	91.1	2.32*	-0.100	23.00	1.61	-0.120	
JPN8	19.2	2.42	0.33	5.32	-1.2	0.00	92.1	1.64	-0.065	21.50	0.66	-0.056	
JPN7	19.0	1.35	-0.02	5.36	5.9	0.06**	92.1	0.93	-0.10	21.50	0.13*	-0.133	
S5	19.0	0.05	-0.06	5.32	6.7	0.09**	92.1	1.61	-0.03	23.33	0.81	-0.130	
BBE226	17.6	1.43	0.19	5.43	0.0	-0.01	90.3	0.00	-0.10	24.67	0.36	0.401*	
BBI276	17.9	0.64	-0.17	5.45	0.4	0.01	90.3	0.00	-0.10	25.00	0.00	-0.133	
Mean	18.8			5.32			91.6			23.17			

Parameter→	I	Fecundit	y	Yie	eld by nu	ımber	Y	ield by we	ight	Cocoon weight			
Genotype ↓	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	
CSR4	516	0.76	-84.1	9672	0.85	-878.6	17.64	0.474	-0.02	1.845	1.05	0.0017	
CSR6	547	0.95	241.6	9746	1.05	2734.1	18.14	0.502	0.13	1.906	1.09	0.0013	
CSR16	529	0.91	-61.1	9754	0.38	-1874.1	18.15	0.599*	-0.07	1.908	0.93	-0.0015	
CSR26	550	1.28	-84.2	9723	0.71	-465.0	17.97	1.262	0.17	1.910	1.00	0.0042	
S1	544	0.84	103.5	9472	1.72	6024.7	18.05	1.324	-0.05	1.816	0.76	-0.0016	
S9	555	1.53	-85.7	9723	1.03	2312.1	18.08	1.294	0.07	1.896	0.68	-0.0014	
D13	562	1.04	251.7	9653	0.19*	-2099.9	18.43	0.481*	-0.07	1.902	1.38	-0.0003	
5HT	526	0.98	-84.5	9437	1.37	-1075.3	17.91	1.941	-0.04	1.820	1.16	-0.0017	
BBE247	516	1.09*	-90.4	9370	1.97	21112.1**	16.90	1.212	0.29	1.748	0.90	-0.0030	
BBE267	527	0.61	-73.5	9382	0.74	21063.9**	16.83	0.911	-0.04	1.781	1.04	0.0179**	
Mean	537			9593			17.81			1.853			

Table 4: Mean values of different seasons on S	Stability parameters analysis for Dumbbell genotypes
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Parameter→	$\rightarrow$ Shell weight			Coc	oon sh	ell ratio	Fi	lament	length	Denier			
Genotype ↓	Mean	bi	S <sup>2</sup> di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	
CSR4	0.412	0.86	0.0000	22.4	1.38	1.01**	959.6	1.54	-1734.1	2.79	1.47	-0.02	
CSR6	0.423	0.99	-0.0001	22.26	1.51	0.30	970.4	0.46*	-1768.9	2.85	0.95	-0.06	
CSR16	0.424	1.13	0.0000	22.18	0.51	0.06	965.0	1.13	588.2	2.78	1.24	-0.01	
CSR26	0.419	1.41	0.0001	21.95	-0.03	-0.07	966.1	0.78	-1446.7	2.84	0.61*	-0.06	
S1	0.404	0.64	0.0000	22.23	1.09	-0.08	1022.6	0.79	-1628.3	2.65	1.54	-0.05	
S9	0.442	0.85	0.0000	23.32	0.47	0.15	1111.6	0.98	-1149.3	2.67	0.74	-0.05	
D13	0.404	0.93	0.0000	21.37	2.3	0.38*	950.0	1.46*	-1761.8	2.69	0.90	-0.06	
5HT	0.424	1.64	0.0001	23.22	0.15	0.06	960.0	1.38	-1437.5	2.94	1.44	-0.06	
BBE247	0.387	1.21	0.0000	22.04	0.02	0.16	895.7	1.01	-1333.2	3.08	0.29*	-0.06	
BBE267	0.321	0.35*	-0.0001	18.62	2.61	2.14***	920.6	0.46	-1677.7	3.16	0.79	-0.06	
Mean	0.406			21.96			972.15			2.85			

Parameter→	R	aw silk %	6	Renditta			] ]	Neatness		Boil-off l	OSS	
Genotype ↓	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di
CSR4	17.50	0.97	-0.40	6.40	1.141	0.0044**	91	0.39	-0.063	24.33	0.690	-0.078
CSR6	18.193	0.48	-0.52	6.43	1.351	0.0071	92	0.97	-0.054	23.33	1.962*	-0.155
CSR16	18.121	1.04	-0.53	6.43	0.494	-0.0005	92	1.46	-0.007	23.00	1.265	-0.096
CSR26	18.322	1.44	-0.25	6.39	-0.07	-0.0051	92	0.80	-0.091	22.67	1.394	0.156
S1	16.90	1.41*	-0.53	6.47	0.098	-0.0049	92	3.16	-0.057	22.67	0.568	0.118
S9	19.223	0.65	-0.53	6.32	0.397	0.0016	93	-0.01*	-0.095	22.33	0.697	-0.078
D13	17.50	1.46	-0.48	6.33	2.179	0.0267*	92	1.46	-0.007	23.00	1.265	-0.096
5HT	17.623	1.09	-0.17	6.41	0.08	-0.007	92	0.88	-0.084	23.00	1.265	-0.096
BBE247	16.35	1.13	-0.49	6.55	-0.01	0.0039	90	0.39	-0.063	24.67	0.568	0.119
BBE267	16.30	0.32	-0.52	6.45	3.491	0.1438***	90	0.39	-0.063	24.67	0.318	0.239
Mean	17.60			6.42			92			23.36		

Parameter→	Parameter→ Fecundity		Yield by number		Yield by weight		Coc Wei	oon ight	Shell Weight		Cocoon shell ratio	
Genotype ↓	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di
CSR2	2	5	2	4	8	7	10	4	3	7	5	4
CSR3	3	8	5	2	7	4	6	6	2	4	8	7
CSR12	4	7	4	6	2	6	2	1	7	8	6	5
CSR17	1	3	9	8	9	3	9	8	8	1	3	3
CSR27	6	1	10	10	4	2	7	7	5	9	4	8
JPN8	5	2	1	9	10	8	8	9	6	3	7	1
JPN7	7	6	7	3	3	5	1	10	9	5	9	9
S5	8	10	8	1	6	9	4	3	10	10	10	10
BBE226	10	9	6	7	5	10	3	2	1	2	2	6
BBI276	9	4	3	5	1	1	5	5	4	6	1	2

Parameter→	Filaı Ler	ment ngth	De	nier	Raw (%	Silk	Ren	ditta	Neat	ness	Boil- los	off s	Total
Genotype↓	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di	
CSR2	5	9	7	3	9	5	5	2	5	3	2	9	136
CSR3	6	10	8	4	1	4	8	7	2	5	4	4	140
CSR12	9	7	4	7	2	3	6	5	6	9	10	8	138
CSR17	8	3	6	10	7	8	2	3	7	10	6	2	149
CSR27	2	5	1	2	6	7	4	8	10	4	5	3	138
JPN8	1	4	3	8	10	10	7	1	4	2	3	1	136
JPN7	4	2	2	6	3	1	9	9	1	6	8	6	137
S5	10	1	5	5	8	2	10	10	3	1	1	5	164
BBE226	7	6	10	1	5	9	3	6	8	7	7	10	155
BBI276	3	8	9	9	4	6	1	4	9	8	9	7	137

$\begin{array}{c c} Parameter \\ \rightarrow \\ v \end{array}$		Yiel nun	ld by nber	Yiel we	ld by ight	Cocoon Weight		Shell Weight		Cocoon shell ratio		
Genotype↓	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s <sup>2</sup> di	bi	s²di
CSR4	7	3	3	2	9	1	6	4	3	8	4	3
CSR6	3	9	2	7	7	8	4	2	5	3	1	8
CSR16	4	1	7	4	6	6	10	1	4	5	3	1
CSR26	8	4	5	1	3	9	3	5	1	9	8	9
S1	6	8	8	8	5	4	8	6	8	6	7	6
S9	10	6	1	6	4	7	2	7	9	4	5	4
D13	2	10	9	5	8	5	9	8	10	2	2	2
5НТ	1	5	6	3	10	3	5	3	7	7	9	10
<b>BBE247</b>	5	7	10	10	2	10	7	9	6	1	6	5
BBE267	9	2	4	9	1	2	1	10	2	10	10	7

Parameter →	Fila Ler	ment Igth	Der	nier	Ra Si (%	aw ilk %)	Ren	ditta	Nea	tness	BOL (%)		Total
Genotype↓	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di	bi	s²di	
CSR4	10	8	8	2	1	3	2	9	8	5	5	1	126
CSR6	9	10	1	8	9	6	3	7	1	3	10	8	145
CSR16	3	1	4	1	2	8	4	1	4	1	1	3	89
CSR26	5	5	6	9	7	2	8	6	3	9	6	9	151
S1	4	6	9	3	6	10	1	5	10	4	7	6	156
S9	2	2	5	4	5	9	5	3	9	10	4	2	135
D13	7	9	2	7	8	4	9	8	5	2	2	4	156
5НТ	6	4	7	5	3	1	6	2	2	8	3	5	129
BBE247	1	3	10	10	4	5	7	4	6	6	8	7	162
BBE267	8	7	3	6	10	7	10	10	7	7	9	10	181

## DISCUSSION

The prime objective of the study is to identify potential genotypes showing stability in performance and to serve as resource material, the pre-requisite for the success of the breeds, under the given environment. It is important to measure the phenotypic expression of the major contributing traits of economic importance in the silkworm genotypes under diversified environmental conditions to understand the genetic endowment pertaining to adaptability and productivity [8]. Seasonal variations in manifestation of phenotypic traits of the genotypes are also ascribed to the genetic differences among different silkworm strains and an interaction with changing environmental conditions [9-11]. Further, prevailing environmental conditions influence variable expression of traits during different seasons of the tropics as observed by many researchers [12-14]. The observations made on the variable

responses of different economic traits to different seasons are in agreement with the earlier findings [13, 16, 17]. Environment-wise analysis of variance of interaction during three seasons measured shows significant differences in yield parameters between the genotypes.

The ultimate goal of breeding is to identify potential genotypes suitable for wide range of environments, fluctuations of which highly influence the yield traits. The genotypes that can adjust to the varying environmental conditions and gives maximum output of economic traits are considered as stable. To identify such genotypes, G x E interactions was studied by subjecting the data to environment-wise analysis of variance by following the standard model of Eberhart and Russel [7]. The combined analysis of variance (mean sum of squares) for the oval and dumbbell parental genotypes for twelve economic traits was estimated (Table 1 & 2).

The Stability is defined as adoption of genotype with relatively constant yield despite unpredictable and transcient environmental conditions to select stable genotypes unaffected by environmental changes [18-20]. Further, a genotype can be considered highly stable if all the important parameters of stability (Mean, bi and s<sup>2</sup>di) are satisfied. Mean performance stability analysis was carried out for the economic traits of oval and dumb-bell parental genotypes reared under three seasons (summer, rainy and winter). Two stability parameters, namely, regression coefficient (bi) and deviation from regression (s<sup>2</sup>di) were analyzed. Among the oval and dumb-bell genotypes analyzed, CSR2, JPN8 (oval) and CSR16 (dumb-bell) genotypes with regression coefficient (bi) showing significant value is as in Tables 3 & 4. S5 (oval) and BBE267 (dumb-bell) genotypes which showed less mean values were identified as poorly adapted to all environments though their regression coefficients were nearer to 1.

From the present study, oval (JPN8, CSR2) and dumb-bell (CSR16) genotypes selected showed the presence and type of GxE interactions with high mean yield values, regression coefficient approaching to unity (bi=1) and non-significant deviation from regression nearer to zero (s2di=0) secured superior cumulative ranks and were considered as the most stable genotypes. These potential genitors if utilized as parents in bivoltine silkworm breeding plan may transmit the genetic basis of their stability and diversity parameters to next generation.

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