

ANALYSIS OF VARIABILITY AND GENETIC PARAMETERS FOR YIELD ATTRIBUTES IN SABITA/SAMBAMAHSURI DERIVATIVES OF RICE (*Oryza sativa* L.) GENOTYPES

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ABSTRACT

Study on variability analysis and genetic parameters for yield attributing characters was carried out using twenty-three recombinant inbred lines of Sabita/Sambamahsuri derivatives with four check varieties viz. Swarna sub-1, Dhanarasi, Sambamahsuri and Sabita in RBD with two replications. Statistical analysis carried out for the estimation of GCV, PCV, heritability (BS) and genetic advance for all characters. The genotypes S_{11} (32.52), S_{23} (31.63), S_{16} (31.25), S_{12} (30.74), S_{13} (30.68) and S_2 (30.06) were superior in grain yield per plant (g) with the margin of 11.36%, 8.32%, 7.02%, 5.27%, 5.06% and 2.95% respectively as compared to best check varieties. S_{17} , S_{27} , S_3 , S_{11} , S_{19} and S_{23} were superior for most of the yield determining traits viz., grain yield per plant, panicle weight, panicle length, number of secondary branches per panicle, number of florets per panicle, number of grains per panicle, harvest index as compared to check varieties. High estimates of GCV and PCV were obtained for panicle weight (15.019 and 17.632) followed by number of floret per panicle (10.285 and 11.122). High heritability was observed for most of the characters under study. High heritability coupled with high GA% was observed for panicle weight and number of floret per panicle. These characters are governed by additive gene action and one should go for direct selection for these traits.

INTRODUCTION

Rice is the most consumed cereal grain in the world. It is staple food crop for more than half of the world's human population. India is one of the world's largest producers of rice, just after China. It is being consumed by almost two-thirds of the population and it plays a pivotal role in Indian economy. The strategy in the present agriculture is to produce adequate quantity of food from the available acreage to meet the requirement of ever expanding world population and the success of the breeding strategies relies heavily on the genetic diversity of the crop. A successful breeding programme will depend on the genetic diversity of a crop for achieving the goals of improving the crop and producing high yielding varieties (Padulosi, 1993). To improve the yield, evaluation of germplasm is the most important aspect (Yadav, 2000) because grain yield is a complex polygenic character controlled by many genes interacting with the environment and it is the product of many factors called yield components. Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement (Kishore *et al.*, 2015). A critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adopting of appropriate selection techniques (Dhanwani *et al.*, 2013). The present study is to find out superior genotypes of rice suitable for the gangetic plains of West Bengal. In this context, keeping the prior points in view,

the present objective is to evaluate 23 rice genotypes along with four check varieties with the view of selecting those that have better yield attributes for incorporation into hybridization programme. Thus, the present experiment was carried out to estimate the genetic variability parameters for various yield attributing traits in rice.

MATERIALS AND METHODS

The experimental materials consisted of twenty-three F_8 recombinant inbred lines (RILs) of Sabita/Sambamahsuri derivatives designated S_1 to S_{23} and four check varieties viz. Swarna sub1, Dhanarasi, Sambamahsuri and Sabita. RILs were developed at RRS, NAZ, Bidhan Chandra Krishi Vishwavidyalaya, SC-Chakdaha, Nadia. Each genotype was grown in 5 m² plot with the spacing of 20 × 20 cm and recommended management practices were followed to obtain good harvest. Observations were recorded from each entry on 20 morpho-physiological characters, which are listed in the following table.1. The data were used for statistical analysis following appropriate computer based statistical software (OPSTAT) for the estimation of analysis of variance, mean, range, genotypic, phenotypic and environmental variance, GCV, PCV, heritability (BS) and genetic advance.

The analysis of variance (ANOVA) was computed based on randomized block design as per standard statistical procedure. Genotypic and phenotypic coefficients of variation were estimated following Burton and De Vane (1953). Heritability in broad sense and genetic advance as percent of mean were

calculated as per Johnson *et al.* (1955) and Al-jibouri *et al.* (1958).

RESULTS AND DISCUSSION

Mean performance of 23 RILs of Sabita/Sambamahsuri derivatives along with check varieties i.e. Swarna sub 1, Dhanrasi and parents i.e. Sambamahsuri and Sabita are presented in table.2. The genotypes S_{11'}, S_{23'}, S_{16'}, S_{12'}, S₁₅ and S₂ were superior in grain yield per plant with the margin of 11.36%, 8.32%, 7.02%, 5.27%, 5.06% and 2.95% respectively as compared to best check varieties. S_{9'}, S_{10'}, S_{12'}, S_{15'}, S_{16'}, S_{17'}, S_{18'}, S_{19'}, S₂₀ reported earliness with respect to the best check varieties. S_{1'}, S_{2'}, S_{3'}, S_{11'}, S_{19'} and S₂₃ were superior for

most of the yield determining traits viz., grain yield per plant, panicle weight, panicle length, number of secondary branches per panicle, number of florets per panicle, number of grains per panicle, harvest index as compared to check varieties.

Variability in population is prerequisite especially for the characters where improvement is required. Analysis of variance (table.3) showed significant differences among the genotypes against all of the characters under study except days to maturity and fertility percentage indicating the existence of sufficient variation among the genotypes for yield and yield component characters studied in the present investigation. So, there is a large scope for improving the characters through selection.

The mean, range, phenotypic, genotypic and environmental variances, coefficient of variance (CV), genotypic coefficient

Table1: Yield attributing characters in rice:

S. N.	Characters	S. N.	Characters
1	Days to 50% flowering	11	Fertility percentage (%)
2	Days to maturity	12	1000 grain weight (g)
3	Plant height (cm)	13	Grain length (mm) (L)
4	Number of panicles per plant	14	Grain breadth (mm) (B)
5	Panicle weight (g)	15	Grain L/B Ratio
6	Panicle length (cm)	16	Kernel length (mm) (L)
7	Number of primary branches per panicle	17	Kernel breadth (mm) (B)
8	Number of secondary branches per panicle	18	Kernel L/B Ratio
9	Number of florets per panicle	19	Harvest index (%)
10	Number of grains per panicle	20	Grain yield per plant (g)

Table2: Mean Performance of 23 RILs of Sabita/Sambamahsuri derivatives for different yield attributing characters.

S. N.	Selection number	Days to 50% flower	Days to maturity	Plant height (cm)	No. of panicle per plant	Panicle weight (g)	Panicle length (cm)	No. of primary branches per panicle	No. of secondary branches per panicle	No. of florets Per Panicle
1	S ₁	115	141	138	10.5	4.11	26.94	13.8	48.8	213.6
2	S ₂	110	140	135.9	11.2	4.47	27.79	14.1	49.1	214.8
3	S ₃	106	139	138.4	12	4.14	27.31	14.6	49.1	209.7
4	S ₄	112	140	139	10.2	3.62	26.52	13.7	47.6	197.5
5	S ₅	111	139	140	11.1	4.09	26.34	13	45.6	157.4
6	S ₆	103	139	135.7	10.5	3.65	26.37	14.9	50.8	210.5
7	S ₇	111	139	148.3	11	3.05	26.04	13.3	46.2	181
8	S ₈	110	139	133.8	10.9	3.75	26.35	13.1	47.2	208.4
9	S ₉	113	133	132.7	9.9	2.61	26.05	14.6	50.2	156.3
10	S ₁₀	102.5	133	127.4	9.9	4.06	25.51	12.5	43	200.4
11	S ₁₁	119	138	127.7	9.7	4.53	26.41	12.1	45.4	219
12	S ₁₂	110	137	129.6	10.9	3.94	25.26	13.6	48.6	203.3
13	S ₁₃	119	143.5	128.4	11.3	3.6	26.14	12.1	45.5	177.4
14	S ₁₄	109	139	123	11.3	3.75	27.31	12.5	47.2	195.8
15	S ₁₅	109	125.5	134.1	11.5	3.81	26.47	11.2	41	205.5
16	S ₁₆	102	131	137.4	11.8	3.39	26.25	11.9	42.3	224.2
17	S ₁₇	104	132	125.7	9.5	3.32	27.23	12.1	42.9	190.4
18	S ₁₈	103	132	127	11.5	4.18	25.43	11.4	40.8	176.7
19	S ₁₉	101	133	129.7	9.7	3.58	26.22	12.3	46.3	204.1
20	S ₂₀	109	137.5	131.3	11.7	3.67	25.94	11.5	43.5	193
21	S ₂₁	114.5	139	140.8	11.4	3.87	27.31	11.4	42.2	215.6
22	S ₂₂	112	139	123.5	9.1	2.32	24.5	12.9	49.4	213.1
23	S ₂₃	114	139	127.9	11	3.92	24.36	11.7	44.7	219.8
24	Swarna sub 1	112	138	115.4	10.1	3.08	24.29	13.8	44.5	203.2
25	Dhanrasi	111	140	138.8	11	3.41	25.42	12.4	39.9	163
26	Sambamahsuri	113.5	141	116.9	9	2.16	22.14	10.2	34.5	160
27	Sabita	116.5	146.5	170.3	11.4	3.12	25.48	12.7	40.6	165.8
	Mean	110.07	137.52	133.21	10.71	3.99	25.98	12.72	45.07	195.54
	C.D.	6.09	6.677	2.468	0.598	0.687	0.786	0.633	2.16	17.104

Table 2 : Continue..

S. N.	Selection number	No. of grains per panicle	Fertility percent (%)	1000 grain weight (g)	Grain length (mm)	Grain Breadth (mm)	Grain L/B ratio	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Harvest index (%)	Grain yield per plant (g)
1	S ₁	155.4	72.75	21.39	8.58	2.78	3.09	6.16	2.09	2.96	34.37	29.9
2	S ₂	163.8	76.26	20.28	8.68	2.75	3.16	6.8	2.28	2.98	33.58	30.06
3	S ₃	149.2	71.14	18.8	8.81	2.87	3.09	6.84	2.35	2.92	32.13	29.5
4	S ₄	145.3	73.67	18.17	8.08	2.49	3.26	6.63	2.19	3.03	31.85	28.68
5	S ₅	134.9	85.72	17.95	8.74	2.67	3.28	6.89	2.25	3.08	28.59	25.36
6	S ₆	143	67.94	18.01	7.92	2.8	2.83	5.7	2.09	2.73	29.63	26.66
7	S ₇	146.5	80.95	19.35	8.03	2.89	2.78	6.05	2.28	2.66	26.46	23.79
8	S ₈	159.5	76.63	20.62	8.41	2.49	3.38	6.68	2.24	2.98	33.09	28.92
9	S ₉	124.2	79.48	19.64	8.77	2.64	3.32	6.57	2.31	2.84	28.16	23.45
10	S ₁₀	151.8	76.06	19.51	7.71	2.48	3.12	5.84	2.29	2.55	29.79	27.1
11	S ₁₁	165.2	75.71	19.26	8.53	2.66	3.21	5.82	2.54	2.3	37.2	32.52
12	S ₁₂	164.7	81.02	20.99	8.9	2.99	2.98	5.8	2.74	2.12	35.64	30.74
13	S ₁₃	140.3	79.28	17.97	8.54	3.02	2.83	5.66	2.42	2.35	31.63	27.27
14	S ₁₄	150	76.67	18.83	8.33	2.59	3.23	5.81	2.3	2.53	29.45	25.09
15	S ₁₅	159.8	77.99	18.95	8.36	2.66	3.15	6.25	2.36	2.65	33.83	30.68
16	S ₁₆	161.8	72.1	17.62	7.95	2.52	3.17	6.25	2.19	2.88	33.38	31.25
17	S ₁₇	139.6	73.34	20.01	8.1	2.99	2.71	6.49	2.39	2.72	32.93	29.87
18	S ₁₈	142.9	80.88	22.05	8.77	2.79	3.14	6.72	2.36	2.85	30.05	27.95
19	S ₁₉	163.8	80.34	19.46	8.29	2.38	3.48	6.58	1.94	3.4	32.95	30.7
20	S ₂₀	155.1	80.37	17.39	8.37	2.53	3.31	6.44	2.02	3.21	29.85	27.91
21	S ₂₁	147.5	68.41	22.04	8.93	2.98	3	6.61	2.33	2.84	29.88	28.95
22	S ₂₂	126.2	59.22	17.63	8.61	2.94	2.93	6.67	2.42	2.76	29.11	24.11
23	S ₂₃	163.2	74.23	17.79	8.19	3.06	2.68	6.33	2.6	2.44	35.69	31.63
24	Swarna sub 1	143.8	70.77	17.36	8.81	3.04	2.9	6.69	2.52	2.66	30.56	29.08
25	Dhanrasi	136.8	83.92	20.3	8.89	3.02	2.94	6.74	2.59	2.61	31.12	28.63
26	Sambamahsuri	121.5	75.94	21.44	8.45	2.19	3.86	5.96	1.91	3.12	26.23	22.05
27	Sabita	136.4	82.31	22.66	10.09	3.01	3.36	7.74	2.42	3.21	29.91	29.2
	Mean	147.86	76.04	19.46	8.51	2.75	3.12	6.39	2.31	2.79	31.37	28.18
	C.D.	15.833	9.229	1.251	0.141	0.104	0.146	0.481	0.334	0.161	3.111	3.367

Table 3 : Analysis of variance for different yield attributing characters of Sabita/Sambamahsuri derivatives (Mean Sum of Square)

S. No.	Characters	Source of Variance with d.f.		
		Replication (1)	Genotype (26)	Error (26)
1.	Days to 50% flowering	0.2960	50.4500*	8.6810
2.	Days to maturity	42.6670	37.5950	10.4360
3.	Plant height (cm)	0.2670	221.1760**	1.4120
4.	Number of panicle per plant	0.0070	1.4230**	0.0840
5.	Panicle weight (g)	3.7820	0.6940*	0.1100
6.	Panicle length (cm)	0.2190	2.7990**	0.1450
7.	No. of primary branches per panicle	0.3590	2.7120**	0.0940
8.	No. of secondary branches per panicle	3.7340	28.9740**	1.0930
9.	Number of florets per panicle	359.8540	877.3770**	68.4710
10.	Number of grains per panicle	254.3670	328.8710*	58.6580
11.	Fertility percentage (%)	0.7730	64.0520	19.9350
12.	1000 grain weight (g)	0.0210	4.9410**	0.3660
13.	Grain length (cm)	0.0070	0.4230**	0.0050
14.	Grain breadth (cm)	0.0030	0.1120**	0.0030
15.	Grain L/B ratio	0.0020	0.1340*	0.0050
16.	Kernel length (cm)	0.0910	0.4480**	0.0540
17.	Kernel breadth (cm)	0.0001	0.0770**	0.0040
18.	Kernel L/B ratio	0.0340	0.1790*	0.0270
19.	Harvest index (%)	38.7600	15.0530*	2.3510
20.	Grain yield per plant (g)	45.9450	14.7330**	2.6590

of variation (GCV), phenotypic coefficient of variation (PCV), heritability (BS), genetic advance (GA) and genetic advance as percentage of mean of 23 RILs including two check varieties and two parents are presented in table.4. The genotypic coefficient of variance means the range of variability available in crop and also enable breeder to compare the amount of

variability present among different character. The GCV and PCV were classified as low (Less than 10%), moderate (10-20%) and high (More than 20%) as suggested by Sivasubramanian and Madhavamenon, (1973).

A wide spectrum of variation was found among the genotypes against all the characters. This would offer a large scope of

Table 4: Variability and genetic parameters for yield attributing characters of Sabita/Sambamahsuri derivatives

S. N.	Characters	Mean	Range	Variance		CV	GCV	PCV	h ² (BS)	GA	GA (%)
				Pheno typic	Genotypic Environ ment						
1.	Days to 50% flowering	110.074	101.00-119.00	29.536	20.855	2.677	4.152	4.940	70.638	7.912	7.188
2.	Days to maturity	137.519	125.50-146.50	24.016	13.580	2.349	2.680	3.564	56.545	5.708	4.151
3.	Plant height (cm)	133.211	115.40-170.30	111.292	109.880	0.896	7.869	7.919	98.731	21.456	16.107
4.	No. of panicle per plant	10.707	9.00-12.00	0.746	0.662	2.701	7.643	8.106	88.903	1.590	14.845
5.	Panicle weight (g)	3.598	2.16-4.53	0.402	0.292	0.110	9.238	15.019	72.553	0.948	26.353
6.	Panicle length (cm)	25.977	22.14-27.79	1.972	0.827	1.145	4.463	4.671	90.150	2.253	8.674
7.	No. of primary branches per panicle	12.719	10.20-14.90	1.403	1.309	0.094	2.409	8.996	93.308	2.277	17.902
8.	No. of secondary branches per panicle	45.070	34.50-50.80	15.034	13.941	1.093	2.319	8.284	92.732	7.407	16.434
9.	No. of florets per panicle	195.537	156.30-224.20	472.921	404.450	68.471	4.232	10.285	85.522	38.312	20.159
10.	No. of grains per panicle	147.859	121.50-165.20	174.405	154.470	19.935	5.181	7.861	69.727	19.994	13.523
11.	Fertility percentage (%)	76.037	59.22-85.72	41.994	22.059	19.935	5.872	6.177	52.529	7.012	9.222
12.	1000 grain weight (g)	19.460	17.36-22.66	2.654	2.288	0.366	3.109	7.772	86.199	2.892	14.865
13.	Grain length (cm)	8.510	7.71-10.09	0.214	0.209	0.005	0.803	5.376	97.795	0.932	10.952
14.	Grain breadth (cm)	2.746	2.19-3.06	0.058	0.055	0.003	1.837	8.509	95.543	0.471	17.134
15.	Grain L/B ratio	3.116	2.68-3.86	0.070	0.065	0.005	2.271	8.153	92.804	0.504	16.180
16.	Kernel length (cm)	6.394	5.66-7.74	0.251	0.197	0.054	3.642	6.942	78.435	0.810	12.665
17.	Kernel breadth (cm)	2.309	1.91-2.74	0.041	0.037	0.004	2.650	8.282	90.711	0.375	16.249
18.	Kernel L/B ratio	2.790	12.12-3.40	0.093	0.087	0.006	5.815	9.900	74.026	0.490	17.547
19.	Harvest index (%)	31.369	26.23-37.20	8.702	6.351	2.351	4.954	8.034	72.979	4.435	14.138
20.	Grain yield per plant (g)	28.184	22.05-32.52	8.696	6.037	2.659	5.775	8.718	69.422	4.217	14.963

selection for evolving promising and desirable plant types. The highest estimates of phenotypic and genotypic variances were observed for number of florets per panicle followed by number of grains per panicle and plant height. Grain length, grain breadth, grain L/B ratio, kernel breadth, kernel L/B ratio, panicle weight and panicle length showed low genotypic and phenotypic variance. The magnitude of PCV was higher than the corresponding GCV for all the characters indicated the influence of environment on the expression of these characters. The difference between PCV and GCV for the studied characters was very less also reported by Sandhya *et al.* (2014) indicating low sensitivity to environment and consequently greater role of genetic factors influencing the expression of these characters; hence they could be improved by following phenotypic selection. Highest estimates of GCV and PCV were obtained for panicle weight followed by number of florets per panicle in this regard. Singh and Choudhary (1996) for number of panicles per plant, number of grain per panicle, grain yield per plant and 1000 grain weight; Nayak *et al.* (2002) for number of panicles per plant, number of spikelet per panicle, number of grains per panicle and grain yield per plant; Sarkar *et al.* (2005) for number of panicles per plant, number of tiller per plant and grain yield per plant; Senapati *et al.* (2008) for panicle number per plant, grain number per panicle, floret number per panicle and panicle weight; Raut *et al.* (2009) for seed yield per plant, 1000 grain weight, grains per panicle and effective tiller per plant; Kumar and Senapati (2013) for grain yield per plant, panicle weight, number of panicles per plant, number of secondary branches per panicle, number of grains per panicle, 1000 grain weight and florets number per panicle and Dhanwani *et al.* (2013) for biological yield.

Heritability estimates indicate relative degree at which character is transmitted from parents to offspring. The heritability estimates was classified as low (Less than 30%), moderate (30-60%) and high (More than 60%) as suggested by Johnson *et al.* (1955). High heritability was observed for all the characters under study except for days to maturity and fertility percentage. The characters having high heritability can be improved by simple selection. Among all of them, Plant height, grain length, grain breadth, number of primary branches per panicle, grain L/B ratio and number of secondary branches per panicle recorded more than 90% heritability. These findings were earlier corroborated by Yadav *et al.* (1992) for plant height, yield per plant, harvest index, days to maturity; Bihari *et al.* (2004) for days to 50% flowering and test weight; Panwar *et al.* (2007) for days to 50% flowering, days to maturity and 1000 grain weight and Karthikeyan *et al.* (2009) for days to 50% flowering, days to maturity and 1000 grain weight; Kumar and Senapati (2013) for plant height, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, days to 50% flowering, fertility percentage, days to maturity, 1000 grain weight and kernel L/B ratio. Fertility percentage and days to maturity showed moderate heritability in this regard.

Genetic advance denotes the improvement in the genotypic value of the new population over the original population. Number of florets per panicle recorded the highest GA followed by plant height. These findings were in agreement with that of Viswakarma *et al.* (1989) for grains per panicle. Lowest GA was observed in kernel breadth followed by grain breadth, kernel L/B ratio and grain L/B ratio. The estimates of genetic

advance as percent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. The range of genetic advance as percent of mean was classified as low (Less than 10%), moderate (10-20%) and high (More than 20%), suggested by Johnson *et al.* (1955). Most of the character showed moderate GA as a percentage of mean. It was highest for panicle weight followed by number of florets per panicle, number of primary branches per panicle, kernel L/B ratio and grain breadth respectively. These findings were earlier corroborated by different workers for one or more characters e.g., Chaubey and Singh (1994) for grain yield per plant followed by panicle weight and total number of spikelets; Sarma *et al.* (1996) for effective tillers per meter row length and panicle weight; The lowest GA as percentage of mean was observed for days to maturity followed by days to 50% flowering, panicle length and fertility percent respectively. Kumar and Senapati (2013) recorded highest GA% for grain yield per plant and lowest for days to maturity under the character they study. High heritability coupled with high genetic advance was obtained for panicle weight and number of floret per panicle. These findings were reported by Singh *et al.* (2005) for plant height; Sanker *et al.* (2006) for days to 50% flowering, plant height, productive tiller per plant, panicle length, grains per panicle, 1000 seed weight and single plant yield; Kishore *et al.* (2008) for days to 50% flowering and plant height. It indicated the predominance of additive gene action for controlling these characters. Therefore, these characters can be improved simply through selection.

High heritability with moderate genetic advance is observed for plant height, number of panicle per plant, number of primary branches per panicle, number of secondary branches per panicle, number of grain per panicle, 1000 grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio, harvest index and grain yield per plant indicating the role of additive as well as non additive gene action for controlling these characters. Thus, these characters can be improved by hybridization followed by selection. High heritability with low genetic advance was observed for days to 50% flowering, days to maturity, and fertility percentage. These findings were earlier reported by Madhavilatha *et al.* (2005) for days to maturity and fertility percentage. It indicated nonadditive gene action for expression of these characters. The high heritability was being exhibited due to favourable environment rather than genotype. So there is little scope for improvement simply through selection.

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