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Estimation of genetic parameters for physico-chemical and nutritional traits in rice

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ABSTRACT

Variability and heritability studies in seven parents and their hybrids revealed the existence of significant differences for all the characteristics and indicated wide variability among the genotypes. In general, the parents exhibited high mean values for most of the quality traits studied, suggesting that parents were superior in quality than the hybrids. The heritability estimates were high which ranged from 88.00 to 99.10. Low to moderate estimates of variability high heritability and low to high genetic advance for all the quality traits indicated the preponderance of both additive and non additive gene effects in conditioning these traits. Variability was found high for iron content, while it was low for hulling percent in the genotypes under study. High heritability along with low genetic advance was exhibited for hulling percent only indicating that this traits was under the influence of environment. Remaining traits exhibited high heritability along with moderate to high genetic advance suggesting that these characters could be of great importance for selecting better genotypes in rice improvement programmes.

Key words: rice, genetic parameters, quality parameters, variability

Super fine varieties of rice with desirable grain dimensions like length:breadth ratio and cooking quality get a premium price in the market. Quality of rice is determined by a combination of many physico-chemical properties and these are largely influenced by the environment. Many high yielding rice varieties and hybrids have been developed in India, in most cases quality is not upto the desirable extent and therefore, lacked acceptability by consumers. The increased demand of quality rice in the local as well as in international market has paid great attention on quality breeding programme. Improving rice quality has become prime objective of most breeding programmes. The quality characters of rice include physical attributes like kernel length:breadth ratio, cooking and eating qualities like elongation ratio, volume expansion ratio, amylose content, gelatinization temperature and nutritional qualities like protein content, iron content and zinc content. Incorporation of these characters into high yielding semi dwarf varieties has met only with partial success. High level of genotypes and phenotypic coefficients of variation is essential for selection of desirable genotypes in every crop improvement programme. Moreover, heritability along with genetic advance are important selection parameters in predicting the grain yield under selection. Hence the present study was undertaken to estimate different genetic parameters in rice.

MATERIAL AND METHODS

The experimental material comprising of 7 genotypes (Table 1) of rice viz., Samba mahsuri, Polasa prabha, Jagtial samba, Nellore mahsuri, Indra, Vijetha and Prabhat were crossed in diallel mating design (without reciprocals) during dry season 2006 and studied during wet season, 2007. These parents were selected based on their attributes for grain quality, cooking quality, reaction to pests and diseases and high yield. These varieties showed diversity for morphological and physiological traits. The twenty one F_1s and seven parents were grown at the experimental farm of Andhra Pradesh Rice Research Institute and Regional Agricultural Research station, Maruteru, during wet season 2007 in randomized block design (RBD) with

three replications having 3m row length and 20x15 cm spacing. Each replication comprised of one row of parent and three rows of F_1s. Recommended agronomic practices were followed. Mean values on yield components viz., hulling percent, milling percent, head rice recovery, length: breadth ratio, volume expansion ratio (VER), elongation ratio (ER), gelatinization temperature (GT), amylose content, protein content, iron content, zinc content and yield per plant. The data were analyzed by using standard methods (Murthy and Govind Swamy, 1967, Julioano *et al.,* 1965 and Little *et al.*1958), iron and zinc content were estimated by using Atomic Absorption Spectrophotometer (Tandon *et al.*, 1993). Mean data were used for calculating the genetic parameters. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed according to the formula given by Burton and Dewane (1952) and heritability (ns) expected genetic advance and genetic advance percent over mean were computed as per Allard (1960).

RESULTS AND DISCUSSION

In general, the parents exhibited high mean values for most of the quality traits studied, suggesting that parents were superior in quality than the hybrids (Table 2). Analysis of variance in parents and hybrids revealed that significant difference were observed for all the quality characters indicated wide variability among genotypes involved in the crossing programme (Table 3).

The considerable range of variation expressed for the traits studied indicated good scope for genetic improvement (Table 4). The genotypes showed wide range of variability for all the characters. In general phenotypic coefficient of variation is higher in comparison to genotypic under study, but the difference is low indicating the influence of environment is very low (Kumar *et al.,*2006). The genotypic coefficient of variation ranged from 1.88-51.61 (the genotypic coefficient of variation of hulling percent and iron content, respectively). Hulling percent registered low genotypic coefficient of variation and Phenotypic coefficient of variation followed by head rice recovery and length : breadth ratio. Low coefficient of variation for length-breadth was reported by Deo sarkar *et al.* (1989). This is in accordance with the present study, while milling percent, volume expansion ratio, elongation ratio, amylose content, protein content and yield per plant exhibited moderate genotypic coefficient of variation and phenotypic coefficient of variation. Kumar *et al. (*2006) reported moderate genotypic coefficient of variation for protein content.

The heritability estimates were high which ranged from 88.00 to 99.10 (heritability estimates for elongation ratio and iron content, respectively). High estimates of heritability for length:breadth ratio was reported by Deo Sarkar *et al.* (1989) and Lalitha and Sreedhar (1999). Pathak and Sharma (1996) and Krishna Veni *et al.* (2006) reported higher estimates for length:breadth ratio, elongation ratio and alkali spreading value, which was in agreement with the present results. In the present study amylose content and protein content also showed high heritability estimates confirming the findings of Deo Sarkar *et al.* (1989) and Lalita and Sreedhar (1999).

Table 1. Salient features of the parents used in the study

Name	Pedigree	Duration (days)	Grain type	Special features
Samba mahsuri (BPT 5204)	(GEB 24/T(N)1) /Mahsuri	150	Fine grain	Excellent cooking quality
Polasa prabha (JGL 384)	BPT 5204/Kavya	130	Fine grain	Resistant to gall midge
Jagtial samba (JGL 3844)	Samba mahsuri/ARC 5984/Kavya	120	Fine grain	High yielding, resistant to gall midge cold tolerance
Nellore mahsuri (NLR 34449)	IR 72/BPT 5204	125	Fine grain	High yielding suitable for wet and dry seasons
Indra (MTU 1061)	PLA 1100/MTU 1010	145	Medium slender	Resistant to BPH, BLB and Gallmidge
Vijetha (MTU 1001)	Vajram/MTU 7014	145	Medium slender	Resistant to BPH tolerant to blast and strong dormancy
Prabhat (MTU 3626)	IR 8/MTU 3	135	Medium bold	High yielder

Table 2. Mean values of quality characters of seven parents and their F_1s (without reciprocals)

Character	Hulling percent (%)	Milling percent (%)	Head Rice Recovery (%)	L/B Ratio	Volume Expansion ratio	Elongation Ratio	Gelatinization Temperature (°C)	Amylose content (%)	Protein content (%)	Iron content (ppm)	Zinc content (ppm)	Grain yield plant^{-1} (g)
Samba mahsuri/Polasa prabha	80.20	69.48	65.56	3.44	5.34	1.91	3.53	25.13	9.15	25.17	20.24	32.26
Samba mahsuri/Jagtial samba	76.86	64.47	57.85	2.97	6.40	1.59	1.67	25.03	9.04	84.13	19.57	28.62
Samba mahsuri/Nellore mahsuri	81.36	78.12	66.10	2.96	6.62	1.76	4.50	25.00	8.17	21.70	22.21	33.75
Samba mahsuri/Indra	79.43	69.06	67.10	2.93	4.80	1.45	1.89	30.13	9.22	23.87	11.37	29.13
Samba mahsuri/Vijetha	79.04	64.34	61.38	2.86	5.07	1.41	3.40	28.10	9.04	55.97	12.37	30.97
Samba mahsuri/Prabhat	79.28	69.88	66.65	2.72	6.41	1.53	2.85	26.33	7.43	33.50	13.60	27.39
Polasa prabha/Jagtial samba	77.98	63.19	56.82	2.96	5.56	1.68	2.67	24.10	8.91	54.77	12.83	22.69
Polasa prabha/Nellore mahsuri	79.10	66.23	59.56	3.16	5.14	1.41	1.98	25.60	9.18	26.13	22.63	27.09
Polasa prabha/Indra	79.10	68.49	64.55	3.11	5.05	1.32	3.60	25.27	9.41	35.33	14.30	31.99
Polasa prabha/Vijetha	77.99	63.71	52.77	2.84	5.69	1.55	5.40	22.13	8.67	22.20	14.73	26.02
Polasa prabha/Prabhat	78.12	62.47	56.71	2.78	7.33	1.37	2.33	24.17	8.79	22.93	12.03	25.73
Jagtial samba/Nellore mahsuri	78.71	63.32	56.67	3.16	5.20	1.43	3.50	22.10	9.10	24.33	11.50	25.24
Jagtial samba/Indra	78.79	64.45	61.39	2.96	4.42	1.36	2.45	22.33	9.24	25.93	11.43	27.48
Jagtial samba/Vijetha	79.09	63.03	51.62	2.78	5.15	1.56	3.63	22.37	10.47	41.00	17.13	31.67
Jagtial samba/Prabhat	80.01	69.59	61.16	2.71	5.50	1.45	3.43	16.33	6.35	27.53	13.57	26.70
Nellore mahsuri/Indra	79.35	67.30	62.74	3.54	4.93	1.43	4.18	15.80	9.60	21.13	10.23	32.75
Nellore mahsuri/Vijetha	79.73	69.05	64.52	3.06	4.53	1.19	2.43	21.77	9.45	27.43	11.57	27.48
Nellore mahsuri/Prabhat	78.59	34.76	62.85	2.42	4.09	1.75	3.30	24.30	7.74	32.27	11.93	25.01
Indra/Vijetha	78.32	61.43	55.08	3.57	5.14	1.63	2.53	16.33	9.25	58.13	12.93	31.67
Indra/Prabhat	79.63	66.88	62.84	2.55	5.69	1.43	2.47	24.13	8.73	86.77	22.60	31.89
Vijetha/Prabhat	77.28	64.85	60.14	2.71	4.82	1.17	3.33	22.20	7.18	43.73	22.83	31.11
Mean	78.95	66.17	60.67	2.96	5.38	1.49	3.10	23.27	8.77	39.14	15.31	28.89
Samba mahsuri	74.99	64.91	57.96	2.89	3.97	1.79	4.68	23.23	7.35	39.41	20.87	22.00
Polasa prabha	80.06	68.10	62.53	3.10	5.24	1.51	3.57	25.87	8.93	70.94	14.97	22.80
Jagtial samba	74.80	64.89	54.55	3.01	4.38	1.65	4.47	22.40	9.28	51.87	13.47	25.28
Nellore mahsuri	77.00	68.31	59.91	2.80	5.55	1.51	5.33	23.30	9.04	63.83	11.17	23.51
Indra	78.35	66.77	64.05	2.83	4.15	1.26	6.27	28.27	5.83	39.23	15.57	24.55
Vijetha	76.72	62.33	51.99	2.67	5.77	1.31	7.20	28.90	8.34	62.77	17.50	22.77
Prabhat	80.02	68.16	58.07	2.51	5.20	1.50	3.20	26.10	8.52	54.00	12.27	27.48
Mean	77.42	66.21	58.44	2.83	4.89	1.50	4.96	25.44	8.18	54.58	15.12	24.06
General Mean	78.5682	65.2702	60.1124	2.9286	5.2540	1.4975	3.5640	23.8118	8.6211	43.0006	15.2648	27.6795
CD (5%)	0.7101	1.2419	1.1654	0.1660	0.2964	0.1063	0.3169	0.4939	0.3366	3.3905	1.3004	1.8937

Table 3. Analysis of variance for quality characters and yield in seven parents and their progenies

Source	df	Mean sum of squares											
		Hulling (%)	Milling (%)	Head Rice Recovery (%)	L/B Ratio	Volume Expansion ratio (g)	Elongation ratio	Gelati-nization Temperature	Amylose content (%)	Protein content (%)	Iron content (ppm)	Zinc content (ppm)	Grain yield plant^{-1}
		1	2	3	4	5	6	7	8	9	10	11	12
Replications	2	0.79*	1.80	1.566	0.03*	0.15*	0.006	0.009	0.29*	0.22**	42.92**	4.27**	0.99
Genotypes	27	6.75**	141.97**	60.07**	0.23**	1.84**	0.10**	5.25**	36.21**	3.10**	1481.74**	50.79**	37.38**
Parents	6	13.99**	15.26**	53.80**	0.12**	1.54**	0.10**	6.11**	19.63**	4.42**	446.72**	32.71**	10.61**
Hybrids	20	3.07**	185.85**	61.03**	0.27**	1.84**	0.10**	2.52*	39.29**	2.59**	1678.67**	58.72**	28.89**
Parents vs hybrids	1	36.95**	24.78**	78.45**	0.27**	3.64**	0.001	54.53**	74.06**	5.37**	3753.39**	0.63	367.69**
Error	54	0.19	0.58	0.51	0.01	0.03	0.004	0.04	0.09	0.04	4.29	0.63	1.34**
CV %		0.5521	1.1624	1.1843	3.4621	3.4463	4.338	5.4311	1.2671	2.385	4.8167	5.204	4.1794

* significant at 5 % level ** significant at 1% level

Table 4. Mean, Coefficient of variation, Heritability and Genetic Advance for 23 characters in F_1 progenies

Character	Range		Variance		Coefficient of variation (%)		Heritability (Broad Sense)	Genetic Advance	
	Parents	F_1s	Genotypic	Phenotypic	Genotypic	Phenotypic	%	Value(k=206)	as % of mean
Hulling percent	74.99-80.06	76.86-81.36	2.19	2.38	1.88	1.96	92.10	2.92	3.72
Milling percent	62.33-68.31	61.43-69.88	47.13	47.71	10.52	10.58	98.80	14.06	21.54
Head rice recovery (%)	51.99-62.53	51.62-66.65	19.85	20.36	7.41	7.51	97.50	9.06	15.08
L/B ratio	2.51-3.10	2.42-3.54	0.07	0.09	9.34	9.96	87.90	0.53	18.04
Volume Expansion Ratio	3.97-5.77	4.09-7.33	0.60	0.63	14.76	15.16	94.80	1.56	29.61
Elongation ratio	1.26-1.79	1.17-1.79	0.03	0.04	11.72	12.50	88.00	0.34	22.65
Gelatinization Temperature	3.20-7.20	1.67-5.40	1.74	1.77	36.97	37.37	97.90	2.69	75.36
Amylose content (%)	22.40-28.90	15.80-25.60	12.04	12.13	14.57	14.63	99.20	7.12	29.90
Protein content (%)	5.83-9.28	6.35-10.47	1.02	1.06	11.72	11.96	96.00	2.04	23.66
Iron content (ppm)	39.23-70.94	21.13-86.77	92.48	96.77	51.61	51.83	99.10	28.52	45.85
Zinc content (ppm)	11.17-20.87	10.23-22.83	16.72	17.35	26.79	27.29	96.40	8.27	54.17
Grain yield plant^{-1} (g)	22.00-27.48	25.01-33.75	12.01	13.35	12.52	13.20	90.00	6.77	24.47

The traits *viz.,* volume expansion ratio, elongation ratio, gelatinization temperature, amylose content, protein content, iron content, zinc content and yield per plant exhibited high heritability along with high genetic advance indicating the presence of additive genes. Similar results were also reported by Sinha *et al.* (2004) and Choudhary *et al.* (2004) for grain yield. It was suggested that these characters of great importance for selecting better genotypes in rice improvement programme with good cooking quality and nutritional quality. Head rice recovery and length : breadth ratio revealed high heritability along with moderate genetic advance. These results are in accordance with Roy *et al.* (2001) and Kumar *et al,* (2006). High heritability along with low genetic advance was exhibited by hulling percent suggesting that the selection for this character must be taken up in advance generation and intermating of the selected superior segregants.

All the quality characters under study indicated low to moderate variability (both genotypic and phenotypic coefficient of variation) high heritability accompanied with low to high genetic advance which suggested that all these quality traits were under the influence of both additive and non-additive genetic components in their expression. Hence improvement of all these characters could be attained by following recurrent or reciprocal recurrent selection to exploit both additive and non-additive genetic components effectively.

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