



Studies on Genetic Variability, Heritability and Genetic Advance for Yield Components and Grain Quality Parameters of Rice (*Oryza sativa* L.)

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ABSTRACT

The analysis of variance revealed significant differences among the 64 genotypes for the all the 17 characters studied except for protein content indicating that enough variability is present in the studied material. The genetic parameters revealed moderate to high variability coupled with high heritability and high genetic advance as percent of mean for grain yield per plant (g), panicle length (cm), number of grains per panicle, head rice recovery per cent, volume expansion ratio, water uptake, L/B ratio and protein per cent suggesting the predominance of additive type of gene action in controlling these traits and scope for improvement of these characters through simple selection.

Key words : Genetic advance, Heritability, Quality parameters, Rice, Variability, Yield components.

Rice (*Oryza sativa* L.) is the world's second most important cereal crop and staple food for more than 60% of the global population providing about 75% of the calorie and 55% of the protein intake in their average daily diet and aptly describes the slogan "Rice is life". In India, rice is grown in area of 45.5 m ha with a production and productivity of 106.54 m t and 2424 k ha⁻¹ respectively (Ministry of Agriculture, Directorate of Economics and Statistics, Government of India 2014). Maintaining stable rice production is extremely important to feed the constantly growing population. For the estimated population of 1.63 billion people by the year 2050 with a per capita rice consumption of 225 to 275 g/day, country would require 133 to 162 m t of rice (Directorate of Rice Research, 2013). At present the rice productivity has reached to a plateau and there is a need to develop varieties with higher yield potential by breaking the existing yield plateau through utilizing more divergent lines in the breeding programmes.

It is known that yield of rice is complex quantitative trait and under pleiotropic gene control, at the same time it is highly influenced by environment and contributed by many other traits. So, selection based on yield alone is misleading. Success of crop improvement in rice therefore depends largely on the selection of parents with

high magnitude of genetic variability for different characters present in the plant population. Heritability and genetic advance are important selection parameters and when considered together help the breeders in determining the traits having better response to selection. Therefore, the present investigation was undertaken to study the heritability, genetic advance and variability of 64 genotypes of rice.

MATERIAL AND METHODS

Sixty four genotypes (Table 1) obtained from Indian Institute of Rice Research (IIRR), Ranjendranagar, Hyderabad, Telengana were evaluated in a Simple Lattice Design (SLD) with two replications during *Kharif* 2014 at Agriculture College Farm, Bapatla, Andhra Pradesh. Each genotype was raised in two rows of five meter length with a spacing of 20 cm x 15 cm between and within the rows, respectively. Standard agronomic practices and recommended fertilizer doses were adopted for normal crop growth. Observations were recorded on ten randomly selected plants from each replication for five yield components *viz.*, plant height, number of productive tillers, panicle length, number of total grains per panicle. However grain yield per plant and the characters; days to 50% flowering, days to maturity and test weight were recorded on plot

Table 1. The rice genotypes employed in the present study along with their pedigree.

S. No.	Designation	Cross combination/ Pedigree	S. No.	Designation	Cross combination/ Pedigree
1	CR 3819-8-1-13-1	Dandi/NLR33892	33	RNR 17462	MTU 1001/JGL 3855
2	NP 7060	NC 495/IR 36//Sita	34	BPT 2658	MTU 7029/Moroberakan
3	CN 1443-5-2-5	Patnai 23/ Swarna	35	CN 1477-19-5-3	Swana/Bhasamanik
4	CR 2826-1-1-1-3B-1	Swarna/ARC 10075	36	CR 3813-4-4-4-3-1-2	C 780-1937-1-3/DRR 1702
5	BPT 2507	BPT 1235/BPT 5204//BPT 5204	37	CR 2712-15-4	Sambha Mahsui/Salakathi
6	AD 11024	CR 1009/I.W.Ponni	38	OR 2545-11	Birupa/IR 62957
7	PAN 828	NA	39	RP 5865-300-4-1-1-1-3-3	MTU 1075/MTU 1010
8	MTU 1180	PLA 1100/NLR 145	40	PAU 3835-12-1-1-1	PR 116//PAU 3075-3-38/PR 106-P3
9	OR 2344-1	Jagannath/IR 21567-1-18-3	41	RNR 17472	Kavya/NLR 34449
10	NP-9560	IET 23078/IET 23088	42	RP 5895-61-19-8-4-3-2	Mahsuri/Vijaya//IR 64
11	CRHR101	NA	43	CN 1406-10-2-2-1-MLD-14	Tilakkachhari/IR 42
12	PRNP-9553	NP 9207-20-2/PRN 3941	44	CR 3697-4-4-2-2-3	CR 662-2-2-1-1-1/Sarala// CR 780-1937-1-3/DRR 1702
13	RP 5714-111-34-3-1-2	IR 60937-40-3-1-3/BM 71	45	OR 2555-5	MTU 1001/IR 65629-22-1
14	PAU 3842-52-1-2-1-1	PR 116//PR 108//1RR1 76//PR 106-P2	46	CB 11161	CO(R)50/Kavuni
15	RP 5878-ZGY1	Fengaizhan1/Yuanjing7// Fengaizhan1/Guang122	47	CRHR 32	NA
16	MTU 7029	Vasista/ Mahsuri	48	CR 2681-3-2-1-1-2	Gayatri/Warda2
17	RNR 11481	MTU 1010/JGL 3855	49	CN 2028-5-1	Selection frm CN 1769
18	RP 5893-136-69-17-8-7-1	Swarna 3/O.longistaminata	50	CR 3723-3	BG 90-2/IR 67962-84-2-2-2
19	CR 3727-12-1	IR 66159-164-5-3-5/IR 64	51	CR 3863-41-3-1	Pusa 44/PTB 33
20	CR 3861-37-5-3	Sambha Mahsui/Phalguna	52	RP 5896-88-50-9-2-2-1	IR 50/C14-8//IET 9993
21	CB 09154	BPT 1788/GEB 24	53	CR 3605-4-2-1-2-1	Gayatri/Jalmagna
22	BPT 5204	GEB 24/TN 1//Mahsuri	54	CR 2711-76	Tapaswini/Dhobanambari
23	BPT 2595	Mutant of BPT 2270	55	CR 3813-4-10-1-1-1	CR 778-1937-1-3/DRR 1702
24	CRH 102	NA	56	CR 2690-2-2-1-1-3	Chakaakhi/Ac.38687
25	CB 09 128	BPT 5204/IR 20	57	CR 3862-25-7-3	Swarna/Sarasa
26	NLR 3130	BPT 5204/NLR 33359	58	CR 3847-1-1-2-2-1	Pooja/Hanseswari//CRMAS 2232-85
27	OR 2394-22	Pathara/Vandana	59	OR (T) 20	Daya Mutant
28	NLR 3135	NLR 33892/WGL 20471/RNR 19994	60	BPT 2270	BPT 5204/CRM 1523
29	PAN 830	NA	61	OR (T) 21	Daya Mutant
30	RP 5709-100-22-6-5-1	RP Bio 226/MTU 1064	62	R (T) 22	Daya Mutant
31	PAU 4332-30-3-3-1	PAU 3418-11-10-2/PAU 3409-37-5	63	RP 5897-211-69-15-9-2-2	Tuzu Mochi (TJP)/I 66// IR 50400-64-1-2-2-2
32	RP 5894-251-47-19-4-2-2	IC 115376/BPT 5204//RP Bio 226	64	WGL-737	P 4616-3-6/Kavya

basis. The grain quality parameters *viz.*, milling percentage, hulling percentage, head rice recovery, L/B ratio, water uptake, kernel elongation ratio, volume expansion ratio, amylose content and protein percentage were estimated replication-wise on plot basis as per the standard procedures delineated by DRR Laboratory Manual on Rice Grain Quality Procedures (Directorate of Rice Research, 2006). The data were analyzed by using ANOVA (Raghavarao, 1983) and the genetic parameters such as PCV and GCV were calculated by the formula given by Burton and De Vane (1953), heritability in broad sense (h^2) by Allard (1960) and genetic advance as per cent of mean (genetic gain) were worked out as suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The 64 genotypes of rice studied in the present investigation differed statistically for all the characters studied. Analysis of variance revealed significant differences among the genotypes for all the characters except protein content, indicating presence of sufficient amount of variability among the varieties (Table 2). Thus, there is ample scope for selection of different quantitative and qualitative characters for rice improvement. The data on mean, range, variability, heritability and genetic advance as per cent mean for 17 characters are presented in Table 3. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association

Table 2. Analysis of variance for yield, yield components and quality characters for 64 genotypes of rice (*Oryza sativa* L.).

Source	Replications	Treatments	Error
Degree of freedom	1	63	63
	MEAN SUM OF SQUARES		
Days to 50% flowering	7.0312	89.7891**	7.0947
Days to maturity	3.1250	89.6428**	25.9821
Plant height (cm)	140.2813	169.8129**	13.8685
Productive tillers per plant	4.1328	0.9367**	1.0548
Panicle length (cm)	1.2051	23.1550**	2.8796
Number of grains per panicle	223.1328	2672.5752**	109.0534
Test weight (g)	0.0069	7.8516**	0.1487
Hulling per cent	1.2051	23.1550**	2.8796
Milling per cent	0.5050	12.8076**	0.7188
Head rice recovery per cent	1.3965	14.0809**	0.5028
Volume expansion ratio	1.1063	75.2176**	0.8543
Water uptake	0.2583	0.7115*	0.0205
L/B ratio	212.6953	4007.1397**	684.9175
Kernel elongation ratio	0.0395	0.4582*	0.0471
Protein per cent	0.0022	0.0479	0.0064
Amylose content	0.0007	2.0907**	0.1820
Grain yield per plant (g)	0.7781	7.0871**	1.4833

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

with the characters at genotypic level. The genetic parameters revealed that moderate to high PCV coupled with moderate to high GCV for the characters number of grains per panicle (25.608 and 24.584), grain yield per plant (g) (21.636 and 21.749), panicle length (cm) (16.585 and 14.636), head rice recovery per cent (10.551 and 10.432), volume expansion ratio (13.991 and 13.592), water uptake (18.899 and 15.903), kernel elongation ratio (11.891 and 10.393), L/B ratio (16.729 and 15.087) and protein per cent (14.017 and 12.845). These results are in agreement with the findings of Dhurai *et al.* (2014) for number of grains per panicle; Bornare *et al.* (2014) for grain yield per plant (g); Umadevi *et al.* (2010) for head rice recovery per cent and kernel elongation ratio; Shejul *et al.* (2013) for L/B ratio and Chakraborty *et al.* (2010) for protein per cent.

The estimates of heritability and genetic advance can be utilized for the prediction of genetic gain, which indicates the genetic improvement that

would result from the selection of best individuals. High broad sense heritability coupled with high genetic advance as percent of mean was recorded for the traits grain yield per plant (g) (83.3 and 37.13), panicle length (cm) (77.90 and 26.60), number of grains per panicle (92.2 and 48.61), head rice recovery per cent (97.8 and 21.24), volume expansion ratio (94.4 and 27.20), water uptake (70.8 and 27.56), L/B ratio (81.3 and 28.02) and protein per cent (84.00 and 24.24). These results are in accordance with the findings of Neha *et al.* (2014) for grain yield per plant (g); Dhurai *et al.* (2014) for panicle length (cm) and number of grains per panicle; Pandey *et al.* (2013) for head rice recovery per cent and volume expansion ratio; Shejul *et al.* (2013) for water uptake and Bhavana (2003) for protein per cent.

CONCLUSION

Present investigation suggested that there is adequate variability present in the material

Table 3. Mean, Variability, Heritability and Genetic advance as per cent of mean for yield , yield components and grain quality parameters in rice (*Oryza sativa* L.).

Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as percent of mean
		Minimum	Maximum	PCV (%)	GCV(%)		
Days to 50% flowering	116.797	103.00	132.00	5.959	5.505	85.4	10.47
Days to maturity	146.813	133.00	161.00	5.179	3.843	55.1	5.87
Plant height (cm)	107.828	90.00	138.00	8.888	8.189	84.9	15.54
Productive tillers per plant	12.994	9.80	15.00	7.678	1.864	15.9	19.3
Panicle length (cm)	21.755	14.61	29.40	16.585	14.636	77.9	26.60
Number of grains per panicle	145.633	90.00	246.00	25.608	24.584	92.2	48.61
Test weight(gm)	21.174	17.58	25.40	9.446	9.268	96.3	18.73
Hulling per cent	75.669	68.85	80.72	3.437	3.249	89.4	6.32
Milling per cent	69.044	60.91	74.38	3.911	3.774	93.1	7.50
Head rice recovery per cent	58.452	37.28	69.40	10.551	10.432	97.8	21.24
Volume expansion ratio	4.324	3.37	5.84	13.991	13.592	94.4	27.20
Water uptake	256.289	142.50	360.00	18.899	15.903	70.8	27.56
L/B ratio	3.005	2.03	4.10	16.729	15.087	81.3	28.02
Kernel elongation ratio	1.387	1.08	1.81	11.891	10.393	76.4	18.71
Protein per cent	7.605	5.60	9.50	14.017	12.845	84.0	24.24
Amylose content	21.925	16.86	27.72	9.442	7.635	65.4	12.71
Grain yield per plant (g)	44.383	30.09	72.67	21.636	21.749	83.3	37.13

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

studied. Moderate to high GCV, PCV coupled with high heritability and moderate to high genetic advance as percent of mean were observed for plant height, number of productive tillers per plant, panicle length, number of grains per panicle, L/B ratio and kernel elongation ratio suggesting the predominance of additive type of gene action in controlling these traits and scope for improvement of these characters is possible through simple selection.

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