



Studies on Genetic Variability in Rice (*Oryza sativa* L.)

Key words : Genetic advance, Genetic variability, Heritability, Rice.

Rice is the most important staple food crop and a primary food source meeting the dietary requirements of the people living in the tropics and sub-tropics. Quantum jump in yield improvement has been achieved in rice with the development of high yielding varieties under commercial cultivation. However, being the staple food of the population in India, improving its productivity has become a crucial importance (Subbaiah *et al.*, 2011). A systematic evaluation and characterization of the genotypes not only helps in identification of superior and genetically divergent lines but also provides information on the utility of the genetic resources. Knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effecting genetic improvement. Estimates of heritability and genetic advance play an important role in exploiting future research programmes for crop improvement. Hence, the present investigation was undertaken to study the genetic variability for yield and its component characters in the popular rice varieties of India.

A field experiment was conducted with eighty seven genotypes of rice collected from Plant Breeding Division, Crop Improvement Section, Directorate of Rice Research (DRR), Rajendranagar, Hyderabad in a randomized block design with three replications at DRR, Hyderabad, Andhra Pradesh, India. The eighty seven popular rice varieties of India used in the present investigation include MO 4, Bhudeb, CN-1039-9, Dandi, PR-113, WGL-14, DL-184, VRM 44-1, KMP-101, Dharitri, RAU3043, Varalu, Birupa, Phalguna, Nagrey Dubraj, Gayatri, VRS-15, MTU-1010, Pooja, Purnendu, MSS-5, Vijetha, PSD-1, BPT-11711, Pusa basumathi, Savitri, Nalini, NDR-359, Manoharsali, Manika, Mandya Vijaya, PR-118, Erramallelu, White ponny, Sahyadri-2, Swarna, Indravathi, MSE-9, Ranjeet, PTB-39, Gouri, IR-64, VRM-3, Jagabandu, Karjal-2, Surendra, Barhavarodhi, Basumathi-386, Harsha, Durga, Madhukar, Jaya, Lalat, Tarouri Basumathi, Champakala, Kanchana, AS-100, Paritdhan, KKP-2, NLR-33654, PR-115, Jalpriya, VRM-31, Sahyadri, Jalanidhi, Mahalaxmi, Matta triveni, VRS-25, Aishwarya, Kalanamak, Shakti, CN-1233-33-9, MSE-12, Konark, Baghiradhi, Pratap, Bhubam,

Varsha, CN 72035-32-8, Kavya, Dinesh, Ramchandi, Gajpathi, DL-183, Basumathi-370, Samba Mahsuri and SGT-1. Single plant observations were recorded on five randomly selected plants in each genotype from the middle row in each replication as per standard techniques for plant height, number of productive tillers per plant, panicle length, single plant yield and spikelet fertility. Days to 50 % flowering was computed on plot basis. Seed weight was recorded by weighing 100-grains of each genotype. Mean kernel length and breadth of ten polished kernels from their bulk sample from each replication of each genotype were measured using a steak grain shape tester. L/B ratio was computed by dividing mean kernel length with mean kernel breadth. Protein content was determined by the Micro-Kjeldhal method described by Pregl (1930). The mean data after computing for each character was subjected to standard methods of analyses of variance following Panse and Sukhatme (1957). Phenotypic (PCV) and Genotypic (GCV) coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean were estimated by the formulae suggested by Burton (1952) and Johnson *et al.* (1955).

In the present investigation, analysis of variance (Table 1) indicated the existence of highly significant differences among the genotypes for all the traits except 100-grain weight, kernel length, kernel breadth and L/B ratio. Plant height and days to 50% flowering exhibited high genotypic and phenotypic variances, followed by single plant yield and spikelet fertility (Table 2). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Among the yield attributing characters, highest PCV and GCV values were obtained for single plant yield (34.22 and 33.61) followed by plant height (21.70 and 21.45), while the least PCV and GCV were recorded for spikelet fertility (4.71 and 3.81). Among the grain quality characters, highest and lowest PCV and GCV values were found with L/B ratio (20.06 and 19.95) and protein content (10.98 and 10.96), respectively.

Table 1. ANOVA for important morphological characters and yield in different rice varieties.

S.No.	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=149)	Error (d.f.=258)
1.	Plant height (cm)	13.01	1816.40**	14.51
2.	Days to 50% flowering	3.69	399.32**	0.98
3.	Number of productive tillers per plant	0.99	7.84**	1.57
4.	Panicle length (cm)	1.71	19.14**	2.04
5.	Spikelet fertility (%)	20.60	42.87**	6.36
6.	Single plant yield (g)	4.42	80.88**	0.97
7.	100-grain weight (g)	0.29	0.40	0.02
8.	Kernel length (mm)	0.003	1.87	0.001
9.	Kernel breadth (mm)	0.001	0.18	0.001
10.	L/B Ratio	0.001	1.28	0.004
11.	Protein content	0.003	2.83**	0.002

** Significant at 1 per cent level *Significant at 5 per cent level

Table 2. Mean, variance, heritability (broad sense), genetic advance and genetic advance as percent of mean for various characters in rice varieties.

S.No.	Character	Mean	Variance		Coefficient of variation		Herita-bility (h ²) (%)	GA (5%)	GA as per cent of mean
			Pheno type	Geno type	Pheno type	Geno type			
1.	Plant height (cm)	114.25	615.145	600.62	21.70	21.45	97.60	49.88	43.66
2.	Days to 50% flowering	102.24	133.76	132.78	11.31	11.27	99.00	23.65	23.13
3.	Number of productive tillers per plant	10.34	3.66	2.09	18.49	13.97	57.00	2.24	21.73
4.	Panicle length (cm)	24.24	7.75	5.70	11.48	9.84	73.00	4.21	17.39
5.	Spikelet fertility (%)	91.36	18.53	12.17	4.71	3.81	65.70	5.82	6.37
6.	Single plant yield (g)	15.35	27.61	26.63	34.22	33.61	96.50	10.44	68.00
7.	100-grain weight (g)	2.16	0.17	0.17	19.58	19.49	99.10	0.86	39.99
8.	Kernel length (mm)	6.24	0.62	0.62	12.67	12.65	99.80	1.62	26.04
9.	Kernel breadth (mm)	1.94	0.06	0.06	12.84	12.69	97.70	0.50	25.85
10.	L/B Ratio	3.24	0.43	0.42	20.06	19.95	99.00	1.34	40.90
11.	Protein content	8.85	0.94	0.94	10.98	10.96	99.70	1.99	22.56

All the characters exhibited high heritability, which ranged from 57 % to 99.80 % (Table 2). Among the yield contributing characters, highest heritability was obtained for 100-grain weight (99.10%) followed by days to 50 % flowering (99.00 %). However, lowest heritability was noticed with number of productive tillers per plant (57.00 %). All the grain quality characters exhibited high heritability ranging

from 97.70 % to 99.80 %. Plant height recorded highest genetic advance (49.88), while the lowest genetic advance was recorded for 100-grain weight (0.86) among the yield contributing characters. Genetic advance for grain quality characters was found to be low with a range of 0.50 to 1.99. Genetic advance as per cent of mean was found to be highest for single plant yield (68.00), while lowest

genetic advance as per cent of mean was recorded for spikelet fertility (6.37). Among the grain quality characters, the highest and least genetic advance as per cent of mean were recorded for L/B ratio (40.90) and protein quality (22.56), respectively.

High heritability along with high genetic advance was noticed for plant height, single plant yield, 100-grain weight and days to 50% flowering, which indicated that these traits were governed by additive gene action. Similar results were also recorded by Padmaja *et al.* (2008). Thus, selection for these traits is likely to accumulate more additive genes leading to further improvement. The characters like panicle length and spikelet fertility exhibiting high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding. These results were in agreement with the earlier findings of Mehetre *et al.* (1996).

All the grain quality parameters exhibited low difference between the estimates of PCV and GCV indicating the stability of these traits over environments. The heritability estimates for kernel length, kernel breadth and L/B ratio were very high coupled with high genetic advance as per cent of mean indicating the influence of additive gene action. Hence, response of these traits to selection would be effective. These findings are in conformity with the observations of Vanaja and Babu (2006) and Bharadwaj *et al.* (2007). Protein quality showed significantly high genetic variability and moderate GCV and PCV. The heritability estimate for this character was very high along with very low genetic advance and high genetic advance as per cent of mean indicating that the expression of this trait was influenced by additive type of gene action. Sangeeta and Borah (2008) earlier recorded high heritability for this trait.

Department of Genetic and Plant Breeding
College of Agriculture, ANGRAU,
Hyderabad -30
Andhra Pradesh

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G Shobha Rani
K Radhika
V Ravindra Babu
V Padma
G Usharani