



## Genetic Diversity Studies in Popular Rice (*Oryza Sativa L.*) Varieties of India

G. Shobha Rani<sup>1</sup>, K. Radhika<sup>1\*</sup>, V. Ravindra Babu<sup>2</sup>, V. Padma<sup>3</sup> and G. Usharani<sup>1</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, <sup>2</sup>Crop Improvement Section,  
Directorate of Rice Research, Rajendranagar, Hyderabad, <sup>3</sup>Department of Plant Physiology,  
College of Agriculture, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

**The success of any breeding programme depends upon the selection of suitable parents for developing elite recombinants. The eighty seven popular rice varieties of India were grouped into ten clusters using Mahalanobis  $D_2$  statistics which revealed the presence of substantial diversity among the genotypes. The characters *viz.*, kernel length, protein content, days to 50 per cent flowering, 100-grain weight, kernel breadth, single plant yield, plant height, number of grains per panicle and L/B ratio contributed maximum towards divergence. Maximum intra cluster distance was observed in cluster X. Cluster II showed maximum inter cluster distance with cluster IX. Most of the long slender grain types are included in the cluster X, which is having highest desirable mean values for most of the characters. The superior performing genotypes from the divergent clusters II, III, VI, VIII, IX and X can be used as parents to exploit maximum heterosis for improving productivity along with fine grain quality.**

**Key words:** Cluster analysis,  $D_2$  statistics, genetic divergence, rice

Rice is the most important staple cereal foodstuff which forms the daily bread for more than three billion people around the world. Thus, the slogan "Rice is Life" aptly suits to the present day scenario where roughly half of the planet's population depends on rice. To meet the demands of increasing population and to maintain self-sufficiency, the present production level needs to be increased enormously which is possible through heterosis breeding and other innovative breeding approaches. To increase the present levels of heterosis for yield, there is a need to identify and utilize genetically divergent parents for inter and intra sub-specific crosses in rice.

A systematic evaluation and characterization of germplasm lines not only help in identification of superior and genetically divergent germplasm lines but also provide information on the utility of the genetic resources. Success of any breeding programme depends upon the amount of genetic variability available in the crop species besides the efficiency of selection techniques adopted by the plant breeder. Quantification of degree of divergence in a given material is of immense value in identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis  $D_2$  statistics has been proved to be a powerful tool for quantifying genetic diversity in a given population. Divergent genotypes could be obtained by collection from different eco-geographical regions or it could be induced by combination breeding. Therefore, the present investigation was carried out to generate

the information on genetic divergence in the popular rice varieties cultivated in different regions of India.

### Materials and Methods

A field experiment was conducted with eighty seven genotypes of rice collected from Plant Breeding Division, Crop Improvement Section, Directorate of Rice Research, Rajendranagar, Hyderabad in a randomized block design with three replications at Directorate of Rice Research Farm, ICRISAT, Patancheru, Hyderabad, Andhra Pradesh, India, situated at 17.53°N latitude, 78.27°E longitude and altitude of 545 m above mean sea level. Thirty days old seedlings were transplanted 20 cm apart between rows and 15 cm within the row in three blocks. All the necessary precautions were undertaken to maintain uniform plant population in each treatment. All the recommended package of practices was adopted besides providing necessary prophylactic plant protection measures to raise a good crop. Single plant observations on yield and its contributing characters 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, spikelet fertility. Days to 50 per cent 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

\*Corresponding author email: rrsunkara@yahoo.co.in

Micro-Kjeldhal method described by Pregl (1930). The mean data after computing for each character was subjected to standard methods of statistical analysis. The genetic divergence between the rice varieties was estimated using Mahalanobis (1936)  $D_2$  statistics and grouping of genotypes into different clusters was carried out by using Tocher's method as described by Rao (1952).

## Results and Discussion

Genetic divergence analysis quantifies the genetical distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence. The genetic divergence among the genotypes is very much essential since a cross involving genetically divergent parents is likely to produce high heterotic effects and variability in the segregating generations. Analysis of variance indicated the existence of significant variability for all the characters studied except 100 grain weight, kernel length, kernel breadth and L/B ratio. Based

**Table 1. Clustering Analysis of different rice varieties under study**

Cluster No.	No. of varieties	Name of the varieties
I	18	MO4, Sahyadri-2, Shakti, Pratap, Dandi, Dharietri, DL-184, WGL-14, IR-735-CN-328, Mahalaxmi, Gouri, Bhubam, Sahyadri-2, Indravalli, Harsha, VRM44-1, Champakala, Jagabandu.
II	2	ASG-4013, AS-100.
III	3	CN-1039-9, ASG-4022, Dinesh.
IV	8	Manoharsali, MSE-9, Jalpriya, PR-118, Mandya Vijaya, Paritdhan, MSE-12, Phalgun.
V	11	KMP-101, Kavya, Ranjeet, Manika, VRM-3, VRS-25, Aishwarya, Nalini, VRM-33, Bhagirathi, Jalanidhi.
VI	4	Gajapathi, Ramchandi, Jaya, Varalu
VII	13	Pooja, Gayatri, Whiteponny, CN-1233-33-9, Purnendu, Bhudeb, Swarna, Durga, DL-183, Savitri, Samba Mahsuri, BPT-11711, Varsha.
VIII	2	Birupa, Nagarey Dubraj.
IX	19	MSS-5, Vijetha, PR-113, PSD-1, Matta triveni, KKP-2, Karjal-2, Sahyadri, Madhukar, PTB-39, Lalat, PR-115, Erramallelu, NDR-359, IR-64, MTU-1010, NLR-33654, Konark, Kanchana.
X	7	VRS-19, SGT-1, Barhavarodhi, Basumathi-386, Tarouri Basumathi, Pusa Basumathi, Basumathi-370.

cluster X can be selected as parents in hybridization programme for developing superior hybrids having high yield coupled with fine grain quality.

Cluster IX had highest mean for number of productive tillers per plant (11.80), 100-grain weight (2.61) and kernel length (8.08) and least mean value for number of grains per panicle (53.60). The cluster II was found to exhibit highest cluster mean values for panicle length (27.83) and least cluster mean

on relative magnitude and  $D_2$  estimates, all the genotypes under study were grouped into ten clusters (Table 1). Among the different clusters, cluster IX consisted of a maximum of 19 varieties and cluster II and VIII contained a minimum of 2 varieties each. A wide range of variation was observed in cluster means for all the characters studied (Table 2). Clusters with high cluster mean and high genetic divergence should be considered while selecting parents for hybridization programme. Most of the genotypes with long slender grains were included in Cluster X, which was found to be the superior group by recording highest cluster mean values for maximum number of yield contributing characters *viz.*, number of grains per panicle (106.00), number of filled grains per plant (970.00), number of chaffy grains per plant (80.50), total number of grains per plant (1050.50), single plant yield (19.95) and L/B ratio (4.84) and lowest cluster mean value for two traits *i.e.*, spikelet fertility (82.13) and kernel breadth (1.63). Hence, genotypes of

value for 100-grain weight (1.50), kernel length (4.37) and L/B ratio (2.35). Maximum cluster mean value for plant height (170.67) and days to 50 per cent flowering (124.89) were recorded in cluster III. Cluster I and cluster VI showed maximum mean values for kernel breadth (2.03) and protein content (11.16), respectively. Minimum cluster mean values for plant height (100.98) and days to 50 per cent flowering (94.68) were recorded in cluster VI and cluster V, respectively. Cluster IV was found to exhibit

**Table 2. Cluster means for different characters (in cluster analysis)**

Cluster	Plant height (cm)	Days to 50 per cent flowering	No. of productive tillers / plant	Panicle length (cm)	No. of grains per panicle	No. of filled grains per plant	No. of chaffy grains per plant	Total no. of grains per plant yield (g)	Single plant yield (g)	Spikelet fertility (%)	100-grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Protein content (%)
Cluster I	102.24	96.22	9.80	23.87	76.13	645.54	65.43	705.96	14.40	91.42	2.051	5.73	2.03	2.87	8.17
Cluster II	131.50	100.33	10.83	27.83	96.65	966.00	55.83	1021.83	14.77	94.91	1.502	4.37	1.88	2.35	8.02
Cluster III	170.67	124.89	10.22	24.78	67.89	671.67	50.11	724.00	17.37	92.25	2.562	6.52	1.98	3.29	8.85
Cluster IV	127.25	105.67	10.50	25.79	77.83	671.29	80.21	747.58	17.21	99.52	2.261	6.23	2.01	3.12	7.49
Cluster V	128.52	94.67	10.64	23.55	73.18	704.15	61.39	765.46	15.28	91.39	2.025	5.74	2.01	2.90	9.72
Cluster VI	100.92	101.00	10.83	23.17	62.17	592.92	59.25	652.17	15.41	90.73	2.275	6.69	2.03	3.35	11.16
Cluster VII	106.67	118.82	10.08	23.10	72.18	649.90	65.64	717.33	11.99	91.01	1.718	5.69	1.78	3.29	9.44
Cluster VIII	105.83	98.33	10.30	24.24	72.95	584.94	49.19	633.43	16.96	91.65	2.462	6.76	1.94	3.53	8.82
Cluster IX	125.20	94.80	11.80	25.93	53.60	586.67	59.07	638.07	14.92	92.11	2.609	8.08	1.87	4.38	9.14
Cluster X	127.17	106.83	10.50	26.50	106.00	970.00	80.50	1050.50	19.95	82.13	1.905	7.77	1.63	4.84	7.70

highest mean for spikelet fertility (99.52) and least cluster mean for protein content (7.49), while cluster VII was characterized by its lowest mean for panicle length (23.10) and single plant yield (11.99). However, lowest mean values for number of filled

grains per plant (584.94), number of chaffy grains per plant (49.19) and total number of grains per plant (633.43) were noticed in cluster VIII. Therefore, genotypes with high mean values for the above yield contributing traits from different clusters may be used

as parents to develop high yielding rice varieties. The inter cluster distances were higher than the intra cluster distances reflecting the presence of wider diversity among the genotypes of the distant group. Similar results were obtained by Anuradha and Reddy (2003), Rao (2004) and Raghuwanshi and Duhoon (2005). The greater the distance between two clusters, the wider will be the genetic diversity among the genotypes of those clusters. Maximum intra cluster distance (1836.70) was

**Table 3. Intra (diagonal) and Inter cluster average of D values of 87 genotypes of rice (in cluster analysis)**

	ClusterI	ClusterII	ClusterIII	ClusterIV	ClusterV	ClusterVI	ClusterVII	ClusterVIII	ClusterIX	ClusterX
Cluster I	624.34	2345.64	2634.61	1313.61	1823.04	5046.28	2097.43	1894.80	5219.85	4530.33
Cluster II		995.01	5484.15	3896.09	3523.41	9004.19	3263.04	6000.19	11942.41	9876.63
Cluster III			1064.66	2215.20	2840.38	4254.82	2464.46	2250.00	4078.59	4484.93
Cluster IV				996.02	3386.11	6720.34	3311.66	2078.63	4513.08	3167.19
Cluster V					1025.66	2551.07	1781.20	2426.64	5396.90	6704.13
Cluster VI						1456.24	3563.74	3501.53	4630.21	8185.60
Cluster VII							1080.65	3060.75	6615.37	6546.87
Cluster VIII								1245.08	2432.179	3249.22
Cluster IX									1032.90	2727.76
Cluster X										1836.70

divergence between the varieties belonging to these clusters. Lowest divergence was noticed between cluster I and IV (1313.61). Nayak *et al.* (2004) pointed out that genetic divergence among the genotypes played an important role in the selection of parents having wider variability for various agronomic and quality characters. Sarawgi and Bisne (2007) recommended that selection of parents should be done from two clusters having wider inter cluster distance to get more variability and high heterotic effect. Hence, the selection of genotypes from cluster II and cluster IX (Table 2) as parents in hybridization programme would help in generating novel recombinants.

**Table 4. Relative contribution of different traits to genetic diversity in rice**

Character	Times ranked	Contribution
	first	(%)
Plant height (cm)	55	1.47
Days to 50 per cent flowering	485	12.96
Number of productive tillers per plant	0	0.00
Panicle length (cm)	0	0.00
Number of grains per panicle	53	1.42
Number of filled grains per plant	16	0.43
Number of chaffy grains per plant	4	0.11
Total number of grains per plant	0	0.00
Single plant yield (g)	64	1.71
Spikelet fertility (%)	0	0.00
100-Grain weight (g)	184	4.92
Kernel length (mm)	1418	37.90
Kernel breadth (mm)	112	2.99
L/B ratio	22	0.59
Protein content	1328	35.50

The selection and choice of parents mainly depends upon contribution of characters towards divergence (De *et al.*, 1988). Relative contribution of different characters towards genetic divergence among the popular rice varieties (Table 4) revealed that the contribution of kernel length was highest (37.90 %), followed by protein content (35.50 %),

observed in cluster X (Table 3) indicating that some genetic divergence still existed among these genotypes and hence these can be used for yield improvement through recombination breeding. The intra cluster distance was minimum (624.34) for cluster I revealing greater uniformity as a consequence of less divergence among the genotypes of this group. Highest inter cluster distance was noticed between cluster II and IX (11942.41) indicating the existence of maximum

divergence between the varieties belonging to these clusters. Lowest divergence was noticed between cluster I and IV (1313.61). Nayak *et al.* (2004) pointed out that genetic divergence among the genotypes played an important role in the selection of parents having wider variability for various agronomic and quality characters. Sarawgi and Bisne (2007) recommended that selection of parents should be done from two clusters having wider inter cluster distance to get more variability and high heterotic effect. Hence, the selection of genotypes from cluster II and cluster IX (Table 2) as parents in hybridization programme would help in generating novel recombinants.

## References

- De, R.N., Seetharaman, R., Sinha, M.K. and Banerjee, S.P. 1988. Genetic divergence analysis in rice. *Indian J. Genet.*, **48**: 189-94.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Natl. Inst. Sci., India*. **12**: 49-55.
- Nayak, A.R., Chaudhary, D and Reddy, J. N. 2004. Genetic divergence in scented rice. *Oryza*, **41**: 79-82.
- Preg, I.F. 1930. Quantitative Organic Microanalysis. 2nd English ed. Translated by Ernest Fyleman.
- Raghuwanshi, K.M.S. and Duhoon, S.S. 2005. Genetic diversity and adaptability in Indian germplasm collection of sesame (*Sesamum indicum* L.). *J. Oilseeds Res.*, **22**: 29-36.
- Rao, C.R. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc., New York. pp.236-272.
- Sarawgi, A.K. and Bisne, R. 2007. Studies on genetic divergence of aromatic rice germplasm for agromorphological and quality characters. *Oryza*, **44**: 74-76.