

### Depiction of genetic divergence in rice (*Oryza sativa* L.)

Praveen Pandey, and P. John Anurag

Department of Genetics and Plant Breeding,  
Allahabad Agricultural Institute-Deemed University, Allahabad (U.P.)-211007, India.  
Corresponding author: P. Pandey, pandeypraveen1986@yahoo.com

**Abstract.** The nature and magnitude of genetic divergence in 40 rice (*Oryza sativa* L.) genotypes for twelve yield and yield component were assessed using Mahalanobis  $D^2$ -statistics. The analysis of variance revealed highly significant differences for all the characters under studied, indicating that there is an ample scope for isolation of promising lines from present gene pool for yield improvement. On the basis of  $D^2$  values the genotypes were grouped into seven clusters. Cluster VI was the largest containing 11 genotypes followed by cluster III with 9 genotypes. The composition of clusters indicated non existence of correspondence between genetic diversity and geographical distribution. Plant height, biological yield and test weight contributed considerably, accounting for 86.16 % of total divergence. The highest intercluster distance was observed between cluster II and VII therefore the genotypes from cluster II (Triguna, MAUB-15, Pant dhan-6) having desired mean values for characters like days to 50% flowering, panicle length and harvest index, were more divergent from the genotypes of cluster VII (Sonachur & Mala) having desired mean values for plant height, flag leaf width, spikelets per panicle, biological yield and test weight, may be used in hybridization programme to achieve desired segregants with higher yield.

**Key words:** rice, Genetic diversity, yield component and  $D^2$ - statistics.

**Introduction.** Rice (*Oryza sativa* L.) is one of the most important food crops of the world. India is the largest rice growing country in the world. However, its productivity per unit area by world standard is very low. In order to increase rice productivity, high yielding and disease resistant varieties should be developed. Genetic improvement of crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. Seed yield is the most important economic character and very complex in nature because it is governed by polygenes and greatly influenced by environmental factors. Therefore direct selection for yield on the basis of *per se* performance may not be effective, hence it is necessary to consider the yield contributing traits during selection. In any crop, the germplasm serves as a valuable source of base population and provides scope for wide variability. Heterosis has been commercially exploited in rice with a yield advantage of 20-25% over the best purelines (Rather et al 2001). Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam 1981). This analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation. The relative contribution of different yield components to total divergence helps in the identification of selection parameter to be used as criteria for the improvement in the yield. Therefore, an attempt was made in the present studies to estimate the extent of variability and genetic divergence in rice genotypes.

**Material and Methods.** The experimental material for the present study consisted of 40 rice genotypes were evaluated in randomized block design in two replications at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, Allahabad

Agricultural Institute, Deemed University, Allahabad during *Kharif*, season (June-November) 2007. Seed were sown in the nursery on 22<sup>nd</sup> June, 2007 and 24 days old seedlings were transplanted into the main field. All types of facilities necessary for cultivation of successful crop including field preparation, inputs, irrigation facilities and laborers were provided from the Department of Genetics and Plant Breeding. The data were recorded on 10 randomly selected plants from each replication for 12 quantitative characters studied were *viz.*, plant height (cm), number of panicles per hill, panicle length(cm), flag leaf length (cm), flag leaf width (cm), number of spikelets per panicle, 1000 grain weight (g), biological yield, grain yield per hill (g), harvest index. However days to 50% flowering was recorded on per plot basis. Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse & Sukhatme (1967). The genetic divergence was estimated by Mahalanobis (1936)  $D^2$  statistics and the grouping of the genotypes into clusters were done by using Tocher's method (Rao 1952).

**Results and Discussion.** The analysis of variance revealed highly significant differences among the genotypes for the entire test characters, indicating the existence of variability among the varieties (Table 1). Considerable genetic divergence was also present among the genotypes. This suggested that adequate scope is available for selection of superior and diverse genotypes for use in a programmed aimed at enhancing genetic yield potential of rice.

Based on relative magnitude of  $D^2$  statistics the 40 genotypes of rice were grouped into 7 clusters (Table 2). Among the different clusters cluster VI consisted maximum number of genotypes (11 genotypes) followed by cluster III (9 genotypes), cluster V (8 genotypes) and cluster I (4 genotypes), while cluster II and IV (each 3 genotypes) and cluster VII included 2 genotypes. The pattern of group constellation proved the existence of significant amount of variability. Similar findings also reported by Sarawgi & Bisne (2007). The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning with respect to the origin. The distribution of genotypes also indicated that the genotypes originated from different states were grouped into same clusters and genotypes of same states into different clusters. Therefore the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions. Similar findings of non-correspondence of genetic divergence with geographic diversity were also reported in rice by Maurya & Singh (1977), De & Suriya Rao (1987), and Vivekanandan & Subramanian (1993). Murty & Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances.

The average intra cluster distance between the members of cluster-VII (1805.04 cm) was recorded highest followed by cluster III (1206.70 cm) and lowest for cluster I (532.62 cm) (Table 3). Maximum intra cluster distances in cluster VII indicating that genotypes in this cluster were relatively more diverse than the genotypes within other clusters. Hybridization programme involving genetically diverse parents belonging to different distant clusters would provide analysis opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. The highest intercluster distance was observed between cluster II and VII (11235.93cm), followed by II and VI (8045.04cm) and I and VII (7566.33cm) and lowest for IV and V (1619.34cm) (Table 3 and see Figure). The genotypes from cluster II (Triguna , MAUB-15, Pant dhan-6) having desired mean values for characters like days to 50% flowering, panicle length and harvest index, were more divergent from the genotypes of cluster VII (Sonachur & Mala) having desired mean value for plant height, flag leaf width, spikelets per panicle, biological yield and test weight, thus these genotypes may be used in hybridization programme to achieve desired segregants for early rice varieties with higher yield.

The utility of  $D^2$ -statistics is enhanced by its applicability to estimate the relative contribution of the various characters to genetic divergence. The selection and choice of parents mainly depends upon contribution of characters towards divergence. Highest contribution in manifestation of genetic divergence was exhibited by plant height

(47.82%) followed by biological yield (30.13%), test weight (8.21%) and spikelets per panicle (2.56 %) (Table5). Usha-Kumari & Rangasamy (1997) also reported that the characters grain yield per hill and plant height have contributed maximum to divergence and should form the basis of selection for genotypes. Tillers per hill (0.64 %), flag leaf length (1.41%), panicle length, grain yield (1.67%) and harvest index (1.67%), and contributing least among all the characters towards genetic divergence (Table4). Nayak et al (2004) also reported that the minimum contribution of panicle length among all the characters. Whereas Naik et al (2006) reported the maximum contribution of grain yield per hill towards genetic divergence.

Based on cluster means (Table5), the cluster have been identified for selecting parents for future hybridization programme and accordingly, cluster II has been identified for selecting parents for incorporating early maturity, Cluster IV for grain yield, Cluster VI for Tillers per hill Cluster VII for Plant height, flag leaf width, number of spikelets per panicle, biological yield and test weight and Cluster V for panicle length, panicles per hill and flag leaf length. The genotypes superior in the above cluster may be involve in a multiple crossing programme to recover transgressive segregants with high genetic yield potential and early maturity. The promising genotypes selected from diverse clusters are listed in table 6 and such genotypes should be involved in the hybridization programme in order to transfer some of the desirable yield contributing characters consisted by them for crop improvement.

Table 1

Analysis of variance for 12 quantitative characters of 40 rice genotypes

S.No.	Characters	Mean sum squares		
		Replication (df=01)	Treatment (df=39)	Error (df=39)
1.	Days to 50 % flowering	3.615	31.5612*	3.3048
2.	Plant height	0.1117	1838.3114*	1.4078
3.	No. of tillers/hill	0.4950	12.2933*	0.1463
4.	Panicle length	0.0911	11.5621*	0.1360
5.	No. of panicles/hill	0.0084	11.9829*	0.0930
6.	Flag leaf length	0.3511	32.3275*	0.4548
7.	Flag leaf width	0.0052	0.0318*	0.0036
8.	No. of spikelets/panicle	18.6245	1748.0723*	15.1747
9.	Biological yield/hill	0.6212	615.3066*	1.1991
10.	Grain yield/hill	0.1436	65.5331*	0.6330
11.	Harvest index	2.4465	176.7697*	0.8609
12.	Test weight (1000 seed weight)	0.6444**	23.7324*	0.1466

df= Degree of freedom; \*\*- significance at 1% level of significant; \*- significance at 5% level of significant.

Distribution of 40 genotypes of rice into different clusters

Table 2

Cluster No.	Name of genotypes included	Number of genotypes
I	Narendra-359, Sarjoo-52, Pusa-44, Indrani	4
II	Triguna , MAUB-15, Pant dhan-6	3
III	OR-7141, Rasi, China, IET-15833-02, HKR-20-436, HUR-3022, Sambha mahsuri, Dudagi, NDR-2070	9
IV	Pusa basmati-1, NDR-6117, Pant dhan-4	3
V	Chinikamini,Chaita-4, Judi-578, Mahsuri, Golden,UPR-2581-21-1-2, CRAC-2221-423, HUBR-02-01	8
VI	Bayalu, Bhata Swarna, Jhumeri, Ranikajar, Tulsimuni, Chullai, Lohandi, Bala, IET-15358, Vishnubhog, Dubraj	11
VII	Sonachur, Mala	2

Intra (diagonal, bold) and inter cluster average distance ( $D^2$ ) in rice genotypes

Table 3

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7
Cluster1	<b>532.62</b>	1631.56	2144.58	1729.60	2467.70	6052.86	7566.33
Cluster2		<b>845.28</b>	2536.50	2983.64	4471.74	8045.04	11235.93
Cluster3			<b>1206.70</b>	2274.50	1996.88	3513.58	5821.70
Cluster4				<b>986.54</b>	1619.34	5018.56	6348.25
Cluster5					<b>722.58</b>	3045.92	3511.75
Cluster6						<b>896.09</b>	2040.87
Cluster7							<b>1805.04</b>

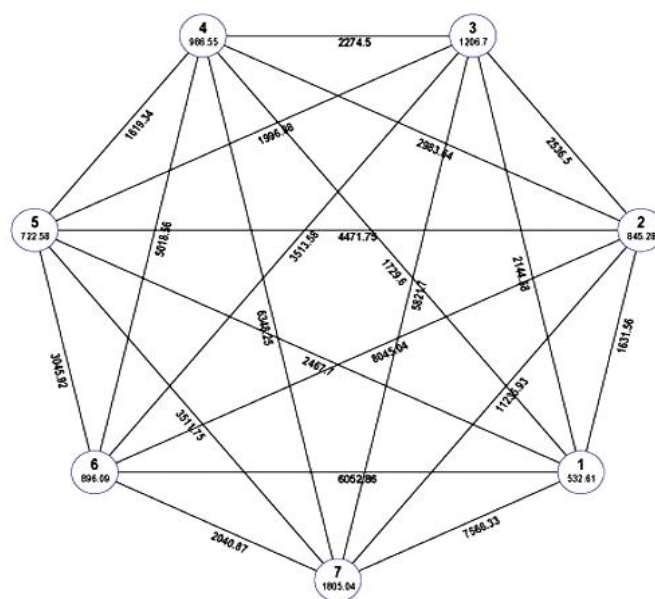


Figure 1. Cluster distance.

Table 4

Percent contribution of each character towards genetic divergence in 40 rice genotypes

<i>S.No.</i>	<i>Characters</i>	<i>Times Ranked 1<sup>st</sup></i>	<i>Contribution %</i>
1.	Days to 50% flowering	0	0.00
2.	Plant height	373	47.82
3.	Tillers per hill	5	0.64
4.	Panicle length	13	1.67
5.	Panicles per hill	33	4.23
6.	Flag leaf length	11	1.41
7.	Flag leaf width	0	0.00
8.	Spikelets per panicle	20	2.56
9.	Biological yield	235	30.13
10.	Grain yield	13	1.67
11.	Harvest index %	13	1.67
12.	Test weight (1000 seed weight)	64	8.21

Table 6

Promising genotypes selected from diverse cluster

<i>S.No.</i>	<i>Cluster</i>	<i>Desirable characters and mean values in parentheses</i>
1	VII	Plant height (166.08 cm), flag leaf width (1.71 cm), No. of spikelets per panicle (234.25), biological yield (114.77g) and test weight (24.49g)
2	V	Panicle length (25.68 cm), panicles per hill (13.75) and flag leaf length (35.20 cm)
3	II	Days to 50% flowering (93.50 days) and harvest index (45.12 %)
4	IV	Grain yield (28.08 g)
5	VI	Tillers per hill (14.90)

Table 5

Mean values of seven clusters for 12 quantitative characters in 40 Rice genotypes

<i>Cluster No.</i>	<i>Days to 50% flowering</i>	<i>Plant height (cm)</i>	<i>Tillers per hill</i>	<i>Panicle length (cm)</i>	<i>Panicles per hill</i>	<i>Flag leaf length (cm)</i>	<i>Flag leaf width (cm)</i>	<i>Spikelets per panicle</i>	<i>Biological yield (g)</i>	<i>Grain yield (g)</i>	<i>Harvest index%</i>	<i>Test weight (g)</i>
I	95.25	97.82	10.09	25.65	9.26	33.04	1.47	142.08	69.55	27.48	39.33	24.41
II	93.50	87.72	9.25	24.89	9.27	32.19	1.45	173.60	54.71	24.58	45.12	17.64
III	96.00	115.34	13.61	22.34	13.61	34.45	1.55	182.48	70.38	17.14	24.84	17.41
IV	94.50	95.89	13.06	24.87	10.47	28.89	1.46	159.38	88.52	28.08	32.33	16.09
V	98.50	113.95	12.61	25.68	13.75	35.20	1.61	205.72	101.30	23.39	23.23	19.33
VI	98.22	165.08	14.90	24.18	12.64	34.53	1.66	202.97	86.52	16.84	19.68	17.57
VII	97.00	166.08	13.30	22.85	13.52	32.77	1.71	234.25	114.77	23.17	19.67	24.49

## References

- Arunachalam V., 1981 Genetic divergence in plant breeding. *Indian Journal of Genetics* **14**:226-236.
- De R. N., Suriya-Rao A. V., 1987 Genetic divergence in rice under lowland situation. *Crop Improvement* **14**:128-131.
- Naik D., Sao A., Sarawgi A. K., Singh P., 2006 Genetic divergence studies in scented rice. *Journal of Plant Science* **5**(2):197-200.
- Mahalanobis P. C., 1936 On the generalized distance in statistics. *Proc Natl Inst Sci India* **2**:49-55.
- Maurya D. M., Singh D. P., 1977 Genetic divergence in rice. *Indian Journal of Genetics* **37**(3):395-402.
- Murty B. R., Arunachalam V., 1966 The nature of genetic divergence in relation to breeding system in crop plants. *Indian Journal of Genetics* **26A**:188-198.
- Nayak A. R., Chaudhury D., Reddy J. N., 2004 Genetic divergence in scented rice. *Oryza* **41**(384):79-82.
- Panse V. G., Sukhatme P. V., 1967 *Statistical methods for agricultural workers*, 2<sup>nd</sup> edition, pp-381, I.C.A.R., New Delhi.
- Rao C. R., 1952 *Advanced Statistical Methods in Biometrical Research*. John Wiley & Sons publishers, New York.
- Rather A. G., Zargar M. A., Sheikh F. A., 2001 Genetic divergence in rice (*Oryza sativa* L.) under temperate conditions. *Indian Journal of Agricultural Sciences* **71**:344-345.
- Sarawgi A. K., Bisne R., 2007 Studies on genetic divergence of aromatic rice germplasm for agromorphological and quality characters. *Oryza* **44**(1):74-76.
- Usha-Kumary R. U., Rangasamy P., 1997 Studies on genetic diversity in international early rice genotypes. *Annals of Agricultural Research* **18**(1):29-33.
- Vivekanandan P., Subramanian S., 1993 Genetic divergence in rainfed rice. *Oryza* **30**:60-62.

Received: 18 July 2010. Accepted: 03 September 2010. Published online: 14 October 2010.

Authors:

Praveen Pandey, Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad (U.P.)-211007, India. E-mail: pandeypraveen1986@yahoo.com

P. John Anurag, Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad (U.P.)-211007, India. E-mail:pjohnanurag@yahoo.co.in

How to cite this article:

Pandey P., Anurag P. J., 2010 Depiction of genetic divergence in rice (*Oryza sativa* L.). *AAB Bioflux* **2**(3):285-291.