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Estimation of genetic diversity for yield and yield attributing traits in rice (*Oryza sativa* L.)

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Abstract
The present investigation was carried out in Agricultural and Horticultural Research Station, Kattalagere. The nature and magnitude of genetic divergence were estimated in 23 rice genotypes in six environments using Mahalanobis D2 – statistics by considering 13 quantitative characters. D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into six clusters. Cluster I constituted maximum number of genotypes (16). The genotypes falling in cluster II had the maximum divergence. The inter cluster distance was maximum between cluster I and IV (10.34) followed by cluster III and V (9.82), suggesting that the genotypes constituted in these clusters may be used as parents for future breeding programme. Traits like; days to maturity, plant height(cm), Number of grains per panicle, Test weight (g), Harvest Index (%), Days to 50% flowering, Panicle length (cm) were the major contributors to genetic divergence.

Keywords: Estimation of genetic attributing traits in rice horticultural *Oryza sativa* L

Introduction
Rice (*Oryza sativa* L.), belongs to the family Graminae, recognized as "millennium crop" expected to contribute towards food security in the world, as it is one of the staple cereal crops of the world and a primary source of food for more than half the world's population. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future. Therefore, rice breeders across the world aim at increasing the grain yield of rice (Song *et al*., 2007). Genetic diversity is pre-requisite for any crop improvement programme, as it helps in the development of superior recombinants (Manonmani and Fazlullah Khan, 2003) [3]. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different characters (Nayak *et al.* 2004) [4]. Genetic divergence is the total number of genetic characteristics in the genetic makeup of a species. It serves as a way for populations to adapt to changing environments. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding program. The D2 technique based on multivariate analysis developed by Mahalanobis (1936) [2] had been found to be a potent tool in quantifying the degree of divergence in germplasm.

Material and methods: The present investigation was carried out in Agricultural and Horticultural Research Station, Kathalagere. The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications in puddle field at all locations. Seeds of rice genotypes were sown on 22nd of June 2018 at Kattalagere in raised beds of one sq m each. Twenty days old seedlings were transplanted to the main field at the rate of one seedling per hill by following Randomized Complete Block Design. The recommended packages of practice were followed to get a normal healthy crop. List of advanced breeding lines (F6) used under present investigation including checks (Table 1). Genetic diversity was assessed using Mahalanobis' (1936) [2] D2 statistics using WINDOSTAT software.

Results and discussion: The amount of diversity available in the crop decides the success of any crop improvement programme with manifold objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. Improvement in grain yield is normally attained through involvement of the genetically diverse parents in breeding programmes. For identifying such diverse parents for crossing, by means of Mahalanobis's D2 statistics has been used in several crops. It is a powerful tool used to quantify the genetic divergence between the genotypes and to relate clustering pattern with the geographical origin. The present study was focused to assess the genetic diversity in twenty

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three rice advanced breeding lines using Mahalanobis' D2 statistics. Of the several methods available, Mahalanobis' generalized distance estimated by D2 statistic (Rao, 1952) [5] is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco- geographical diversity and phylogenetic relationship. So as to enumerate the diversity in twenty advanced breeding lines of rice, thirteen quantitative characters were studied and their fitness was assessed using the concept of Mahalanobis' generalized distance (D2). Genetic diversity analysis assists in studying nature of diversity among the advanced breeding lines. With the purpose of finding the genetically diverse genotypes for their uses in recombination breeding programme, Mahalanobis' generalized (D^2) analysis was carried out with thirteen characters studied. Advanced breeding lines distributed into five clusters. This cluster pattern showed that cluster I consists of maximum of sixteen number of advanced breeding lines, cluster II consists of three, cluster IV consists two and remaining two clusters are solitary. The distribution pattern of rice advanced breeding lines into five clusters is shown in Table 2. Intra and inter relation of clusters judged by average D2 values. The maximum intra cluster distance noticed in cluster IV (1.58). Diversity among the clusters was in the range of 1.47 to 10.34. Cluster I and cluster IV showed maximum inter cluster distance (10.34) followed by the cluster III and cluster IV (9.82). The lowest inter cluster distance was observed between cluster I and cluster III (1.47). The average D^2 values of intra and inter clusters distances are mentioned in Table 2. The cluster means regarding thirteen characters across the five clusters are mentioned in Table 3. The advanced breeding lines with respect to days to fifty per cent flowering belongs to cluster IV showed highest mean value of (104.63), while cluster III showed the least mean value days to fifty per cent flowering (85.75). The advanced breeding lines belong to cluster III showed the least mean value days to maturity (125.00). While cluster IV showed highest mean value for days to days to maturity (131.63). With respect to plant height, advanced breeding lines belongs

to cluster I showed highest mean value of (86.06 cm), while cluster II showed the least mean value of plant height (76.72 cm) Table 4. Across the thirteen characters with the five clusters, the cluster II with total score of 36 secured first rank followed by cluster III and cluster V with 38 score secured second rank. Cluster IV with two advanced breeding lines is the most divergent group with a maximum intra-cluster distance (1.58) and these results are on par with the results of Tuhina *et al.* (2012) [7] as they obtained five clusters for forty three upland rice accessions and they had noted the highest number of advanced breeding lines (14) in cluster I and lowest in cluster II, III and IV (01). The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning clustering with respect to the origin (Ushakumari and Rangaswamy, 1997). It is desirable to select advanced breeding lines from these clusters showing high inter cluster distance and also with high grain yield as parents in recombination breeding programme for obtaining wide variability and desirable segregants. Sixteen advanced breeding lines were present in cluster I. likewise in cluster II, two in cluster IV and one genotype each were present in III and V clusters. These results are in conformity with the observations made by Sohrabi *et al.* (2012) [6].

Proportion of contribution of each character to total D2 statistics showed significant differences and they are mentioned in Table 2 The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004) [4]. The most important character contributing to the divergence among the thirteen quantitative characters studied was days to maturity which is more responsible for increasing grain yield. This was followed by plant height (cm), number of grains per panicle, test weight, harvest index, days to fifty per cent flowering,), panicle length (cm), number of tillers per plant, number of spikelets per panicle, panicle fertility (%), straw yield (kg/ha), grain yield (kg/ha), days to maturity and number productive of tillers per plant. These observations are in accordance with the findings of Banumathy *et al.* (2010) [1].

Table 1: List of advanced breeding lines (F6) used under present investigation including checks.

Cross combinations	Code	Advanced breeding lines	Grain shape	Grain color
Jyoti X Biliya	G1	JB-1-11-7	Medium slender	Light red
	G2	JB-1-20-2	Medium slender	Light red
	G3	JB-1-22-1	Medium slender	Light red
	G4	JB-1-22-2	Medium slender	Light red
	G5	JB-1-22-3	Medium slender	Light red
Jyoti X Kesari	G6	JK-1-7-5	Medium bold	Dark red
	G7	JK-1-11-8	Medium bold	Light red
	G8	JK-1-12-1	Medium bold	Light red
	G9	JK-1-13-1	Medium bold	Light red
	G10	JK2-2-1-8-1	Medium bold	Light red
	G11	JK2-1-12-1	Medium bold	Light red
Jyoti X Akkalu	G12	JA-4-1	Medium slender	Light red
	G13	JA-4-2	Medium slender	Light red
	G14	JA-4-3	Medium slender	Light red
	G15	JA-6-2	Medium slender	Light red
	G16	JA-6-3	Medium slender	Light red
	G17	JA-6-4	Medium slender	Light red
Jyoti X Tunga	G18	JT-2-15-1	Medium slender	Light red
	G19	JT-2-16-1	Medium slender	Light red
	G20	JT-2-22-5	Medium slender	white
Jyothi	G21		Bold	Red
KHP-2	G22		slender	Red
Tunga	G23		Bold	white

Table 2: Per cent contribution of character towards divergence of twenty advanced breeding lines of rice.

S. No.	Characters	Contribution (%)
1.	Days to maturity	54.1
2.	Plant height (cm)	9.88
3.	Number of grains per panicle	5.14
4.	Test weight (g)	5.14
5.	Harvest Index (%)	4.74
6.	Days to 50% flowering	4.35
7.	Panicle length (cm)	4.35
8.	Number of tillers per plant	3.16
9.	Number of spikelets per panicle	2.37
10.	Panicle fertility (%)	2.2
11.	Straw yield (kg/ha)	1.8
12.	Grain yield (kg/ha)	1.58
13.	Number of productive tillers per plant	1.19

Table 3: Distribution of twenty advanced breeding lines of rice into different clusters.

Clusters	Number of advanced breeding lines	Advanced breeding lines
I	16	JB-1-20-2, JB-1-22-1, JB-1-22-2, JB-1-22-3, JK-1-7-5, JK-1-11-8, JK-1- 12-1, JK-1-13-1, JK2-2-1-8-1, JK2-1-12-1, JA-4-1, JA-4-2, JA-4-3, JA-6-2, JA-6-3, JA-6-4.
II	3	JT-2-15-1, JT-2-16-1, JT-2-22-5.
III	1	JB-1-11-7.
IV	2	KHP-2, Tunga.
V	1	Jyothi

Table 4: Average intra and inter cluster distance values of twenty advanced breeding lines of rice

Cluster	I	II	III	IV	V
I	0.65	6.34	1.47	10.34	4.84
II		0.33	7.86	3.56	8.12
III			0.00	9.82	5.37
IV				1.58	7.44
V					0.00

References
1. Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D. Genetic diversity analysis of rice germplasm lines for yield attributing traits. Electron. J. Plant. Breed. 2010; 1(4):500-504.
2. Mahalanobis PC. A statistical study at Chinese head measurement. J Asiatic society Bengal. 1936; 25:301:77.
3. Manomani S, Fazlullah khan AK. Analysis of genetic diversity for selection of parents in rice. Oryza. 2003; 40:54-56.
4. Nayak AR, Chaudhury D, Reddy JN. Genetic divergence in scented rice. Oryza. 2004; 41(384):79-82.
5. Rao CR. Advance statistical methods in biometric research. John Wiley and Sons Inc., New York, 1952.
6. Sohrabi MY, Rafii, Latif MA. Genetic Diversity of Upland Rice Germplasm in Malaysia Based on Quantitative Traits. Scientific World J. 2012; 15:416-491.
7. Tuhina K, Mohamed H, Mohd RY, Wong MY, Faezah M Sallesh, Jannatul F. Genetic Variation, Heritability, and Diversity Analysis of Upland Rice (*Oryza sativa L.*) Genotypes Based on Quantitative Traits. BioMed Res. Int. 2012; 7(2):1-7.
8. Usha Kumary RU, Rangasamy P. Studies on genetic diversity in International early rice genotypes. Annl. of Agric Res. 1997; 18(1):29-33.