



GENETIC DIVERGENCE ANALYSIS FOR CERTAIN YIELD TRAITS IN RICE (*Oryza sativa* L.)

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ABSTRACT

Genetic diversity among 34 rice genotypes was worked out using Mahalanobis D^2 statistic. On the basis of genetic distance, these genotypes were grouped into seven clusters. Cluster II was the largest, consisting of 14 genotypes, followed by cluster I with nine genotypes and cluster VII with three genotypes, while clusters III, IV V and VI contained two genotypes each. There was no parallelism between genetic diversity and geographical distribution. The maximum inter cluster distance (140.17) was highest between Cluster II and cluster VII, followed by clusters VI and VII. Among the different characters studied, grain yield per plant, number of grains per panicle, days to fifty per cent flowering and grain length contributed significantly for the genetic diversity. The genotypes (AUR-3, CO-43, ASD-19 and Manavari) from these clusters may be used as potential donors for future hybridization programme to develop higher grain yield.

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INTRODUCTION

Rice (*Oryza sativa* (L.)) the prime, most essential grain food stuff which forms an important part of the diet of more than three billion people around the world and popularly called as “Global grain”. It is being cultivated in 155.13 million hectares with an annual production of about 646 million tonnes globally. In India, it is grown in an area of about 44 million hectares with annual production of around 90 million tones. However, the yield level of most of high yielding varieties of rice particularly under irrigated condition is being palteued since two decades. Thus, to meet the demands of rice particularly 145 million tonnes by 2025 A.D. to meet the demand of ever increasing population and maintaining its self-sufficiency under the present scenario of declining and deteriorating resource base such as land, water, labour and other inputs adversely affecting the quality of environment is a big challenge. The major objective in rice breeding programme is to maintain the desirable traits with an increase in the yield potential of the selected germplasm.

Genetic improvement mainly depends on the amount of genetic variability present in the population. The estimation of genetic diversity between different genotypes in the crop of interest is the first and foremost process in any plant breeding programme. Genetic divergence is an useful tool for an efficient choice of parents for hybridization to develop high yield potential cultivars. Such a study also permits to select the genetically divergent parents to obtain the desirable

recombinants in the segregating generations. A detailed understanding about the extent structure of genetic variation in different varieties of the same species is important for the development of appropriate and efficient strategies for collection, conservation, and preservation of cultivar relatives. With the development of advanced biometrics techniques such as multivariate analysis based on Mahalanobis Statistic, quantification of degree of divergence among the biological population and assessing of relative contribution of different components to the total divergence intra and inter cluster levels have now become possible. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Arunachalam, 1981; Samsuddin, 1985; Shukla et al. (2006) and Sarawgi and Rita Binse(2007).

MATERIALS AND METHODS

The experiment was conducted at the experimental farm of Department of Genetics and Plant Breeding, Annamalai University, Annamalai Nagar, Tamil Nadu, India during 20010-11. Thirty four genotypes of rice were planted in a randomized block design with three replication at the rate of one seedling per hill adopting spacing of 15cm within the row and 20 cm between the rows. Each genotype was planted in five rows with each row consisting of 20 hills. Data were collected for days to first flowering, days to 50% flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, grain length, grain breadth, hundred seed weight and grain yield per plant. The genetic divergence was estimated using Mahalanobis's

D2 statistics (Mahalanobis, 1949). All the genotypes were grouped into clusters on the basis of D2 values, as suggested by Tocher (Rao, 1952).

RESULTS AND DISCUSSION

The germplasm is the reservoir of genetic variability which often exploited to meet the changing needs for developing improved varieties of a crop (Hawkes, 1981). A proper knowledge of the genetic make-up and diversity of flora will help us in the management, improvement and conservation of endangered varieties. A lack of knowledge about the genetic structure of these varieties/populations may result in the differential harvest of the varieties/populations that will ultimately have a drastic and long-term effect. The importance of genetic diversity for selecting parents for recombination in an autogamous crop like rice and to recover transgressive segregates is worth prime. The genetic divergence existing in 34 rice genotypes was studied by employing D² analysis for 10 quantitative characters. The 34 genotypes were grouped into seven distinct clusters. The pseudo F-test revealed that seven cluster arrangements was the most appropriate for materials under studied, therefore, 34 genotypes were accepted to be grouped into seven different non overlapping clusters. The distribution of 34 genotypes in seven clusters has been given in Table 1. Among the seven clusters the highest 14 genotypes were appeared in cluster II followed by cluster I of nine genotypes. Cluster VII had three genotypes and the remaining clusters possessed two genotypes each (Clusters III, IV, V and VI).

The estimates of intra and inter cluster distances for 34 rice genotypes for seven clusters are presented in Table 2. The highest intra cluster distance was recorded for the cluster II(100.97) followed by cluster VII (85.70), cluster I (80.13) and cluster VI (63.13). The maximum inter cluster distance was recorded between the clusters II and VII(140.17). This was followed by the clusters VI and VII (131.69) and the clusters V and VII (125.36). The minimum inter cluster distance was observed between the clusters IV and VI(58.09).

An examination of average intra and inter cluster distance indicated that genotypes of within cluster had little divergence from each other with respect to aggregate of effects of 10 characters under study. Similar findings were also reported by Nayak *et al.*, (2004), Chaturvedi and Maurya (2005) and Yadav *et al.*, (2011). Therefore, the chance of obtaining recombinants in segregating generations by crossing the members of same cluster are very low. It is therefore, suggested that crosses should be attempted between the genotypes belonging to cluster separated by large inter cluster distances. In this consequences, the highest inter cluster distance was observed between clusters II and VII, followed by cluster VI and VII and V and VII respectively. The lowest inter cluster distance between cluster IV and VI that genotypes present in these cluster pairs were genetically close to each other and the crosses between genotypes belonging to this clusters are unlikely to generate promising recombinants in later generations.

Table 1 Composition of D² Clusters for 34 rice Genotypes

Cluster	Number of genotypes	Name of genotypes
Cluster I	9	IR-72,IR-66,ADT-41,KeralaKaruna, IR-50,Swarna,ASD-18,ASD-20 and AUR-12
Cluster II	14	CO-33,IR-36,ADT-37,ASD-16,CO-46, AD-95-319,Triguna,Co-43,Bhavani,Co-47, White Ponni, Co-45,TKM-11 and MDU-5
Cluster III	2	IR-58190-40-3-1-2 and AUR-3
Cluster IV	2	ASD-19 and IR-104-014-44962
Cluster V	2	Manavari and PMK-2
Cluster VI	2	ADT-38 and ADT-45
Cluster VII	3	MDU-4,ADT-36 and AUR-4

Table 2 Estimates of average inter (D2) and intra (D) cluster values for 34 rice genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	6421.26 (80.13)	11910.96 (109.13)	5938.47 (77.06)	7723.93 (87.88)	9952.91 (99.76)	9638.05 (98.17)	8118.87 (90.10)
Cluster II		10196.15 (100.97)	7949.52 (89.16)	5994.48 (77.42)	11441.55 (106.96)	6537.90 (80.85)	19649.16 (140.17)
Cluster III			1048.83 (32.38)	4133.52 (64.29)	4216.66 (64.93)	5454.43 (73.85)	12166.67 (110.30)
Cluster IV				1626.73 (40.33)	10070.58 (100.35)	3375.50 (58.09)	14867.47 (121.93)
Cluster V					2197.13 (46.87)	9193.77 (95.88)	15716.90 (125.36)
Cluster VI						3985.65 (63.13)	17342.42 (131.69)
Cluster VII							7345.21 (85.70)

Table 3 Cluster means of 34 rice genotypes for ten morphological traits

Cluster	Days to first Flowering	Days to fifty per cent flowering	Plant height	Number of productive tillers	Panicle length	Number of grains per panicle	Grain length	Grain breadth	Hundred grain weight	Grain yield per plant
I	68.64	75.00	84.18	11.29	18.04	81.64	7.65	2.61	1.64	15.90
II	73.45	79.28	96.88	14.62	19.85	106.25	6.98	2.59	1.98	21.71
III	73.85	78.75	79.05	10.85	18.10	85.61	7.46	2.55	2.14	38.53
IV	73.21	73.25	89.15	13.61	20.33	108.48	7.80	3.03	1.99	32.43
V	80.28	86.28	114.81	12.83	18.15	81.36	7.45	2.98	1.50	27.73
VI	73.60	79.36	84.53	20.30	18.30	109.16	9.08	2.65	2.16	17.80
VII	65.57	71.56	75.17	15.76	15.22	69.74	7.84	2.52	1.02	19.31
Grand Mean	71.90	77.50	90.43	13.79	18.69	94.14	7.46	2.64	1.80	21.70

Table 4: Contribution of different characters to genetic divergence

S.No	Characters	Contribution (%) of each characters
1.	Days to first Flowering	0.35
2.	Days to fifty per cent flowering	7.48
3.	Plant height	0.55
4.	Number of productive tillers	3.94
5.	Panicle length	0.55
6.	Number of grains per panicle	33.51
7.	Grain length	7.13
8.	Grain breadth	1.24
9.	Hundred grain weight	4.09
10.	Grain yield per plant	41.17

The genotypes in the cluster VI had the highest mean performance for number of productive tillers, number of grains per panicle, grain length and hundred grain weight for cluster mean (Table 3). Similarly the genotypes in the cluster V had highest mean performance for days to first flowering, days to fifty per cent flowering and plant height. This trend indicated that none of the cluster contained genotypes with all the desired characters which could be directly selected and utilized. In addition most of the minimum and maximum clusters mean values were distributed in relatively distant clusters.

During the selection of parents, the advantage of characters that played important role in group constellation and the cluster showing greater genetic divergence should be considered (Nayak *et al.*, 2004). Accordingly, grain yield per plant, number of grains per panicle, days to fifty per cent flowering and grain length played substantial contribution towards the total genetic divergence while remaining characters had low or negligible role in conditioning the genetic diversity (Table 4). Thus, the crossing of genotypes belonging to clusters separated by high inter cluster distances and differing markedly for characters having high contribution towards total genetic divergence would be more fruitful for isolating superior segregates in segregating generations.

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