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Genetic diversity studies in Rice (*Oryza sativa* L.)

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Abstract
The nature and magnitude of genetic divergence were estimated in 30 rice genotypes in six environments using Mahalanobis D2 – statistics by considering 12 quantitative characters. ANOVA revealed the presence of considerable amount of variability among the genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for fertile grains followed by flag leaf area and tillers per hill. High heritability coupled with high genetic advance was recorded for plant height. Mahalanobis D2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into six clusters. Cluster I constituted maximum number of genotypes (19). The genotypes falling in cluster II had the maximum divergence. The inter cluster distance was maximum between cluster II and V (228.14) followed by cluster III and V (214.44), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. Traits like; plant height, fertile grains, panicle length and plot yield were the major contributors to genetic divergence.

Keywords: rice, GCV, PCV, heritability, genetic advance, D2 analysis and genetic divergence

Introduction
Knowledge about germplasm diversity and genetic relationships among breeding materials could be an invaluable aid in crop improvement strategies. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population. Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996 and Rahman, 1997) [11, 14]. The use of Mahalanobis D2 statistics for estimating genetic divergence has been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008) [17, 15]. Hence, in this study 30 genotypes of rice were evaluated to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programmes.

Material and Methods
The experimental material for the present study comprised of 30 genotypes of rice laid in randomized block design (RBD) with three replications at Experimental Block 1 of Department of Plant Breeding and Genetics, College of Agriculture and Technology, Bhubaneswar, Odhisa, and National Rice Research Institute, Cuttack, Odhisa. during kharif (2015-16). Rabi (2015- 16), kharif (2016-17) each with two fertilizer doses. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for, plant height (cm), number of tillers per hill, panicle length (cm), chlorophyll content index at tillering, chlorophyll content index at days to 50 % flowering, flag leaf area (cm), harvest index (%), test weight (g), fertile grains (g), and fertility percentage. Yield observations days to maturity were recorded on plot basis. The data was subjected to Mahalanobis D2 statistics to measure the genetic divergence as suggested by Rao (1952) [16].

Results and Discussions
Analysis of variance showed significant differences for all the characters studied except for flag leaf width, suggesting the existence of high genetic variability among the genotypes. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. Similar findings were reported by Mishra *et al* (2003) [10]. Both PCV and GCV estimates were highest for fertile grains followed by

flag leaf area and tillers per hill.(Table 1) for plant height.. The results are in confirmation with the findings of Deosarkar *et al*. (1989) [5]. High estimates of heritability (above 60%) in broad sense were recorded for all the twelve characters under study. which ranged from 93% (chlorophyll content index at 50 % flowering) to 97% (plant height). Johnson (1955) [6] reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion.

Therefore, genetic advance was also computed. A perusal of genetic advance for all the quantitative characters under study ranged from 0.11% (harvest index) to 37.89 % (fertile grains). These findings were in agreement with Bihari *et al*. (2004) [1]. High heritability coupled with high genetic advance was registered for plant height, suggesting predominance of additive gene action in the expression of these traits. Similar findings were reported by Krishna *et al*. (2010) [7].

The thirty genotypes under study were grouped into six clusters using Mahalanobis D2 analysis (Table 2). Cluster I constitutes of 19 genotypes each, forming the largest cluster followed by cluster III (4 genotypes), cluster II (3 genotypes), cluster IV (2 genotypes), clusters V and cluster VI (2 genotypes), cluster I intra clustural 35.72, cluster II intra clustural 39.47, cluster III intra clustural 40.79, cluster IV intra clustural 24.55, cluster V and VI intra clustural is zero.The pattern of group constellation proved the existence of significant amount of variability. 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).

The inter and intra average distances among six clusters were computed and have been given in Table 3. The intra cluster distance ranged from 50.15(cluster V) to 228.14 (II). The inter cluster distance was maximum between cluster II and V (228.14) and minimum inter cluster distance was observed between cluster IV and cluster V (50.15). To realize much variability and high heterotic effect, Mishra *et al*. (2003) [10] and Chaturvedi and Maurya (2005) [4] recommended that parents should be selected from two clusters having wider inter cluster distance.

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4). Cluster V exhibited highest mean value for fertile grains while cluster IV contained genotypes with highest mean value for plant height. Cluster V recorded highest value for days to 50% flowering, flag leaf area, chlorophyll content index at 50% flowering, panicle length, fertile grains and plot yield. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al*., 2004) [12]. Contribution towards genetic divergence is presented in table 4. The highest contribution in manifestation of genetic divergence was exhibited by fertile grains (23.60%) followed by days to 50% flowering (17.65 %) and moderately for plant height (11.30%) and Fertility percentage (11.25%)

It is well known that crosses between divergent parents usually produce greater heterotic effect than between closely related ones. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that parental lines selected from cluster IV (Gajapati, Samanta) for plant height, cluster V (Gouri) for fertile grains and next to that cluster III (Jogesh, Kalinga-3,Vandana, Heera) showing high genetic distance. Lowest gentic distance was recorded from cluster III range from (0.35-0.5) for harvest index could be used in crossing programmes to achieve desired segregates.

Table 1: Estimation of component of variance and genetic parameters for 12 quantitative characters in rice genotypes under study:

S. No	Characters	PCV	GCV	H (bs)	G.s	G s %
1	Days to 50% flowering	13.57	13.26	95.38	12.783	22.78
2	Plant Height	12.3	12.12	97.1	19.301	21.02
3	Flag leaf area	24.78	24.25	95.83	11.813	41.79
4	Chlorophyll Content Index at tillering	18.56	17.48	88.64	3.062	28.96
5	Chlorophyll content index at 50% flowering	21.97	21.23	93.41	3.72	36.12
6	Total number of tillers	22.23	20.33	83.63	3.386	32.73
7	Panicle length	10.05	9.22	84.19	3.583	14.89
8	Fertile grains	28.35	27.92	97	37.898	48.4
9	Fertility percentage	13.72	13.15	91.82	16.333	22.17
10	100 seed weight	11.64	10.85	86.86	0.528	17.79
11	Harvest Index	19.45	17.56	81.54	0.114	27.91
12	Plot yield	13.29	12.45	87.83	0.345	20.54

Note:
GCV = Genotypic coefficient of variation,
PCV = Phenotypic coefficient of variation
h2 (bs) = Heritability (broad sense)
GA = Genetic advance

Table 2: Distribution of the 30 rice genotypes into different clusters

Cluster	Cluster size	Cluster composition	Intra Cluster Avg. D2	Yield range (Kg/plot)	Cluster Mean yield	Range of b's	Mean of b's	Range of S2d	Mean of S2d
I	19	3,10,11,12,13,14,15,16 17,18,19,20,21,23,24, 25,27,28,30	35.72	1.56-1.98	1.75	0.570-1.757	1.141	0-0.061	0.014
II	3	1,2,6	39.47	1.37-1.61	1.5	0.160-1.019	0.562	0-0.013	0.019
III	4	5,7,8,9	40.79	1.32-1.75	1.46	0.024-1.025	0.58	0-0.150	0.038
IV	2	26,27	24.55	1.54-1.59	1.57	1.288-1.345	1.317	0.023-0.026	0.025
V	1	22	0	1.86	1.86	1.19	1.19	0.004	0.004
VI	1	4	0	1.83	1.83	0.504	0.504	0.006	0.006

Table 3: Average D- square between clusters

Clusters	I	II	III	IV	V	VI
I	1	103.73	113.66	74.55	62.28	65.54
II		1	70.02	190.71	228.14	55.97
III			1	145.4	214.44	93.15
IV				1	50.15	177.75
V					1	167.94
VI						1

Table 4: Cluster mean values of 6 clusters for different quantitative characters in rice and their contribution to total divergence

Characters	I	II	III	IV	V	VI	Contribution %
Days to 50% flowering	58.7	51	43.64	59.67	61.67	59.17	17.65
Plant Height	90.84	88.57	94.32	106.42	94.39	78.56	11.30
Flag leaf area	29.71	19.93	25.18	33.06	35.42	21.6	9.12
Chlorophyll Content Index at tillering	11.04	9.44	9.25	10.15	10.94	10.92	5.07
Chlorophyll content index at 50% flowering	11.08	7.68	8.35	9.66	11.98	10.66	6.97
Total number of tillers per hill	9.82	12.52	11.53	9.84	10	10.39	1.29
Panicle length	24.05	21.52	24.42	25.42	26.94	24.67	2.04
Fertile grains	84.38	63.58	50.94	90.47	111.72	58.56	23.60
Fertility percentage	76.6	81.26	61.97	58.08	67.39	79.14	11.25
100 seed w eight	2.95	2.61	3.15	3.38	2.88	2.94	4.80
Harvest Index	0.43	0.38	0.35	0.34	0.45	0.5	3.49
Plot yield	1.75	1.5	1.46	1.57	1.86	1.83	3.41

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