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Genetic diversity studies among rice (*Oryza sativa* L.) Genotypes for grain yield, yield components and nutritional traits in rice

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Abstract
Genetic divergence was assessed among 38 rice genotypes to study the nature and magnitude of genetic divergence using D^2 statistics. The experimental material was divided in to eight clusters based on D^2 values with cluster I containing the maximum of 20 genotypes. Maximum intra cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. The cluster V and cluster VIII had highest average compared to other groups in terms of five traits. Maximum inter cluster distance was recorded between cluster II and VI followed by II and V and II and III indicating wider genetic diversity and it may be used in rice hybridization programme for improving grain yield. The maximum contribution of individual trait to the divergence among genotypes recorded in protein content followed by number of filled spikelets per panicle, days to 50 per cent flowering and 1000 grain weight. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters.

Keywords: genetic diversity, among rice, *Oryza sativa*, nutritional traits, rice

Introduction
Rice (*Oryza sativa* L.) is the most important food crop of world grown under 159.81 Million ha area (FAOSTAT, 2016) [3]. Being grown worldwide, it is the staple food for more than half of the world's population. As a cereal grain, it is the most widely consumed staple food for a large part of the population, especially in Asia. It is the agricultural commodity with the third-highest worldwide Therefore, even a small increase in the grain yield and nutritive value of rice can be highly significant for human nutrition.

Genetic diversity is one of the key factors in tailoring the effective breeding programme in any crop. Success of hybridization followed by selection depends largely on the selection of parents with high genetic variability for different characters. The genetically diverse parents are likely to produce heterotic effects and desirable seggregants. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents. Therefore, the magnitude of genetic divergence and characters contributing to the genetic divergence were studied using Mahalanobis D^2 statistic among 38 germplasm lines of rice.

Material and Methods
Thirty eight diverse rice genotypes from different geographic origin were transplanted in randomized block design with three replications during *kharif, 2017* at the College farm of Agricultural College, Mahanandi of Acharya N.G. Ranga Agricultural University. In each replication single seedling was transplanted per hill in 3 rows of 5meters length with 20 x 15 cm spacing. Recommended package of practices were followed to obtain a normal crop. The observations were recorded on five randomly taken plants from each plot for days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, panicle weight, number of filled spikelets per panicle, kernel length, kernel breadth, kernel L/B ratio, 1000 grain weight, harvest Index, grain yield, protein content, iron content and zinc content. The analysis of genetic divergence was done using Mahalonobis D^2 (1936) statistics. The genotypes were grouped into different clusters by Tocher's method described by Rao (1952) [6].

Results and Discussions

Based on D^2 values, seventeen traits clustered 38 rice genotypes in to eight major groups (Table.1). The genotypes within each cluster were closer to each other than the genotypes in different clusters. From Fig.1 and Table.1 it is found that cluster I was the largest (20) followed by cluster II (12). While clusters III, IV, V, VI, VII and VIII comprised of only one genotype each. These six genotypes maintained separate identity and they were not included with any other cluster and exhibited higher genetic distance with most of the other clusters. Random genetic drift and selection for specific characters in specified environments cause greater diversity than geographical distance (Murthy and Arunachalam, 1966) [5]. Similar results of greater genetic diversity for the genotypes in the monogenotypic clusters were also reported by Beevi and Venkatesan (2015) [1].

In the present study, clustering pattern revealed that the genotype from different sources or origin clustered together. This pattern of grouping indicated that there was no association among the geographical distribution of genotypes and their genetic divergence. It might be attributed to the free exchange of genetic material among the breeders from different places or unidirectional selection adopted by breeders while exercising selection process. The highest number of 20 genotypes in cluster I and 12 genotypes in cluster II showed lesser divergence, this might be due to having some similar characteristics or common parentage among the genotype which led to their grouping in the same cluster. This study also revealed that genotypes from same origin were distributed in different clusters. This could be understood that these genotypes might be exposed to different environmental conditions resulting in enhanced divergence and represented selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity.

Average intra and inter cluster distances have been shown in Table 2. The maximum intra cluster distance was recorded in cluster I (77.07) followed by cluster II (69.72). Thus, the genotypes from those clusters had higher degree of divergence that would produce more desirable segregants for achieving greater genetic advance. In contrary, the minimum was noticed in the clusters III, IV, V, VI, VII and VIII as they included single genotype each, signifying that some genetic divergence still existed among the genotypes. Selection within such clusters might be executed based on maximum mean value for the desirable characters. This could be exploited in the yield improvement through recombination breeding.

The maximum inter cluster distance was recorded between cluster II and VI (373.87) followed by II and V (346.89), II and III (313.75), II and IV (313.00) and VI and VII (311.16) were found to be divergent in the decreasing order of their magnitude that could be used as parents for crossing programme to obtain high heterotic effects and trangressive segregants with high variability. A cluster diagram was constructed showing the relationship between the different populations (Fig.2). Where the greatest distance between the two clusters was existed between cluster II and VI (373.87), thus showed greater divergence. Whereas, the least distance was measured between cluster III and IV (33.05), which exhibited the lowest genetic divergence between them among the eight clusters formed.

The cluster means for each of the 17 characters are presented in Table.3. From the data it was observed that considerable differences existed for all the characters under study and demonstrated that selection of genotypes having superior performance for a particular trait and average performance for other trait could be made and used in the hybridization programme for improvement of that character. In the present study, it was observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of directly selecting a single genotype for immediate use. Thus, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. The divergent clusters V and VIII having highest average compared to other groups in terms of five traits each *viz*., panicle weight, number of filled spikelets per panicle, SCMR, iron and zinc contents in cluster V and kernel length, kernel L/B ratio, 1000 grain weight, grain yield per plant and protein in cluster VIII. Therefore, the genotypes in these clusters having high mean values may be directly used for adaptation or inter crossing could be suggested to generate a wide spectrum of variability followed by effective selection for these characters.

The contribution of individual trait to the divergence among genotypes is presented in Fig.3. Protein content contributed maximum towards genetic divergence (25.32 %) followed by number of filled spikelets per panicle (23.47%), days to 50 per cent flowering (21.19%) and 1000 grain weight (15.93%). Similar observations were noted by earlier workers Ahmed *et al*. (2015) for protein content; Beevi and Venkatesan (2015) [1] for number of filled spikelets per panicle and Chamundeswari (2016) [2] for days to 50 per cent flowering and 1000 grain weight. However, remaining traits showed very little or no contribution towards genetic divergence which is suggestive of lack of diversity for this trait in the present genetic material which might be due to the operation of directional selection adopted by the breeders in the development of these genotypes.

Therefore, D^2 analysis revealed the concept of non correspondence of genetic divergence and geographic diversity and summarized that the genotypes NLR 3304, NLR 3251, MTU 1081, RNR 15048 and NLR 4002 from cluster III, IV, V, VI and VII, respectively were found to be promising and found to be genetically divergent. Hence, these genotypes could be utilized in the hybridization programme to produce transgressive segregants. Nutritional traits are the most important strategy in rice, in view of that clusters with more nutritional content were estimated. The genotypes of cluster VI and VIII had high protein, cluster V had high iron and zinc content. Hence, these genotypes may be utilized in further breeding programmes to improve the nutritional characters in addition to higher yields.

Table 1: Cluster composition of 38 rice genotypes based on Tocher's method.

Cluster number	No. of genotypes	Genotypes
I	20	BPT 5207, BPT 4358, NDLR 8, NDLR 7, RP Bio 226. MCM 111, NLR 3346, NLR 3296, NLR 4001, NLR 3354, NLR 3041, MTU 7029, SWARNA Sub 1, MTU 2076, MTU 1032, BPT 2698, MTU 1075, MTU 1078, BPT 2673, NLR 3391.
II	12	MTU 4870, MTU 5293, PLA 1100, MTU 2077, BPT 2270, MTU 1061, MTU 5182, BPT 2295, BPT 2231, MTU 1031, BPT 3291, MTU 1064.
III	1	NLR 3304

IV	1	NLR 3251.
V	1	MTU 1081
VI	1	RNR 15048
VII	1	NLR 4002
VIII	1	PD 10

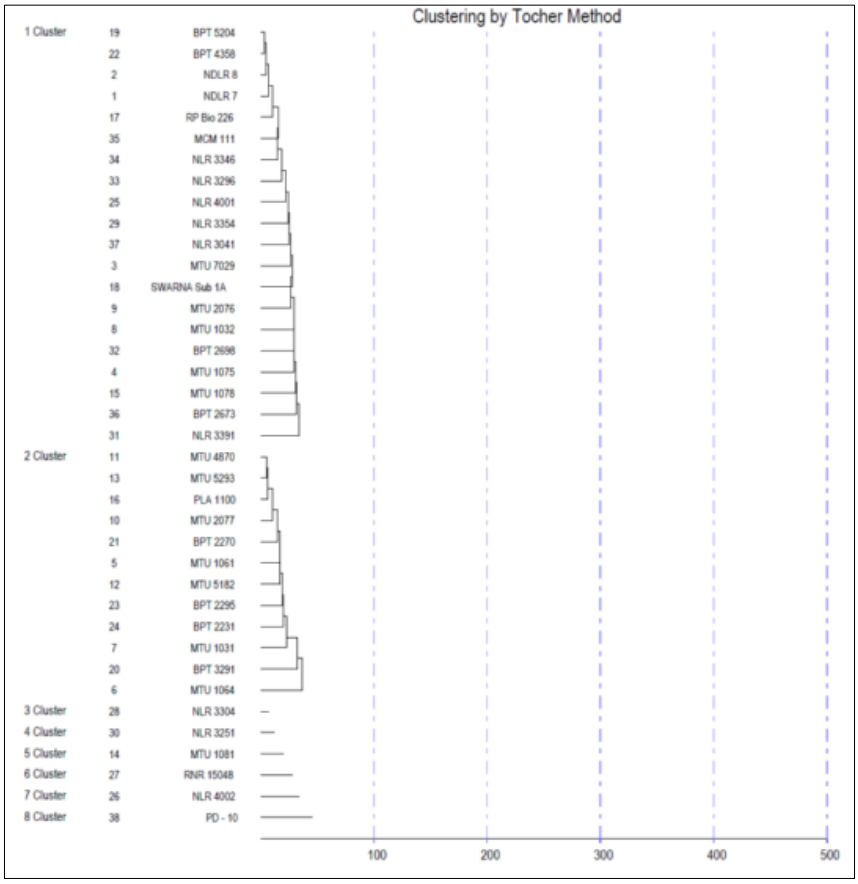

Fig 1: Grouping of genotypes into clusters using Tocher's method

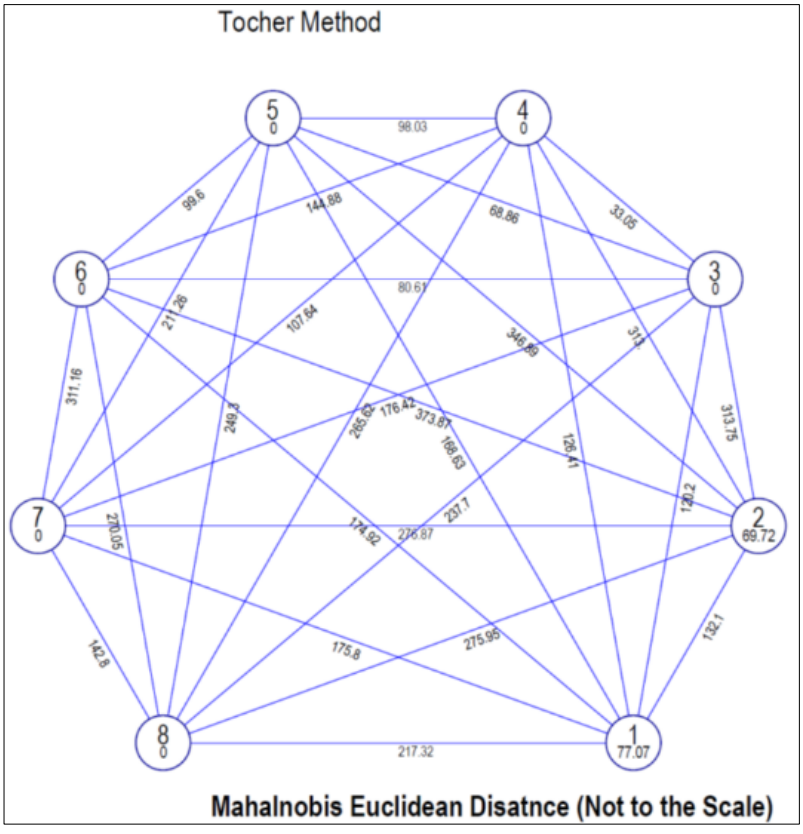

Fig 2: Cluster diagram showing average intra and inter cluster distance

Table 2: Average intra and inter cluster distances for the rice genotypes studied.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	77.07	132.10	120.20	126.41	168.63	174.92	175.80	217.32
II		69.72	313.75	313.00	346.89	373.87	276.87	275.95
III			0.00	33.05	68.86	80.61	176.42	237.70
IV				0.00	98.03	144.88	107.64	265.62
V					0.00	99.60	211.26	249.30
VI						0.00	311.16	270.05
VII							0.00	142.80
VIII								0.00

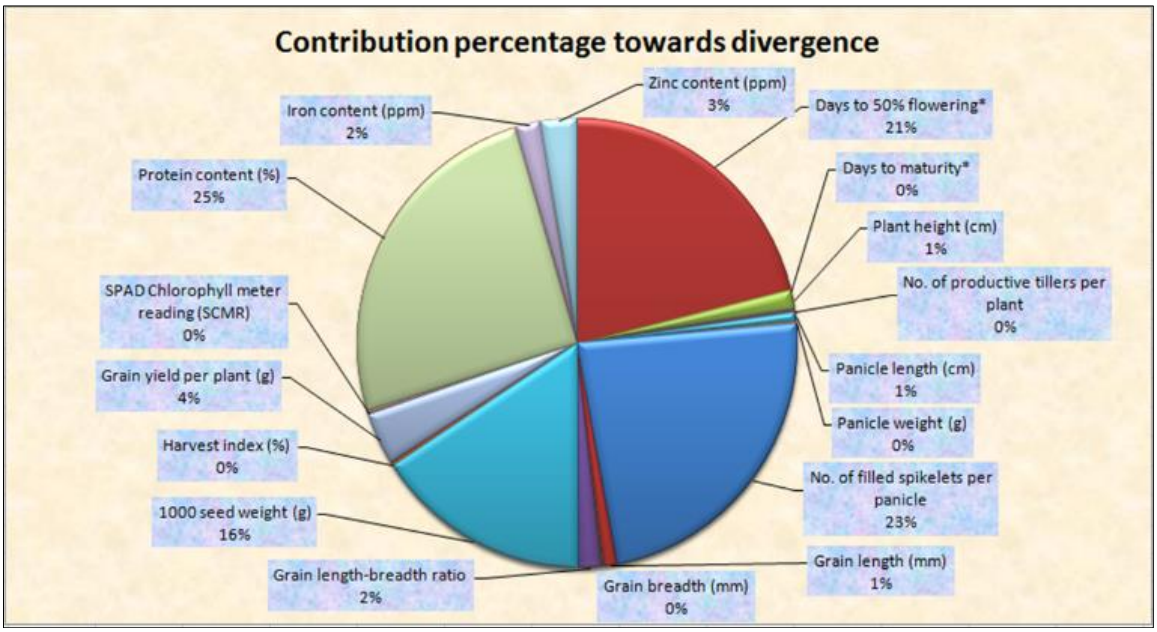

Fig 3: Relative contribution of seventeen characters to total genetic diversity in 38 genotypes of rice

Table 3: Cluster means with respect to yield and its attributes among 38 rice genotypes

Character Cluster	DFF	DM	PH	NPT	PL	PW	NFS	KL	KB	LBR	TW	HI	GY	SCMR	Protein	Iron	Zinc
1 Cluster	107.03	137.07	115.34	13.04	23.73	3.07	167.29	5.36	1.91	2.82	15.80	29.84	29.75	39.91	2.87	4.98	9.80
2 Cluster	120.08	150.08	118.43	11.58	24.18	3.00	119.84	5.40	2.08	2.64	17.58	25.44	25.16	39.02	2.87	5.37	10.66
3 Cluster	94.00	124.00	108.60	17.47	23.07	3.87	218.73	5.50	2.02	2.74	14.92	35.78	38.00	41.51	2.93	5.90	9.57
4 Cluster	90.00	120.00	108.87	16.27	23.32	3.78	201.93	5.54	2.15	2.58	15.40	42.62	40.66	40.80	2.66	4.83	10.13
5 Cluster	97.67	124.00	116.30	13.13	26.47	4.86	231.57	5.71	1.60	3.58	14.96	40.11	43.90	42.93	2.87	6.40	12.53
6 cluster	94.00	124.00	121.40	13.87	27.87	3.00	220.73	5.01	1.39	3.60	11.83	35.83	38.29	41.16	3.21	4.10	8.33
7 Cluster	90.67	120.67	112.73	17.80	24.83	3.35	162.67	6.53	1.91	3.43	21.69	39.86	41.47	42.29	2.51	5.13	9.07
8 Cluster	92.00	123.00	114.00	14.93	26.46	4.34	144.80	6.68	1.73	3.86	24.13	40.88	45.47	37.22	3.21	5.63	9.27

DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height, NPT-Number of productive tillers per plant, PL-Panicle length, PW-Panicle weight, NFS-Number of filled spikelets per panicle, KL-Kernel length, KB-Kernel breadth, LBR-Kernel length breadth ratio, TW-1000 grain weight, GY-Grain yield per plant, HI-Harvest index, SCMR-SPAD chlorophyll meter reading.

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