Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Genetic diversity analysis in elite rice (*Oryza sativa* L.) germplasm using agro-morphological traits

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Abstract
Thirty two genotypes of rice were evaluated to assess the genetic divergence. The data were recorded for 13 quantitative characters. Analysis of variance showed highly significant differences for all the characters under study. Based on relative magnitude of D^2 values, the genotypes were grouped into seven clusters. Cluster II constituted maximum number of genotypes with 15 genotypes. Maximum inter-cluster distance (D^2) was observed between cluster VII and III, followed by cluster VII and IV, suggesting that the genotypes from these clusters can be selected to yield superior segregants and further genetic improvement. Maximum genetic divergence was exhibited by days to maturity (49.19%) followed by plant height (17.54%), spikelets per panicle (16.33%) and biological yield (11.29%).Therefore, days to maturity, plant height, spikelets per panicle and biological yield contributing to 83.06% of the total divergence need to be focused in selection of parents for hybridization programme.

Keywords: D^2 analysis, Genetic diversity, Cluster, Rice

Introduction
Rice is a cereal crop belonging to genus *Oryza* of family Poaceae. About half of the world's population depends on rice for their survival (Bhati *et al*., 2015) [3]. It contributes significantly in Indian Economy and also serves as staple food for more than 70 per cent of the people dwelling in Asia. The slogan 'Rice is life' aptly describes the importance of rice in food and nutritional security. Rice is the most important food crop of India covering about one-fourth of the total cropped area and providing food to about half of the Indian population. India has the largest area (43.39 mt) under rice cultivation with a production of 104.32 million tons and a productivity of 2404 kg per hectare (Ministry of Agriculture, 2016-2017).

In the present scenario the rice productivity has reached a plateau. In order to achieve the expected targets, we have to develop the varieties with higher yield potential by breaking the existing yield plateau and by utilizing more diversified parents in breeding programmes. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Beevi and Venkatesan, 2015) [2]. This helps in the choice of parents for hybridization in yield improvement programmes.

Genetic diversity is a prerequisite for any crop improvement program as it helps in the development of superior recombinants. The crosses between parents with maximum genetic divergence are responsive for genetic improvement. Recently diversity in rice has been well utilized with respect producing high yielding genotypes along with another desirable back ground to solving the food problems.

Mahalanobis D^2 statistics for estimating genetic divergence had been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008) [13]. The multivariate analysis developed by Mahalanobis (1936) [6] has been found to be most suitable in quantifying the degree of divergence in germplasm.

Recognizing the Importance of genetic diversity in plant breeding experiments, present research work was undertaken to study genetic divergence and to identify divergent parents for future hybridization programmes in 32 elite rice germplasm for yield and quality traits.

Materials and methods
The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, SHUATS, Allahabad, U.P during *Kharif* -2017. The site of experiment is located at 25.57^0 N latitude, 81.51^0 E longitude and 98 meter above the sea level. This region has subtropical climate with an average rainfall of around 1013.4 mm annually. The experimental material consist of thirty two IRRI rice genotypes along with two checks

(Table 1). These genotypes were evaluated in Randomized Block Design (RBD) with three replications. Each genotype was transplanted in three rows of 5x2 m length adopting a spacing of 20x15 cm. Normal package of practices and need based plant protection measures were followed. The observation data were recorded randomly from five selected plants from each genotype per replication for Days to 50% flowering, Plant height (cm), Flag leaf length (cm), Flag leaf width (cm), Panicle length (cm), No. of tillers per plant, No. of panicles per plant, No. of spikelets per panicle, Days to maturity, Harvest index (%), Biological yield (g), Test weight (g) and Grain yield (g).

Data of each character was subjected to statistical analysis to measure genetic divergence which includes Analysis of variance (Panse and Sukhatme, 1961) [9] and Genetic divergence (Mahalanobis, 1936) [6]. D^2 statistics for 13 quantitative characters.

Table 1: List of Experimental Materials (32 Rice Genotypes)

S. No	Name of Genotypes	S. No	Name of Genotypes
1	IRRI – 6	17	IRRI – 8
2	IRRI – 23	18	IRRI – 39
3	IRRI – 12	19	IRRI – 15
4	IRRI – 35	20	IRRI – 37
5	IRRI – 2	21	IRRI – 10
6	IRRI – 9	22	IRRI – 21
7	IRRI – 11	23	IRRI – 3
8	IRRI – 5	24	IRRI – 24
9	IRRI – 4	25	IRRI – 1
10	IRRI – 30	26	IRRI – 29
11	IRRI – 36	27	IRRI – 31
12	IRRI – 25	28	IRRI – 7
13	IRRI – 20	29	IRRI – 14
14	IRRI – 17	30	IRRI – 22
15	IRRI – 26	31	NDR – 359 (Check)
16	IRRI – 16	32	SHIATS DHAN – 1 (Check)

Results and discussion
The analysis of variance showed highly significant for all 13 quantitative characters under study (Table 2). This indicates that there was an ample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. These findings are in accordance with the findings of Ashok *et al.* (2017) [1]. And Kumar *et al.* (2017) [5]. Who also observed significant variability for yield and its components traits in rice.

Genetic divergence is of greatest interest to plant breeder as it plays a vital role in farming a successful breeding programme. Mahalanobis D^2 statistics was used for the quantitative assessment of genetic divergence for all the 13 characters. The thirty two genotypes were grouped into seven clusters by Non-Hierarchical Euclidean cluster analysis (Table 4). Cluster II has the highest no. of genotypes (15), cluster III consists of 9 genotypes, cluster I with 4 genotypes and cluster IV, V, VI and VII each had only 1 genotype.

A comparison of the mean value of thirteen characters of different clusters has been presented in Table 5. Considerable differences in cluster mean values were evident for all the characters. Considering the cluster mean, it was observed that test weight (22.71g) and grain yield (37.47g) exhibited the highest mean values in cluster I. While cluster II showed moderate mean values for all the characters under study. Cluster III recorded the lowest mean values for days to maturity (115.48 days), days to 50% flowering (84.59 days) and flag leaf width (1.26 cm). Cluster IV characterized for high mean value of days to 50% flowering (96.40 days) and low mean values for plant height (87.80 cm), flag leaf width (1.26 cm), panicle length (25.10 cm), tillers per plant (13.40), panicles per plant (12.20), spikelets per panicle (117.53), biological yield (59.56g) and grain yield (18.73). Cluster V had the highest mean value for days to maturity (134.76 days) and low mean value for harvest index (29.90%). Cluster VI had the lowest mean value for flag leaf length (28.76 cm). Cluster VII exhibited highest mean values for plant height (127.50 cm), flag leaf length (40.93 cm), flag leaf width (1.50 cm), panicle length (26.53 cm), spikelets per panicle (260.06) and harvest index (43.93%) and low mean value for test weight (17.93g). Therefore, more emphasis should be given on clusters with high mean values for yield and yield contributing characters for selecting genotypes as variety as well as parents in future breeding programme. The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning clustering with respect to the origin. Similar findings were also reported by Priyanka *et al.* (2015) [11]. and Kumar *et al.* (2017) [5].

The intra and inter cluster average distances among seven clusters were variable (Table 5).The maximum intra-cluster (D^2) was registered for, cluster III (121.94), followed by cluster II (109.15) and cluster I (37.63). The inter-cluster distance (D^2) was found maximum between cluster VII and III (1250.00) followed by distance between cluster VII and IV (1218.62). The lowest inter-cluster distance was observed between cluster V and IV (103.58).The inter distances in all the clusters were higher than the intra cluster distances indicating wider genetic diversity among genotypes of different groups. Therefore, the genotypes from the clusters having maximum inter-cluster distances can be selected to yield superior segregants and further genetic improvement. The results were in agreement with Ashok *et al.* (2017) [1]. and Priya *et al.* (2017) [10].

The percent contribution of thirteen characters towards total genetic divergence is presented in Table 5. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004) [7].The highest contribution in the manifestation of genetic divergence was exhibited by days to maturity (49.19%) followed by plant height (17.54%) and spikelets per panicle (16.33%). Garg *et al.* (2011) [4]. reported the maximum contribution of days to maturity among other characters. Ovung *et al.* (2012) also reported maximum contribution of plant height and spikelets per panicle. Therefore, days to maturity, plant height and spikelets per panicle contributing to 83.06% of the total divergence need to be focused in selection of this traits for hybridization programme.

Table 2: Analysis of Variance for Thirteen Quantitative Characters in 32 Rice Genotypes.

S. No	Parameter	Mean Squares		
		Replications (Df=2)	Treatments (Df=31)	Error (Df=62)
1.	Days to 50% Flowering	0.20	60.13**	0.69
2.	Plant Height	3.13	301.12**	1.35
3.	Flag Leaf Length	8.01	34.45**	1.40
4.	Flag Leaf Width	0.0066	0.02**	0.0030
5.	Panicle Length	22.62	5.08**	0.98
6.	Tillers per Plant	17.12	13.38**	2.11
7.	Panicle per Plant	19.06	13.06**	1.67
8.	Spikelets per Panicle	39.41	2514.90**	19.39
9.	Days to Maturity	0.74	118.19**	0.41
10.	Harvest Index	16.25	64.49**	3.72
11.	Biological Yield	11.12	385.76**	5.58
12.	Test Weight	0.10	8.02**	0.26
13.	Grain Yield per Plant	16.63	122.58**	2.36

** Significant at 5% and 1% level of significance.

Table 3: Distribution of 32 Rice Genotypes into Different Clusters:

Sl. No.	Cluster No.	No. of Genotypes	Genotypes Included
1	I	4	IRRI-35, IRRI-36, IRRI-9, IRRI-16
2	II	15	IRRI-25, IRRI-10, IRRI-15, IRRI-24, IRRI-5, IRRI-11, IRRI-3, IRRI-1, IRRI-39, IRRI-2, IRRI-14, IRRI-8, IRRI-21, IRRI-23, IRRI-29
3	III	9	IRRI-17, IRRI-31, IRRI-37, IRRI-30, IRRI-6, IRRI-4, IRRI-26, IRRI-12, IRRI-7
4	IV	1	IRRI-20
5	V	1	IRRI-22
6	VI	1	NDR-359 (Check)
7	VII	1	SHIATS DHAN-1 (Check)

Table 4: Intra and Inter cluster average distances in rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	37.63	143.25	342.16	222.90	113.95	215.28	695.73
Cluster II		109.15	198.58	228.03	243.23	428.54	960.29
Cluster III			121.94	531.77	577.59	721.57	1250.00
Cluster IV				0.000	103.58	454.37	1218.62
Cluster V					0.000	163.22	697.84
Cluster VI						0.000	319.66
Cluster VII							0.000

Table 5: Cluster mean values for different component characters in Rice and their contribution to total divergence

Cluster member	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Contribution %
Days to 50% Flowering	93.53	90.39	84.59	96.40	96.20	94.53	96.36	1.61
Plant Height	101.79	93.22	92.23	87.80	101.80	121.80	127.50	17.54
Flag Leaf Length	31.13	32.16	30.46	29.96	31.96	28.76	40.93	1.21
Flag Leaf Width	1.36	1.32	1.26	1.26	1.40	1.43	1.50	0.01
Panicle Length	26.11	25.54	25.54	25.10	26.03	26.43	26.53	0.01
Tillers/plant	19.11	16.40	16.44	13.40	14.80	14.40	16.56	0.01
Panicle/plant	17.95	14.93	14.83	12.20	12.93	13.43	13.60	0.01
Spikelets/panicle	142.23	136.28	133.37	117.53	143.33	178.36	260.06	16.33
Days to Maturity	128.49	123.11	115.48	132.66	134.76	132.56	128.03	49.19
Harvest Index	41.39	38.88	37.94	31.43	29.90	38.43	43.93	0.40
Biological Yield	90.83	70.96	71.86	59.56	75.60	72.56	76.36	11.29
Test Weight	22.71	21.77	20.85	21.16	20.10	18.50	17.93	2.42
Grain Yield/plant	37.47	27.52	27.64	18.73	22.53	27.83	33.26	0.01

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