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## Genetic divergence in mid early rice genotypes

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### Abstract

Rice has a vast genetic resource in the world. To explore the genetic resources for its exploitation in the genetic improvement programme, the current study was done with mid early rice genotypes of Bihar. The research was performed at research farm of Bhola Paswan Shastri Agricultural College, Purnea (Bihar) with thirty- four mid early rice genotypes. The genetic diversity among the genotypes was analysed using Mahalanobis D<sup>2</sup> statistics. The study showed that the intra and inter cluster average distances among six clusters were found variable. The highest intra-cluster distance was recorded for cluster-III (24.44) followed by cluster IV (19.55) and cluster I (17.05). The highest inter-cluster distance was observed between cluster III and V (118.78), followed by cluster I and III (103.90) and cluster V and VI (102.92) indicating wider genetic diversity among the genotypes between these groups. The highest contribution towards genetic divergence was exhibited by days to 50% flowering (37.08%) followed by fertile grains/panicle (27.63%) and 1000grain weight (12.12%). The other traits showed less or no contribution towards divergence.

**Keywords:** Mid early rice, genetic divergence

### Introduction

Rice (*Oryza sativa* L.) is life for more than half of the global population. It is the most important crop of India and it occupies 23.03% of the gross cropped area in the country. In India, rice plays a vital role in providing food security as it contributes 43% of total food grain production and 46% of the total cereal production. India being the second largest producer of rice still lacks behind. The rising demand, saturation of cultivated field and low gross domestic production of rice are likely to cause a supply shortage of a crop in the near future. But the year 2025, about 785 million tons of paddy which is 70% more than current production will be needed to meet the growing demand (Kumar *et al.* 2016)<sup>[1]</sup>. Therefore being the staple food of the population in India, improving its productivity has become a crucial importance. Rice occupies a predominant position in Bihar accounting for 50.5% of total cereal production. In spite of all these, India is still lagging behind in the context of the productivity than world. Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding. Recently diversity in rice has been well utilized with respect producing high yielding genotypes along with another desirable back ground to solve the food problems. The narrow genetic base of rice genotypes is likely to make vulnerable to biotic and abiotic factors. The D<sup>2</sup> technique is based on multivariate analysis developed by Mahalanobis (1936) had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both in inter-cluster and intra-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation (Rao, 1952). In view of all this the present study was done with the objective to study the genetic diversity among the rice genotypes.

### Materials and methods

The present experiment consisted of 34 rice genotypes collected from Rice Research Section of Bihar Agricultural College, Sabour, Bhagalpur and was conducted at Research Farm of Bhola Paswan Shastri Agricultural College, Purnea.

These 34 rice genotypes were grown in randomized block design with three replications. The plant to plant and row to row distance was maintained at 20x15 cm. The recommended agronomical practices were followed to ensure a normal healthy crop. The reading from five tagged plants were averaged replication wise and the mean data of twelve characters namely, days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, flag leaf length, number of spikelets per panicle, fertile grains per panicle, biological yield per plant, grain yield per plant, 1000 grain weight and harvest index was used for statistical analysis. The data thus obtained were subjected to Mahalanobis D<sup>2</sup> Statistics analysis and grouping of genotypes was done according to Tocher method (Rao, 1952).

### Results and discussion

All the 34 genotypes taken for genetic divergence analysis differed significantly for almost all the characters under study showing marked divergence. Based on D<sup>2</sup> values of all the studied traits the 34 rice genotypes were grouped into 6 clusters (Table-1).

#### Clustering Pattern

The clustering pattern reflected the presence of considerable amount of genetic diversity in the genetic material under study. Earlier workers, Reddy *et al.*, (2002) [5], Babu *et al.*, (2003) [3], Sarkar *et al.*, (2006) [6] and Sohrabi *et al.*, (2012) [7] also reported considerable diversity between the clusters in rice genotypes. The intra and inter cluster average distances among 6 clusters were variable, the result represented in Table- 2. The highest intra-cluster distance was recorded for

cluster-III (24.44) followed by cluster IV (19.55) and cluster I (17.05). Genotypes from these clusters could be utilized as parental lines for hybrid breeding programmes owing to their higher mean performance within group. Lowest intra-cluster distance was recorded for cluster-V and VI (0.000). The highest inter-cluster distance was observed between cluster III and V (118.78), followed by cluster I and III (103.90) and cluster V and VI (102.92) indicating wider genetic diversity among the genotypes between these groups. To realize high heterotic effect, Babu *et al.*, (2003) [3], Suman *et al.*, (2005) [8], Sarkar *et al.*, (2006) [6] and Chandra *et al.*, (2007) recommended that parents should be selected from two clusters having wider inter-cluster distance.

The points to be considered while selecting the genotypes during crossing programme is, the genotypes should belong to more divergent clusters, and it should show desirable mean performance for various characters. Mani *et al.*, (2014) suggested that, parents with high yield potential and belonging to distant clusters are likely to yield superior segregants within a short period. Considering the genetic divergence, clustering pattern and mean performance of genotypes for grain yield and other yield contributing characters, BRR0044, BRR0059, BRR0051, BRR0072 and BRR2069 may be considered as elite genotypes and hybridization involving these genotypes is likely to give desirable segregants. Results suggested a possibility for obtaining greater variation in the segregating generations derived from the hybridization of genotypes of Cluster III with Cluster V or Cluster III and Cluster I with Cluster V. Such approach was also advocated by Suman *et al.*, (2005) [8].

**Table 1:** Distribution pattern of 34 rice genotypes into 6 clusters based on D<sup>2</sup> statistic

Clusters	No. of genotypes	Genotypes
I	12	BRR2061, BRR0075, BRR0073, BRR2060, BRR0071, SITA, BRR0072, BRR0057, BRR0056, BRR0014, BRR2057, BRR2025
II	8	BR0060, BRR0059, BRR0058, BRR2068, BRR2005, R.MAHSURI1, BRR0074, BRR0044
III	7	BRR2065, BRR2072, BRR2070, BRR2055, BRR2069, BRR2071, BRR0064
IV	5	BRR2058, BRR2059, BRR2067, BRR2056, BRR2054
V	1	BRR0051
VI	1	BRR2066

Source of genotypes: BAU, Sabour

**Table 2:** Average intra and inter cluster distance among 6 clusters for 34 rice genotypes

Clusters	I	II	III	IV	V	VI
I	17.05	43.70	103.90	32.00	24.71	82.53
II		16.42	62.34	60.45	28.70	55.39
III			24.44	68.75	118.78	60.82
IV				19.55	61.51	76.79
V					0.00	102.92
VI						0.00

**Table 3:** Contribution of different characters towards genetic divergence

S. No.	Characters	Times ranked 1st	% Contribution
1.	Days to 50% flowering	37.08	37.08%
2.	Days to maturity	5.70	5.70%
3.	Plant height(cm)	1.07	1.07%
4.	Number of effective tillers/plant	0.53	0.53%
5.	Panicle length(cm)	3.39	3.39%
6.	Flag leaf length(cm)	5.35	5.35%
7.	Number of spikelets/panicle	1.43	1.43%
8.	Number of fertile grains/panicle	27.63	27.63%
9.	Biological yield/plant(g)	2.50	2.50%
10.	Grain yield/plant(g)	3.21	3.21%
11.	1000 grain weight(g)	12.12	12.12%
12.	Harvest index (%)	0.01	0.00%

### Percentage contribution of characters towards genetic divergence

The percent contribution of 12 characters towards total genetic divergence is listed in Table-3. The selection and choice of parents mainly depends upon contribution of characters towards divergence. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by Days to 50% flowering (37.08%) followed

by fertile grains/panicle (27.63%), 1000grain weight (12.12%), days to maturity (5.70%), flag leaf length (5.35%), panicle length (3.39%), grain yield/plant (3.21%), biological yield/plant (2.50%), spikelets/panicle (1.43%), plant height (1.07%) and effective tillers/plant (0.53%). Only harvest index showed no contribution towards divergence. Similar findings were also observed by Mani *et al.*, (2014) and Chandramohan *et al.*, (2016) [9].

**Table 4:** Mean performance of clusters for different characters towards genetic divergence in 34 rice genotype

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of effective tillers/plant	Panicle length(cm)	Flag leaf length(cm)	Number of spikelet/panicle	Number of fertile grains/panicle	Biological yield/plant(g)	Grain yield/plant (g)	1000 grain weight (g)	Harvest index (%)
I	99.75	128.08	98.94	10.32	23.79	31.20	205.07	183.61	30.22	13.30	26.10	44.13
II	114.58	140.67	106.39	12.04	24.77	35.00	238.85	213.60	34.00	14.96	23.38	44.53
III	121.00	147.05	116.22	8.77	25.42	36.34	169.44	144.47	28.02	10.78	21.11	38.94
IV	100.73	130.53	103.74	8.95	22.83	31.09	159.60	136.48	25.19	11.02	24.60	44.36
V	102.00	129.67	100.60	12.08	26.17	40.73	265.30	228.90	32.80	15.60	24.02	47.86
VI	118.67	146.00	79.60	10.67	21.83	25.17	166.20	141.20	26.60	12.48	32.24	47.17

### Cluster Mean

A comparison of the mean values of Six clusters for 12 characters has been presented in (Table- 4.). Considerable differences in cluster mean values were evident for all the characters studied. The present study revealed that cluster I had highest mean values for spikelets/panicle (205.07), followed by fertile grains/panicle (183.61) and days to maturity (128.08) and lowest mean values for effective tillers/panicle (10.32) followed by grain yield/plant (13.30). Whereas, Cluster II had highest mean values for spikelets/panicle (238.85), followed by fertile grains/panicle (213.60), days to maturity (140.67), days to 50% flowering (114.58) and plant height (106.39) and lowest mean values for characters like effective tillers/panicle (12.04) followed by grain yield/plant (14.96). Cluster III showed highest mean values for characters like spikelets/panicle (169.44), followed by days to maturity (147.05) and fertile grains/panicle (144.47) and lowest mean values for effective tillers/panicle (8.77) followed by grain yield/plant (10.78). However, The highest mean values for spikelets/panicle (159.60), followed by fertile grains/panicle (136.48), days to maturity (130.53), plant height (103.74) and days to 50% flowering (100.73) were the characteristic features of cluster IV, this cluster also showed lowest mean values for effective tillers/panicle (8.95) followed by grain yield/plant (11.02). The cluster V had highest mean value for spikelets/panicle (265.30), followed by fertile grains/panicle (228.90), days to maturity(129.67), days to 50% flowering(102) and plant height (100.60) and lowest mean values for characters like effective tillers/panicle (12.08) followed by grain yield/plant (15.60). Cluster VI showed highest mean values for spikelets/panicle (166.20) followed by fertile grains/panicle (141.20) and days to maturity (146) and lowest mean values for effective tillers/panicle (10.67) followed by grain yield/plant (12.48). However, none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. This shows that the hybridization between genotypes of different cluster is necessary for the development of desirable genotypes.

Selection of genotype with higher mean value may be used for adaptation or may be used as parent in future breeding

programme. The similar result was also reported by Suman *et al.* (2005) [8], Sarkar *et al.* (2006) [6].

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