The Pharma Innovation

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Genetic divergence study in rice (*Oryza sativa* L.) under direct seeded condition

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Abstract
Genetic divergence assessed among 15 rice genotypes using Mahalanobis D^2 statistic. D^2 analysis differed significantly with regard to the character and distributed 15 genotypes into four clusters, of which cluster I was the largest comprising of 12 genotypes and Cluster II, Cluster III and Cluster IV had single genotype each. The pattern of distribution of genotypes from different eco-geographical region into various clusters was at random indicating that geographical diversity and genetic diversity were not related. Cluster I had maximum intra-cluster value of 206.52 and maximum inter-cluster distance was observed between the cluster III and IV (2197.20) followed by cluster I and III (819.96) indicating the importance of the genotypes present in these cluster on genetic divergence for quantitative characters. The genotypes IR-64 of cluster IV, IR-127299-32-2-2 of cluster III and genotype IR-127339-11-1-1-1-1 of cluster 1I are diverse in nature, Hence these genotypes are used as better parent in hybridization programme for direct seeded condition, likely to produced wide variability with desirable segregates. The characters *viz*. Number of grains panicle^{-1}, grain yield plant^{-1}, and 1000 grain weight (g), contributed maximum towards genetic divergence among the genotypes.

Keywords: Rice, genetic divergence, variability, Mahalanobis D^2

Introduction

Rice (*Oryza sativa* L.,) has a short day monocotyledonous, angiospermic, self-pollinated plant belongs to *Oryza* genus, Poaceae family. It is most important cereals crop on the planet, providing food to more than 50 percent world populations. It is staple food in nearly 100 nations across the world and accounts for 20% of direct human calorie intake, making it the most significant crop on the planet. It's widely cultivated in tropical and subtropical areas, where there's a wider diversity of habitats, temperature, and water regime changes.

Rice is often cultivated by sowing seedlings in puddled soil (wet tillage). Rice production is becoming less economical as water and labour become increasingly rare and expensive. Pudding and transplanting need big volume of waters & labour, both are becoming increases scarce and affluent. Rice cultivation in traditional techniques needs a lot of water. One kilogramme of rough rice requires an average of 2500 litres of water, ranging from 800 to over 5000 litres (Bouman, 2009) [1]. In the instance of direct seeded rice (DSR), labour savings were identified from an average of 24 in manual transplanting to two in DSR (Kumar *et al*., 2018). The inefficient use of inputs (water, labour), resource scarcity, particularly water and labour, climate change, the impending energy crisis, and rising rice production costs are all threatening the productivity and sustainability of rice-based systems (Ladha *et al*., 2009) [4].

Many farmers in India have switched from transplanted to DSR culture because to the introduction of early maturing strains & improved fertiliser management strategies. Direct seeded rice is a viable option because to its minimal input requirements. As a result, the adaption of early maturing varieties is favoured. Due to a labour scarcity in Bihar, farmers are being encouraged to use 'Direct seeding of Rice' instead of traditional transplantation. In direct seeded rice areas, most farmers grow land races, which are more resistant to environmental stress but have lesser production potential than contemporary strains. In traditional direct seeded rice regions, modern semi dwarf varieties produced for irrigated soil have not been widely accepted.

In light of the aforementioned difficulties, it is necessary to identifying rice genotypes that are relatively well adapted for the Direct seeded rice situation in Bihar. Genetic diversity is the foundation of genetic improvement of crops. Breeder seek to understand rice genetic diversity and uncover new genes and traits in rice that will help in development of new variety which

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face challenges brought about by climate change, pest and disease and other unfavourable conditions. The present study was undertaken for estimating genetic divergence of selected genotypes as it permits precise comparison among all possible pairs of genotypes in any given group before effecting actual crosses.

Materials and Methods

The experimental materials consisting of 15 diverse rice genotypes with one check were grown during 2020-21 in randomized block design with 3 replications at research farm of Tirhut College Agriculture, Dholi, Muzaffarpur. The farm is located at 85.4 E longitudes and 25.93 N latitude of the experimental site above 52.12 meter mean sea level. Genotypes were sown under direct seeded condition with spacing of 20cm × 15 cm and each genotype grown in six rows of 3m length. Appropriate management and cultural practices were followed to raise a good crop. Observation on 11 important yield components, quantitative traits were recorded based on five randomly selected plants in each genotype in each replication. The genetic diversity was estimated by using Mahalanobis D^2 (1936) [6] statistics analysis as elaborated by Murty and Arurechalam (1966) [8] and grouping of genotype into cluster was done through Tocher`s method (Rao, 1952) [10].

Result and Discussion

The analysis of Variance showed significant differences among the genotypes for all the characters. It is suggested that the variation among these genotypes might have resulted due to differences in their pedigree (Table-1). Adapting Tocher's procedure, group consultation resulted in distribution of 15 genotypes into four diverse clusters. Cluster I recorded the largest among all the clusters comprised of 12 genotypes followed by Cluster II, Cluster III and Cluster IV comprised of single genotype each respectively. The clustering pattern revealed that Cluster-I having 12 genotypes were more similar to each other in yield and yield component with less variation. While in the Cluster II, III, & IV with single genotypes in each cluster had high genetic variation in each genotype (Table-2 and Fig. 2.1). This pattern showed that genotypes collected from the same geographic origin were found to be distributed in different clusters. Similar findings of non-correspondence of genetic divergence with geographic diversity were reported earlier by Sathish et al. (2017) [11], Tandekar et al. (2018) [16], Shanmugasundaram et al. (2000) [13]. Murthy and Arunachalam (1966) Stated that genetic drift and selection in environment could cause greater diversity than geographic distances.

The inter-cluster distance (Table-3 and Fig.-3.1) recorded higher than intra cluster distance, revealing that sizable sum of genetic divergence existed in genotypes studied. The intra-cluster average D^2 values ranged from 0.00 (cluster II, III and IV) to 206.52 (cluster I). The highest intra-cluster distance (206.52) was observed in the cluster I, indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce more desirable breeding materials for achieving maximum genetic advance with regard to yield per se, provided that there is adequate complementation of gene effects of parental lines (Rahman et al., 1997) [9]. Therefore, genotypes from cluster I should be given emphasis while selection of parents for hybridization programme since most of the elite breeding cultivars were

included in the cluster.

The highest inter-cluster distance was found between cluster III and IV (2197.20) indicating maximum divergence of genotypes included in these two clusters. The minimum inter-cluster distance was found among clusters I & cluster II (365.87) indicating that genotypes included in them were closely related. According to Singh et al. (2018) [15], Chandramohan et al. (2016) [2] and Rahaman et al., (1997), crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. Thus, selection of genotypes from these clusters for a crossing programme will produce desirable transgressive segregants.

The cluster mean for 11 characters (Table 4) directed sizable difference between clusters for all traits. Cluster I exhibited maximum mean value for days to maturity while lowest mean value for number of panicles plant[-1]. Highest cluster mean value for number of grains panicle[-1] exhibited by cluster II, while lowest cluster mean value recorded for number of panicle plant[-1]. Cluster III recorded highest mean value for number of grains panicle[-1] and lowest mean value for number of panicle plant[-1]. Cluster IV showed maximum mean value for days to maturity with lowest mean value for number of panicle plant[-1]. The character expressions are the result of continuous selection pressure exerted on the respective genotypes, which has made them to behave a like in respective situations. The promising genotypes with high mean values for above traits from divergent clusters are selected as parents for hybridization programme to develop high yielding rice varieties.

Independent contribution of traits in the direction of total divergence computed in terms of frequencies of characters having rank I times presented in table- 5. Perusal of above table it is evident that characters number of grain panicle[-1] is single major characters for adaptation which contributed highest (39.05) percent towards total divergence. Amongst other characters, grain yield plant[-1] (23.81 percent), 1000 grain weight (12.38) made considerable contribution to discriminate the genotypes in the term of total divergence.

Supreme contribution to genetic divergence was found viz., number of grain panicle[-1] with 41 times ranked followed by grain yield per plant with 25 times ranked first, 1000 grain weight with 13 times ranked first, days to 50% flowering with 10 times ranked first, plant height (cm) with 6 times ranked first, The Lowest contribution was given by traits like panicle length by 2 times ranked followed by harvest index% by 4 times ranked. The maximum contribution of character number of grains panicle[-1] to genetic divergence in rice were reported earlier by Sathish et al. (2017) [11], Tandekar et al. (2018) [16], Singh et al. (2018) [15], Chandramohan et al. (2016) [2], Lakshmi et al. (2014) [5], Shafina et al. (2014) [12] Singh UK et al. (1999) [14] which corroborated the result of the present study.

The greater distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the cluster having maximum inter-cluster distance can be selected to yield superior segregates (Mishra et al. 2003; Chaturvedi and Maurya, 2005 Singh et al. 2018; Chandramohan et al. 2016) [7, 3, 2, 15]. In the present study, IR-64 of Cluster IV and IR-127299-32-2-2 of Cluster III can be selected for crossing programme to get desirable transgressive segregates. The genotypes from Cluster I having desire characters like date of flowering,

Genotype IR-127339-11-1-1-1-1 from cluster II and genotype IR-127299-32-2-2 from cluster III having highest cluster mean for number of grains panicle^{-1} and genotype IR-64 of cluster IV showed highest mean value for character days to maturity can be selected as ultimate parents for inclusion in the hybridisation programme. Thus, the crosses resulting from these divergent parents are expected to throw wide spectrum of variability for yield and its components characters in the segregating generations.

Table 1: Analysis of variance (ANOVA) to 11 morphological traits, 15 genotypes in Rice.

Sl. No.	Characters	Replication (df = 2)	Genotype (df = 14)	Error (df = 28)
1	Days to 50% flowering	9.68	92.80**	0.49
2	Days to maturity	1.75	16.46**	0.73
3	Plant height (cm)	4.97	384.86**	2.74
4	Panicle length (cm)	0.18	10.76**	0.36
5	No. of panicles plant^{-1}	0.27	1.95**	0.06
6	No. of tillers plant^{-1}	1.93	7.09**	0.22
7	1000 grain weight (g)	4.98	42.01**	1.02
8	Biological yield plant^{-1} (g)	3.13	5.85**	0.84
9	Number of grains panicle^{-1}	13.85	1128.66**	3.14
10	Harvest index (%)	4.54	31.98**	1.46
11	Grain yield plant^{-1} (g)	1.71	5.82**	0.24

** Significant of P = 0.05

Table 2: Distribution of 15 genotypes of rice in diverse cluster:

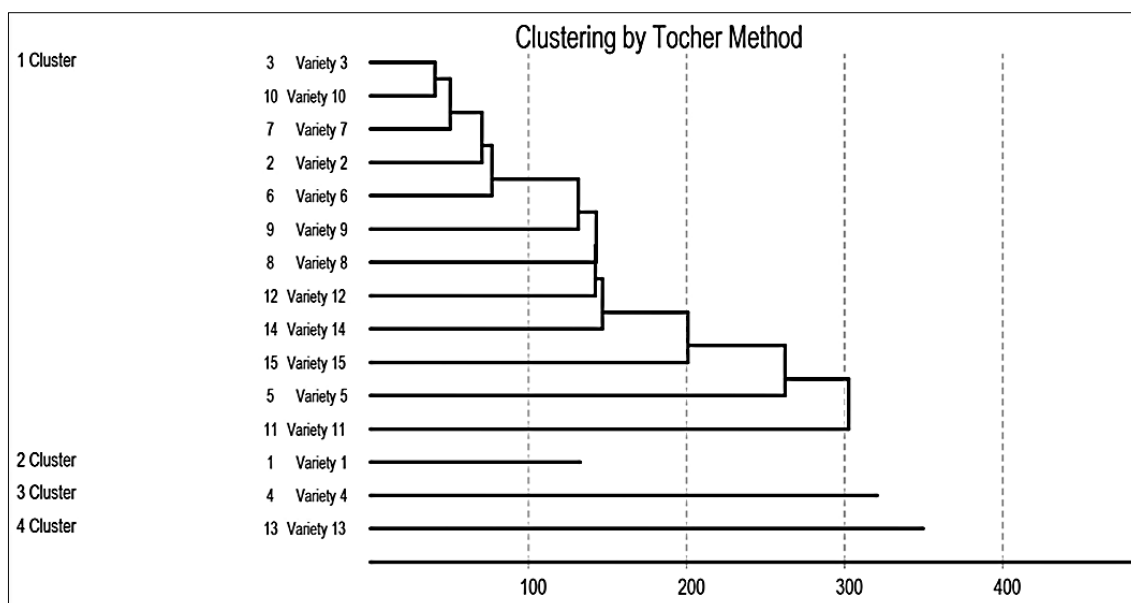| Cluster	No. of Genotypes	Genotypes
I	12	IR-127293-69-1-1, IR-127290-B-B-293-1, IR-127364-46-2-1, IR-125026-108-1-1, IR-127361-196-2-1-B, IR-127335-106-2-2-1-1, IR-127367-107-1-B-B, DRR DHAN-44, IR-154, Rajendra Neelam (C), IR-127285-124 2-1, Sahabhagi Dhan
II	1	IR-127339-11-1-1-1-1
III	1	IR-127299-32-2-2
IV	1	IR-64

Fig 1: Clustering pattern of 15 rice genotypes on the basis of D^2 statistics by Tocher method

Genotype 1-IR-127339-11-1-1-1-1 Genotype 6-IR-127361-196-2-1-B Genotype 11-Sahabhagi Dhan
Genotype 2-IR-125026-108-1-1 Genotype 7-IR-127364-46-2-1 Genotype 12-DRR DHAN-44
Genotype 3-IR-127293-69-1-1 Genotype 8-IR-127367-107-1-B-B Genotype 13-IR-64
Genotype 4-IR-127299-32-2-2 Genotype 9-IR-127335-106-2-2-1-1 Genotype 14-IR-154
Genotype 5-IR-127285-124-2-1 Genotype 10-IR-127290-B-B-293-1 Genotype 15-Rajendra Neelam

Table 3: Intra & inter-cluster distance (Tocher) amongst genotypes of Rice:

Clusters	I Cluster	II Cluster	III Cluster	IV Cluster
I Cluster	206.52	(365.87)	(819.96)	(700.36)
II Cluster		0	(607.65)	(654.05)
III Cluster			0	(2197.2)
IV Cluster				0

Intra-Cluster (D^2): in bold
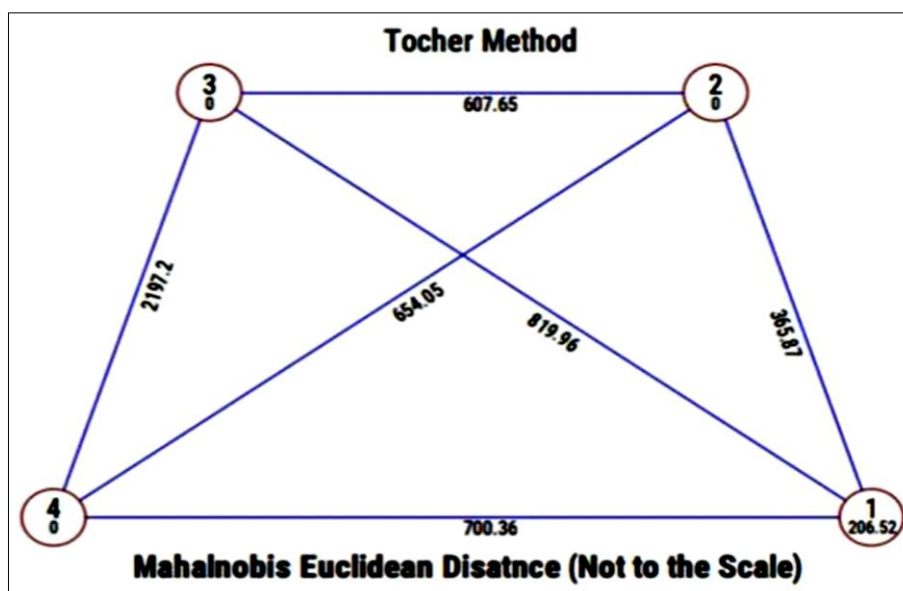Inter-Cluster (D) : in parentheses

Fig 2: Intra & inter cluster distance (D^2) between four clusters in rice by Tocher Methods

Table 4: Mean of cluster for 11 morphological characters among the genotypes in rice.

Sl. No.	Character	I Cluster	II Cluster	III Cluster	IV Cluster	Over all mean
1	Days to 50% flowering	81.25	84.67	92.00	72.67	82.64
2	Days to maturity	119.92	120.33	124.33	118.00	120.64
3	Plant height (cm)	113.93	97.48	99.27	93.75	101.10
4	Panicle length (cm)	23.44	25.20	21.23	20.28	22.53
5	Number of panicles plant^{-1}	7.50	9.53	7.83	7.80	8.16
6	Number of tillers plant^{-1}	12.17	15.83	10.57	13.99	13.14
7	1000 grain weight (g)	30.03	22.53	22.53	30.50	26.39
8	Biological yield plant^{-1} (g)	33.57	31.02	32.87	33.77	32.80
9	Number of grains panicle^{-1}	102.28	120.43	153.57	74.30	122.64
10	Harvest index (%)	59.09	60.57	54.04	57.19	57.72
11	Grain yield plant^{-1} (g)	19.40	19.31	18.11	19.21	19.00

Table 5: Independent character contribution towards total divergence in 11 characters of rice.

Sr. No.	Characters	Times ranked 1st	Percent of Contribution
1	Days to 50% flowering	10	9.52%
2	Days to maturity	0	0.00%
3	Plant height (cm)	6	5.71%
4	Panicle length (cm)	2	1.90%
5	Number of panicles plant^{-1}	0	0.00%
6	Number of tillers plant^{-1}	4	3.81%
7	1000 grain weight (g)	13	12.38%
8	Biological yield plant^{-1} (g)	0	0.00%
9	Number of grains panicle^{-1}	41	39.05%
10	Harvest index (%)	4	3.81%
11	Grain yield plant^{-1} (g)	25	23.81%

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