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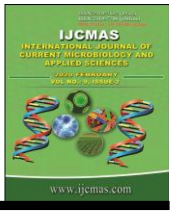

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Study of Genetic Divergence in Lowland Rice Genotypes of Bihar

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ABSTRACT

The present experimental work was carried out at Rice Breeding Section, Pusa, Samastipur, with twenty-two lowland genotypes which were shown in R.B.D. style and were analysed for genetic divergence with the help of Mahalanobis's D^2 statistics.Twenty-two genotypes of rice were grouped into six clusters using Tocher's method. The cluster I consists of maximum number of genotypes forming the largest cluster followed by cluster VI having three genotypes. The intra cluster distance ranged from 0.00 to 84.45. The inter cluster distance ranged from 52. to 282.49.Thehighest intra cluster distance was observed in cluster VI (84.85) followed by Cluster I (67.75). Maximum inter cluster distance was observed between cluster III and Cluster IV followed by cluster III and cluster IV. Per cent contribution of 15 characters and towards total genetic divergence was found maximum for 1000 grain weight (35.5 per cent) followed by days to flowering (22.08 per cent), grain length (17.32 per cent). It was observed that 1000 grain weight ranked 1st maximum times (82) followed by days to flowering (51), grain length (40), plant height (36).The genotype in cluster III and cluster IV due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized in future for heterosis breeding programme for getting high yielding recombinants.

Keywords

Genetic divergence,
Lowland rice,
Genotypes,
Tocher's method

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Introduction

Rice (*Oryza sativa* L.) may be originated at least 130 million years ago and dispersed all around the world with separation of different continent from the single land mass that existed. It is one of the most important food crops of the world particularly Asian countries where it is the staple food. The estimated world rice production for the year 2019-20 is 496.67 million metric tons (USDA, 2020). It is produced in wide range of locations and under different climatic conditions. As it grows in variable climatic condition and having such an extended geographical distribution through out the world it is the crop with maximum germplasm diversity. As the consequence of great geographical distribution and extending its boundaries to various climatic conditions it faces several form abiotic stresses occurring in those environment and flooding being of those. Therefore, study of the diversity of rice in low lying flooded area is of prime importance for the development of new varieties, to sustain the rice production and improve the socioeconomic status of people living in these areas. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004) and it also helps in the development of superior recombinants (Manonmani and Khan, 2003b). Genetic diversity analysis is done with help of D^2 statistics developed by P. C. Mahalanobis. Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence (Iftekharuddaulae *et al.*, 2002).

Materials and Methods

The present research work was conducted at Rice Breeding Section, Pusa Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during kharif 2019. Total of twenty-two lowland rice(table 1) were investigated, which were sown in Randomized Block Design fashion at standard spacing of 15 x 20 cm in three replications. All the recommended packages of practices were followed during the growth period. Observations for fifteen characters were recorded viz., grain length (mm), grain width (mm), kernel length (mm), days to 50% flowering, plant height (cm), root volume (mm^3), panicle length of main axis` (cm), leaf length (cm), leaf width (cm), no. of panicle, days to maturity, stem thickness (mm), 1000 grain weight, kernel width(mm), grain yield per plant (g). Various parameters of genetic diversity like clustering pattern of various genotypes, mean intra and inter-cluster distances among the different clusters, cluster mean, contribution of individual character to divergence and dendrogram of the clustering pattern were analysed using the data recorded for the fifteen characters.

List of genotypes

1	**SANTOSH**	**9**	**VAIDEHI**	**17**	**BRASALI**
2	KANAK	10	JANAKI	18	MEGHNAD
3	RADHA	11	BAROGAR	19	SILHAT
4	PANKAJ	12	MADHUKAR	20	SHYAMALA
5	SATYAM	13	SINGHARA	21	BPT-5204-SUB 1
6	RAJSHREE	14	UJALA DHUSARISA	22	KISHORI
7	SWARNA	15	SAGAR SAMBA		
8	SUDHA	16	JAGANNATH BALLAVA		

Results and Discussion

Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization program. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 22 rice genotypes and to identify the diverse genotypes for future utilization breeding program.

In the present investigation the genotypes were grouped into 6 clusters (table 1, fig. 1) on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance. Cluster I comprised of maximum number of genotypes (15) including check Swarna followed by Cluster VI which included 3 genotypes and Cluster II, III, IV and V comprised of 1 genotype each. Clustering based on the D^2 distances was done by Shivani *et al.,* (2018), Kumari *et al.,* (2018) and Guru *et al.,* (2017). The inter cluster distance (Table 2) ranged from 52.38 to 282.49. The highest intra cluster distance (Table 2) was observed in cluster VI (84.85) followed by Cluster I (67.75). Cluster I, III, IV and V showed intra cluster distance of 0.00. Maximum inter cluster distance was observed between cluster III and Cluster IV followed by cluster III and cluster IV. Minimum inter cluster distance was observed between cluster II and cluster IV followed by cluster II and cluster V, indicating that the genotypes in the clusters were closely related. Similar divergence estimation based on D^2 distances was done by Shivani *et al.,* (2018) and Kumari *et al.,* (2018).

Table.1 Clustering pattern of twenty-two genotypes of rice on the basis of D^2 statistics

Cluster No.	**No. of genotypes within cluster**	**Genotypes in cluster**
I	15	SUDHA, VAIDEHI, SILHAT, MADHUKAR, UJALA DHUSARIA, JANAKI, MEGHNAD, RADHA, SANTOSH, KANAK, SATYAM, SWARNA, SAGAR SAMBA, RAJSHREE, BAROGAR,
II	1	PANKAJ
III	1	SHYAMALA
IV	1	BPT-5204-SUB-1
V	1	KISHORI
VI	3	SINGHARA, JAGANNATH BALLAVA, BRASALI

Table.2 Mean intra and inter cluster distance (D^2) among six cluster in rice

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	67.75	99.46	135.34	187.11	123.42	189.82
Cluster II		0.00	196.03	52.38	52.73	138.25
Cluster III			0.00	282.49	216.60	102.41
Cluster IV				0.00	97.38	141.39
Cluster V					0.00	166.64
Cluster VI						84.85

Table.3 Cluster mean values of 6 clusters of different quantitative characters in 22 rice cultivars

	GL	GW	KL	DFL	PLH	RV	PLMA	LW	NP	DTM	ST	TW	KW	LL	YLD
Cluster I	8.66	2.66	6.47	113.53	144.35	17359.51	23.72	1.23	16.07	144.56	4.21	23.55	2.02	57.97	25.80
Cluster II	7.67	2.83	5.93	119.33	104.87	21833.97	24.57	1.57	14.00	142.00	3.73	16.65	2.00	46.43	29.74
Cluster III	8.77	2.30	6.60	149.33	185.37	13667.28	23.93	1.30	18.17	181.67	4.27	26.55	1.93	65.83	20.53
Cluster IV	7.17	1.70	5.07	125.00	102.07	20137.33	24.00	1.20	16.22	142.33	3.97	9.47	1.67	40.70	23.80
Cluster V	9.07	2.83	6.73	136.00	126.30	20000.46	25.67	1.27	17.53	149.33	3.93	13.29	2.08	50.43	33.17
Cluster VI	7.69	2.34	5.67	148.56	179.41	16111.73	24.12	1.19	14.77	170.67	4.02	17.06	1.91	61.89	29.57

G.L.= GRAIN LENGTH, GW= GRAIN WIDTH, KL= KERNEL LENGTH, DFL= DAYS TO 50% FLOWERING, RV= ROOT VOLUME, PLMA= PANICLE LENGTH OF MAIN AXIS, LW= LEAF WIDTH, NP= NUMBER OF PANICLES, DTM= DAYS TO MATURITY, ST= STEM THICKNESS, TW=1000 GRAIN WEIGHT, KW =KERNEL WIDTH, LL= LEAF LENGTH, YLD= GRAIN YIELD PER PLANT

Table.4 Ranking and contribution of character towards divergence

S.NO.	SOURCE	TIMES RANKED 1^{ST}	CONTRIBUTION (%)
1	GRAIN LENGTH (mm)	40	17.32
2	GRAIN WIDTH (mm)	0	0.00
3	KERNEL LENGTH (mm)	1	0.43
4	DAYS TO 50% FLOWERING	51	22.08
5	PLANT HIEGHT (cm)	36	15.58
6	ROOT VOLUME (mm^3)	0	0.00
7	PANICLE LENGTH OF MAIN AXIS (cm)	0	0.00
8	LEAF WIDTH (cm)	0	0.00
9	NO. OF PANICLE	0	0.00
10	DAYS TO MATURITY	0	0.00
11	STEM THICKNESS (mm)	6	2.60
12	1000 GRAIN WEIGHT (g)	82	35.50
13	KERNEL WIDTH (mm)	1	0.43
14	LEAF LENGTH (cm)	5	2.16
15	GRAIN YIELD PER PLANT (g)	9	3.92

Fig.1 Clustering pattern of 22 rice cultivars on the basis of D^2 statistics by Tocher's method

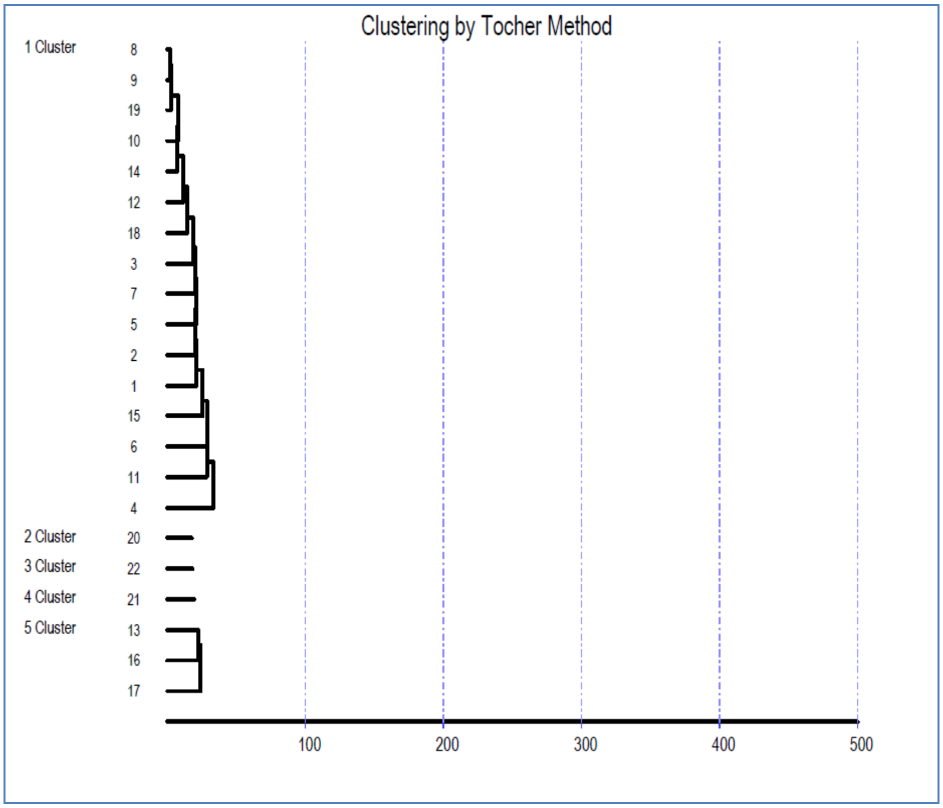
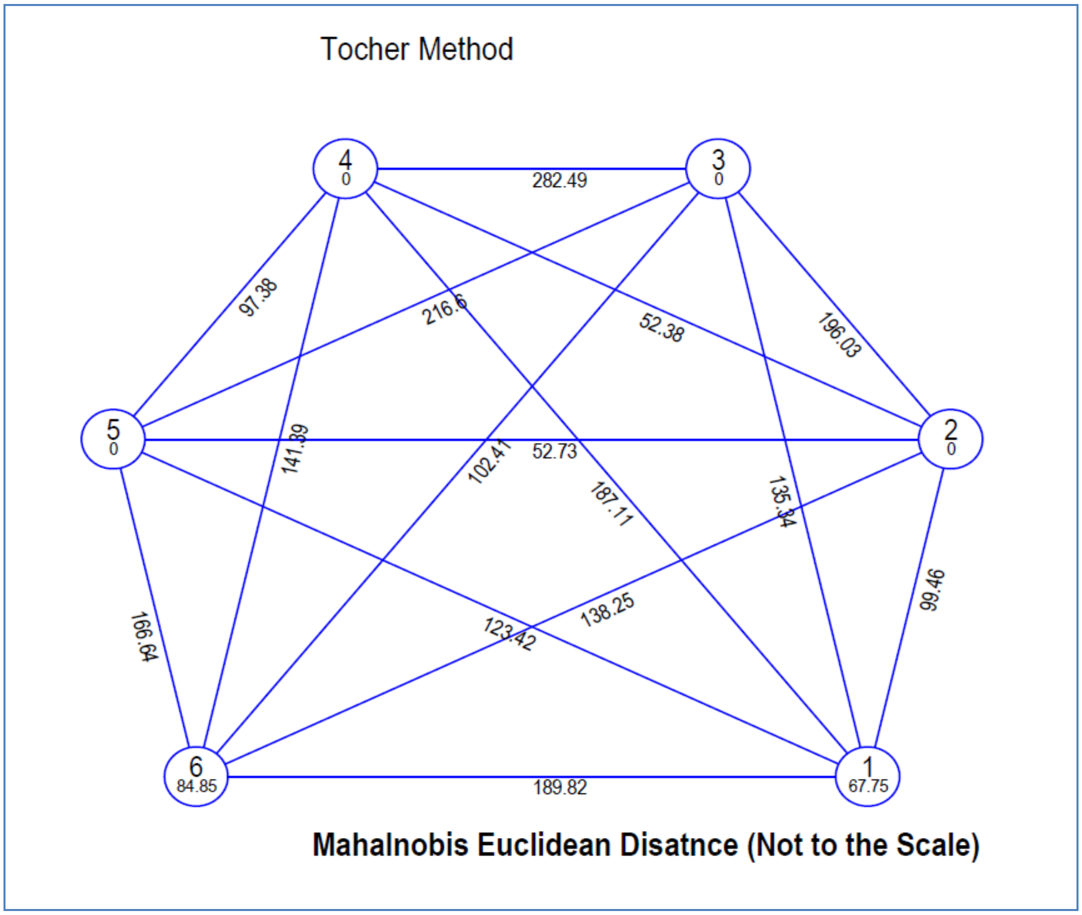


Fig.2 Intra and Inter cluster distances on the basis of D^2 statistics



Cluster mean analysis

Cluster means (Table 3) with respect to 15 characters and 22 genotypes along with check was evaluated with help D^2 values. It was evident that cluster mean for grain length was highest in cluster V and lowest in cluster IV while cluster mean for grain width was recorded maximum for cluster II and minimum for cluster. Kernel length recoded highest cluster mean value for cluster V and lowest cluster mean value for cluster V while cluster mean for days to 50 per cent flowering was recorded highest for cluster III and lowest for cluster I. Cluster mean performance for plant height was observed maximum for cluster III and minimum for cluster IV while maximum value for cluster mean for root volume was recorded for cluster II and minimum for cluster III. Cluster mean for panicle length of main axis was recorded highest for cluster V and minimum for cluster I whereas cluster mean values for leaf width was observed maximum for cluster II and cluster VI. Cluster mean values for number of panicles per plant was recorded highest for cluster and lowest for cluster II while cluster mean for days to maturity was recorded highest for cluster III and recorded minimum for cluster II. Observation of cluster mean of stem thickness showed that it was highest for cluster I and lowest for cluster II whereas cluster mean for 1000 grain weight was recorded highest for cluster III and recorded minimum cluster IV. Cluster mean for kernel width was observed maximum for cluster I and lowest for cluster IV while cluster mean for leaf length was recorded highest for cluster III and lowest for cluster. Cluster mean for yield per plant was observed highest for cluster V and minimum for cluster III. Cluster mean analysis was also done by Shivani *et al.*, (2018), Kumari *et al.*, (2018) and Guru *et al.*, (2017) for selection of genotypes.

Percent contribution of character towards total genetic diversity

Per cent contribution (table 4) of 15 characters towards total genetic divergence was found maximum for 1000 grain weight followed by days to 50 per cent flowering, grain length, plant height, yield per plant, stem thickness, leaf length, kernel length and kernel width. These findings were in accordance with the finding of Shivani *et al.*, (2018), Kumari *et al.*, (2018) and Guru *et al.*, (2017).Character contribution to total divergence was based on number of times character ranked first. It has been presented in the table 4. From the table it was observed that 1000 grain weight ranked 1st maximum times followed by days to flowering and grain length (40), plant height (36),

In conclusion, twenty-two genotypes of rice were grouped into six clusters using Tocher's method. The cluster I consists of maximum number of genotypes forming the largest cluster followed by cluster VI having three genotypes and rest of the clusters i.e. II, III, IV, V were found to be mono-genotypic. The genotype in cluster III and cluster IV due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized in future for heterosis breeding programme for getting high yielding recombinants.

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