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GENETICS AND PLANT BREEDING

Genetic Divergence Analysis for Quantitative Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was conducted with 64 rice germplasm to investigate the nature and magnitude of genetic divergence during *Rabi* 2016. The analysis of variance showed significant differences for all the characters studied among the genotypes. Based on the analysis, the genotypes were grouped into 3 clusters. Maximum number of 58, 4 and 2 genotypes was grouped under cluster II, III and I respectively. Maximum inter cluster distance was observed between cluster II and III (45.279) followed by cluster II and I (37.703) indicates wider the genetic diversity between genotypes. Cluster I showed highest mean for seed yield per plant (26.60 g) followed by cluster III. Milling percentage, panicle length and panicle weight (0.05%), number of productive tillers per plant and number of grains per panicle were failed to contribute significantly towards genetic diversity. Plant height (39.51%), kernel breadth after cooking (14.48%), kernel length after cooking (7.59%) were found to be the most contributing traits towards genetic diversity. Hence these traits could be focused for selection while improving grain quality and yield.

Highlights

- Maximum inter cluster distance was observed between cluster II and III (45.279)
- Cluster I showed highest mean for seed yield per plant (26.60 g)
- Plant height (39.51%), kernel breadth after cooking (14.48%), kernel length after cooking (7.59%) were found to be the most contributing traits towards genetic diversity

Keywords: Clusters, Genetic Diversity, Milling Quality and Quality traits

Rice (*Oryza sativa* L.) is one of the most important food cropof the world for more than half of the global populations. It is primary food source for more than one third of world's population. India is the second largest producer and consumer of rice next to China. As the population is increasing alarmingly, in order to meet the indispensable demand, improvement through genetic manipulation is the only way. The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent (Daniel 2000). Even though self-pollinated crops are highly homozygous there is every possibility of genetic variation among the parents collected from different eco-geographicalregions. In the present study, an attempt was made to assess the genetic divergence using Mahalanobis D^2 statistics and different clustering procedures, based on yield and quality characters and assessing the relative contribution of different components to total divergence. In order to meet the food requirement of growing population, development of high yielding varieties are essential. The success of any breeding programme depends on the selection of parents for hybridization. The germplasm provides immense scope for wide variability. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding

programme (Vivekananda and Subramaniam 1993). Keeping this in view, the presentstudy was focused to assess the genetic diversity among 64 ricegermplasm using Mahalanobis D^2 statistics.

MATERIALS AND METHODS

The experimental material for the present study comprised of 64 rice germplasm laid in square lattice design with three replications at the Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during *Rabi* 2016. The genotypes were raised in plot of 5rows with each row of 3 meters length. Row to row and plant to plant spacing was maintained at 10 x 15 cm. All the recommended agronomic practices were followed. Five plants were selected at random for each genotype in each replication to record the data on all yield and yield attributing characters *viz*., days to 50% flowering, plant height, tillers per plant, number of productive tillers per plant, panicle length, panicle weight, number of grains per panicle, 1000 grain weight and single yield per plant and 15 quality traits like hulling percentage, milling percentage, head rice recovery (%), kernel length(mm), kernel breadth(mm), L/B ratio, kernel length after cooking(mm), linear elongation ratio, kernel breadth after cooking(mm), breadth wise expansion ratio, volume expansion ratio, water uptake, amylose content (%), gelatinization temperature and gel consistency(mm).The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochersmethod suggested by Rao, 1952.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the characters studied among the genotypes (Table 1). This suggested that the genotypes were genetically diverse and considerable amount of variability existed among them. Thus,indicated the better scope for selection of different parents for further hybridization programme to get the high heteroticcombinations in terms of various quantitative characters.Based on D^2 values, all the genotypes were grouped into three clusters (Table 1). Maximum number of genotypes (58genotypes) was grouped in cluster II. It was followed by cluster III (4 genotypes), and cluster I (2 genotypes).The intra and inter cluster distance are presented in (Table 2.). The maximum inter cluster distance was observed between cluster IIand cluster III (45.279) followed by cluster I and cluster II(37.703) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would desirable.

Table 1: Distribution of genotypes to different clusters based on Tocher's method

Cluster Number	Total Number of Genotypes	Genotypes	Origin
I	2	KR 15016	Karaikal
		KR 1510	Karaikal
II	58	KKLR 1	Karaikal
		Vallan samba	Tamil Nadu
		Garudan samba	Tamil Nadu
		ADT 50	Tamil Nadu
		AD09067	Tamil Nadu
		CR 1009 sub1	Tamil Nadu
		CR1009	Tamil Nadu
		ADT 45	Tamil Nadu
		PY-3	Puducherry
		PY-4	Puducherry
		PY-6	Puducherry
		TKM 10	Tamil Nadu
		Gopalbhog	West Bengal
		Athurkichadi	Tamil Nadu
		Bhavani	Tamil Nadu
		Mapillai samba	Tamil Nadu
		Swarna	Andhra Pradesh
		Jaya	Tamil Nadu
		IR 20	Phillippines
		Kuzhiadichan	Tamil Nadu
		ADT 38	Tamil Nadu
		Karupukavuni	Tamil Nadu
		ADT 49	Tamil Nadu
		CO 45	Tamil Nadu
		Kaiviral samba	Tamil Nadu
		CO 48	Tamil Nadu
		CO 49	Tamil Nadu
		CO 50	Tamil Nadu
		TRY 1	Tamil Nadu
		ADT 46	Tamil Nadu
		Samba Mashuri	Andhra Pradesh

		I W Ponni	Tamil Nadu
		KR 15092	Karaikal
		Kichadi Samba	Tamil Nadu
		CO 46	Tamil Nadu
		ADT 39	Tamil Nadu
		IR 36	Phillippines
		Rasi	Tamil Nadu
		KR15077	Karaikal
		Kullakar	Tamil Nadu
		CO 45	Tamil Nadu
		CO 47	Tamil Nadu
		ASD 20	Tamil Nadu
		ASD 19	Tamil Nadu
		ASD 18	Tamil Nadu
		ASD 17	Tamil Nadu
		ASD16	Tamil Nadu
		MTU 1010	Andhra Pradesh
		IR 64	Pillippines
		IR 50	Pillippines
		TKM 11	Tamil Nadu
		ADT 36	Tamil Nadu
		ADT 47	Tamil Nadu
		ADT 43	Tamil Nadu
		CO 41	Tamil Nadu
		MDU 5	Tamil Nadu
		CO 39	Tamil Nadu
		ADT 48	Tamil Nadu
III	4	RNR 15048	Telangana
		ADT 45	Tamil Nadu
		KR 15066	Karaikal
		KR 15007	Karaikal

The minimum inter cluster distance was found between cluster I and cluster III (30.66) indicatingthat closeness and hence, hybridization among the varietieswill not give effective results. The maximum intra cluster distance was observed for cluster III (45.37) followed by cluster II (43.21), and cluster I (6.497) indicating the considerable variation present within the clusters. The diversity in the present material was also supported by the appreciable amount of variation among cluster means for different characters (Table 3), which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster I showed highest mean for seed yield per plant (26.60g) followed by cluster III (23.58g).

Table 2: Average intra and inter cluster D^2 values

Cluster No	I	II	III
I	42.213	1421.52	940.043
	(6.497)	(37.703)	(30.66)
II		1867.241	2050.148
		(43.212)	(45.279)
III			2057.998
			(45.365)

Intra cluster divergence: Diagonal values, Inter cluster divergence: Off-diagonal values, D values : Values in parameters

None of clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Most of the minimum and maximum mean values were distributed in relatively different clusters. Cluster I exhibited maximum cluster mean value for seed yield per plant as well as hulling percentage, head rice recovery, volume expansion ratio and amylose content; cluster II for days to flowering, plant height, grains per panicle, panicle length, panicle weight, 1000 grain weight, milling percentage, kernel length, kernel breadth, kernel breadth after cooking and gelatinization temperature and cluster III for number of tillers per plant, number of productive tillers per plant, L/B ratio, kernel length after cooking, linear elongation ratio, breadth wise expansion ratio, water uptake and gel consistency. Thus, based on cluster means, the various these clusters have been identified for selecting parents for future hybridization programme.

The maximum inter cluster distance exhibited by cluster II-III also identified for selecting parents for incorporating the high quality characters with yield attributing traits; whereas, cluster I also identified for selecting parents for incorporating the single plant yield, head rice recovery, and hulling percentage. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety and also suggested to create variability for developing the varieties involving a large number of different lines instead of closely related ones. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values

were distributed in relatively distant clusters. The contribution of each trait to total divergence is presented in table 4. Among the traits studied, plant height had maximum contribution towards the genetic divergence (39.51%) (Rajesh *et al.* 2010; Iftekharuddaula *et al.* 2010; Devi 2016) followed by kernel breadth after cooking (14.48%), kernel length after cooking (7.59%), 1000 grain weight (6.94%), water uptake (5.51%) and gelatinization temperature (4.37%) whereas number of productive tillersper plant and grains per panicle had no contribution towards thegenetic divergence.

Table 3: Cluster mean for productive and quality traits

Sl. No.	Character	Clusters		
		I	II	III
1	Days to 50 per cent flowering	85.83	**99.12**	83.00
2	Plant height	86.53	**103.46**	92.41
3	Number of tillers per plant	17.55	18.29	**19.66**
4	Number of productive tillers per plant	17.55	18.25	**19.66**
5	Grains per panicle	142.28	**143.32**	140.67
6	Panicle length	21.51	**22.55**	21.18
7	Panicle weight	2.12	**2.66**	2.32
8	1000 grain weight	2.18	**2.21**	2.02
9	Hulling percentage	79.33	73.56	76.79
10	Milling percentage	62.33	**64.34**	63.42
11	Head rice recovery	**60.20**	59.63	60.15
12	Kernel length	5.99	**6.18**	6.03
13	Kernel breadth	2.00	**2.33**	1.96
14	L/B ratio	3.01	2.69	**3.12**
15	Kernel length after cooking	7.92	8.73	**8.75**
16	Linear elongation ratio	1.33	1.42	**1.46**
17	Kernel breadth after cooking	2.37	**2.97**	2.74
18	Breadth wise expansion ratio	1.37	1.29	**1.40**
19	Volume expansion ratio	**3.25**	3.23	2.96
20	Water uptake	197.50	203.10	**220**
21	Amylose content	**28.00**	25.80	23.71
22	Gelatinization temperature	3.50	**4.09**	2.83
23	Gel consistency	72.76	73.32	**84.05**
24	Single plant yield	**26.60**	22.81	23.58

Note - (Bold faced) **-** *Indicates maximum cluster mean values;* —— *Indicates minimum cluster mean values.*

Table 4: Contribution of characters towards genetic divergence

Sl. No.	Character	Times ranked first	Contribution (per cent)
1	Days to 50 per cent flowering	14	0.91
2	Plant height	815	39.51
3	Number of tillers per plant	6	0.30
4	Number of productive tillers per plant	0	0.00
5	Grains per panicle	0	0.00
6	Panicle length	1	0.05
7	Panicle weight	1	0.05
8	1000 grain weight	140	6.94
9	Hulling percentage	3	0.15
10	Milling percentage	1	0.05
11	Head rice recovery	5	0.25
12	Kernel length	5	0.25
13	Kernel breadth	3	0.15
14	L/B ratio	24	1.19
15	Kernel length after cooking	153	7.59
16	Linear elongation ratio	8	0.04
17	Kernel breadth after cooking	292	14.48
18	Breadth wise expansion ratio	43	2.13
19	Volume expansion ratio	30	1.49
20	Water uptake	111	5.51
21	Amylose content	18	0.89
22	Gelatinization temperature	88	4.27
23	Gel consistency	46	0.28
24	Single plant yield	224	11.11

CONCLUSION

Results of the present study indicated maximum inter cluster distance exhibited by cluster II– III identified for selecting parents for incorporating high quality characters with yield attributing traits; whereas, cluster I also identified for selecting parents for incorporating the single plant yield, head rice recovery, and hulling percentage. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield

potential. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety and also suggested to create variability for developing the varieties involving a large number of different lines instead of closely related ones. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety.

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