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Studies on genetic divergence among rice (*Oryza sativa* L.) genotypes

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Abstract

An experiment was conducted with 50 genotypes of rice to estimate the nature and magnitude of genetic divergence, using Mahalanobis' D^2 statistic. Observations were recorded on ten agronomic traits *viz.*, plant height at maturity, number of productive tillers per plant, panicle length, seeds per panicle, seed length, seed breadth, thousand seed weight, flag leaf length, flag leaf breadth and seed yield per plant. The genotypes were grouped into as many as six clusters. Cluster III encomposed thirty three genotypes followed by cluster I with eight genotypes. Cluster V included three genotypes. Clusters II, IV and VI each comprised of two genotypes. The intra-cluster distance was maximum with cluster V. The inter-cluster distance was maximum between the clusters II and V. Highest mean value for plant height at maturity, number of productive tillers per Plant, panicle length, seeds per panicle, flag leaf length, flag leaf breadth and seed yield per plant was recorded with the Cluster V. Seed yield per plant followed by seeds per panicle and thousand seed weight contributed maximum towards the total genetic divergence. Hybridization among the genotypes grouped in the clusters II and V, may produce high yielding heterotic hybrids and/or wider variability in segregating generations.

Keywords: cluster analysis, quantitative, quality, rice

Introduction

Rice (*Oryza sativa* L. 2n=24) is one of the major food crops of the world, covering 11 per cent of the arable land in the world. It is a major source of the food energy for more than half of the human population. The world rice production was 497.7 million tonnes from 162.06 million hectares of area with a productivity of 3.07 t ha^{-1} (http://www.statista.com, 2019) [5]. More than 75% of the world's rice supply comes from 80 million hectares of irrigated land in Asia (http://ricepedia.org, 2019) [4]. Rice provides 49 per cent of the calories and 39 per cent of the proteins in Asian diet (FAO STAT, 2011) [2]. About 92% of the Worlds rice is produced and consumed in Asia. In India, rice is cultivated in an area of about 43.8 million hectares with a production of 118.87 million tones, and productivity level of 2.71 t ha^{-1} (http://www.statista.com, 2019) [5]. Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D^2 statistic developed by Mahalanobis (1936) [8]. 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 among 50 rice genotypes and to identify and suggest the diverse genotypes for future crop improvement programme through plant breeding.

Materials and Methods

Fifty diverse genotypes of rice from different eco-geographical origin were evaluated in Randomized Block Design with three replications at Plant Breeding Farm (11°24′ N latitude and 79°44′E longitude ±5.79 M MSL), Annamalai University, Annamalainagar, Tamilnadu, during December 2015. The seedlings were transplanted to the main field at the rate of one seedling per hill, after 25 days, with a spacing of 20 cm × 15 cm in two rows plots of 3 m length. Recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomly selected competing plants per replication per entry. Ten agronomic traits *viz.*, plant height at maturity (cm), number of productive tillers per plant, panicle length (cm), seeds per panicle, seed length (mm), seed breadth (mm), thousand seed weight (g), flag leaf length (cm), flag leaf breadth (cm) and seed yield per plant (g) were recorded. Mahalanobis' (1936) [8] D^2 statistic was used to estimate the genetic divergence among the 50 genotypes. Grouping of genotypes into clusters was carried out following Tochers Method (Rao, 1952) [12].

Results and discussion

The analysis of variance revealed significant difference among the fifty genotypes for al the ten characters indicating the existence of high genetic variability among the genotypes for all the traits (Table 1). The fifty genotypes were grouped into as many as six clusters by employing Tocher's method (Rao, 1952) [12] (Table 2). Out of the six clusters, cluster III was the largest, comprising of thirty three genotypes, followed by cluster I with eight genotypes. The cluster V consisted of three genotypes and the clusters II, IV and VI each comprised of two genotypes. From the clustering pattern, it was clear that the distribution of genotypes from different geographical regions in to these clusters was apparently random. Genotypes of similar origin were grouped into different clusters and *vice versa*, thereby indicating no relationship between geographical and genetic diversity. The tendency of genotypes to occur in clusters cutting across eco-geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. It was recorded that the genotypes collected from different regions were independent of their genetic origin. Genetic diversity and geographic diversity was mainly due to the free exchange of genotypes from one region to another and also may be due to the character constellation that practiced in several regions resulting in segregation of genotypes irrespective of their geographic region. Similar findings were earlier reported by Sabesan and Saravanan (2008) [14], Satheeshkumar and Saravanan (2012[15]), Bhati *et al.* (2015) [1], Radha *et al.* (2018) [11] and Ponsiva *et al.* (2019) [10]. The average intra and inter-cluster distance analysis indicated that the maximum intra-cluster distance was observed with cluster V (13.90) followed by cluster III (12.44), cluster VI (12.17) and cluster I (11.78) (Table 3). This suggested that the genotypes in cluster V were relatively more diverse among themselves. However, in all the cases, the inter-cluster distances were greater than the intra-cluster distances implying the presence of greater degree of genetic diversity among the genotypes of two clusters than the genotypes present within the cluster. From the inter-cluster distance for six clusters (Table 2), it could be seen that the highest divergence was observed between the clusters II and V (19.02) followed by cluster IV and V (16.34) and cluster I and V (16.21), indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between these genotypes belonging to these clusters might result in high heterosis, which could be exploited in crop improvement programme. This result is supported by earlier findings in rice Sabesan *et al.* (2009) [13], Padmaja *et al.* (2010) [9], Garg *et al.* (2011) [3], Bhati *et al.* (2015) [1], Kamlesh kumar *et al.* (2015) [6], Radha *et al.* (2018) [11] and Ponsiva *et al.* (2019) [10]. The cluster mean values showed a wide range of variation for all the traits of interest (Table 4). Cluster V was characterized with high mean values for plant height at maturity, number of productive tillers per plant, panicle length, seeds per panicle, flag leaf length, flag leaf breadth and seed yield per plant. Cluster II exhibited a low mean for plant height at maturity, panicle length and seeds per panicle. Cluster IV had high mean for seed length and thousand seed weight. Cluster VI had high mean for seed breadth. Seed yield per plant (46.78 per cent) followed by seeds per panicle (19.00 per cent) and thousand seed weight (11.27 per cent) contributed maximum for the discrimination among the genotypes tested (Table 5). Similar finding were made by Sabesan and Saravanan (2008) [14], Satheesh kumar and Saravanan (2012) [15], Kumari Priyanka *et al.* (2015) [7] and Ponsiva *et al.* (2019) [10]. Hence, these traits could well be declared as choice of traits for crop improvement through breeding.

Table 1: Analysis of variance for 10 agronomical traits in 50 rice genotypes of rice

Source	Df	MSS									
		PHT	**NPT**	**PL**	**SPP**	**SL**	**SB**	**TSW**	**FLL**	**FLB**	**SYD**
Replication	2	0.26	27.69	1.98	203.58	0.21	0.08	15.61	0.02	2.54	0.74
Genotype	49	839.97**	58.90**	13.99**	4488.96**	1.52**	0.28**	46.83**	101.19**	0.10**	154.00**
Error	98	23.84	14.79	2.79	67.86	0.12	0.03	8.02	0.01	3.39	3.97

**Significant at 1 per cent level

Table 2: Composition of D^2 clusters for 50 rice genotypes

Cluster	Number of genotypes	Name of genotypes
I	8	G1, G2, G3, G4, G5, G6, G26, G30
II	2	G17, G28
III	33	G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G18, G19, G20, G21, G22, G23, G24, G25, G27, G29, G31, G32, G33, G34, G35, G36, G37, G38, G39, G40, G41, G42, G43
IV	2	G45, G47
V	3	G44, G49, G50
VI	2	G46, G48

Table 3: Average intra and inter (D^2) cluster values for 50 rice genotypes

Cluster	I	II	III	IV	V	VI
I	138.81 (11.78)	130.45 (11.42)	169.15 (13.01)	193.26 (13.90)	262.67 (16.21)	252.66 (15.90)
II		7.77 (2.79)	163.70 (12.79)	77.88 (8.83)	361.90 (19.02)	217.95 (14.76)
III			154.67 (12.44)	151.84 (12.32)	222.21 (14.91)	212.67 (14.58)
IV				29.63 (5.44)	267.12 (16.34)	111.19 (10.55)
V					193.33 (13.90)	213.17 (14.60)
VI						148.00 (12.17)

Table 4: Cluster means of 50 rice genotypes for various traits

Cluster	PHT (cm)	NPT	PL (cm)	SPP	SL (mm)	SB (mm)	TSW (g)	FLL (cm)	FLB (cm)	SYD (g)
I	69.83	13.67	19.18	77.75	7.55	2.51	18.03	17.52	0.94	9.09
II	66.50	8.33	17.42	36.83	8.01	2.72	22.25	15.23	0.72	10.12
III	90.95	13.37	21.02	81.80	7.93	2.58	19.52	23.02	0.81	11.45
IV	96.67	9.67	20.95	52.50	8.39	3.40	23.93	21.07	0.61	10.36
V	107.33	16.90	21.37	127.89	7.79	2.81	22.27	27.76	1.02	20.44
VI	107.30	7.33	17.67	68.33	7.43	3.55	22.04	27.62	0.76	17.66
General mean	89.77	11.54	19.60	74.18	7.85	2.93	21.34	22.04	0.81	13.18

PHT: Plant height at maturity
NPT: Number of productive tillers per plant
PL: Panicle length
SPP: Seeds per panicle
SL: Seed length
SB: Seed breadth
TSW: Thousand seed weight
FLL: Flag leaf length
FLB: Flag leaf breadth
SYD: Seed yield per plant

Table 5: Contribution of different traits to genetic divergence

S. No.	Characters	Contribution of each characters (%)
1	Plant height at maturity	0.16
2	Number of productive tillers per plant	0.26
3	Panicle length	3.35
4	Seeds per panicle	19.00
5	Seed length	3.67
6	Seed breadth	5.88
7	Thousand seed weight	11.27
8	Flag leaf length	1.47
9	Flag leaf breadth	8.16
10	Seed yield per plant	46.78

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