

Research Note

Determination of genetic divergence based on biometrical traits in rice (*Oryza sativa* L.)

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Abstract

Genetic divergence was studied for ten biometrical traits in 99 rice genotypes using Mahalanobis D² statistics. The analysis of variance revealed presence of significant differences among the genotypes for all the characters studied. Based on genetic distance, all the 99 genotypes were grouped under ten different clusters. The characters like grains per panicle contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster II and VIII. Selection of genotypes in these clusters may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with different quality traits.

Keywords

Clusters, diversity analysis, genetic divergence, rice

Rice (*Oryza sativa* L. $2n = 2X = 24$) is one of the most important cereal crops. It is a source of food to over three and a half billion people and it contributes more than 20% of total dietary calories (Khush, 2013). Rice has become a commodity of strategic significance and the fastest growing food source in India, any reduction in the rice production will have large scale implications on food security (Rathod *et al.*, 2017). In India, it covers the largest area of about 44.6 million ha of land with a production of about 90.2 million tons. Rice is unique because it can grow in wet environments that other crops cannot survive in.

Genetic diversity available in any crop forms the basis of crop improvement. For crop improvement and to plan various breeding strategies, the knowledge on nature and magnitude of genetic variability in a crop is important. Genetically diverse germplasm is an important source for identification of parental lines. Assessment and identification of diverse parents having desired traits is a tedious work in crop improvement. This is made easy with the help of tools like Mahalanobis D² statistics (Mahalanobis, 1936). Once the parents are identified, they may be used for hybridization in order to transfer the desired traits into cultivars and develop improved varieties. Because of diverse nature of parents, there is a chance for getting heterotic effects. The performance and heterosis of hybrids are associated with genetic divergence between their parental lines (Ashok Kumar Meena *et al.*, 2017). The spectrum of variability in segregating generations largely depends on the genetic divergence of the

parents involved in the hybridization (Toshimenla *et al.*, 2016)

Keeping these points in view, the present study was formulated to assess the genetic diversity among 99 genotypes for ten quantitative traits in rice germplasm. This study was undertaken to determine the genetic diversity in rice for the maximum utilization of the genetic resources.

The experimental material consisted of 99 rice genotypes from different geographical regions. All the genotypes were evaluated in RBD design with two replications during *Kharif* 2017 at Rice Research Station, Ambasamudram, Tamil Nadu Agricultural University, Tamil Nadu. The seedlings were transplanted to main field at the rate of one seedling per hill with a spacing of 20 cm between rows and 10 cm within plants. Recommended agronomic practices and need based plant protection measures were taken up.

Field observations were taken for 10 quantitative traits viz. days to 50 per cent flowering, plant height (cm), productive tillers, panicle length (cm), filled grains per panicle, total grains per panicle, brown rice length (mm), brown rice breadth (mm), test weight- 1000 grain weight (g), single plant yield (g). These 99 genotypes were utilized to assess genetic diversity by Mahalanobis D² statistics using GENRES software.

Analysis of variance showed significant differences among the 99 genotypes for all the characters taken for the study, indicating their wide genetic

divergence. Clustering of germplasm was done for ten quantitative traits using Mahalanobis D^2 statistics. A total of ten clusters were identified with cluster VI being the largest having 23 genotypes, followed by cluster I having 20 genotypes. Clusters IV and VII had two genotypes each.

The intra and inter cluster distances are included in Table 3. The intra-cluster distance was found to be highest for cluster VIII (12.80) followed by cluster VI (11.96) and cluster V (11.61). However, least intra-cluster distance was for cluster IV (4.09).

The inter-cluster distance was recorded highest between clusters II and VIII (19.23) followed by clusters II and IX (17.32), I and VIII (16.16). This indicates the divergence between cluster II and cluster VIII is highest. The least inter-cluster distance was between cluster I and VII (7.12). When the inter-cluster distance between clusters is higher, the genotypes in those clusters would be more diverse. Genotypes from these diverse clusters may be selected for crossing programme as parents in order to have high heterotic effects in the hybrid combinations. From the results of the present study, it may be inferred that the genotypes belonging to clusters II and VIII may be used as parents for crossing.

Cluster means for ten quantitative traits have been listed in Table 4. Cluster means for days to 50% flowering was lowest for cluster VIII (72.37) followed by cluster IV (74.25) and highest for cluster II (102.6) followed by cluster X (91.18) and cluster I (91.07). Cluster III (144.78) showed highest cluster mean values for plant height (cm) followed by clusters VI (142.85) and X (142.73).

In case of productive tillers per plant, cluster V (8.39) was followed by clusters VI (7.08) and VII (7.00) possessing high cluster mean values.

Cluster X (26.31) was observed to have highest cluster mean for panicle length (cm) followed by cluster I (25.39) and cluster II (23.56). In case of improvement for a particular trait, genotypes from those clusters having high cluster mean values for that trait may be used as parents for crossing.

Cluster means for filled grains per panicle was highest for cluster X (100.06) followed by cluster IV (95.25) and cluster VI (93.32). Cluster X (165.87) showed highest cluster mean values for total grains per panicle followed by clusters VII (157.75) and I (134.75).

In case of test weight (g), cluster VIII (26.42) was followed by clusters X (25.05) and VII (24.14) possessing high cluster mean values. Cluster means for brown rice length (mm) was highest for cluster VII (6.46) followed by cluster IX (6.45) and cluster I (6.43).

Cluster VIII (2.51) showed highest cluster mean values for brown rice breadth (mm) followed by clusters X (2.04) and VI (2.01). In case of single plant yield (g), cluster X (15.66) was followed by clusters VI (13.95) and V (13.17) possessing high cluster mean values.

Considering the trait days to 50 per cent flowering, cluster with lowest cluster mean may be selected as those genotypes will be early flowering. Here the genotypes of cluster VIII will take least number of days for achieving 50 per cent flowering, as indicated by their low cluster mean value (72.37).

While considering percentage contribution of each character to genetic diversity (Table 5), single plant yield (g) was found to have highest contribution (28.86%) followed by days to 50% flowering (22.44%) and brown rice length (mm) (20.14%). The present study revealed that the selection of parents must be based on wider inter cluster distance and superior mean performance for yield.

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Table 1. Analysis of variance (ANOVA) for quantitative traits in rice

Source of Variation Source	Degrees of Freedom	Mean sum of squares									
		Days to 50% Flowering	Plant Height (cm)	Productive Tillers Per Plant	Panicle length (cm)	Filled Grains Per Panicle	Total Grains Per Panicle	Test Weight (g) (1000 grains)	Brown Rice Length (mm)	Brown Rice Breadth (mm)	Single plant yield (g)
Replications	1	6.80	55.84	2.67	42.15	1082.63	42.63	0.5	0.01	0.06	0.25
Treatments	98	186.68**	1482.38**	6.29**	20.39**	2297.63**	214.93**	44.57**	1.26**	0.25**	52.94**
Error	98	4.29	80.19	0.47	2.16	211.93	261.98	8.12	0.04	0.03	4.26

**Significance at 0.01% probability

Table 2. Classification of genotypes into clusters based on Tocher's method in ricegermplasm

Cluster Number	Genotypes in Cluster	Total Number of Genotypes
I	T 3094, T 3095, T 3096, T 3098, T 3099, T 3101, T 3102, T 3105, T 3108, T 3109, T 3110, T 3112, T 3116, T 3117, T 3122, T 3123, T 3129, T 3134, T 3137, T 3140	20
II	T 3143, T 3150, T 3155, T 3157, T 3158, T 3156, T 3412, T 3413, T 3539, T 3597	10
III	T 3406, T 3407, T 3408, T 3409, T 3418, T 3440, T 3008	7
IV	T 3520, T 3816	2
V	T 3421, T 3431, T 3432, T 3436, T 3437, T 3023, T 3004, T 3005, T 3013, T 3450, T 3451, T 3453, T 3454, T 3482, T 3483, T 3505, T 3609, T 3753, T 3007	19
VI	T 3521, T 3538, T 3555, T 3506, T 3556, T 3598, T 3608, T 3634, T 3635, T 3692, T 3693, T 3706, T 3706, T 3752, T 3817, T 3818, T 3888, T 3889, T 3910, T 3911, T 3950, T 3951, T 3774	23
VII	T 4209, T 4386	2
VIII	T 3966, T 3967, T 4027, T 4030	4
IX	T 4044, T 4108, T 4212, T 4385	4
X	T 4109, T 4254, T 4255, T 4275, T 4358, T 4366, T 3145, T 3146	8

Table 3. Inter and intra (bold) cluster distances among rice germplasm

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	8.679	11.670	13.546	12.069	11.578	11.679	7.120	16.168	12.468	11.399
II		9.556	15.008	15.794	13.000	12.727	11.252	19.239	17.328	11.911
III			10.660	8.633	12.103	12.695	13.067	12.571	13.948	12.242
IV				4.099	11.095	11.799	10.968	9.818	10.191	11.751
V					11.614	11.953	10.712	15.121	14.325	11.366
VI						11.965	11.026	15.869	14.798	11.264
VII							5.204	14.870	10.758	10.395
VIII								12.808	13.869	15.235
IX									11.255	15.148
X										10.342



Table 4. Cluster means for each character in rice germplasm

Cluster no	Days to 50% Flowering	Plant Height (cm)	Productive Tillers Per Plant	Panicle Length (cm)	Filled Grains Per Panicle	Total Grains Per Panicle	Test Weight (g) (1000 Grains)	Brown Rice Length (mm)	Brown Rice Breadth (mm)	Single Plant Yield (g)
1	91.075	110.468	6.875	25.391	49.525	134.750	22.429	6.435	1.869	8.501
2	102.600	129.035	6.350	23.561	85.700	119.350	19.881	5.638	1.741	11.301
3	80.357	144.786	6.571	22.476	82.000	108.143	19.899	5.144	1.841	11.494
4	74.250	129.675	7.000	21.725	95.250	129.750	17.982	5.725	2.005	11.727
5	87.474	126.479	8.395	23.553	71.211	130.684	21.762	5.742	1.841	13.179
6	88.739	142.852	7.087	22.828	93.326	131.783	21.592	6.063	2.018	13.958
7	91.000	95.375	7.000	22.900	69.750	157.750	24.140	6.455	2.020	10.085
8	72.375	123.012	5.750	20.253	80.125	121.875	26.425	5.240	2.517	11.894
9	77.500	86.750	5.625	20.233	77.250	122.500	20.642	6.450	1.870	9.110
10	91.188	142.731	6.813	26.311	100.063	165.875	25.051	5.730	2.042	15.666

Table 5. Percentage contribution of each character to genetic diversity in rice germplasm

Traits	% CONTRIBUTION
Days to 50 % flowering	22.4490
Plant height (cm)	5.9988
Productive tillers	5.3391
Panicle length (cm)	0.7009
Filled grains/panicle	1.6491
Total grains/panicle	3.3395
Test weight -1000 grain weight (g)	2.0614
Brown rice length (mm)	20.1402
Brown rice breadth (mm)	9.4620
Single plant yield (g)	28.8600