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Assessment of Genetic Divergence in Rice for Grain Yield and Quality Traits

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Abstract Forty elite rice genotypes were evaluated for their genetic diversity with respect to yield, yield components and quality traits. The genotypes were grouped into seven distinct clusters based on their genetic diversity using Mahalanobis D^2 statistic. The results revealed no relation between geographical and genetic diversity. Maximum inter-cluster distance was observed between cluster IV and VII, followed by cluster I and VII and cluster IV and cluster VI. Intra-cluster distance was maximum for cluster IV, indicating high variability within the cluster. Analysis of cluster means revealed highest grain yield per plant, in addition to higher grains per panicle, high panicle length and high test weight for cluster IV. Genotypes included in this clusters can therefore be used for development of high yielding varieties. Further, the traits, namely, test weight and panicle length were observed to contribute 52.05% to the total divergence and hence, need to be stressed in selection of parents for hybridization. Crosses between the genotypes grouped in cluster IV (NLR 3390) having high *per se* performance in addition to maximum genetic distance with the genotypic placed in the cluster VII (BPT 2658) are expected to be heterotic and also result in superior and desirable recombinants.

Keywords D^2, Rice, Genetic diversity, Quality, Yield.

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Introduction

Rice (*Oryza sativa* L. 2n = 2x = 24) is the principal staple cereal food and source of calories for more than half of the world's population. It offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative characters [1]. It is the staple food for 65% of the global population and forms the cheapest source of food energy and protein. To meet the food demands of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tonnes every year, which is possible through heterosis breeding and other innovative breeding approaches [2].

Genetic divergence is an efficient tool for an effective choice of parents for hybridization program.

Table 1. Clustering pattern of 40 rice [*Oryza sativa* L.] genotypes by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype (s)
I	9	BPT 2675, BPT5204, JMP 43, NLR 5785-12-2-1, JMP24, BPT 2650, MTU 2244-47-15-6-77, MTU PS 257-1-1-1, MTU 2035-18-1-2-7
II	12	RGL 7014, BPT 2660, NLR 3379, MTU 335-19-1-1-1, NLR 3380, BPT 2743, MTU 20601-1-1-1-1, BPT 2661, BPT 2757, BPT 2571, BPT 2763, BPT 2741
III	13	MTU 2035-12-2-4-3, MTU 2111-13-1-2, BPT 2595, MTU 2127-35-1-1-1, MTU 2127-48-1-1-1, MTU 7029, MTU 2022-8-3-3, BPT 2587, BPT 2644, BPT 2774, BPT 2758, BPT 2593, BPT 2772
IV	3	MTU 2195-201-1-3, NLR 3390, MTU 2195-105-1-5
V	1	MTU 2071-13-1-1
VI	1	NLR 3385
VII	1	BPT 2658

Such study selects the genetically divergent parents to obtain desirable combinations in the segregating generations [3]. Genetic diversity plays an important role in plant breeding in the choice of parents, either to exploit heterosis or to generate productive recombinants. Assessment of germplasm for genetic diversity is of immense importance in selection of diverse genotypes for hybridization program. Realizing the importance of germplasm in the development of desirable varieties, breeders are now looking for more diverse forms from various sources to further augment the yield potential of the genotypes. Mahalanobis's D^2 statistic is a powerful and widely used tool for quantifying genetic divergence among the available genotypes with respect to various characters. In this context, the present investigation was undertaken to classify and understand the nature and magnitude of genetic diversity of elite rice genotypes from different rice research station of Andhra Pradesh state for yield and quality traits.

Materials and Methods

The experimental material for the present investigation consisted of 40 elite genotypes of rice collected from different rice research stations of Andhra Pradesh state, namely, Bapatla (BPT), Ragolu (RGL), Maruteru (MTU), Nellore (NLR) and Jangamaheswarapuram (JMP). These genotypes were evaluated during *kharif*, 2015 at Agricultural College Farm, Bapatla in a randomized complete block design with three replications. The seeds were raised on nursery bed and seedlings were transplanted in main field after 28 days. Each genotype was planted in two rows of 4 m length with a spacing of 20 cm between rows and 15 cm between the plants. Observations were recorded on 10 randomly chosen plants for 11 quantitative characters, namely, days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio and grain yield per plant. Mean value of the recorded data was subjected to analysis of variance. Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis D^2 and the varieties were grouped into different clusters according to Tocher's method.

Results and Discussion

Univariate analysis of variance revealed significant difference for all 11 characters studied indicating the existence of sufficient variability for effective selection. Hence, D^2 analysis was undertaken to classify and understand the nature and magnitude of genetic diversity among the genotypes with respect to the traits studied in the present investigation. The results based on the relative magnitude of D^2 values revealed grouping of the 40 genotypes studied into seven clusters (Table 1). Among these, cluster III was the largest, comprising of 13 genotypes from Maruteru and Bapatla, while cluster V, VI and VII were monogenotypic and comprised of single variety from Maruteru, Nellore and Bapatla, respectively, indicating uniqueness of the genotypes. The clusters, I II and IV comprised of nine, 12 and three genotypes, respectively, developed from different rice research stations of the state, namely, Bapatla,Jangamaheswarapuram, Nellore, Maruteru and Ragolu. The mode

Table 2. Average intra and inter-cluster D^2 values among seven clusters with 40 rice [*Oryza sativa* L.] genotypes. Diagonal values are intra-cluster distances. Off the diagonal values are inter-cluster distances.

Cluster No.	I	II	III	IV	V	VI	VII
I	5.02	24.06	22.09	35.97	39.81	63.95	116.15
II		11.83	20.29	65.40	16.01	23.68	53.11
III			19.36	61.52	32.73	41.74	80.31
IV				34.99	76.15	97.62	173.85
V					0.00	21.21	35.37
VI						0.00	20.45
VII							0.00

of distribution of genotypes from different geographic regions into various clusters was thus observed to be random indicating that geographic diversity and genetic diversity are not related. Genotypes chosen from the same eco-geographical region were observed to be present in different clusters as well as in the same cluster, while genotypes from diverse geographical regions were included in the same cluster. Similar results were reported in rice earlier [4]. The production of greater diversity by genetic drift and selection, compared to that produced by geography was also observed in the present study. Genotypes from Maruteru were observed to be distributed over five clusters (Cluster I, II, III, IV and V), while genotypes from diverse geographical regions of the state were planced in the same clusters (Clusters I, II and II). Similar results were reported earlier [5].

An analysis of the inter and intra cluster distances (Table 2) revealed maximum inter-cluster distances between clusters IV and VII (173.85) followed by I and VII (116.15) ; and IV and VI (97.62) indicating that genotypes from these clusters were highly divergent meriting their consideration in selection of parents for hybridization. Similar greater diversity between genotypes from different clusters based on their inter-cluster distance has also been reported earlier in the crop [6]. Minimum inter-cluster distance was observed between the clusters, II and V (16.01) indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be minimum for cluster I (5.02) and maximum for cluster IV (34.99), while it was zero for the monogenotypic clusters, namely, clusters V, VI and VII as they included only single genotype. The genotypes included in cluster IV exhibiting maximum intra-cluster distance are inferred to be more divergent than those in other clusters.

A perusal of the results on cluster means for yield and yield components (Table 3) revealed con-

Table 3. Mean values of seven clusters estimated by Tocher's method from 40 rice (*Oryza sativa* L.) genotypes. Bold figures indicate minimum and maximum values in each character.

Cluster No.	Days to 50% flowering	Days to maturity	Productive tillers per plant	Plant height (cm)	Panicle length (cm)	Grains per panicle	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)
I	111.40	145.80	10.40	117.43	24.97	211.20	18.97	5.80	2.21	2.64	21.30
II	110.56	144.28	10.33	105.61	26.22	220.33	21.39	5.44	1.95	2.81	19.72
III	111.33	146.24	8.38	113.38	21.86	187.29	19.39	5.60	1.84	3.05	17.38
IV	113.17	150.17	9.50	127.67	27.50	225.33	26.64	6.00	2.27	2.65	24.87
V	110.50	144.69	7.83	107.89	23.03	164.92	16.13	5.58	1.95	2.87	14.16
VI	112.00	148.33	6.33	123.67	22.33	203.00	16.07	6.99	2.55	2.74	17.33
VII	105.33	141.50	5.50	101.67	16.33	91.50	14.70	5.51	2.09	2.64	10.77

Table 4. Contribution of different characters towards genetic divergence in 400 rice (*Oryza sativa* L.) genotypes.

Sl. No.	Source	No. of times ranked first	Percent contri-bution
1	Days to 50% flowering	19	2.44%
2	Days to maturity	2	0.26%
3	Productive tillers per plant	9	1.15%
4	Plant height (cm)	47	6.03%
5	Panicle length (cm)	141	18.08%
6	Grains per panicle	25	3.21%
7	Test weight (g)	265	33.97%
8	Kernel length (mm)	115	14.74%
9	Kernel breadth (mm)	82	10.51%
10	L/B ratio	64	8.21%
11	Grain yield per plant (g)		

siderable differences between the clusters for all characters under study. Cluster means indicate average performance of all genotypes present in a particular cluster. The data indicated a wide range of mean values between the clusters. Days to 50% flowering had a range of 105.33 days for cluster VII to 113.17 days for cluster IV ; days to maturity had a range of 141.50 days for cluster VII to 150.17 days for cluster IV ; productive tillers per plant had a range of 5.50 for cluster VII to 10.40 for cluster I ; plant height had a range of 101.67 cm for cluster VII to 127.67 cm for cluster IV ; panicle length had a range of 16.33 cm for cluster VII to 27.50 cm for cluster IV ; grains per panicle had ranged from 91.50 for cluster VII to 225.33 for cluster IV ; test weight had a range of 14.70 g for cluster VII to 26.64 g for cluster IV ; kernel len gth had ranged from 5.44 mm for cluster II to 6.99 mm for cluster VI ; kernel breadth had a range of 1.84 mm for cluster III to 2.55 mm for cluster VI ; L/B ratio had a range of 2.64 mm for cluster I and VII to 3.05 mm for cluster III ; and grain yield per plant ranged from 10.77 g for cluster VII to 24.87 g for cluster IV. In conclusion, cluster IV had recorded highest grain yield per plant (24.87 g) and was characterized by higher grains per panicle (225.33), panicle length (27.50 cm) and test weight (26.64 g), while cluster VII was early for days to 50% flowering with lowest value (105.33). The cluster IV showed highest grain yield per plant followed by cluster I and cluster II. Genotypes included in these clusters can therefore be used as diverse sources in breeding programs aimed at the development of high yielding varieties.

Information on the relative contribution of various plant characters towards divergence has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations [7]. In the present study, test weight contributed maximum (33.97%) followed by panicle length (18.08%), kernel length (14.74%) and kernel breadth (10.51%) towards the total divergence (Table 4). Contribution of the remaining characters to the total divergence was, however, relatively low. Therefore, test weight and panicle length contributing to 52.05% of the total divergence need to be stressed in selection of parents for hybridization.

In conclusion, the study revealed existence of genetic diversity among the genotypes studied for different traits. However, no relation was observed between geographic and genetic diversity. Further, crosses between the genotypes grouped in cluster IV (NLR 3390, MTU 2195-201-1-3 and MTU 2195-105-1-5), having maximum genetic distance with the genotypes placed in the cluster VII (BPT 2658) are expected to be heterotic. However, genotypes, MTU 2195-201-1-3 and MTU 2195-105-1-5 being poor yielders, cannot be utilized in the crossing programs aimed at obtaining high yielding hybrids. Therefore, cross between NLR 3390 and BPT 2658 alone may produce superior and high yielding hybrids or transgressive segregants.

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