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RESEARCH ARTICLE

GENETIC DIVERGENCE STUDIES IN RICE GENOTYPES UNDER SALINE CONDITION

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ABSTRACT

Genetic divergence was assessed among 60 rice genotypes from different eco – geographical regions of India using Mahalanobis D² analysis. The experimental materials were evaluated during 2013-2014 at Plant Breeding Farm, Annamalai University, Annamalai nagar, Tamil Nadu, India. The 60 rice genotypes were grouped into six clusters. Cluster I was found to be the largest comprising of 50 genotypes followed by cluster II had four genotypes. The clusters IV and V had two genotypes each while cluster III and VI are monogenotypic in nature. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters grain yield plant⁻¹, number of grains panicle⁻¹ and plant height contributed maximum towards genetic divergence among the genotypes. Cluster III recorded highest mean value for grain yield plant⁻¹ and lowest mean value for days to first flower. The highest inter-cluster distance (D² = 7925.46) was recorded between clusters III and VI. Selection of genotypes in these clusters which may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with desirable traits.

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INTRODUCTION

The success of any plant breeding programmes largely depends on the existence of diversity among the genotypes (Allard, 1960). This helps in the choice of parents for hybridization in yield improvement programmes. Hence, estimation of genetic diversity for yields and its components among genotypes is important for planning the future crossing programme. The use of Mahalanobis D² statistic for estimating genetic divergence has been emphasized by Shukla *et al.* (2006) and Sarawgi and Rita Bisne (2007). Hence, the present investigation was carried out in the saline lowland of Annamalai nagar to ascertain the value and magnitude of genetic diversity of 60 rice genotypes and to select suitable genotypes for further utilization in breeding programme.

MATERIALS AND METHODS

The experimental materials consisted of 60 diverse rice genotypes and were grown in a randomized block design with three replications at the Plant Breeding Farm of Annamalai University, Annamalai nagar during 2013-2014. The 25-days old seedlings were transplanted with a spacing of 20 x 20 cm to the main field and each genotype was grown in three rows of 3m length. These genotypes were grown in saline soil with electrical conductivity (EC) of 2.83 dsm⁻¹. Appropriate management and cultural practices were followed to raise a good crop. Observations on 11 morphological and quality characters were recorded based on ten randomly selected

plants in each genotype in each replication. The genetic diversity between the genotypes was worked out using Mahalanobis D² (1936) statistics and grouping of genotypes into clusters was done using Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters. All the 60 genotypes were grouped into six clusters (Table 1). Cluster I was found to be the largest comprising of 50 genotypes followed by cluster II had four genotypes. The clusters IV and V had two genotypes each while cluster III and VI are monogenotypic in nature. The clustering pattern showed that genotypes collected from same geographical origin were found to be distributed in different clusters. Similar findings of non-correspondence of genetic divergence with geographic diversity were reported earlier in rice by Vivekanandan and Subramanian (1993), Rahman *et al.* (1997) and Shanmugasundaram *et al.* (2000). Murthy and Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances.

The intra-cluster average D² values ranged from 0.00-16.82 (Table 2). The highest intra-cluster distance (16.82) was observed in the cluster IV, indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce more desirable breeding materials

Table 1 Clustering pattern of 60 rice genotypes

Cluster No	Number of Genotypes	Name of the genotypes
I	50	CARI 1, CARI 2, CARI 3, CARI 4, CARI 5, ANR 16, ANR 21, ANR 37, ADT 36, ADT 38, ADT 43, ADT 45, Shali, Porimol, Sampada, Shabagidhan, CSR 10, CSR 36, CSR 43, Co 43, Co 47, Ranjith, Gayathri, Swarna, Jaya, PY 1, BPT 5204, MTU 1010, CR 1009, STBN 1, STBN 2, STBN 3, STBN 4, STBN 5, STBN 6, STBN 7, STBN 8, STBN 9, STBN 10, STBN 11, STBN 12, STBN 13, STBN 14, STBN 15, STBN 16, STBN 17, STBN 18, STBN 19, Pokkali
II	4	Bora, Chhatoki, Pusa Basmati, Supermoti
III	1	IR 64
IV	2	NDR 59, Basmati SPS
V	2	Burmadhan Black, C 14-8
VI	1	Pusa Basmati 1121

Table 2 Inter-cluster and Intra-cluster (diagonal) average of D² and D values (parenthesis) of 60 rice genotypes

Cluster No	I	II	III	IV	V	VI
I	214.34 (14.64)	354.34 (18.82)	1859.22 (43.11)	1426.62 (37.77)	2235.09 (47.27)	5864.49 (76.57)
II		251.14 (15.84)	421.09 (20.52)	887.08 (29.78)	1858.61 (43.11)	5433.60 (73.71)
III			0.00 (0.00)	1203.73 (34.69)	2568.53 (50.68)	7925.46 (89.02)
IV				283.21 (16.82)	688.36 (26.23)	1955.16 (44.21)
V					200.10 (14.14)	1444.63 (38.00)
VI						0.00 (0.00)

Table 3 Cluster means and per cent contribution of eleven characters for divergence in 60 genotypes of rice

Cluster No	Days to first flower	Plant height (cm)	No. of tillers plant ⁻¹	No. of panicles plant ⁻¹	Panicle length (cm)	No. of grains panicle ⁻¹	Thousand grain weight (g)	Grain Length (mm)	Grain breadth (mm)	Grain L/B ratio	Grain yield plant ⁻¹ (g)
I	81.35	103.73	18.42	9.99	25.41	122.28	16.93	8.39	3.16	2.67	20.28
II	74.17	107.00	18.92	7.25	24.34	66.92	14.99	7.15	3.17	2.29	7.59
III	65.67	100.67	24.00	11.00	20.33	153.67	14.30	5.87	3.20	1.83	24.15
IV	70.00	112.17	19.00	7.00	20.17	63.84	25.14	10.57	3.43	3.15	11.82
V	98.33	154.17	13.84	6.00	24.50	70.00	25.29	8.89	3.70	2.00	10.40
VI	80.33	94.33	15.00	5.67	22.00	54.00	12.47	9.45	2.67	3.53	5.49
C.V. (%)	4.57	16.44	0.90	3.16	7.68	17.34	9.60	3.16	7.90	7.06	22.14

for achieving maximum genetic advance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines (Rahman *et al.*, 1997). Therefore, genotypes from cluster IV should be given emphasis while selection of parents for hybridization programme since most of the elite breeding cultivars were included in this cluster.

The highest inter-cluster distance was observed between clusters III and VI (D² = 7925.46) indicating high divergence of genotypes included in these two clusters. The lowest inter-cluster distance was observed between I and II (354.34) indicating that genotypes included in them were closely related (Table 2). According to Rahman *et al.*, 1997, crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. Thus, selection of genotypes from these clusters for a crossing programme will produce desirable transgressive segregants.

The genotypes of cluster III had recorded the highest grain yield plant⁻¹ while the genotypes of cluster VI recorded the lowest grain yield (Table 3). Further, the genotypes of cluster VI recorded the lowest thousand grain weight, grain breadth and dwarf in nature. Relatively taller genotypes were included in cluster V. The genotypes of cluster III had more number of tillers plant⁻¹, number of panicles plant⁻¹ including grain yield

and were earlier to flower. Cluster I included the genotypes having longest panicle length. The promising genotypes *viz.*, with high mean values for above traits from divergent clusters were STBN 13, CSR 10, CARI 2 and CARI 3 may be selected as parents for hybridization programme to develop high yielding rice varieties.

Among all the characters, grain yield plant⁻¹ (22.14%) contributed the maximum towards genetic divergence followed by number of grains panicle⁻¹ (17.34%) and plant height (16.44%). The maximum contribution of grain yield plant⁻¹ and number of grains panicle⁻¹ in rice were reported by Arivoli *et al.* (2009) which corroborated the results of the present study.

The greater the distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the clusters having maximum inter-cluster distance can be selected to yield superior segregants (Mishra *et al.*, 2003; Chaturvedi and Maurya, 2005). In the present study, genotypes from cluster I, II, III and VI can be selected for crossing programme to get desirable transgressive segregants.

Thus from the present study, it is inferred that STBN 13 of cluster I recorded desirable number of panicles per plant, number of grains per panicle and grain yield plant⁻¹ with short stature. The other genotypes *viz.*, CSR 10, CARI 2 and CARI 3 were also found superior for yield and most of the component characters studied. Hence, these genotypes were selected for further improvement through hybridization and selection.

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