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STUDIES ON GENETIC DIVERSITY IN RICE (*ORYZA SATIVA* L.) UNDER SALINE ECOSYSTEM

K.R. Saravanan, M. Venkatesan, S. Vennila and S. Suganthi
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar 608 002.
***- Corresponding Author**
Email: saravan_rangan@rediffmail.com

Abstract

Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits. The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing one. The experiment was conducted to assess genetic divergence among 100 genotypes were evaluated using mahalanobis d^2statistics. Observations were recorded on 100 rice genotypes for eleven characters *viz.* Days to 50 per cent flowering, plant height at maturity, number of tillers, number of productive tillers per plant, panicle length, number of seeds per panicle, seed length, seed breadth, seed length and breadth ratio, seed yield per plant. The ANOVA indicated significant differences among all the traits of interest. The genotypes namely G98(NDRK 11-27) and G67(CSR-RIL-01-IR-165) were adjudged as potential parent based on mean performance. D^2 analysis of the 100 genotypes based on eleven characters confirmed the presence of high genetic diversity among the genotypes by their resolution into as many as seven clusters. Genotypes of different eco-geographic origins were grouped in a single cluster as well as different clusters. The germplasms falling in different clusters with high mean for grain yield and other component characters can be utilized for hybridization programme. Thus the pattern of clusters demonstrated that the genetic diversity was not fully related to geographical diversity.
***Keywords*:** Genetic Diversity, Rice, Saline condition, STBN Genotypes.

Introduction

Rice is one of the most important food crop and a primary food source for more than one third of world's population (Singh and Singh, 2008). In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Knowledge about germplasm diversity and genetic relationships among breeding materials could be an invaluable aid in crop improvement strategies. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as parents diversity in optimum magnitude is required to obtain superior genotypes in segregating population. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996 Rahman *et al.,* 1997). The use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Thirugnanakumar, 1991, Ramya and Senthilkumar, 2008).Keeping the above all aspects into consideration, the present investigation was undertaken with the following specific objectives to assess the nature and magnitude of genetic divergence among the 100 rice genotypes, study the relative contribution of individual character towards the expression of genetic diversity and also identify suitable parents for hybridization programme based on diversity and *per se* performance.

Materials and Methods

The experiment was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during Kuruvai 2018. The experimental material for this genetic divergence study comprised of 100 genotypes collected from various places. The details of the materials are presented in Table 1.Seeds were sown in raised nursery beds. In each genotypes, one seedling per hill was transplanted in the main field after 25 days with the spacing of 20 cm between rows and 15 cm between plants in 3m lengthy rows. The experiment was carried out in Randomized Block Design with three replications. A uniform population of 20 plants per row was maintained.

Observations were recorded five randomly selected plants for each genotypes from each replication on 100 rice genotypes for 11 characters *viz.* Days to 50 per cent flowering, plant height at maturity, number of tillers, number of productive tillers per plant, panicle length, number of seeds per panicle, seed length, seed breadth, seed length and breadth ratio, seed yield per plant.

The mean values were computed for each genotypes over three replication for each genotype. Analysis of variance was carried out by using the method of Panse and Sukhatme. Mahalanobis D^2 statistic was used for estimating the genotypic divergence. For grouping the genotypes into different clusters, the criterion suggested by Rao (1952) was followed. Each character was ranked on the basis of values in all combinations of genotype for estimation of contribution of individual character towards divergence.

Results and Discussion

Analysis of variance was based on the mean values of eleven quantitative traits observed for 100 rice genotypes. The results were represented in Table-2 show significant difference for all the 11 characters observed, indicating that the genotypes selected for the present study were genetically different. Similar studies were reported by Padmaja *et al* (2010), Pandey *et al.* (2011). Employing Mahalanobis, generalized distance the divergence in 100 genotypes of rice was assessed for 11 yield contributing character. 100 genotypes of rice were grouped in seven clusters they were grouped into seven clusters using clustering technique. The

results are presented below Tables (3). Clustering pattern indicated that, The cluster I comprised of eighty four genotypes where as cluster II comprised of eleven genotypes and clusters III,IV,V,VI,VII each comprised of one genotypes. The inter and intracluster distance was maximum in the clusters I (17.77) and minimum .Inter cluster distance was minimum between the clusters VI,VII and maximum between the clusters II and III (41.65), The highest inter-cluster distance was indicating that hybridization between the most diverse genotypes would yield desirable segregants with the accumulation of favorable genes in the segregating generations.

Analysis of cluster means indicates existence of considerable differences in the mean values of different traits (Table 4). The highest mean values for number of tillers per panicle, number of productive tillers per panicle, panicle length, seed length, seed L/B ratio were observed in cluster IV. The highest mean values for number of tillers per panicle, seed length, seed breadth, seed L/B ratio with lowest values for days to 50% flowering, plant height were observed in cluster II. cluster VI indicated highest value for number of tillers per panicle, number of productive tillers per panicle, number of seeds per panicle, panicle length, seed length, seed L/B ratio, single yield per plant with lower values in days to 50% flowering, plant height, seed breadth. Thus, various characters contributes to the total divergence in cluster I, II, III, V, VI and VII.

The relative contribution of individual character towards the expression of genetic diversity estimated over character wise D^2 value, the analysis are furnished Days to 50% flowering (92.383%), Plant height at maturity (93.078%), Number of tillers (15.743%), Number of productive tillers (12.561%), Panicle length (21.088%), Number of seeds/panicle (147.191%), Seed length (0.888), Seed breath (0.249%), Seed l/b ratio (3.633%), 100 seed weight (2.735%), Seed yield per plant (33.582%).Relative ranking of the contribution of thirteen characters towards genetic diversity based on D^2 statistic revealed that number of seeds per panicle contributed maximum towards genetic diversity followed by plant height and Days to 50 % flowering.

Conclusion

A significant range of variation was evident among 100 genotypes of rice were evaluated. ANOVA indicated significant differences among all the traits of interest. The genotypes namely G98 and G67 were adjudged as potential parent based on mean performance.D^2 analysis of the 100 genotypes based on eleven character confirmed the presence of high genetic diversity among the genotypes by their resolution into as many as seven clusters. Genotypes of different eco-geographic origins were grouped in a single cluster as well as different clusters. Thus the pattern of clusters demonstrated that the genetic diversity was not fully related to geographical diversity.

Table 1: Analysis of variance for eleven morphological characters in 100 rice genotypes

Sources of Variation	CHARACTERS										
	DFF	PLHT	NTPP	NPT	PL	NSPP	SL	SB	SBR	HSW	SYPP
Replication	8.185	9.16	2.33	3.07	6.26	23.24	0.004	0.003	0.06	0.02	24.29
Treatment	125.12	156	22.36	33.52	41.36	34.55	0.015	0.046	0.91	0.26	422
Error	6.53	6.55	1.83	3.02	4.83	18.32	0.002	0.015	0.34	0.002	19.32

Table 2: Composition of D^2 clusters for 100 genotypes

Clusters	Number of Genotypes	Name of genotypes
I	84	IR 84649-81-4-1-3B /CR 3397-S-B-4-B-1, CR 3903-161-1-3-2, CS RIL-01-IR75, PAU 3835-36-6-3-3-4, CS RIL-01-IR75, PAU 5563-23-1-1, ASD-16, CST 7-1, RP 5680-110-52-4-3, KR-15075, CSR-3883-7-1-6-2-2-1, USAR DHAN-6, CSAR-839-3, CSAR-1610, CSAR 17817, CSR-2016-IR-18-7, CSR 2016-IR-18-10, KS-12, CSR-17135, RP-5706-120-72-2, KR-15100, CR 2851-S-B-1-2B-1, CSR-2748-4441-66, CSR-36, TRY-1, CSR-2016-IR-18-12, TRY-3, CSR-2016-IR-18-9, GOA DHAN-2, C0-43, TRY-2, CR 3881-M-3-1-5-1-1-1, RAU 1397-14, CSR 2016 IR-18-1, CSR-27, PAU 7114-3480-1-1-1-0, CARI DHAN -8, CSR-2748-4441-15, CSR-2748-4441-22, IRRI-147, RAU-1526-1-2, PUSA-44, CSR-2748-444-72, CSR-RIL-01-IR-165, NDRK-11-26, CSAR-1604, CR 3887-15-1-2-1, CSR 2016-IR-18-14, NDRK-11-24, ADT-39, CSR 2711-103, CSR 2016 IR-18-12, CSR-89-IR-15, CR-2851-S-1-6-2B-4-1, NDRK-11-30, CR 3884-244-8-7-4-1-3, CSR-2014-IR-18-11, CSR-2748-4441-193, PAU 3835-36-6-3-3-4, CSR-TPB-2, CR 3884-244-8-5-6-1-1, NDRK-25, PAU 3835-12-1-1-1, IR 83421-6-B-3-1-1/CR 3364-15-2B-14-2B, CR 3883-3-1-5-2-1-2, CR 3890-35-1-3-4, CR 3881-4-1-3-7-2-3, CSR-2016-IR-18-15, CSR-2748-4441-15, BL 10, CSR-2711-171, JK – 238, NDRK-11-27, CSR-2016-IR-18-2, ADT-36, USAR DHAN-3, CSR 11-121, KR-15005, CSAR-1620, CSR 2016-IR-18-8, KR-15003, NDRK-11-29, CSR 2748-197, PAU 1114-3480-1-1-0, NDRK-11-28
II	11	NSICRC 222, CARIDHAN-6, RP 5683-101-30-2-3-1, CR 3903-161-1-3-2, RP 5694-36-91-5-1-1, CARI DHAN-9, KR 15103, CSR 2016-IR-18-3, CSR-RIL-01-IR-165, PAU 5563-23-1-2, CSR-C27 SM-117
III	1	CSR 2016-IR-18-6
IV	1	KR-15075
V	1	PAU 5564-18-1-2
VI	1	ADT-42
VII	1	RP-5683-101-30-2-3-1

Table 3: Inter and intra cluster average of D^2 and D (Values in parantheses) and the extent of diversity among the cluster

Clusters	I	II	III	IV	V	VI	VII
I	315.77 **(17.77)**	461.39 **(21.48)**	483.56 **(21.99)**	594.87 **(24.39)**	622.50 **(24.95)**	610.09 **(24.70)**	67.25 **(27.45)**
II		245.54 **(15.67)**	1734.72 **(41.65)**	1372.70 **(37.05)**	1568.16 **(39.60)**	1066.02 **(32.65)**	945.56 **(30.75)**
III			0.00 **(0.00)**	538.24 **(23.20)**	332.69 **(18.24)**	885.65 **(29.76)**	1310.44 **(36.20)**
IV				0.00 **(0.00)**	754.05 **(27.46)**	1404 **(37.47)**	1664 **(40.80)**
V					0.00 **(0.00)**	730.08 **(27.02)**	1431 **(37.84)**
VI						0.00 **(0.00)**	198.81 **(14.10)**
VII							0.00 **(0.00)**

Table 4 : Cluster means of 100 rice genotypes

Clusters	Days to fifty % flowering	Plant height	No. of tillers per plant	No. of Productive Tillers per plant	Panicle Length	No of seeds per Panicle	Seed Length	Seed Breadth	Seed Length /Breadth Ratio	Hundred Seed weight	Seed Yield Per Plant
I	95.044	93.361	15.083	11.536	20.866	126.730	0.892	0.263	3.672	2.539	29.411
II	68.576	89.848	16.788	12.394	19.424	138.636	0.907	0.254	3.602	2.539	31.682
III	116.333	89.333	12.667	7.667	20.667	136.667	0.910	0.213	4.292	2.430	18.640
IV	105.333	89.000	22.000	21.000	23.333	118.667	0.947	0.227	4.200	2.013	42.257
V	91.777	88.666	14.000	12.000	23.000	257.000	0.823	0.257	3.208	2.613	31.357
VI	89.666	109.667	14.667	12.333	23.000	167.667	0.833	0.280	2.981	3.460	42.663
VII	80.000	91.667	15.000	11.000	17.333	85.000	0.870	0.250	3.486	3.550	39.067
General Mean	**92.383**	**93.078**	**15.743**	**12.561**	**21.088**	**147.191**	**0.888**	**0.249**	**3.633**	**2.735**	**33.582**

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