

Original Research Article

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Exploration of Genetic Diversity in Traditional Landraces of Rice for Yield and Its Attributing Traits under Saline Stress Condition

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ABSTRACT

Genetic divergence study of 144 rice landraces using Mahalanobis D² statistics revealed the presence of considerable genetic diversity. The 144 diverse landraces were grouped into 13 clusters with the cluster VI consists of maximum of 17 landraces followed by cluster XII which has 16 landraces. The maximum intra cluster distance was recorded in cluster V (969.20) followed by cluster II (917.05) indicating that the landraces included in these cluster were relatively more diverse. Among the inter cluster distances highest was recorded for cluster V and XII (5989.69) followed by cluster XI and XII (5155.12). The inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes of different groups. For grain yield per plant, the highest cluster mean was recorded in cluster X (49.50gm) and lowest (14.50gm) was recorded in cluster VIII. The highest contribution towards total divergence was recorded by plant height (52.37%) followed by spikelet per panicle (24.88%), grain yield /plant (11.05%). These characters are highly genetic variable and genotype having these characters in different cluster could be used in breeding programme to develop high yielding cultivars in rice under saline condition.

Keywords

Rice, D² analysis, Genetic diversity analysis, Landraces and Salinity

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Introduction

Rice (*Oryza sativa* L.) is a one of the most important cereal crops and serves as the staple food for over one-third of the world's population (Chanbeni *et al.*, 2012). The tremendous variation for salt tolerance within

Oryza species provide opportunities to improve rice for salt-stress tolerance through genetic means. Soil salinization is a serious problem in the entire world and it has grown substantially causing loss in crop productivity (FAO, 2006). It is a major constraint limiting agricultural productivity on nearly 20% of the

cultivated and irrigated area worldwide (Zheng *et al.*, 2001). The major inhibitory effect of salinity on plant growth has been attributed to osmotic effect, ion toxicity and nutritional imbalance leading to reduction in photosynthetic activities and other physiological disorders. Salt stress has been reported to cause an inhibition of growth and development, reduction in photosynthesis, respiration and protein synthesis in sensitive species. According to the classification of crop tolerance to salinity, the rice crop is within the sensitive division from 0 to 8 ds m⁻¹. The susceptibility of rice to salinity stress varies with growth stages. It was reported that the panicle formation and tillering stages were the most sensitive stages to salinity.

It was hypothesized that rice yield decreased by 12 per cent for every unit (dSm⁻¹) increase in EC above 3 dSm⁻¹. The highest yield was obtained from fresh water (no salinity) while salinity treatments of 2, 4, 6 and 8 dSm⁻¹ represented 21, 25, 37 and 47 per cent yield losses. (Ologundudu *et al.*, 2014). Therefore, the present study is planned to exploit the diversity of landraces for salinity tolerance and their characterization. The strength and value of germplasm depends on two factors, the number of accessions it contains and the diversity present in those accessions (Sridhar *et al.*, 2016). For the balanced use of plant genetic resources, characterization and quantification and information on the genetic diversity within and among closely related crop varieties is essential. Genetic diversity is prerequisites for any successful breeding programme. Use of genetically diverse parents in recombination breeding supposed to give maximum heterosis in F₁'s and the importance of genetic diversity in selecting the parents has been continually emphasized by lot of workers (Thippeswamy *et al.*, 2016, Anandan *et al.*, 2011, Dushyanthakumar and Anand, 2010). Thus, the evaluation of genetic diversity of rice genotypes could provide valuable

information for genetic improvement of salt tolerant rice.

Materials and Methods

Experimental location

The material for the present investigation contained 144 landraces of rice conserved at the in the Department of Genetics and Plant breeding, UAHS, Shivamogga, Karnataka. The experiment was carried out in natural saline field (pH: 8.14, EC: 5.81 dsm⁻¹, ESP: 9.21) condition during *kharif* season of 2016.

Field evaluation and data collection

The experiment was laid out in augmented design with three replications. For each landrace, 20 plants with row to-row spacing of 25 cm and plant-to-plant spacing of 10 cm. Recommended package of practices were followed to raise a healthy crop. The data on ten quantitative characters were recorded on five competitive plants of each landrace. Data were collected on Days to 50% flowering, SPAD reading, total number of tillers /plant, productive tillers /plant, plant height at maturity (cm), panicle length(cm), panicle weight (g), number of spikelet's/panicle, spikelet fertility (%) and grain yield /plant (g). Data analysis was carried out using WINDOSTAT software (Version 9.2) with D² statistics given by Mahalanobis (1936). The mean values were computed to calculate D² values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952).

Results and Discussion

Genetic divergence among 144 landraces for 10 characters was studied by using Mahalanobis D² analysis as per Rao (1952). Based on Mahalanobis D² analysis, the 144 landraces for yield and related characters were

grouped in to 13 clusters. The distribution pattern of landraces in 13 clusters are presented in Table 24. The cluster pattern revealed that cluster VI consists of maximum of 17 landraces followed by cluster XII which has 16 landraces. The lowest number of landraces *i.e*, four were included in cluster VIII. Similarly Dushyanthakumar (2008), Kaliyamoorthy *et al.*, (2013) and Kumari *et al.*, (2018) observed diversity among the rice genotypes for yield and its attributing traits.

The distances for the landraces with respect to yield within the cluster and also the distance of two clusters were assessed. The average D^2 values of intra and inter clusters distances were presented in Table 2. The maximum intra cluster distance was recorded in cluster V (969.20) followed by cluster II (917.05) indicating that the landraces included in these cluster were relatively more diverse and the lowest intra cluster distance was observed in cluster IX (148.21) followed by cluster XII (286.13) indicating that landraces present in these clusters were relatively less diverse. Among the inter cluster distances highest was recorded for cluster V and XII (5989.69) followed by cluster XI and XII (5155.12), cluster VII and XII (5107.60) indicating that landraces in these 2 respective clusters were highly diverse. Whereas, the lowest inter cluster distance were recorded between cluster IV and cluster V (660.56) followed by cluster XI and XIII (857.26) indicating that the landraces belong to these two respective clusters were relatively less diverse. Similar pattern of diversity was reported by Dushyanthakumar (2008), Kaliyamoorthy *et al.*, (2013) and Kumari *et al.*, (2018). The higher the intra cluster distance indicates that the landraces present in respective clusters and inter cluster distances between respective clusters have wider genetically distance between them and landraces which falls under the more far distance showing clusters had wider diversity between them. Importantly,

the genotypes belonging to the highly diverged clusters should be used in hybridization programme for obtaining a wide spectrum of variations in the breeding population Nirosha *et al.*, (2016). On the other hand, Shahidullah *et al.*, (2009) suggested the selection of genotypes belonging to moderate diversity in order to exploit benefits of heterosis. Above all, the selection of genotypes is dependent on the objectives of the breeding programme.

Cluster mean analysis

The cluster means with respect to ten yield and yield related traits were calculated using touchers method and are presented in Table 3. For days to 50% flowering higher cluster mean was recorded for cluster XI and XIII (136.00) and lowest cluster mean was recorded in cluster IX (81.00). Regarding the SPAD reading, highest cluster mean was recorded for cluster VII (17.50) and lowest cluster mean was recorded in cluster X. For total no. of tillers/plant, highest cluster mean was observed in cluster X (25.00) on the contrary, the lowest cluster mean was recorded for cluster XI (7.50). However, in productive tillers/plant, the highest cluster mean was recorded for cluster X (24.80) and lowest cluster mean was recorded for cluster XI (7.42). Whereas, for plant height, the highest cluster mean was recorded for cluster XII (139.50cm) and lowest cluster mean was observed in cluster V (75.29cm). Similarly, for panicle length, highest cluster mean was recorded for cluster XII (24.67cm) and lowest cluster mean was recorded in cluster XIII (18.00). Whereas, for panicle weight, highest cluster mean was recorded in cluster VI (2.92gm) and lowest cluster mean was recorded in cluster VIII (0.74gm). For spikelets/panicle, the highest cluster mean was recorded for cluster VII (178.60) and lowest cluster mean was recorded for cluster VIII (121.00).

Table.1 Grouping of 144 landraces based on D² clustering method evaluated during *Kharif* 2016 for yield and related traits under saline condition

Cluster	Number of Landraces	Landraces*
I	11	SGRL1, SGRL8, SGRL11, SGRL19, SGRL43, SGRL53, SGRL62, SGRL160, SGRL162, SGRL169, SGRL177
II	12	SGRL6, SGRL17, SGRL22, SGRL31, SGRL34, SGRL74, SGRL94, SGRL109, SGRL130, SGRL133, SGRL148, SGRL150
III	14	SGRL10, SGRL23, SGRL25, SGRL29, SGRL33, SGRL47, SGRL48, SGRL50, SGRL67, SGRL69, SGRL73, SGRL 91, SGRL115, SGRL124
IV	9	SGRL24, SGRL56, SGRL78, SGRL84, SGRL105, SGRL123, SGRL151, SGRL155, SGRL159
V	10	SGRL9, SGRL15, SGRL20, SGRL26, SGRL60, SGRL70, SGRL125, SGRL134, SGRL142, SGRL144
VI	17	SGRL5, SGRL7, SGRL16, SGRL18, SGRL30, SGRL37, SGRL39, SGRL71, SGRL77, SGRL83, SGRL111, SGRL113, SGRL116, SGRL122, SGRL138, SGRL167, SGRL175
VII	7	SGRL45, SGRL46, SGRL64, SGRL65, SGRL68, SGRL82, SGRL85
VIII	4	SGRL32, SGRL72, SGRL98, SGRL135
IX	12	SGRL12, SGRL44, SGRL51, SGRL52, SGRL54, SGRL57, SGRL59, SGRL79, SGRL96, SGRL108, SGRL121, SGRL176
X	5	SGRL2, SGRL35, SGRL97, SGRL132, SGRL140
XI	13	SGRL3, SGRL4, SGRL36, SGRL93, SGRL119, SGRL126, SGRL145, SGRL147, SGRL149, SGRL156, SGRL158, SGRL171, SGRL174
XII	16	SGRL14, SGRL27, SGRL41, SGRL42, SGRL49, SGRL61, SGRL76, SGRL81, SGRL95, SGRL100, SGRL120, SGRL129, SGRL153, SGRL154, SGRL 161, SGRL164
XIII	14	SGRL13, SGRL 21, SGRL38, SGRL63, SGRL75, SGRL80, SGRL 92, SGRL127, SGRL128, SGRL131, SGRL152, SGRL168, SGRL172, SGRL173

Table.2 Average intra and inter cluster distance values of landraces of rice for yield and related traits under saline condition
Kharif 2016

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII
Cluster I	773.00	1526.04	1281.25	1226.31	1951.21	1245.03	2308.11	1404.69	1235.87	1731.52	1636.39	2624.83	2700.00
Cluster II		917.05	1879.66	3307.36	4220.96	2505.57	2925.93	1826.51	1479.61	2062.06	2014.87	1767.90	3624.80
Cluster III			297.42	1470.98	1931.33	2628.28	265.81	3441.12	1053.43	1723.08	1781.39	3623.71	1617.67
Cluster IV				391.81	660.56	1062.99	2123.71	2721.78	2047.20	1603.37	2414.93	4391.81	2297.01
Cluster V					969.20	2154.41	2397.33	3407.45	3247.96	2654.34	2504.94	5989.69	2201.53
Cluster VI						426.15	3943.36	1842.41	1942.83	1353.60	3169.97	1988.19	4493.80
Cluster VII							649.46	5033.97	2142.96	2116.20	2217.88	5107.60	1301.46
Cluster VIII								842.13	2715.21	2988.49	1856.24	2871.08	4196.99
Cluster IX									148.21	1973.23	3402.89	1673.75	4401.13
Cluster X										341.28	2735.38	1889.45	2768.74
Cluster XI											326.45	5155.12	857.26
Cluster XII												286.13	7232.85
Cluster XIII													304.62

*Diagonal values indicate intra cluster distances and above diagonal values indicate inter cluster distances

Table.3 Cluster means for yield and yield related traits of 144 landraces under saline condition

	Days to 50% flowering	SPAD reading	Total tillers	Productive tillers	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Spikelet per panicle	Spikelet fertility (%)	Grain yield/plant (g)
Cluster I	102.78	9.61	11.90	11.83	108.06	21.11	2.03	140.76	83.43	22.40
Cluster II	109.88	10.04	13.19	13.01	129.95	22.04	2.29	153.30	83.08	27.13
Cluster III	101.00	16.60	10.50	10.24	97.50	21.83	1.90	167.50	80.20**	20.00
Cluster IV	97.00	4.30	13.00	12.81	81.00	18.50	2.10	137.00	85.20	27.25
Cluster V	104.42	10.85	13.52	13.22	75.29**	19.83	1.49	137.44	81.88	20.05
Cluster VI	94.00	10.35	15.00	14.30	104.00	22.17	2.92*	124.00	80.20**	43.75
Cluster VII	107.00	17.50*	12.00	11.73	88.00	23.90	1.85	178.60*	81.50	22.25
Cluster VIII	115.00	5.95	19.50	19.16	124.00	24.00	0.74**	121.00**	88.50*	14.50**
Cluster IX	81.00**	8.55	11.50	11.25	117.50	22.15	2.04	157.00	88.20	23.50
Cluster X	106.00	2.74**	25.00*	24.80*	102.00	20.50	1.98	154.00	83.51	49.50*
Cluster XI	136.00*	12.15	7.50**	7.42**	104.00	24.50	2.27	147.00	86.51	17.00
Cluster XII	88.00	10.90	24.50	24.21	139.50*	24.67*	1.97	145.00	80.50	48.21
Cluster XIII	136.00*	6.25	11.00	10.73	82.00	18.00**	1.66	163.00	82.80	18.25

*Highest cluster mean and ** Lowest cluster mean

Table.4 Per cent contribution of yield and related characters towards divergence in landraces of rice under saline condition

Sl.no.	Characters	Contribution (%)
1	Plant height	52.37%
2	Spikelet per panicle	24.88%
3	Grain yield	11.05%
4	Days to 50% flowering	7.70%
5	Total tillers	1.78%
6	SPAD reading	1.07%
7	Spikelet fertility	0.77%
8	Panicle weight	0.18%
9	Panicle length	0.11%
10	Productive tillers	0.09%

For spikelet fertility, the highest cluster mean was recorded in cluster VIII (88.50) and lowest cluster mean in cluster III, cluster IV and cluster VI (80.20). Whereas, for grain yield per plant, the highest cluster mean was recorded in cluster X (49.50gm). Whereas, lowest (14.50gm) was recorded in cluster VIII. Similarly, Supriya *et al.*, (2017), Sridhar *et al.*, (2016) and Rathod *et al.*, (2017) also reported varied cluster means for yield and related characters in rice genotypes. Analysis of cluster means helps to identify clusters having different levels of variability for different characters. It is possible to identify clusters having higher diversity for more no of characteristics and it also helps to identify clusters having less diversity for more number of characteristics. Utilization of higher mean recorded clusters in breeding programme is expected to yield desirable lines in advanced generation of selection.

Contribution of different characters towards divergence

Contribution of different yield and yield related traits studied towards total divergence was assessed and presented in Table 4. The highest contribution towards total divergence

was recorded by plant height (52.37%) followed by spikelet per panicle (24.88%), grain yield /plant (11.05%), days to 50% flowering (7.70%) and the productive tillers/plant (0.09%) was lowest percent contributed. These findings are in close correspondence with Chanbeni *et al.*, (2012), Sowmiya and Venkatesan (2017) and Kumari *et al.*, (2018).

From the above all findings it can be concluded that, The landraces studied were found to be highly diverse under saline stress, landraces from high divergent clusters contain wide genetic diversity for different traits studied and are expected to yield potential F₁s and transgressive seggregants for further exploitation.

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