



Genetic Divergence Studies for the Quantitative Traits of Paddy under Coastal Saline Ecosystem

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Twenty six genotypes of paddy were evaluated for the quantitative traits under coastal saline ecosystem to study the diversity pattern and were grouped into 6 clusters. Maximum of 7 genotypes were grouped in cluster 6 followed by 5 genotypes in cluster 5. Maximum inter cluster distance was observed between cluster 2 and cluster 6 while highest intra cluster distance was observed in cluster 1 followed by cluster 6. The percentage contribution towards divergence is highest for the trait potassium content of the stem followed by sodium content of the stem, test weight and calcium content of the stem. Highest plant height, more number of productive tillers and high shoot calcium content and lowest shoot sodium content of the stem of the genotype MCM 225 in cluster 3 and high potassium content represented by genotype viz., NLR 20017 in cluster 6 indicate the importance of the genotypes for the parental selection in hybridization program for development of high yielding genotypes coupled with salinity tolerance considering the importance of the traits low sodium content and high potassium content of the stem for breeding saline tolerant genotypes with high yield.

(**Key words:** Genetic divergence, Paddy, Coastal salinity)

Soil salinity is a global phenomenon adversely affecting the productivity of millions of hectares of land, compromising the ability of a large number of countries to maintain the agricultural production and productivity targets. Salt tolerance of a plant varies with environmental and biological factors and response to salinity in terms of morphology, anatomical adaptation and changes in various physiological and biochemical processes under salt stress facilitate the formulation of agro techniques and development of salt tolerant varieties through conventional as well as biotechnological approaches. Generally, salinity tolerance is a polygenic trait. Screening rice germplasm to locate salt tolerant genes for use in improving the currently grown varieties is of continuous importance to plant biotechnologists (Flowers, 2004). One major approach in plant breeding is to maximize the genetic diversity between parental genotypes for hybridization. There are rice varieties which yield high under normal condition, they fail to perform in salt affected soils. Therefore, use of salt-tolerant rice varieties is essential to minimize chances of crop failure (Sarangi *et al.*, 2014). So, genetic diversity screening for trait of interest is an essential part of the commencement of a breeding program.

In addition to intergenetic variation of different crops to tolerate salinity, there is wide variation in the inherent

salt tolerance for various physiological traits in addition to the morphological and agronomic characters. Of late, Krishna Western delta of Andhra Pradesh where problematic areas of soil salinity spread over 0.25 million hectares where rice is the only crop of choice, suffer problems such as poor crop establishment reduced crop growth finally resulting in lower crop yields. Low success in rice salt tolerance breeding may be due to the low selection efficiency using only agronomic characters, lack of effective evaluation methods for the salt tolerance among the genotypes and complexity of the salinity tolerance genotypes. Rice being the sole crop in the coastal saline soils, 26 germplasm lines were evaluated and analyzed for the degree of genetic divergence with regards to various salinity tolerance and yield traits under saline conditions.

MATERIALS AND METHODS

The trial was conducted at Machilipatnam Agricultural Research Station, Krishna District of Andhra Pradesh representing coastal saline ecosystem with pH 7.35, EC 14.21 dS m⁻¹ and ESP 17.57% with 26 germplasm. The experiment was laid out in a Randomized Block Design with two replications and a good crop was raised as per the recommended agronomic practices under main field conditions duly maintaining the EC and ESP% naturally by sea water infringement

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Table: 1. Mean performance of the genotypes

S. No.	Genotype	Plant Height	Days to 50% flowering	Productive tillers plant ⁻¹	Filled grains panicle ⁻¹	Unfilled grains panicle ⁻¹	Panicle length (cm)	Root length (cm)	Root dry weight (g)	Test weight (g)	Sodium content of the stem	Potassium content of the stem	Calcium content of the stem	Yield t ha ⁻¹
1	FL449 (IR 66946-3R149-1-1)	86.92	75.00	9.0	92.60	13.20	22.96	14.16	6.40	24.00	2.03	4.07	3.60	3.58
2	IR 11T 265	81.20	80.00	8.4	62.80	14.00	22.86	14.74	3.90	23.50	1.14	2.11	2.80	3.28
3	IR 11T258	90.98	79.00	8.5	117.20	10.40	25.18	17.50	6.70	22.00	2.49	0.59	2.40	2.04
4	RGL 11416	91.32	76.00	11.0	88.60	13.40	17.94	16.54	12.80	21.00	2.36	0.85	2.80	3.16
5	IR 11T 261	85.04	75.00	13.2	116.80	16.40	25.62	15.22	5.70	23.50	3.40	1.06	4.80	2.35
6	IR 11T 262	92.42	70.00	12.0	92.60	6.20	23.88	13.20	9.34	24.00	3.64	1.38	3.20	2.74
7	BPT 2270	85.24	80.00	14.2	91.00	5.60	25.02	17.56	5.50	20.50	3.65	1.25	4.00	3.57
8	IR 11T 164	78.16	70.00	9.8	67.20	8.80	22.78	16.56	9.80	23.50	1.81	1.44	4.40	2.82
9	MCM 220	74.88	76.00	7.9	55.80	15.60	20.24	17.00	5.90	21.50	2.58	1.37	4.80	2.46
10	IR 11T 235	75.08	84.00	9.5	74.20	12.60	22.48	13.40	5.60	24.50	1.73	1.36	2.40	2.42
11	NLR 20017	75.32	75.00	11.0	162.80	29.60	23.32	16.18	6.80	20.50	2.38	6.00	8.40	2.28
12	IR 11T193	68.36	70.00	13.0	73.20	4.40	21.88	15.04	3.10	25.00	2.65	6.00	4.40	2.28
13	IR 11T 179	66.30	75.00	13.8	76.60	15.00	20.54	14.22	6.50	24.00	2.82	0.83	3.60	2.05
14	IR 11T 206	73.52	70.00	13.7	67.80	6.20	20.62	18.98	3.60	23.50	5.63	1.50	4.40	1.58
15	NLR 40024	65.22	70.00	12.8	64.00	4.60	19.12	17.24	6.60	23.00	0.74	2.32	4.00	2.14
16	IR 11T 222	77.26	75.00	10.9	67.60	7.80	20.44	13.90	5.30	22.50	1.71	1.99	2.40	1.96
17	MTU 1001	66.62	75.00	11.4	48.80	2.80	18.80	11.30	3.60	21.50	0.45	0.20	4.00	1.91
18	IR 11T207	63.20	80.00	12.1	59.20	5.20	20.30	12.44	5.40	23.50	0.37	1.36	4.40	2.36
19	MCM 225	93.78	80.00	15.0	78.20	10.60	20.74	12.98	6.00	20.50	0.35	2.30	4.20	4.22
20	IR 11T 205	61.68	80.00	9.3	45.20	5.20	25.96	14.62	2.60	23.50	9.18	1.20	4.80	1.82
21	AT 401	66.14	67.00	6.5	51.40	16.60	21.54	12.62	4.60	24.00	3.72	1.75	5.20	1.65
22	IR 11T242	80.82	67.00	7.3	71.40	17.20	20.04	11.12	4.30	23.50	3.12	1.72	5.20	1.04
23	IR 29	66.46	70.00	10.2	64.00	4.60	18.78	11.78	4.60	23.00	1.88	1.54	3.20	2.32
24	IR28	63.54	67.00	10.7	51.40	7.60	17.64	10.06	2.50	23.00	0.57	1.04	3.60	1.82
25	IR66946-3R-178-1-1 (FL 478)	57.70	71.00	7.9	101.60	13.60	24.26	14.72	2.30	23.50	5.65	0.51	4.40	1.16
26	CSR 28	99.16	87.00	10.4	158.40	24.20	29.34	16.70	9.70	23.50	3.96	1.21	2.80	1.83

due to proximity to the sea shore. Data were recorded on 10 random and competitive plants on the 10 quantitative parameters viz., plant height, days to 50% flowering, tillers per plant, sodium, potassium and calcium content of the stem, panicle length, grains per panicle, test weight (1000 grain weight) and grain yield. Multivariate analysis of genetic divergence among genotypes was done using Mahalanobis D^2 statistic and grouping into clusters done by Tochers method (Rao,1952) for yield and yield contributing characters under saline conditions.

RESULTS AND DISCUSSIONS

Grouping of genotypes and their characterization provided useful information about their relatedness and possible use in crop improvement programme. The analysis of variance and results indicated significant differences among genotypes for all the ten characters indicating high variability. Twenty six genotypes studied in the present investigation were grouped into six clusters based on the relative magnitude of D^2 values such that, the genotypes belonging to same cluster had an average smaller D^2 value than those belonging to different clusters.

The distribution pattern of genotypes into different clusters revealed no parallelism between genetic and geographic diversity as genotypes chosen from same eco-geographical region were found 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 by Anandan *et al.* (2012) and Venkatlaxmi, (2013).

The distribution of genotypes into various clusters is presented in Table 1. Among the six clusters, cluster 6 was the largest comprising of 7 genotypes followed by cluster 5 with 5 genotypes while smallest cluster (cluster 3) comprised of 2 genotypes. Baburam Singh *et al.* (2010) assessed the genetic divergence in twenty aromatic rice genotypes for seven biometrical characters. The genotypes were classified into five clusters. The cluster means indicated that the cluster mean for potassium (4.79) and calcium content of the stem (6.40) plant height (105.72) and tillers per plant (11.70) was highest in cluster 3 while cluster 4 represented by cultures with lowest sodium content of the stem (0.748) while highest grain yield (3.25 t ha⁻¹) and panicle length (22.95) represented by cluster1 (Table 2).

The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes (Table3) Highest intra cluster distance is observed in cluster1 (8154.34) followed by cluster 6 (4477.59). Highest inter cluster distance was observed between cluster 2 and cluster 6 (Table 3) followed by clusters 5 and 2 indicating wide genetic diversity among the genotypes within these groups.

Table 2. Clustering pattern based on D^2 Analysis

Cluster Number	Number of Genotypes	Cluster Members
1	4.	9 (MCM 220 INDIA), 15 (NLR 40024 INDIA), 21 (AT 401 SRILANKA), 22 (IR 11T242 IRRI)
2	4.	3 (IR 11T258 IRRI), 13 (IR 11T 179 IRRI), 25 (IR66946-3R-178-1-1 FL 478) IRRI), 26 (CSR 28IRRI)
3	2.	12 (IR 11T193 IRRI), 19 (MCM 225 INDIA)
4	4.	16 (IR 11T 222 IRRI), 17 (MTU 1001 INDIA), 18 (IR 11T207 IRRI), 24 (IR28 IRRI)
5	5.	1 (FL449 (IR 66946-3R149-1-1), IRRI), 2 (IR 11T 265 IRRI), 6 (IR 11T 262 IRRI), 14 (IR 11T 206 IRRI) , 20 (IR 11T 205 IRRI)
6	7.	4 (RGL 11416 INDIA), 5 (IR 11T 261 IRRI), 7(BPT 2270 INDIA), 8 (IR 11T 164 IRRI), 10 (IR 11T 235 IRRI), 11 (NLR 20017 INDIA), 23 (IR 29 IRRI).

Table 3. Intra and inter cluster distances for six clusters

1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
8154.347	13061.11	13968.05	20363.77	17402.03	18964.990
	0	13518	18703.02	27528.08	30442.510
		2738.656	10675.78	6959.652	10204.140
			0	21198.62	26825.960
				3457.989	6671.720
					4477.592

Table 4. Mean performance of different clusters with respect to different traits

	Plant height (cm)	Days to 50% flowering	Tillers plant ⁻¹	Sodium content of the stem	Potassium content of the stem	Calcium content of the stem	Panicle length (cm)	Grains panicle ⁻¹	Test weight (g)	Grain yield (t ha ⁻¹)
Cluster 1	95.24	103.25	10.50	2.54	1.79	4.80	22.95	164.00	23.00	3.50
Cluster 2	73.70	105.00	8.75	3.73	0.79	3.30	20.33	93.45	23.35	1.32
Cluster 3	105.72	107.00	11.70	1.58	4.79	6.40	21.63	136.90	22.75	2.53
Cluster 4	95.83	107.00	11.42	0.75	1.15	3.60	18.79	99.35	22.62	3.25
Cluster 5	82.90	96.40	8.20	4.32	2.05	3.76	19.92	168.44	23.70	1.62
Cluster 6	91.22	105.86	10.12	2.46	1.20	3.49	21.78	148.83	22.35	2.40

Table 5. Relative contribution of different traits

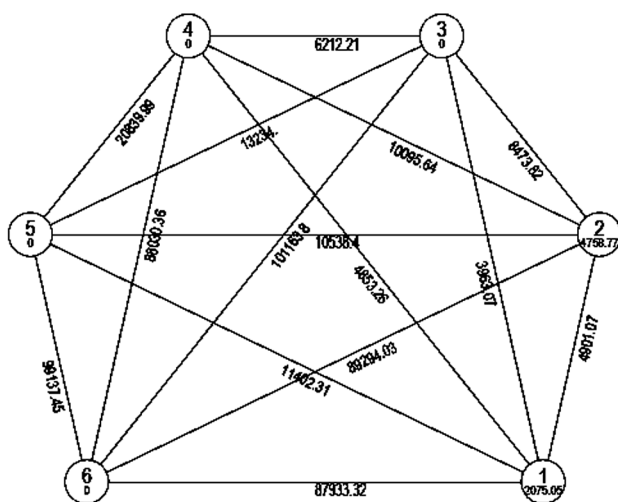
Source	Times Ranked 1st	Contribution %
1 Plant height	0	0.00
2 Days to 50% flowering	0	0.00
3 Tillers plant ⁻¹	8	2.46
4 Sodium content of the stem	49	15.08
5 Potassium content of the stem	62	19.08
6 Calcium content of the stem	15	4.62
7 Panicle length	4	1.23
8 Grains panicle ⁻¹	2	0.62
9 Test weight (g)	51	15.69
10 Grain yield plant ⁻¹ (g)	134	41.23

stem (4.62) among the salinity tolerance traits while maximum contribution was done by grain yield (41.23). and as such due weight age be given for these traits as they together contribute 95.7% towards total divergence. Out of the six clusters, cluster 5 is represented by genotypes with low sodium content and high calcium content of the shoot while cluster 5 is represented by the genotypes with high potassium content of the stem among the salinity parameters (Table 4). Linghe Zeng *et al.* (2003) opined that sodium and calcium selectivity could be one salt tolerance component and an useful selection criterion in screening for salt tolerance.

Physiological studies of rice suggest that a range of characteristics (such as low shoot sodium concentration would increase the ability of the plant to cope with salinity) vigor was strongly correlated with survival shoot sodium concentration, which a priority expected to be important, accounted for only a small proportion of the variability in the survival of salinity. Perusal of results revealed that there was no cluster with at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Highest plant height, more no. of productive tillers and high shoot calcium content and lowest shoot sodium content of the only genotype MCM 225 in cluster 3 and high potassium content represented by only genotype viz., NLR 20017 in cluster 6 indicate the importance of these genotypes for the parental selection in hybridization program for development of high yielding and salinity tolerant genotypes.

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**Fig. 1.** Cluster Diagram

Information on the relative contribution of various plant characters towards divergence was reported to aid the breeder in choice of parents for hybridization and effective selections. Relative contribution of the traits towards divergence was maximum for potassium content of the stem (19.08%), sodium content of the stem (15.08%), test weight (15.69) and calcium content of the

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