

*Full Length Research Paper*

## Genetic divergence of Indica rice genotypes in saline and non-saline environmental conditions

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Rice is staple food for Asian people and there is urgent need to produce more rice per unit area, which can be enhanced by possibly utilizing the unexplored germplasm for adverse climatic and soil conditions. Among the stress, salinity is profound and gaining prime importance in upcoming years; only possible way is breeding for salt tolerance by utilizing available genetic resources. This study was undertaken to identify promising genotypes based on its genetic diversity evaluated under saline and normal conditions. In the present study, Pokkali showed better visual salt injury score and IR 72593 showed highest grain yield under salinity condition. Cluster analysis is effective in identifying selection of better parents to harness heterosis in germplasm. Among 127 genotypes, cluster analysis resulted in 28 clusters following Tochers method. Cluster VII comprising of 10 genotypes had the highest intra cluster distance indicating the high genetic divergence among the genotypes. The genotypes in Cluster VIII and IX showed minimum inter cluster distance, which is obvious that, these clusters would have been evolved by similar evolutionary procedure. Maximum inter cluster distance was noticed between Cluster XXIV and XXVII. Hybridization among divergent clusters in all possible combinations will exhibit good heterosis for yield and tolerance to salinity.

**Key words:** Rice, salt tolerance, genetic diversity.

### INTRODUCTION

Genetic diversity in crop species is the gift of nature. The increase in productivity is mainly depending on exploitation of genetic resources already present in the ecosystem. It is estimated that, not even 15% of the genetic diversity has been utilized, it may be underutilized or overexploited for a particular trait. With the advent of scientific principles over the past decades, the plant

breeders have been increasingly cognizant of the importance of genetic diversity in crop plants. An insight into the extent and magnitude of variability present in the crop species is of utmost importance as it forms the basis of selection and thus, enables execution of any effective crop improvement programme. Besides, its quantitative estimation would indicate the potentiality of the

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germplasm from where the selection of desirable types with desirable traits can be done for maximizing the yield level. The yield and yield components of a breeding population are highly influenced by the environment, which renders it difficult to conclude whether the observed variability is heritable or not. It is therefore essential to partition the observed variability into heritable and non-heritable components, by looking at the genotypic as well as phenotypic variations existing among the germplasm.

Success in any breeding programme largely depends upon the choice of parents and the ability of parents to produce desirable recombinants. It is also dependent to a greater extent on the knowledge of genetic architecture of the population handled by the breeders (Tai, 1979). Germplasm is the basic material with which a plant breeder has to initiate any breeding programme. Land races are one of the important components of the germplasm and serve as the basic material for launching any crop improvement programme. Moreover, the land races are primitive cultivars, they have broad genetic base, which provides them wider adaptability and protection from various stresses (Jeyaprakash et al., 1998).

Screening for salt tolerance has been accomplished in a number of crops for some genotypes (Grieve and Maas, 1988; Royo and Aragues, 1999). Screening is an essential part of the commencement of a breeding program. Though, there are rice varieties which yield better under normal condition, they fail to perform in salt affected soils. The *in situ* performance of a variety and its reduction in grain yield at defined stress levels can be used as criteria in the screening and evaluation of rice breeding materials and varieties under salinity. The symptoms of salt injuries are stunted growth, rolling and withering of leaves, occurrence of white blotches, browning and drying of older leaves (Akbar, 1986).

Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996). In conventional breeding, that is, the approaches based on genetic variation existing for a character in the gene pool, and screening for genetic diversity within extant genotypes is the first step towards the genetic improvement of crops and cluster group ranking of genotypes based on multiple agronomic characters, can be applied in salt tolerance breeding (Zeng et al., 2002). Babu et al. (2006) reported that, genetic improvement mainly depends on the amount of genetic variability present in the population; hence, estimation of genetic diversity for salt tolerance parameters among genotypes is important for planning the future crossing programme. Cultivars with wide genetic distance can be crossed to widen the genetic base and exploit heterosis (Bhuyan et al., 2007). The present study focused on identification of promising genotypes among the germplasm resources based on its performance in contribution to genetic divergence

under saline and non-saline environment.

## MATERIALS AND METHODS

The study materials consisted of 127 medium and long duration rice germplasm viz., 8 maintainer lines, cultivars from IRRI, some indigenous cultivars and landraces from Tamilnadu, Andhra Pradesh, and Kerala.

### Details of experiment

The field experiment to screen 127 genotypes for salinity was carried out in two environments (control and salinity condition) in Tamil Nadu. One being naturally occurring salt stress at Anbil Dharmalingam Agricultural College and Research Institute, Trichy and the other was Tamilnadu Agricultural University, Coimbatore, where the experiment was conducted under normal condition. The experimental design followed was Randomized complete block design with 3 replications. The seedlings were germinated in the nursery and transplanted to the main field at 28 days after sowing (DAS). Single seedlings per hill were planted following a spacing of 20 × 20 cm. In both environments, various biometrical measurements were recorded both at the seedling and maturity stage.

### Cluster analysis (HCA)

The data on 14 quantitative traits for all the 127 medium and long duration rice genotypes were subjected to multivariate hierarchical cluster analysis. The ANOVA, mean calculation and combined analysis over locations were computed using SAS (1999) program Proc GLM. For hierarchical cluster analysis, the computer software INDOSTAT was used.

## RESULTS

### Genetic diversity based on morphological characters

The genetic divergence within the genotypes was tested by Wilk's criterion and was found to be significant. Thus, the analysis of genetic divergence among the genotypes taken from saline condition for the study was considered to be relevant.

### D<sup>2</sup> analysis

By the application of clustering technique, the genotypes were grouped into 28 clusters (Figure 1). Cluster I consisted of 75 genotypes, Cluster II consisted of 5 genotypes, Cluster IV consisted of 8 genotypes, Cluster VI consisted of 6 genotypes, Cluster VII consisted of 10 genotypes, Cluster III, V, and VIII to XXVIII consisted of 1 genotype each.

### Intra and inter cluster distances

The intra and inter cluster distance are presented in Table 1. Cluster VII had the highest intra cluster

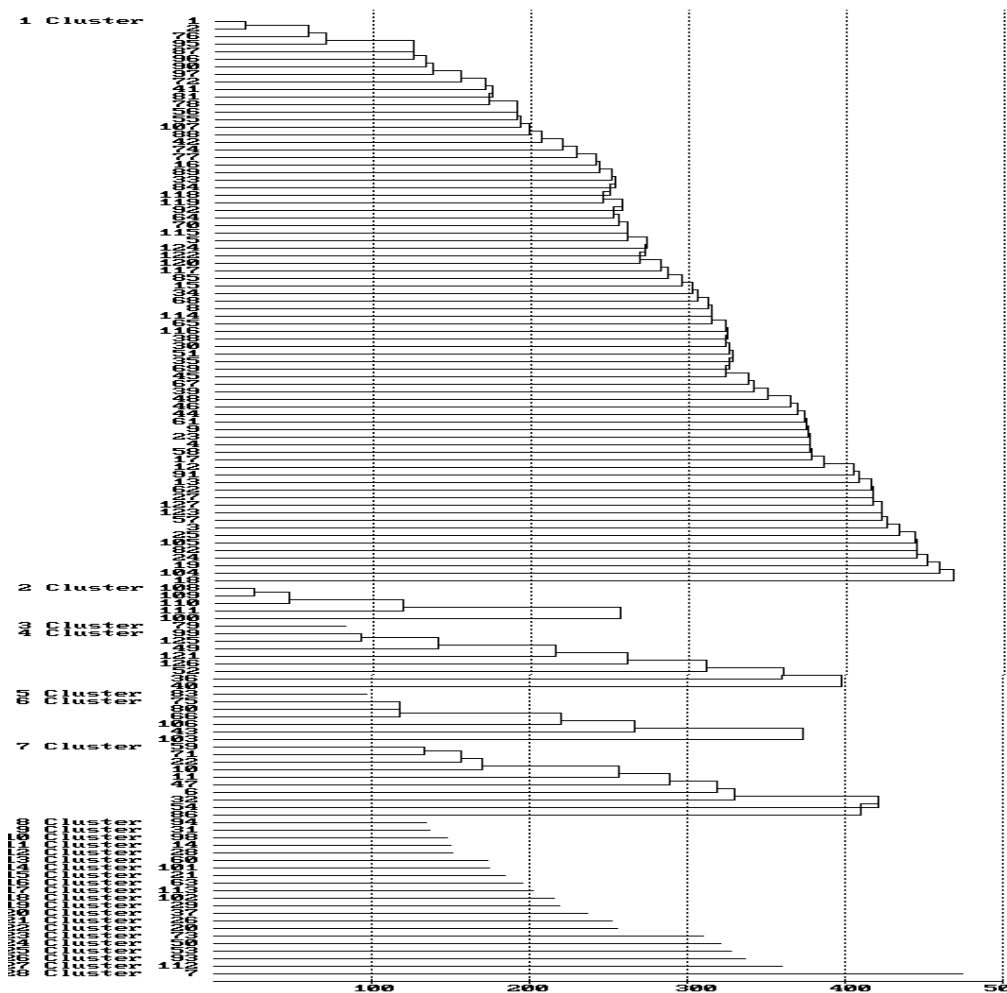


Figure 1. Clustering for 127 rice genotypes.

generalized distance of 376.4. The Clusters III, V, and VIII to XXVIII had single entries with no cluster distance. The inter cluster distance was the highest between Cluster XXIV and XXVII (4070.4), followed by Cluster XXIII and XXVII (3906.3), XXVI and XXVII (3612.0), II and XXIII (3457.4), II and XXIV (3434.0) and least between Cluster VIII and Cluster IX (139.9).

### Cluster mean values of characters

The clusters mean values for the different characters are presented in Table 2. Among the clusters, Cluster XXVII showed high mean value for plant height and days to 50% flowering (128.5 cm and 111.0 days), Cluster V for number of tillers (12.00), productive tillers (11.66) and panicle length (27.50), and Cluster XVIII for spikelet fertility (83.44). Cluster XXV showed highest mean value for grains per panicle (148.6), Cluster XI had highest mean value for harvest index (55.33), Cluster XV had higher grain yield (2.94) and least mean value for  $\text{Na}^+/\text{K}^+$

ratio (0.10), Cluster XVII had highest mean value for straw yield, XVIII had highest mean value for spikelet fertility (83.44) and Cluster XXVI for highest SES for visual salt injury (7.25).

The least mean value clusters are cluster XXIV for plant height (51.50), spikelet fertility (50.37) and SPAD reading (29.85), cluster XXV for number of tillers (6.0), productive tillers (5.66), cluster III for straw yield (10.44), cluster XIV for days to fifty per cent flowering (70.66), cluster XIX for panicle length (17.50) and cluster XXI for hundred grain weight (1.75).

### Contribution of characters to genetic divergence

The relative contribution made by each character to genetic divergence is presented in Table 3. Maximum contribution of traits towards genetic divergence was from plant height (25.55%) followed by  $\text{Na}^+/\text{K}^+$  ratio (18.35%), number of grains per panicle (14.79%), days to 50% flowering (14.02%), SES for visual salt injury

**Table 1.** Average intra (in bold) and inter cluster D<sup>2</sup> distances.

Parameter	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIV	XX	XXI	XXII	XXIII	XXIV	XXV	XXVI	XXVII	XXVIII
I	<b>361.0</b>	1413.8	479.6	625.0	561.7	542.9	557.0	529.0	542.9	501.8	524.4	580.8	524.4	557.0	510.8	533.6	734.4	795.2	670.8	571.2	789.6	590.5	846.8	1062.8	1162.8	1082.4	1797.8	1361.6
II	1413.8	<b>190.4</b>	2430.5	1901.0	835.2	967.2	1239.0	1738.9	2052.1	506.3	1528.8	2410.8	1608.0	1383.8	2097.6	1089.0	750.8	795.2	2209.0	1190.3	1849.0	745.3	3457.4	3434.0	2672.9	2959.4	519.8	712.9
III	479.6	2430.5	<b>0.0</b>	841.0	942.5	894.0	1030.4	645.2	484.0	1011.2	424.4	506.3	841.0	470.9	299.3	723.6	1513.2	1505.4	795.2	1024.0	1218.0	1024.0	309.8	812.3	1218.0	973.4	2787.8	2304.0
IV	625.0	1901.0	841.0	<b>364.8</b>	1043.3	686.4	745.3	670.8	681.2	1122.3	1115.6	479.6	818.0	1082.4	924.2	1043.3	1036.8	1369.0	998.6	718.2	605.2	906.0	739.8	650.3	739.8	492.8	2601.0	1474.6
V	561.7	835.2	942.5	1043.3	<b>0.0</b>	357.2	852.6	324.0	557.0	252.8	331.2	1129.0	620.0	864.4	823.7	739.8	590.5	475.2	1451.6	368.6	823.7	334.9	1681.0	1814.8	1592.0	1624.1	812.3	1089.0
VI	542.9	967.2	894.0	686.4	357.2	<b>327.6</b>	778.4	547.6	734.4	488.4	590.5	912.0	888.0	691.7	841.0	846.8	852.6	852.6	1421.3	519.8	734.4	557.0	1346.9	1369.0	1149.2	1075.8	1339.6	761.8
VII	557.0	1239.0	1030.4	745.3	852.6	778.4	<b>376.4</b>	954.8	1017.6	557.0	1122.3	702.3	488.4	948.6	900.0	670.8	515.3	585.6	566.4	600.3	739.8	772.8	1391.3	1339.6	1303.2	1513.2	1849.0	1142.4
VIII	529.0	1738.9	645.2	670.8	324.0	547.6	954.8	<b>0.0</b>	136.9	756.3	400.0	686.4	441.0	1169.6	635.0	942.5	852.6	882.1	1211.0	445.2	650.3	510.8	882.1	948.6	1082.4	812.3	1672.8	1764.0
IX	542.9	2052.1	484.0	681.2	557.0	734.4	1017.6	136.9	<b>0.0</b>	888.0	492.8	580.8	428.5	1149.2	615.0	739.8	986.0	1069.3	986.0	650.3	986.0	625.0	625.0	894.0	1169.6	784.0	1953.6	2061.2
X	501.8	506.3	1011.2	1122.3	252.8	488.4	557.0	756.3	888.0	<b>0.0</b>	542.9	1149.2	590.5	595.4	784.0	408.0	388.1	222.0	967.2	484.0	1075.8	408.0	1806.3	2025.0	1772.4	2025.0	620.0	778.4
XI	524.4	1528.8	424.4	1115.6	331.2	590.5	1122.3	400.0	492.8	542.9	<b>0.0</b>	1135.7	852.6	524.4	529.0	640.1	1108.9	1049.8	1232.0	864.4	1303.2	497.3	1049.8	1616.0	1755.6	1354.2	1505.4	1764.0
XII	580.8	2410.8	506.3	479.6	1129.0	912.0	702.3	686.4	580.8	1149.2	1135.7	<b>0.0</b>	615.0	1183.4	620.0	1089.0	1135.7	1156.0	723.6	501.8	479.6	1211.0	441.0	364.8	576.0	835.2	2926.8	1909.7
XIII	524.4	1608.0	841.0	818.0	620.0	888.0	488.4	441.0	428.5	590.5	852.6	615.0	<b>0.0</b>	1274.5	818.0	542.9	404.0	441.0	484.0	542.9	806.6	640.1	1190.3	1310.4	1528.8	1451.6	1689.2	1764.0
XIV	557.0	1383.8	470.9	1082.4	864.4	691.7	948.6	1169.6	1149.2	595.4	524.4	1183.4	1274.5	<b>0.0</b>	625.0	561.7	1339.6	1383.8	1075.8	1225.0	1552.4	888.0	1149.2	1722.3	1730.6	1552.4	2016.0	1398.8
XV	510.8	2097.6	299.3	924.2	823.7	841.0	900.0	635.0	615.0	784.0	529.0	620.0	818.0	625.0	<b>0.0</b>	942.5	1466.9	1142.4	888.0	784.0	1102.2	1075.8	557.0	750.8	823.7	1296.0	2294.4	1874.9
XVI	533.6	1089.0	723.6	1043.3	739.8	846.8	670.8	942.5	739.8	408.0	640.1	1089.0	542.9	561.7	943.1	<b>0.0</b>	538.2	784.0	557.0	1030.4	1624.1	428.5	1376.4	1980.3	2106.8	1689.2	1376.4	1592.0
XVII	734.4	750.8	1513.2	1036.8	590.5	852.6	515.3	852.6	986.0	388.1	1108.9	1135.7	404.0	1339.6	1466.9	538.2	<b>0.0</b>	299.3	835.2	497.3	882.1	346.0	2106.8	2134.4	1980.3	1962.5	1062.8	1310.4
XVIII	795.2	795.2	1505.4	1369.0	475.2	852.6	585.6	882.1	1069.3	222.0	1049.8	1156.0	441.0	1383.8	1142.4	784.0	299.3	<b>0.0</b>	1011.2	412.1	967.2	670.8	2218.4	2143.7	1892.3	2450.3	745.3	1030.4
XIV	670.8	2209.0	795.2	998.6	1451.6	1421.3	566.4	1211.0	986.0	967.2	1232.0	723.6	484.0	1075.8	888.0	557.0	835.2	1011.2	<b>0.0</b>	1176.5	1376.4	1122.3	961.0	1317.7	1849.0	1640.3	2683.2	2237.3
XX	571.2	1190.3	1024.0	718.2	368.6	519.8	600.3	445.2	650.3	484.0	864.4	501.8	542.9	1225.0	784.0	1030.4	497.3	412.1	1176.5	<b>0.0</b>	249.6	615.0	1383.8	1115.6	829.4	1444.0	1436.4	1169.6
XXI	789.6	1849.0	1218.0	605.2	823.7	734.4	739.8	650.3	986.0	1075.8	1303.2	479.6	806.6	1552.4	1102.2	1624.1	882.1	967.2	1376.4	249.6	<b>0.0</b>	1043.3	1325.0	823.7	691.7	1129.0	2520.0	1482.3
XXII	590.5	745.3	1024.0	906.0	334.9	557.0	772.8	510.8	625.0	408.0	497.3	1211.0	640.1	888.0	1075.8	428.5	346.0	670.8	1122.3	615.0	1043.3	<b>0.0</b>	1656.5	1840.4	1648.4	1383.8	1036.8	1406.3
XXIII	846.8	3457.4	309.8	739.8	1681.0	1346.9	1391.3	882.1	625.0	1806.3	1049.8	441.0	1190.3	1149.2	557.0	1376.4	2106.8	2218.4	961.0	1383.8	1325.0	1656.5	<b>0.0</b>	320.4	930.3	580.8	3906.3	2819.6
XXIV	1062.8	3434.0	812.3	650.3	1814.8	1369.0	1339.6	948.6	894.0	2025.0	1616.0	364.8	1310.4	1722.3	750.8	1980.3	2125.2	2143.7	1317.7	1115.6	823.7	1840.4	320.4	<b>0.0</b>	324.0	547.6	4070.4	2580.6
XXV	1162.8	2672.9	1218.0	739.8	1592.0	1149.2	1303.2	1082.4	1169.6	1772.4	1755.6	576.0	1528.8	1730.6	823.7	2106.8	1980.3	1892.3	1849.0	829.4	691.7	1648.4	930.3	327.6	<b>0.0</b>	900.0	3422.3	1962.5
XXVI	1082.4	2959.4	973.4	492.8	1624.1	1075.8	1513.2	812.3	784.0	2025.0	1354.2	835.2	1451.6	1552.4	1296.0	1689.2	1962.5	2450.3	1640.3	1444.0	1129.0	1383.8	580.8	547.6	900.0	<b>0.0</b>	3612.0	2275.3
XXVII	1797.8	519.8	2787.8	2601.0	812.3	1339.6	1849.0	1672.8	1953.6	620.0	1505.4	2926.8	1689.2	2016.0	2294.4	1376.4	1062.8	745.3	2683.2	1436.4	2520.0	1036.8	3906.3	4070.4	3422.3	3612.0	<b>0.0</b>	1176.5
XXVIII	1361.6	712.9	2304.0	1474.6	1089.0	761.8	1142.4	1764.0	2061.2	778.4	1764.0	1909.7	1764.0	1398.8	1874.9	1592.0	1310.4	1030.4	2237.3	1169.6	1482.3	1406.3	2819.6	2580.6	1962.5	2275.3	1176.5	<b>0.0</b>

(9.31%), straw yield (8.10%), single plant yield (4.56%), spikelet fertility (2.37%), panicle length (1.05%), 100 grain weight (0.91%), number of tillers (0.42%), harvest index (0.40%), SPAD (0.10%) and number of productive tillers(0.06%).

## DISCUSSION

### Per se performance of genotypes

Per se performance of the parents is one of the

simplest selection criteria for identifying superior genotypes. The genotypes with high *per se* performance would be much useful as parent for producing better offspring in any breeding programme (Saraswathi et al., 1996). The genotype IR 70868-B-P-20-2 showed superior performance for harvest index. Genotype Pokkali showed superior performance for SES for visual salt injury, CSR 10 showed early flowering, IR 74096-AC-35 showed reduced plant height, IR 74095-AC-1 showed higher tiller number, IR 73104-B-1-1-3-2-1 showed higher number of productive tillers per plants, IR 72046-3R-

2-2-1 showed highest panicle length, IR 74802-3R-7-1-2 showed highest number of grains per panicle, IR 71830-3R-2-3-3 showed with higher spikelet fertility, IR 66401-2B-6-1-3 showed highest hundred grain weight, IR 72593-B-19-2-3-1 showed highest single plant yield, TKM 11 showed highest straw yield. While IR 74095-AC-38 showed highest SPAD readings and IR 72593-B-19-2-3-1 showed lowest Na<sup>+</sup>/ K<sup>+</sup> ratio. Many breeders practically use the *per se* performance of genotypes for choosing superior parents. Such an attempt was also made in the present study to identify suitable parents for

**Table 2.** Cluster mean values for fourteen characters in rice genotypes under salinity condition.

Cluster No.	SES for visual salt injury	Days to 50% flowering	Plant height (cm)	Number of tillers	Number of productive tillers	Panicle length (cm)	Grains per panicle	Spikelet fertility	Hundred grain weight	Single plant yield	Straw yield	Harvest index	SPAD	Na <sup>+</sup> :K <sup>+</sup> ratio
I	5.57	85.50	83.853	10.12	9.66	22.86	78.97	73.8	2.24	14.52	17.68	44.6	43.5	0.175
II	5.19	94.13	132.10	10.06	9.80	24.80	109.6	77.9	2.55	18.49	31.37	36.6	41.4	0.139
III	5.35	79.00	73.500	7.00	6.66	26.50	50.66	74.7	2.27	9.00	10.44	46.0	39.8	0.147
IV	6.61	84.54	75.813	10.83	10.04	21.56	88.87	62.6	2.12	14.69	21.15	40.7	44.5	0.318
V	5.15	102.0	101.00	12.00	11.66	27.50	84.00	77.1	2.31	13.86	15.28	46.7	41.7	0.140
VI	5.47	90.11	101.83	10.83	9.83	26.27	90.11	73.0	2.29	14.80	16.82	46.6	42.6	0.251
VII	5.74	82.96	79.25	10.80	10.13	22.82	112.10	73.9	2.31	22.02	24.43	47.35	43.8	0.171
VIII	5.75	104.6	79.00	9.66	8.66	22.50	60.00	64.3	2.40	11.45	12.12	47.67	41.85	0.213
IX	5.0	5.25	100.66	71.50	9.66	25.00	38.00	63.88	2.41	8.30	16.15	33.90	38.80	0.213
X	4.50	92.00	103.00	10.00	10.00	23.50	94.00	81.98	2.38	15.63	22.13	40.87	44.10	0.110
XI	4.80	94.00	100.00	10.00	8.66	25.50	45.66	67.96	1.79	12.28	9.913	55.33	44.40	0.110
XII	5.65	83.66	51.500	6.66	6.00	26.00	110.66	75.60	1.99	11.96	19.203	37.96	39.50	0.257
XIII	5.55	97.66	64.500	9.00	9.00	24.50	72.67	75.26	2.68	19.09	21.66	46.71	48.50	0.147
XIV	5.15	70.66	107.50	9.00	9.00	23.50	64.67	81.44	2.34	10.62	14.51	42.03	47.15	0.137
XV	4.25	81.000	77.30	9.66	9.00	21.50	91.00	54.93	2.94	10.35	10.54	48.93	40.35	0.100
XVI	5.15	84.667	94.00	9.66	9.66	27.00	40.66	78.86	2.35	15.12	29.09	34.16	43.85	0.107
XVII	6.15	100.00	88.00	11.00	10.66	21.75	99.00	81.58	1.80	19.11	31.57	35.05	44.75	0.140
XVIII	4.15	100.66	86.00	7.66	7.66	24.00	117.0	83.44	2.35	20.65	24.48	45.70	39.95	0.107
XIX	5.250	78.66	62.00	10.66	10.00	17.50	67.00	75.23	2.00	21.71	25.04	46.41	40.20	0.123
XX	5.45	98.66	76.50	10.66	10.00	24.50	139.0	76.00	1.98	12.32	21.23	36.63	38.50	0.187
XXI	7.05	94.00	67.75	10.00	9.66	22.50	152.6	76.35	1.75	17.37	16.16	51.71	42.50	0.267
XXII	6.45	99.66	106.00	8.66	8.66	24.30	64.00	61.77	1.81	14.44	24.37	37.08	36.25	0.120
XXIII	5.35	77.66	56.50	7.66	7.66	21.00	51.66	58.31	2.02	9.15	11.09	45.39	40.10	0.267
XXIV	6.15	81.00	51.50	6.66	6.66	19.00	101.6	50.37	2.50	12.04	12.06	48.79	29.85	0.313
XXV	6.15	82.66	67.50	6.00	5.66	22.50	148.6	37.93	2.75	8.14	15.62	34.27	31.75	0.277
XXVI	7.25	85.66	75.50	10.66	7.00	20.50	43.66	48.93	2.12	13.01	14.20	47.23	39.20	0.410
XXVII	3.00	111.00	128.50	11.00	8.66	24.05	77.00	79.67	2.86	15.07	28.07	35.00	39.79	0.113
XXVIII	3.85	84.00	119.25	10.66	9.66	25.65	127.66	76.43	2.48	23.96	23.29	50.21	44.30	0.333

utilizing in hybrid rice breeding programme.

### Genetic diversity analysis

One major approach in plant breeding is to maximize the genetic diversity between parental

genotypes for inter crosses. Genetic diversity between parental genotypes is usually estimated by measurements of physiological and morphological differences of quantitative and economically important traits (Zeng et al., 2002). Cluster analysis is an effective method for comparing cultivars (Jolliffe et al., 1989). It has

been used to characterize crop germplasm and genotypes grouped into homogeneous clusters when trials were conducted under non-saline conditions at different locations (Crossa et al., 1995; Franco et al., 1999, 2003). Traditional philippine upland rice cultivars have been classified by clusters analysis on growth characters under non-

**Table 3.** Relative contribution of different characters towards divergence in 127 rice genotypes – salinity condition.

S/N	Character	Number of first ranks	Per centage of contribution towards divergence
1	SES for visual salt injury	745	9.31
2	Days to 50% flowering	1122	14.02
3	Plant height (cm)	2044	25.55
4	Number of tillers	34	0.42
5	Number of productive tillers	5	0.06
6	Panicle length (cm)	84	1.05
7	Number of grains per panicle	1183	14.79
8	Spikelet fertility	190	2.37
9	Hundred grain weight	73	0.91
10	Single plant yield	365	4.56
11	Straw yield	648	8.10
12	Harvest index	32	0.40
13	SPAD	8	0.10
14	Na <sup>+</sup> /K <sup>+</sup> ratio	1468	18.35

saline conditions (Schlosser et al., 2000). It has also been reported that, clustering is effective in screening for salt tolerance in rice (Zeng et al., 2002) when agronomic parameters were analyzed.

The Mahalanobis D<sup>2</sup> statistic has been found to be favourable for estimating genetic divergence between genotypes for selection in the breeding programme. The success in obtaining highly heterotic hybrids and creating greater variability for efficient selection of useful recombinants in a breeding programme depends to a large measure on the degree of divergence between the parents chosen (Murthy and Rao, 1967). For exploiting heterosis as a means of increasing production, it is necessary to utilize parents with maximum genetic divergence. The more diverse the parents, the more are the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations.

The cluster analysis suggested the resolution of 127 genotypes into 28 clusters following Tocher's method of clustering, indicating wide diversity in the experimental material for majority of the characters.

Cluster VII comprising of 10 genotypes had the highest intra cluster distance indicating the high divergence among the genotypes of the cluster. Considering the inter cluster distances, it was found that, minimum inter cluster distance was noticed between Clusters VIII and Cluster IX which explain that, the genotypes in these clusters would have been evolved by similar evolutionary procedure. Maximum inter cluster distance was noticed between cluster XXIV and XXVII. The mean performance of grain yield was contributed by Cluster XV, whereas, the Cluster XXVII showed the lowest mean value for SES for visual salt injury, Cluster XXIV had the lowest mean value for plant height, Cluster XIV showed the lowest

mean value for days to 50% flowering, likewise Cluster V for number of tillers, productive tillers and panicle length, and the Cluster XXV showed the highest mean value for grains per panicle, XVIII, XXIV, and XI showed the highest mean values for spikelet fertility, straw yield, and harvest index, respectively. The Cluster XV for highest 100 grain weight and lowest Na<sup>+</sup>/K<sup>+</sup> ratio. Keeping this in mind, it appeared that, the distribution of characters is random between clusters and crossing between all possible combinations would not only exhibit high heterosis but also increase the yield and tolerance level of salinity.

## Conclusion

In addition to general features of variation and divergence indicated, this study also provides the information on the potent characters that contributes to the divergence between the genotypes. The genetic variation in salinity tolerance probably represents adaptation to diverse environments in the regions of origin of these taxa. (Bayuelo-Jimenez et al., 2003). It was found that, the maximum contribution to the genetic divergence was accounted by plant height followed by Na<sup>+</sup>/K<sup>+</sup>. The low contribution to genetic divergence by other characters may be due to the fact that, selection towards uniformity in these characters could have caused an eroding effect on genetic diversity. Because the experimental material used under present investigation were promising genotypes, so there was only minimum contribution of quantitative traits towards genetic divergence. The clustering pattern of genotypes revealed that, the genotypes originated in different locations were clubbed together or genotypes originated from same location were distributed in different clusters. Similar findings have been

reported by Vanaja et al. (2003) and Babu et al. (2006). The kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to difference in adaptation, selection criteria, selection pressure and environmental conditions (Nayak et al., 2004). There is a possibility of operation of a similar phenomenon in clusters showing less contribution towards the genetic divergence. Similar results have been reported by Datt and Mani (2003) and Sobita Devi et al. (2006). Therefore selection of genotypes from different clusters may produce a wide spectrum of variation in progeny and may yield new varieties with desirable traits.

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