



Genetic Divergence Studies for Salinity Tolerance, Yield Components and Grain Yield in Rice Genotypes

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ABSTRACT

Genetic divergence study of fifty genotypes of rice (*Oryza sativa* L.) for twelve characters led to their grouping in to eight clusters. Shoot sodium content (59.67) showed maximum contribution towards genetic divergence followed by shoot potassium content (15.51) and shoot dry weight (9.80). Grain yield plant⁻¹ (4.33), plant height (3.59), days to 50% flowering (3.51), 1000 seed weight (2.86), productive tillers hill⁻¹ (0.49), root length (0.16) and spikelet fertility percent (0.08) each were noticed to contribute less than 5 percent towards the total divergence. The maximum inter cluster D² values was observed between cluster VII and VIII followed by cluster I and VIII.

Key words : Genetic divergence, Tolerance.

Rice (*Oryza sativa* L.) offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various traits. Assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding programme. Genetic variability is the prerequisite for making the progress in crop improvement. As such, inclusion of genetically divergent parents in the breeding programmes is essential to create new variability in any crop. In the present investigation, an attempt was made to classify and to know the genetic diversity for certain yield components, salinity traits and grain yield for use in hybridization programme to develop rice varieties for cultivation in saline soils.

MATERIAL AND METHODS

The material comprised of 50 rice genotypes collected from diverse places were screened at an estimated initial E.C and pH of 14.21 dsm/m² and 7.35 in plot no.1 of Block-E during *kharif* 2010. Thirty-two days old seedlings were transplanted at the rate of two seedlings per hill in the main field. The crop was provided with recommended doses of fertilizers, normal cultural operations and need based plant protection measures. The water was never drained out from

experimental plot to maintain stable soil E.C and pH for the entire experimentation period.

Five plants per genotype were randomly selected from the two central rows for recording data on twelve (12) characters. The six characters pertaining to salinity tolerance like (i) Shoot length at seedling stage (cm), (ii) Dry weight of shoot at seedling stage (g) (iii) Root length at seedling stage (cm), (iv) Dry weight of root at seedling stage (g) (v) Sodium content in shoot at maximum tillering stage and (VI) Potassium content in shoot at maximum tillering stage. The remaining six characters pertaining to the yield components like (i) Days to 50% flowering, (ii) Plant height, (iii) Number of productive tillers plant⁻¹, (iv) Spikelet fertility percent at maturity, (v) 1000 seed weight and (vi) grain yield plant⁻¹. The means of replications were used for statistical analysis. The analysis of genetic divergence using Mahalanobis D² analysis was done as described by Rao (1952) and grouping of genotypes in to different clusters was carried out by using cluster analysis.

RESULTS AND DISCUSSION

Fifty genotypes studied in the present investigation were grouped into eight clusters based on the relative magnitude of D² values such that the genotypes belonging to same cluster had an

Table 1. Clustering of 50 genotypes of rice by Tocher's method under saline conditions.

Sl.No	Cluster Number	Number of genotypes	Genotypes
1	I	8	NLR30491, NLR33636, NLR3042, NLR34450, RGL1880, BPT5204, RGL 2537, MGP2
2	II	14	NLR28600, NLR33892, NLR20017, NLR20083, NLR28523, MTU1061, RGL2332, NLR33057, NLR145, RGL2538, NLR33641, CSR-RIL-06-165, Rp Bio-226, NLR33671
3	III	12	NLR33359, NLR20002, NLR40024, NLR3041, NDRK50016, MGP1, MTU1001, BPT3291
4	IV	11	M.Sughandha, NLR33365, NLR33648, NLR9672 PUSA1121, BPT2270, BPT1768, BPT2231, MGP3, NLR34242, RGL11414, NLR20022 NDRK50015, NLR34449, NLR9672-96
5	V	1	NLR27999
6	VI	1	NLR20084
7	VII	1	NLR33358
8	VIII	2	NLR9674, NLR34452

Table 2. Details of centres from which the genotypes in different clusters studied in rice under saline conditions.

Sl.No	Cluster Number	Number of genotypes	Centres of the genotypes
1	I	8	Nellore, Bapatla, Ragolu, Machilipatnam
2	II	14	Nellore, Maruteru, Ragolu, Hyderabad, Karnal
3	III	12	Nellore, Hyderabad, Mauteru, Bapatla, Machilipatnam, Faizadabad
4	IV	11	Nellore, Machilipatnam, Ragolu, Faizadabad, Hyderabad, Bapatla
5	V	1	Nellore
6	VI	1	Nellore
7	VII	1	Nellore
8	VIII	2	Nellore

average smaller D^2 value than those belonging to different clusters. Among the eight clusters, cluster II was the largest comprising of 14 genotypes (NLR 28600, NLR 33892, NLR20017, NLR 20083, NLR 28523, MTU 1061, RGL 2332, NLR33057, NLR 145, RGL 2538, NLR 33641, CSR-RIL-06-165, RP BIO 226 and NLR 33671), representing collections from different centres of the country (Table.1), viz., Nellore, Maruteru, Ragolu Hyderabad and Karnal while cluster III (NLR33359, NLR20002, NLR40024, NLR3041, NDRK50016, MGP1, MTU1001, BPT3291, M.Sughandha, NLR33365, NLR33648 and NLR9672) had 12 genotypes from

Nellore, Hyderabad, Maruteru, Bapatla Machilipatnam and Faizadabad. Similarly, Cluster IV (PUSA1121, BPT2270, BPT1768, BPT2231, MGP3, NLR34242, RGL11414, NLR20022, NDRK50015, NLR34449, and NLR9672-96) had 11 genotypes from Nellore, Machilipatnam, Ragolu, Faizadabad, Hyderabad and Bapatla. The Cluster I (NLR30491, NLR33636, NLR3042, NLR34450, RGL1880, BPT5204, RGL 2537 and MGP2) had eight genotypes from Nellore, Bapatla, Ragolu and Machilipatnam. While V (NLR27999), VI (NLR20084) and VII (NLR33358) clusters had single genotype from Nellore and cluster VIII

Table 3. Average intra and inter cluster D² values among eight clusters comprising of 50 genotypes of rice under saline conditions.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	48.96	182.29	144.94	769.70	314.98	201.36	165.75	2340.41
II		84.72	188.70	389.97	159.54	207.28	250.05	1492.65
III			179.72	620.19	350.78	310.85	227.30	2025.96
IV				276.90	553.88	816.70	773.76	741.03
V					0.00	72.97	362.90	1603.32
VI						0.00	331.29	2194.03
VII							0.00	2387.65
VIII								207.79

Bold and diagonal values indicate intra cluster distance

(NLR9674 and NLR34452) had two genotypes from Nellore. 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 earlier workers (Kandamoorthy and Govindarasu, 2005; Ravindrababu *et al.* (2006); Rameshchandra *et al.* (2007) and Venkatlaxmi, 2013). The production of greater diversity by genetic drift and selection, compared to that produced by geography was also observed in the present study. Genotypes from a particular centre were observed to be distributed over different clusters, while genotypes from diverse geographical regions of different centers were placed in the same cluster (Table.2). Similar results were also reported earlier (Madhavilatha *et al.* 2005).

Intra-cluster D² values ranged from 0.00 (Cluster V, VI, VII) to 276.90 (Cluster IV), indicating maximum genetic divergence among the genotypes in cluster IV, compared to those in other clusters. Further, the inter-cluster D² values of eight clusters revealed highest divergence between clusters VII (0.00) and VIII (2387.65), followed by cluster I(48.96) and VIII (2340.41) indicating that genotypes from these clusters were highly divergent. Kandhola and Panwar (1999) also reported greater diversity between genotypes from different clusters based on their inter-cluster

distance. Minimum inter-cluster distance was observed between clusters IV (276.90) and VIII (741.03) indicating their close relationship and similarity with regards to the characters studied. (Table.3)

The cluster means for each of the twelve characters are presented in Table.4. The data indicated that the cluster mean for shoot length was highest in cluster V (59.43 cm) and the lowest in cluster III (29.48 cm). Shoot Dry weight was also highest in cluster V (0.57 g) and the lowest was in cluster III (0.26 g). Shoot sodium content was highest in cluster VIII (2.38 %) and the lowest was recorded in cluster I (0.34%). Cluster VII recorded the highest shoot potassium content (0.94%) and the lowest shoot potassium content was in cluster VI and cluster VIII (0.34%). Root length was highest in cluster VI (13.37 cm) and lowest in cluster V (9.60 cm). Cluster VI recorded the highest root dry weight (0.19 g) and the lowest was recorded in cluster I and cluster VIII (0.13 g). Days to 50 percent flowering was highest in cluster V (137.34 days) and the lowest in cluster VII (84.67 days). Plant height was highest in cluster VI (104.50 cm) and lowest in cluster I (83.05 cm). Cluster VII recorded the highest number of productive tillers plant⁻¹ (8.30) and the lowest number of productive tillers plant⁻¹ was in cluster V (4.70). The spikelet fertility percent was also highest in cluster VII (85.61) and the lowest in cluster I (69.92). Highest 1000 seed weight was recorded in cluster V (21.90 g) and the lowest in cluster I (16.59 g). Cluster VII recorded the highest grain yield per plant⁻¹ (11.80

Table 4. Mean values of eight clusters obtained by Tocher's method estimated from 50 genotypes of rice under saline conditions.

Sl.No	Cluster	Shoot length (cm)	Shoot Dry weight (g)	Sodium content (%)	Potassium content (%)	Root length (cm)	Root Dry weight (g)	Dry weight per cent	Days to 50 per cent flowering (Days)	Plant height (cm)	Productive tillers hill ⁻¹ (No.)	Spikelet fertility (%)	1000 seed weight (g)	Grain yield plant ⁻¹ (g)
1	I	29.71	0.27	0.34	0.62	10.74	0.13	105.17	83.05	4.97	69.92	16.59	7.32	
2	II	36.80	0.34	0.77	0.60	12.22	0.16	120.88	89.65	6.26	72.37	18.78	8.31	
3	III	29.48	0.26	0.59	0.71	12.88	0.15	116.50	87.98	7.07	72.19	17.89	9.65	
4	IV	34.79	0.32	1.44	0.66	12.91	0.16	118.76	89.03	6.08	71.07	17.59	9.34	
5	V	59.43	0.57	0.72	0.39	9.60	0.14	137.33	103.97	4.70	74.29	21.90	9.70	
6	VI	52.13	0.51	0.39	0.34	13.37	0.19	134.00	104.50	7.20	75.63	19.23	8.30	
7	VII	48.23	0.47	0.39	0.94	9.90	0.16	84.67	90.57	8.30	85.61	20.17	11.80	
8	VIII	35.82	0.32	2.38	0.34	10.30	0.13	120.00	93.17	7.85	73.78	17.32	10.10	

g) while in cluster I it was low (7.32 g). A perusal of these 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. Therefore, judicious combination of all the targeted traits required hybridization between the selected genotypes from divergent clusters. The results also revealed high grain yield, productive tillers, spikelet fertility percent and shoot potassium content for cluster VII; shoot length, shoot dry weight, number of days to 50 percent flowering and 1000 seed weight for cluster V; plant height, root length and root dry weight for cluster VI; and shoot sodium content for cluster VIII indicating the importance of selection of genotypes from these clusters in hybridization programmes for effecting improvement of the respective traits.

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. The shoot sodium content contributed maximum (59.67%), followed by shoot potassium content (15.51%) and shoot dry weight (9.80%). Grain yield plant⁻¹ (4.33%), plant height (3.59%), days to 50 per cent flowering (3.51%), 1000 grain weight (2.86%), productive tillers hill⁻¹ (0.49%), root length (0.16%) and spikelet fertility percent (0.08%) each were observed to contribute less than 5 per cent towards the total divergence (Table.5).

The present investigation, explicitly indicated the presence of considerable diversity in the material studied for salinity tolerance traits, yield components and grain yield. Crossing among divergent parents having desirable traits is most likely to produce better hybrids and desirable recombinants. The greater distance between the clusters indicate higher genetic diversity between them. Based on the above results, 10 parents ((NLR33057, NLR33358, NLR33359, NLR40024, NLR33671, NLR3041, MTU1061, MTU1001, PUSA1121 and BPT2231) are expected to give promising segregants for grain yield, yield components and salinity tolerance traits under saline conditions.

Table 5. Per cent contribution of each character towards genetic divergence (D^2) in 50 genotypes of rice under saline conditions.

Sl.No	Character	Percentage contribution towards divergence	Number of times ranked first
1	Shoot length (cm) at seedling stage	0.01	0
2	Shoot Dry weight (g) at seedling stage	9.80	120
3	Shoot sodium content at maximum tillering stage	59.67	731
4	Shoot potassium content at maximum tillering stage	15.51	190
5	Root length (cm) at seedling stage	0.16	2
6	Root Dry weight (g) at seedling stage	0.01	0
7	Days to 50 per cent flowering (Days)	3.51	43
8	Plant height (cm)	3.59	44
9	No. of. Productive tillers hill ⁻¹	0.49	6
10	Spikelet fertility (%)	0.08	1
11	1000 seed weight (g)	2.86	35
12	Grain yield plant ⁻¹ (g)	4.33	53

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(Received on 21.02.2014 and revised on 24.11.2014)