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Divergent analysis in rice under sodicity

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Abstract
In the present investigation, 31 genotypes were subjected to pooled analysis of variance for ten characters. The analysis of variance for stability revealed that the genotypes were significant for all the traits. An attempt was made to assess the mean performance in 31 rice genotypes for 10 quantitative traits. Among the 31 genotypes measured, high mean value for alkali injury score at vegetative stage were recorded by the following genotypes CR 2218-41-2-1-1-S-B-1, PNL-4-35-20-4-1-4,CSR 12-B 19, CST 7-1, these genotypes shows high mean performance for some of the traits viz., alkali injury score at reproductive stage, plant height, no. of tillers per panicle, no. of filled grains per panicle. CSR-36, CSR-2K-262, CR 2815-4-26-1-S-3-1-1, CARI Dhan 4,CSR-12-19 showed high mean value for 1000 seed weight whereas RP-4353-MSC-38-43-6-2-4-3, CR 2815-4-23-8-5-4-2-1, CR 2815-4-26-1-S-3-1-1, TNAU RICE TRY 3 shows greater mean value for spikelet fertility. These genotypes would be used in hybridization programme. Highest mean value for days to 50% flowering recorded in CSR 12-B -23, CR 2218-41-2-1-1-S-B-1, CR 2839-1S-13-1-5-B-1, CSR 27, CST 7-1 whereas NDRK 11-1, RP 4353-MSC-38-43-6-2-4-3,PNL 1-1-1-6-7-1, NDRK 11-7, shows lowest mean value. The genotypes showed medium duration was utilized in breeding programme which was highly preferred by the breeders as well as by the farmers. The highest mean value for plant height were measured by the genotypes CSR-2K-219, NDRK 11-3, CSR (D) 7-0-4, CSR-12-B-18, CSR-12-B-19, CST 7-1. Genotypes such as CR 2840-1-3-3B-S-B, NDRK 11-5, CARI Dhan 4, Amalmana showed intermediate mean value. This reveals that genotypes with height would be favored by the researchers. Hence these genotypes can be exploited for further breeding programme.

Keywords: divergent analysis-rice-under sodicity

Introduction
Rice (*Oryza sativa* L.) occupies an essential place in Indian agriculture. It is primary food source for more than one third of world's population. Rice is also called as the "Grain of Life", because it is not only the staple food for more than 70 per cent of the Indians but also a source of livelihood for about 120-150 million rural households. It is the staple food crop for people of the eastern and southern parts of the country. Rice is vital for the nutrition of much of the population in Asia, as well as in Latin America and the Caribbean and in Africa. It is one of the main sources of carbohydrate.

At the current rate of population growth accelerating at 1.8 per cent, rice requirement by the year 2020 would be around 140 million tones. Rice production in 2011-2012 was recorded as 103.41 million tones. Rice has been grown under diverse ecological conditions and gets exposed to different environmental stresses like salinity, alkalinity, drought, cold etc. Soil alkalinity and salinity are widespread problems in a number of rice growing countries. Worldwide 800 million hectares of land are affected by either salinity (397 million hectare) or sodicity (343 million hectare). In India, around 7 million hectares of land are salt affected soil which is distributed in different states and about 3 million hectares are affected by sodicity. Alkali soils are characterized by a relatively less (EC < 4 dS/m at 25°C) salt concentration and/or high (>8.2) pH and Exchangeable sodium percentage of >15 (Abrol *et al*., 1988) [1]. Saline soil are characterized by a relatively less (EC < 4 dS/m) salt concentration and or high (> 9) pH and Exchangeable sodium percentage of >16.

Moreover, most of the land suited to rice production is currently unused because of these soil problems in India. In order to meet the increased food production, development of high yielding varieties under sodicity 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. Genetic diversity is the most important tool to choose the right type of parents for hybridization programme. Breeding for sodicity tolerance requires selection of parents with a wider genetic diversity. A narrow genetic base in the breeding materials

limits genetic gains in breeding. Parents identified on the basis of divergence for any breeding program would be more promising (Arunachalam, 1981) [5]. Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. The divergence can be studied by the technique, D^2 statistics which is developed by Mahalanobis (1936) [25]. It is based on multivariate analysis and grouped into various clusters. This is considered as the most effective method to study the degree of genetic diversity among genotypes. Therefore, an attempt is made to study the magnitude of genetic divergence and characters contributing to the genetic divergence in rice under sodicity. The following objective is framed in the present study:

Materials and Methods

Thirty one diverse rice genotypes were grown in randomized block design with three replications during II season, 2012-13. The experiment plot comprised of single row of 3M length with a spacing of 20 cm between rows and 20 cm between plants. The crop was maintained under irrigated transplanted condition under sodicity. The soil ESP (18.1%); EC (0.46 dS/m) and pH (9.02) were recorded during peak tillering phase. The dataon quantative traits were recorded on five random plants per entry per replication. The genetic divergences were estimated by D^2 analysis (Mahalanobis, 1936) [25]. The analysis of variance was worked out to test the differences among genotypes by F-test. It was carried out according to the procedure of Randomized Complete Block Design for each character as per methodology advocated by Panse and Sukhatme (1967) [30]. The genetic divergence among 40 genotypes was estimated by Mahalanobis (1936) [25] D^2 statistics for12 quantitative traits.

Table 1: Distribution of 31 genotypes of rice among clusters on the basis of D^2 analysis

Cluster	No. of genotypes	Genotypes
I	9	CR 2815-4-23-8-5-4-2-1, CR 2815-4-26-1-S-3-1-1, CSR-2K-255, RP 4353-MSC-38-43-6-2-4-3,CR 2840-1-3-3B-S-B, CSR-2K-262, NDRK 11-5, NDRK 11-2, Check (CSR 36)
II	10	CSR 12-B 18, CSR 12-B 19, NDRK 11-4, CSR-2K-219, CR 2839-1S-13-1-5-B-1, CR 2218-41-2-1-1-S-B-1, CSR 12-B23, CR 2815-4-3-1-1-1-1, NDRK 11-6, Check (CSR 27).
III	6	NDRK 11-1, CARI Dhan 4 Amalmana NDRK 11-3 CSR-2K-242 PNL 1-1-1-6-7-1
IV	1	Check (CST 7-1)
V	2	NDRK 11-7 Local Check
VI	1	PNL 4-35-20-4-1-4
VII	1	CSR(D)7-0-4
VIII	1	PNL 9-1-2-7-4-6-1

Table 2: Intra and inter cluster average distances for different characters in rice:

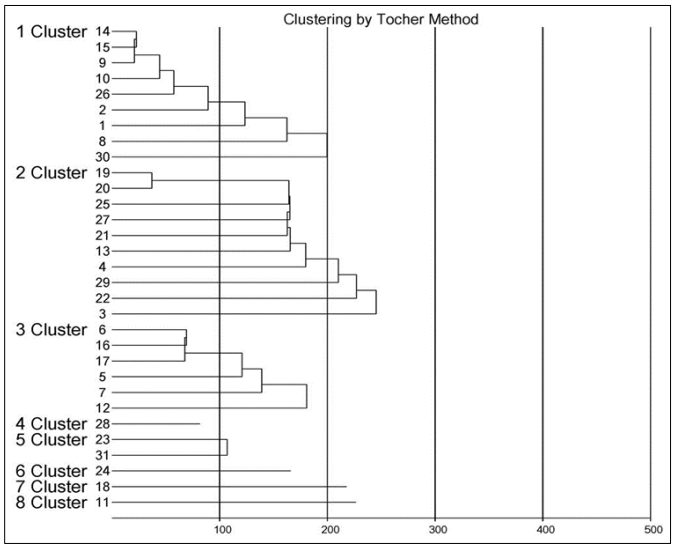
Clusters	I	II	III	IV	V	VI	VII	VIII
I	11.84	17.12	29.59	22.76	21.00	16.71	42.83	50.65
II		15.23	24.31	17.97	26.94	18.14	34.30	43.83
III			13.00	26.03	41.11	34.65	19.61	24.53
IV				0.00	36.97	22.27	30.85	42.29
V					10.34	21.89	54.64	62.63
VI						0.00	44.63	55.09
VII							0.00	15.05
VIII								0.00

The percent contribution of 10 characters towards total genetic divergence is listed in (Table 4). The selection and choice of parents mainly depends upon contribution of characters towards divergence (De *et al*. 1992) [16]. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by spikelet fertility per cent (66.67) followed by no. of tillers per plant (12.69), no. filled grains per panicle (9.68) and plant height (7.10). The lingering character viz., days to 50% flowering, 100 seed weight, panicle length and alkali injury score did not contribute significantly to the total divergence.

Table 3: Per cent contribution of characters towards divergence

Traits	Times ranked 1st	Contribution %
Days to 50% flowering	11	2.37%
Plant height (cm)	33	7.10%
alkali injury score (growth stage:2)	0	0.00%
No. of tillers per plant	59	12.69%
No.of productive tillers per plant	0	0.00%
Panicle length (cm)	2	0.43%
No. of filled grains per panicle	45	9.68%
Spikelet fertility (%)	310	66.67%
alkali injury score (growth stage:5)	2	0.43%
1000 seed weight (gm)	3	0.65%

Table 4: Tocher Methoddiscussion



Discussion

In order to enhance the genetic potential, there must be a comprehensive understanding of the amount and pattern of genetic variation that exists within the available cultivated genotypes of rice. The improvement that can be brought out in a character depends entirely on the magnitude of genetic variability for that character.in recent years, the knowledge of

genetic diversity and the evolutionary history of crop plants resulted major advances in crop improvement. Mahalanobis generalized distance estimated by D^2 statistic and clustering by Tocher's method is a unique tool for discriminating populations by considering a set of parameters together. Assessment of nature and magnitude of genetic diversity is essential for effective choice of parents in hybridization programme. The clustering pattern reflects the closeness between the clusters and the geographical adaptation of the genotypes. In the present investigation, 31 genotypes were subjected to pooled analysis of variance for ten characters. The analysis of variance for stability revealed that the genotypes were significant for all the traits.

The success of any breeding programme depends on the choice of parents based on the mean performance (Anitha and Dorairaj, 1990) [4]. Allard had suggested that the selection should be applied mainly in the lines exhibiting high mean variability. According to the mean performance (Table 2) a wide range of variation was found for most of traits. An attempt was made to assess the mean performance and in rice genotypes represents the mean performance of 31 genotypes for 10 quantitative traits.

Among the 31 genotypes measured high mean value for alkali injury score at vegetative stage were recorded by the following genotypes CR 2218-41-2-1-1-S-B-1, PNL-4-35-20-4-1-4,CSR 12-B 19, CST 7-1, these genotypes shows high mean performance for some of the traits viz., alkali injury score at reproductive stage, plant height, no. of tillers per panicle, no. of filled grains per panicle.CSR-36, CSR-2K-262, CR 2815-4-26-1-S-3-1-1, CARI Dhan 4,CSR-12-19 showed high mean value for 1000 seed weight whereas RP-4353-MSC-38-43-6-2-4-3, CR 2815-4-23-8-5-4-2-1, CR 2815-4-26-1-S-3-1-1, TNAU RICE TRY 3 shows greater mean value for spikelet fertility. These genotypes would be used in hybridization programme. Highest mean value for days to 50% flowering recorded in CSR 12-B -23, CR 2218-41-2-1-1-S-B-1, CR 2839-1S-13-1-5-B-1, CSR 27, CST 7-1 whereas NDRK 11-1, RP 4353-MSC-38-43-6-2-4-3,PNL 1-1-1-6-7-1,NDRK 11-7, shows lowest mean value. The genotypes showed medium duration was utilized in breeding programme which was highly preferred by the breeders as well as by the farmers. The highest mean value for plant height were measured by the genotypes CSR-2K-219, NDRK 11-3, CSR (D) 7-0-4, CSR-12-B-18, CSR-12-B-19, CST 7-1. Genotypes such as CR 2840-1-3-3B-S-B, NDRK 11-5, CARI Dhan 4, Amalmana showed intermediate mean value. This reveals that genotypes with height would be favored by the researchers. Hence these genotypes can be exploited for further breeding programme.

The genotypes with high mean for each trait can be taken into consideration to identify the suitable genotypes for a particular environment. The wide ranges of mean value show the existence of variability among the genotypes. Success of any breeding programme depends upon the availability and accurate description of genetic variation in the breeding material. The greater the genetic variability of the breeding material, better the chances of success to be achieved through selection. However, quantification and classification of the variability in collected genotypes are important in plant breeding since effective utilization of genotypes in breeding program is enhanced if the variation is properly characterized and described (Bezaweletaw *et al*. 2007) [9]. A critical choice of parents from the existing genotypes would be valuable to create segregating progenies with maximum genetic variability for further selection (Barrett and kidwell, 1998) [8]

Genetic diversity arises either due to geographical separation or due to genetic barriers to crossability. Generalized distance analysis among the genotypes of a crop has been used by the researchers under the assumption that cultivars within the group were genetically related whereas diverse cultivars are classified into different clusters. This technique measures the force of differentiation at two levels, namely intra cluster and inter cluster distance. In the present study, genetic divergence was assessed by Mahalanobis D^2 statistics and tocher's method. 31 genotypes were measured for genetic diversity using 10 quantative traits.

A method suggested by tocher (rao, 1952) [16] was used to group the genotypes into different clusters based on D^2 value. Among the different cluster, cluster II consisted number of genotypes (10 genotypes) followed by cluster I (9 genotypes), cluster III (6 genptypes), cluster V (2 genotypes), cluster IV, VI, VII, VIII include one genotype each. Cluster II and I were highly heterogeneous. Cluster I consists of following genotypes CR 2815-4-23-8-5-4-2-1,CR 2815-4-26-1-S-3-1-1,CSR-2K-255,RP 4353-MSC-38-43-6-2-4-3, CR 2840-1-3-3B-S-B, CSR-2K-262,NDRK 11-5,NDRK 11-2,Check (CSR 36). Cluster II consist of genotypes CSR 12-B 18,CSR 12-B 19,NDRK 11-4,CSR-2K-219,CR 2839-1S-13-1-5-B-1,CR 2218-41-2-1-1-S-B-1,CSR 12-B23,CR 2815-4-3-1-1-1-1,NDRK 11-6,Check (CSR 27). Cluster III comprise of genotypes NDRK 11-1, CARI Dhan 4, Amalmana NDRK 11-3, CSR-2K-242, PNL 1-1-1-6-7-1. Cluster IV, VI, VII, VIII consist of Check (CST 7-1), PNL 4-35-20-4-1-4, CSR (D) 7-0-4, PNL 9-1-2-7-4-6-1 respectively. Cluster V encompassed of genotypes NDRK 11-7, TNAU RICE TRY 3.

These result emphasized the necessity of quantative assessment of genetic diversity to identify suitable parents in rice for hybridization program.

In the present study indicated that spikelet fertility contribute maximum per cent towards diversity followed by plant height, no. of tillers per plant and no. of filled grains per panicle. The traits, days to 50% flowering, panicle length, alkali injury score at reproductive stage, 1000 grain weight did not have significant contribution towards the divergence. Alkali score at vegetative stage and no. of productive tillers per plant contribute nothing towards the genetic divergence.

In this study, very high contribution of spikelet fertility per cent alone towards diversity was remarked. In contrast, kumar *et al* (1998) [22] indicated that 1000 seed weight was the major contributor of genetic divergence.

Thirty one genotypes were grouped into eight clusters. The intra and inter cluster average distances among eight clusters were variable (table). The intra cluster distance varied from 10.34(cluster V) to 15.23 (cluster II). The highest intra cluster distance was shown by cluster cluster II (15.23) whereas the minimum intra cluster distance falls in the cluster V (10.34). high cluster D^2 values indicated the significant amount variability among the genotypes within the same cluster.

Diversity among the inter cluster distance varied with D^2 value from 15.05 to 62.63. The highest inter cluster distance showed between the cluster V and cluster VIII (62.63) followed by cluster VI and VIII (55.09), cluster V and cluster VII (54.64), cluster I and cluster VIII (50.65). The minimum inter cluster distance falls in the cluster VII and cluster VIII. Garg (2011) reported that inter cluster D^2 values ranged from 2.46 to 1.60. Chanbeni Y. Ovung (2012) [13] reported that inter cluster varied from 643to 2907. Hybridization programme involving genetically diverse parents belonging to different distant cluster would provide analysis opportunity for bringing together gene constellation of diverse nature,

promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents (Anand and murthy. 1968) [3].

Cluster IV exhibited the highest mean days for 50 per cent flowering (121.33) and cluster III exhibited low mean days to 50 per cent flowering. The highest mean days for 50 per cent flowering (121.33), mean value for plant height (103.00), panicle length (26.00) & 1000 seed weight (24.77) were observed in cluster IV. The highest mean value for No. of tillers per plant (32.67), No. of productive tillers per plant (25.67), No. of filled grains per panicle (127.00) & spikelet fertility percentage (90.78) were observed in cluster V. The highest mean value for alkali injury score (growth stage: 2) (8.33) & alkali injury score (growth stage: 5) (7.67) were observed in cluster VI.

Results of overall cluster means suggested that the selection of genotypes from the clusters IV, V & VI for further breeding work may yield better recombinants.

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