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Studies on genetic diversity of rice (*Oryza sativa* L.) under natural saline condition

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Abstract
The present investigation on genetic diversity was carried out with twenty five rice genotypes including saline tolerant check variety, TRY 1 and TRY(R) 3 during navarai 2018. Twenty five rice genotypes were used to evaluate their response in saline condition for 12 biometrical traits *viz.*, days to first flowering, plant height, number of productive tillers per plant, number of grains per panicle, 100 grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. Genetic divergence was studied based on Mahalanobis D^2 statistic and grouping of cluster was done following Tocher's method. The analysis of variance revealed the presence of significant variability among the genotypes for all the characters studied. Twenty five rice genotypes were grouped into eight clusters based on genetic distance and mean of different characters. The maximum intra cluster distance was recorded by cluster VIII and maximum inter cluster distance was observed between clusters VII and VIII. Parents selected from these clusters could produce superior progenies and hybrids for saline tolerance. In the present study, the distantly related parents belonging to clusters VII and VIII, VI and VII may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregation with high heterotic effects. Thus the genotypes, NLR 34449, ADT 46, ADT 49, BPT 5204 and TRY 3 holds greater potential for improving and stabilizing the productivity of saline prone areas.

Keywords: Genetic diversity, saline condition, D^2 analysis

Introduction
Rice (*Oryza sativa* L.) popularly called as "Global grain" occupies a pivotal place as a primary food source for more than half of the global population. It is a member of grass family (Poaceae) having more than 20 species in which there are two distinct cultivated species having AA genome with diploid level (2n = 24), *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). Asia is known to be rice bowl of the world, as more than 90% of the world's rice is grown and consumed here. India is remarkably rich in rice diversity, including cultivars, landraces, wild and weedy relatives (DRR, Hyderabad).

Among the rice growing countries of the world, India ranks second in production and consumption next to China. In India, it is estimated that rice would be grown in an area of 42949.60 thousand hectares with a production of 112905.50 thousand tonnes and productivity of 2585kg per hectare (Indiastat, 2017) [4].

Many factors are considered for the low production rate in rice, especially the environmental obstacles such as different abiotic stress e.g. drought, flood and salinity (Gregario *et al.*, 2002) [3]. Among these, soil salinity become more alarming as the amount of saline area around the globe is increasing gradually due to higher use of ground water for irrigation and rising of the sea level due to the global warming (Mori and Kinoshita, 1987) [5]. At present, salinity is the second type of stress and is the most predominant hindrance to rice production after drought (Gregario *et al.*, 1997) [3]. In accordance to the above facts and keeping in view the present alarming scenario, development of salt tolerant genotypes is definitely an urgent need of the hour.

Genetic diversity in crop plants is essential to sustain level of high productivity (Tripathi 2013). In the present study D^2 technique based on multivariate analysis developed by Mahalanobis (1936), has been used to quantify the degree of divergence in germplasm. Thus hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature.

Materials and Methods

The experimental material for this genetic divergence study comprised of twenty five rice Genotypes collected from various places were utilized for study. The details of the materials are presented in Table 1. The experiment was carried out at the Experimental Farm of Plant Breeding Department (11°24´N latitude and 79°44´E longitude 5.79 m MSL), Tamilnadu, India during Navarai, 2018 (December - January). Seeds of the 25 rice genotypes were sown in raised nursery bed under saline soil with electrical conductivity (EC) of 2.1 dsm^{-1} and pH 8.5. In each genotype, one seedling per hill was transplanted in the main field after 25 days with the spacing of 20 cm between rows and 15 cm between plants in 3 m long rows. The experiment was carried out in randomized block design with three replications. Recommended agronomic practices and need based plant protection measures were taken up to maintain healthy crop stand.

Table 1: List of Rice Genotypes Selected for D^2 Analysis

Genotype Code	Genotype Names	Origin
G1	Jgl 1798	Krishi Vigyan Kendra, Nellore, Andhra Pradesh
G2	Ir 20	International Rice Research Institute, Philippines.
G3	Adt 43	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G4	Trupthi	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G5	Adt 45	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G6	Adt(r) 49	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G7	Nlr 34449	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G8	Adt(r) 50	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G9	Tkm 9	Rice Research Station, Thirurkuppam.
G10	Co 43	Tamil Nadu Agricultural University, Coimbatore.
G11	Sonam	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G12	Adt 39	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G13	Co(r) 51	Tamil Nadu Agricultural University, Coimbatore.
G14	Adt 46	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G15	Bpt 5204	Agricultural College, Bapatla, Andhra Pradesh, India.
G16	Adt 37	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G17	Akshaya	Banaras Hindu University, Varanasi
G18	Try 1	Agriculture College & Research Institute (TNAU), Trichy
G19	Adt 36	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G20	Swarna sub 1	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G21	White ponni	Tamil Nadu Agricultural University & RI, Coimbatore.
G22	Asd 16	Regional Research Station, Ambasamudram, TN, India.
G23	Try(r) 3	Agriculture College & Research Institute (TNAU), Trichy
G24	Co(r) 50	Tamil Nadu Agricultural University, Coimbatore
G25	Adt 41	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India

Results and Discussion

The genetic divergence of 25 genotypes of rice was studied by using Mahalanobis D^2 analysis. Based on D^2 analysis, the 25 genotypes were grouped into eight clusters (Table 2). Among the eight clusters, cluster V comprised of five genotypes was the largest cluster with maximum number of genotypes. This was followed by clusters I, VII, VIII with four genotypes and clusters II, III, IV, VI which had two genotypes each.

Table 2: Distribution of 25 rice genotypes into different clusters

Cluster No.	Genotypes	Number of Genotypes
Cluster I	Jgl 1798, ir 20, nlr 34449, adt 39	4
Cluster II	Adt(r) 50, sonam	2
Cluster III	Co(r) 51, adt 36	2
Cluster IV	Co 43, white ponni	2
Cluster V	Adt 43, trupthi, adt 45, adt(r) 49, tkm 9	5
Cluster VI	Try 1, co(r) 50	2
Cluster VII	Adt 46, bpt 5204, swarna sub 1, asd 16	4
Cluster VIII	Adt 37, akshaya, try(r) 3, adt 41	4

The highest intra cluster distance was registered in cluster VIII followed by cluster VI (Table 3) (Fig.1). Thus the genotypes from those cluster had high degree of divergence that would produce more desirable segregants for achieving greater genetic advance. The least intra cluster distance was recorded in cluster II followed by cluster III and IV indicating homogenous nature of the genotypes with less deviation between the genotypes. Parallel findings were found by Nirosha *et al.* (2016) [6]. Parents selected from these clusters could able to produce superior progenies and hybrids to overcome saline problem.

The maximum inter cluster distance was found between clusters VII and VIII (206.59) followed by clusters VI and VII (197.56) showing the wider genetic diversity among the genotypes between these clusters. This indicates that the genotypes in these clusters are having broad spectrum of genetic diversity and could be used in hybridization programme. Therefore, genotypes of clusters VII and VIII may be selected as parents in formulating breeding programmes. This is in conformity with the findings of Yadav *et al.* (2011) [7].

Table 3: Average inter (D^2) and intra (D) cluster distance for 25 rice genotypes

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster VI	Cluster VII	Cluster VIII
Cluster-I	5335.697 (73.04)	15142.783 (123.05)	2829.913 (53.19)	4157.878 (64.48)	17491.471 (132.25)	21723.467 (147.38)	10839.973 (104.11)	26758.354 (163.57)
Cluster-II		674.720 (25.97)	13798.920 (117.46)	20917.260 (144.62)	21311.799 (145.98)	22758.004 (150.85)	20683.205 (143.81)	25963.363 (161.13)
Cluster-III			750.864 (27.40)	1814.035 (42.59)	17763.480 (133.27)	23379.283 (152.90)	9109.535 (95.44)	27818.467 (166.78)
Cluster-IV				859.938 (29.32)	21995.551 (148.30)	29798.637 (172.62)	9642.723 (98.19)	33847.090 (183.97)
Cluster-V					18169.004 (42.61)	10637.462 (103.13)	31025.332 (176.14)	17693.826 (133.01)
Cluster -VI						2307.759 (48.03)	39032.281 (197.56)	9765.483 (98.82)
Cluster-VII							18215.240 (134.96)	42681.727 (206.59)
Cluster VIII								22239.604 (149.12)

Intra cluster – Diagonal values
Inter cluster – Off diagonal values

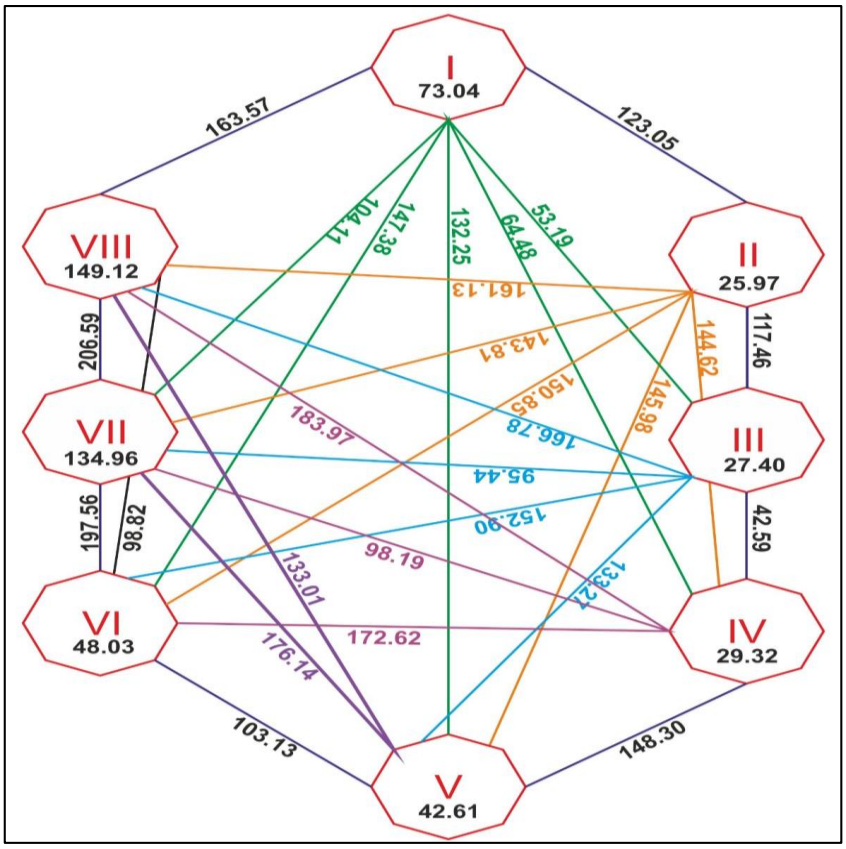

Fig 1: Cluster pattern based on D values (not to Scale in rice Genotypes)

Cluster mean analysis revealed a wide range of variation for all the characters under study (Table 4). Cluster III had lowest cluster mean value for days to first flowering indicating that the genotype in this cluster had earliness in the flowering and may serve as a suitable source for incorporation of earliness in other genotypes. While cluster II shows the highest cluster mean value for days to first flowering indicating that the genotypes in this cluster had late flowering.

Cluster II recorded the maximum cluster mean value for plant height whereas cluster III had minimum value. Thus genotypes from cluster III could be utilized in the breeding programme for obtaining semi dwarf segregants. Similar results were reported by Bhadru *et al.* (2011)

Cluster VI shows the maximum cluster mean value for number of productive tillers per plant while the cluster IV showed the minimum cluster mean value. Number of grains per panicle was found maximum in cluster VII while minimum value was found in cluster IV. The maximum cluster mean value for 100 grain weight was recorded in cluster VII while the minimum value recorded in cluster II for the characters. Obtaining bold grain type segregants would be possible by selecting genotypes from the cluster VII as it had the maximum 100 grain weight.

The maximum cluster mean value for grain length was recorded in cluster VII whereas cluster VI had minimum value. Cluster II had the maximum cluster mean value for grain breadth while cluster VI had minimum value. Grain L/B ratio was found maximum in cluster IV while cluster II had minimum value. Kernel length was found maximum in cluster III while low in cluster VIII. Cluster II recorded maximum

cluster mean value for kernel breadth while cluster IV had minimum value. The maximum cluster mean value for kernel L/B ratio was recorded in cluster IV whereas cluster II had minimum value. For grain yield per plant, maximum cluster mean value recorded in cluster VI and minimum in cluster III. The relative contribution of individual characters towards the expression of genetic diversity were estimated and characters wise D^2 value recorded 35.66 per cent contribution for grain length, 25 per cent contribution for grain yield per plant were the major forces of discrimination among the genotypes tested. Similar findings were reported by Damodar Reddy (2012) [2].

Reference

1. Bhadru DD, Lokanadha Reddy, MS Ramesh. Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. Electronic J Pl. Breed. 2011; 2(1):112-116.
2. Damodar Reddy P. Studies on genetic divergence of some improved rice genotypes under salinity (*Oryza sativa* L.). M.Sc. (Ag.) Thesis, Annamala Univ., Annamalainagar, India, 2012.
3. Gregario GB, Senadhira D, Mendoza RD, Manigbas NL, Roxas JP, Guerta CQ *et al.* Progress in breeding for salinity tolerance and other abiotic associated stresses in rice. Field crops Research. 2002; 76:91-101.
4. Gregorio GB, Tagging salinity tolerance genes in rice using amplified fragment length polymorphism (AFLP). PhD thesis, University of the Philippines, Los Banos, 1997, 118. http://www. indiastat.com
5. Mori I, Koh, Kinoshita T. Salt tolerance of rice callus clones. Rice Genetics Newsletter. 1987; 4:112-113.
6. Nirosha RS, Thippeswamy V, Ravindrababu V, Ram Reddy, Spandana B. Genetic diversity analysis of zinc, iron, grain protein content and yield components in rice. Electronic J. of Plant Breeding, 2016, 371-377.
7. Yadav I, Kumar SS, Jain R, Vimal SC, Yadav VK. Character association and path analysis of vigor index with some important seed vigor contributing traits in barley (*H. vulvgare* L.). Environment and Ecology. 2011, 29:1866-1870.