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PHENOTYPIC DIVERGENCE OF RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER FARMERS FIELD AND COASTAL SALINE FIELD CONDITION

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Abstract

Genetic divergence is a pre-requisite for the production of superior recombinants for the crop improvement program. The nature and magnitude of genetic divergence were estimated in 33 genotypes of rice for ten quantitative characters under normal environment (E_1) and saline field environment (E_2) were considered and evaluated using D^2 statistics from Mahalanobis. The analysis of variance revealed a highly significant difference among the rice genotypes for all the ten traits studied. All the genotypes show significant variations in their mean output for all the ten characters examined. Based on the study of Mahalanobis D^2 33 genotypes were grouped into 6 clusters in E_1 and nine clusters in E_2 and eleven clusters in the pooled analysis. The clustering pattern showed that there is little parallelism exists between geographical origin and genetic diversity, because genotypes from different geographical to source fall within the same cluster and *vice versa.* The intracluster distance ranged from 449.47 in cluster II to a maximum distance of 7829.81 in cluster IV and the inter-cluster distance D^2 values also varied widely between cluster I and IV with a maximum value of 7349.49 and a minimum value of 993.80 between cluster II and cluster III under E1. In E_2 intracluster distance ranged from 279.84 in cluster II to 6149.94 cluster VIII and minimum inter-cluster distance showed between cluster VII and VIII (4768.74) and the minimum was recorded between cluster III and cluster VII (515.65). Among ten characters studied Days to 50 per cent flowering (22.16), 100 seed weight (22.16), number of tillers per plant (18.75), and grain yield per plant (10.04) are the four major contributing traits towards genetic divergence in E1; in E2 three characters days to 50 per cent flowering (11.74), 100 seed weight (26.52) and grain yield per plant (27.08) and in pooled analysis days to 50 per cent flowering (21.40), plant height (11.36), number of tillers per plant (21.40) and grain yield per plant (17.80) are the four major contributors.

Comparison of mean of various characters over normal (E1) and saline field environment (E2) revealed the phenomena of decreased plant height along with the reduced number of tillers per plant, number of panicles per plant, flag leaf length, flag leaf breadth, panicle length, number of grains per panicle and grain yield per plant under saline field environment (E2). When compared to normal crop growth in (E1). Grain yield was drastically affected by an increase in salinity. In our investigation, three genotypes G_7, G_{20}, G_{15} which recorded stable and high yield under salinity.

Therefore, selection of divergent genotypes from the clusters namely III and IV, II and VIII and II and X from E_1, E_2 and pooled analysis respectively would produce a broad spectrum of variability for different traits studied, which may enable further selection and improvement of grain yield along with saline tolerance. The hybrids developed from the genotypes (AURC 2108, AURC 2204, AURC 2117) within the limit of compatibility of these clusters may produce the high magnitude of heterosis or desirable segregants which would be rewarding in a rice breeding programme.

Keywords **:** *Oryza sativa* L., Genetic diversity, Phenotypic Screening, Mahalanobis' D^2 statistics

Introduction

Rice (*Oryza sativa L.* 2n=24) belongs to Poaceae family. It is the most important food crop that provides the staple food for almost half of the world's population (Mahmood-ur-Rahman ANSARI *et al*., 2015). It is originated from South East Asia and has been grown extensively in the humid-tropical and Subtropical regions of the geographical distribution. It is the staple food for 65 per cent of the human population in India. It is the staple food of 65% of India's human population. It is a major source of lively hood for more than 250 million households. Rice is the major calorie intake source and also contributes to the total agricultural income in most of the Asian countries. The area under rice farming in India was during 2016-2017 was 43.5 million hectares with a production of 104.32 million tonnes during (Directorate of Economics and Statistics Report, 2017). However, at the current rate of population growth, rice production has to be enhanced to about 120 million tonnes by 2020 (Survey of Indian Agriculture, 2005). It is well known that rice is grown under different ecologies and water regimes, suffer severe yield losses due to several biotic and abiotic stresses (Samal *et al*., 2016). Rice crop in coastal areas is very often subjected to major abiotic stresses such as submergence, harvest lodging due to heavy rains or cyclones and salinity. To sustain climate change conditions, identification of genotypes tolerance to multiple abiotic stress is required.

Rice is sensitive to salinity at the early seedling and reproductive stages (Tiwari *et al.,* 2016). Salinity in soil and/or water is one of the main abiotic stresses in all over the world, cause reducing plant growth and crop productivity. About 6.5% (831 million ha) of the world's total cultivated area (12.78 billion ha) is plagued by salt in soils (FAO). In India, salt-affected soils currently constitute 6.73 million ha in different agro-ecological regions, which are expected to increase to 16.2 million ha by 2050.

Millions of hectares within the humid areas of South and Southeast Asia are technically fitted to rice production but are left uncultivated or otherwise low productive in terms of yields because of salinity and other abiotic stresses (Boje-Klein, 1986). Thus, it is understood that utilization of the less

productive lands, including salinized lands is an absolute requirement for the growing demand for food. The use of some management options can ameliorate yield reduction under salinity stress. However, implementation of such practice is often limited because of the high cost and less availability of good quality water. Therefore, the need for genetic improvement of salt tolerance of rice plant is of utmost concern, as it is the practical way to meet the ever-growing demand of food for the burgeoning population.

Hence, the study of traits associated with the improved performance of the plants under salt stress conditions will help in screening and selection of tolerant genotypes and using these traits in breeding programs.

Materials and Methods

The present investigation was conducted in two different environments E_1 (Normal field environment) and E_2 (salinity field) during (Kuruvai season) June 2019. The particulars of the two environments are presented in Table 2. Thirty-three rice genotypes (along with 24 culture and 9 popular rice varieties) were used in the present investigation. The seeds of these genotypes were collected from various places. The details of these genotypes are furnished in (Table 1).

Field plot technique

Seeds of thirty-three rice genotypes were sown in raised nursery beds during (Kuruvai season) June 2019. The study was conducted with three replications in two different environments in a randomized block design. In each genotype, one seedling per hill was transplanted into the main field after 25 days aging seedling with the spacing of 20 cm between rows and 15 cm between plants for 6 m row length were maintained per replication. Recommended agronomic practices and need-based plant production measures were carried. Ten agronomic traits *viz*., days to 50% flowering, plant height, number of tillers, number of panicles per plant, flag leaf length, flag leaf breadth, panicle length, number of grains per panicle, 100 seed weight and grain yield per plant were recorded and analyzed statistically by using the software.

Statistical Analysis

Unit analysis : The mean values were computed for each genotype over three replications for each genotype. The variance and the corresponding standard errors of the mean were computed from the deviation of the individual values (Panse and Sukhatme, 1978).

Genetic divergence : Mahalanobis D^2 statistic was used for estimating the genotypic divergence among the thirty-three genotypes. The D^2 statistic between the populations as estimated from the sample on the basis of 'P' character is,

$$D^2p = \sum_{i=1}^{P} \sum_{j=1}^{P} (\lambda i j) \sqrt{}_i \sqrt{}_j$$

where,

ij = Reciprocal matrix to the pooled common dispersion obtained from the error matrix.

i = Difference in mean values for the i^{th} character of the two populations.

j = Difference in mean values for the j^{th} character of the two populations.

Accordingly, error variance and covariance matrix were obtained. The correlated variables were transformed into uncorrelated variables by pivotal condensation method as given by Rao (1952). The actual values of D^2 between any two variables were obtained by squaring and adding differences corresponding to the transformed mean values of the two genotypes.

Table 1 : List of 33 rice accessions and their source.

Name of genotypes	Source
AURC 2102	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2112	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2113	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2107	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2105	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2111	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2108	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2106	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2101	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2115	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2119	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2114	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.

AURC 2110	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2116	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2117	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2103	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2216	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2218	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2213	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2204	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2212	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2201	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2206	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
AURC 2200	Experimental Farm, Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India.
CSR – 27	Central Soil Salinity Research Institute, Karnal, Haryana, India
SWARNA SUB – 1	Directorate of Rice Research Institute, Hyderabad, India
TRY-3	Agricultural College & Research Institute, Trichy, Tamilnadu, India
CSR – 10	Central Soil Salinity Research Institute, Karnal, Haryana, India
PUSA – 44	Punjab Agricultural University, Punjab, India
CSR – 36	Central Soil Salinity Research Institute, Karnal, Haryana, India
ADT – 36	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
ADT – 37	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
ADT – 38	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India

Table 2 : Particulars of two environments

Particulars	**E_1**	**E_2**
Location	Farmer's Field Farmer name: Gnanasekaran Kavarapattu Chidambaram Tamilnadu	Experimental farm Department of Genetics and Plant Breeding Annamalai Nagar Cuddalore dt. Tamilnadu
Latitude		11.3921° N
Longitude		79.7146° E
Season	Kuruvai	Kuruvai
	June 2019	June 2019
Soil type	Clay loam	Clay
Soil Ph	6.8	7.9
EC	0.37	1.34
Soil status		
N	High	High
P	Low	Medium
K	High	High
Climate		
Avg. Temp (°C)	27.4	29.4
Avg. Rainfall (mm)	1075	1298

Results and Discussion

The genotypes under study showed a wide range of variations in both normal and salt stress condition, which provide the plant breeder with the opportunity to select appropriate genotypes for the further breeding program, Genetic divergence between rice genotypes for grain yield and yield attributing traits. Based on D^2 analysis 33 genotypes were grouped into six clusters in E1, while nine clusters in E2 and pooled analysis were grouped into eleven clusters.

In E1, the cluster VI comprised of 13 genotypes had the maximum number of genotypes, whereas cluster I comprised of eight genotypes and cluster IV comprised of six genotypes and cluster II, III, V comprised of two genotypes each (Table 3). In E2, cluster IX comprised of 9 had the maximum number of genotypes, whereas cluster I consists of eight genotypes and cluster VIII comprised of 4 genotypes and cluster II, III, IV, V, VI, VII comprised of two genotypes each (Table 4). In pooled analysis, cluster I comprised of 8 had the maximum number of genotypes, whereas cluster X comprised of 6 genotypes and cluster XI comprised of 3 genotypes and cluster II, III, IV, V, VI, VII, VIII, IX comprised of two genotypes each (Table 5).

Intra and inter-cluster distance

The intra and inter-cluster distance among six clusters in E1, nine clusters in E2 and eleven clusters in pooled analysis were computed and presented in Table (6,7&8) respectively. The intracluster distance for E1, E2 and pooled analysis ranged from 449.47 (cluster III) to 7829.81 (cluster IV), 279.84 (cluster II) to 6149.94 (cluster VIII) and 354.80 (cluster II) to 5188.77 (cluster X) respectively.

The maximum inter-cluster distance in E1 was found between cluster I and IV (7349.49). In E2 it was found between cluster VII and VIII (4768.74) and in the pooled analysis it was found between cluster VIII and X (7571.67).

Table 3 : Composition of D^2 clusters for 33 rice genotypes in E1

Clusters	No. of genotypes	Name of the genotypes
I	8	AUC 2102, AUC 2112, AUC 2113, AUC 2107, AUC 2105, AUC 2111, CSR – 27, ADT – 36
II	2	AUC 2101, AUC 2114
III	2	PUSA – 44, CSR – 36
IV	6	AUC 2108, AUC 2106, AUC 2115, AUC 2119, AUC 2110, SWARNA SUB – 1
V	2	AUC 2103, ADT – 37
VI	13	AUC 2116, AUC 2117, AUC 2216, AUC 2218, AUC 2213, AUC 2204, AUC 2212, AUC 2201, AUC 2206, AUC 2200, TRY-3**,** CSR – 10, ADT – 38

Table 4 : Composition of D^2 clusters for 33 rice genotypes in E2

Clusters	No. of genotypes	Name of the genotypes
I	8	AUC 2102, AUC 2112, AUC 2113, AUC 2107, AUC 2105, AUC 2111, AUC 2213, SWARNA SUB – 1
II	2	CSR – 10, ADT – 36
III	2	AUC 2114, PUSA – 44
IV	2	AUC 2115, TRY-3
V	2	AUC 2218, CSR – 27
VI	2	AUC 2212, ADT – 37
VII	2	AUC 2101, AUC 2119
VIII	4	AUC 2108, AUC 2106, AUC 2110, CSR – 36
IX	9	AUC 2116, AUC 2117, AUC 2103, AUC 2216, AUC 2204, AUC 2201, AUC 2206, AUC 2200, ADT – 38

Table 5 : Composition of D^2 clusters for 33 rice genotypes in the Pooled analysis

Clusters	No. of genotypes	Name of the genotypes
I	8	AUC 2102, AUC 2112, AUC 2113, AUC 2107, AUC 2105, AUC 2111, AUC 2101, CSR-10
II	2	AUC 2114, ADT – 37
III	2	AUC 2218, CSR-36
IV	2	AUC 2115, SWARNA SUB-1
V	2	CSR – 27, ADT – 36
VI	2	AUC 2110, AUC 2216
VII	2	AUC 2212, TRY – 3
VIII	2	AUC 2119, AUC 2103
IX	2	AUC 2213, PUSA – 44
X	6	AUC 2108, AUC 2106, AUC 2116, AUC 2117, AUC 2204, AUC 2201
XI	3	AUC 2206, AUC 2200, ADT – 38

Table 6 : Average inter and intracluster distances for yield and yield attributing characters in 33 rice genotypes under normal field condition (E1)

Cluster no.	I	II	III	IV	V	VI
I	6500.76 (80.63)	5078.41 (71.26)	6709.50 (81.91)	7349.49 (85.73)	3868.82 (62.20)	6351.57 (79.70)
II		449.47 (21.20)	993.80 (31.53)	5155.75 (71.80)	1789.18 (42.30)	4618.56 (67.96)
III			507.84 (22.54)	5518.59 (74.29)	3676.05 (60.63)	6097.07 (78.08)
IV				7829.81 (88.49)	5172.99 (71.92)	6536.41 (80.85)
V					1011.35 (31.80)	4025.22 (63.45)
VI						5837.66 (76.41)

Table 7 : Average inter and intracluster distances for yield and yield attributing characters in 33 rice genotypes under saline field condition (E2)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	3580.13 (59.83)	2531.72 (50.32)	2177.33 (46.66)	2111.01 (45.95)	2389.25 (48.88)	2341.57 (48.39)	2563.58 (50.63)	4317.27 (65.71)	3984.43 (63.12)
II		279.84 (16.73)	580.31 (24.09)	665.64 (25.80)	2437.29 (49.37)	1929.97 (43.93)	667.26 (26.02)	4306.13 (65.62)	4363.12 (66.05)
III			310.25 (17.61)	656.63 (25.63)	1779.50 (42.18)	1165.65 (34.14)	515.65 (22.71)	3837.09 (61.94)	3821.81 (61.82)
IV				311.19 (17.64)	1747.42 (41.80)	1274.23 (35.70)	1336.15 (36.55)	3189.27 (56.47)	3245.54 (56.97)
V					320.67 (17.91)	570.26 (23.88)	1951.68 (44.18)	3501.97 (59.18)	2581.47 (50.81)
VI						350.99 (18.74)	1474.91 (38.41)	3826.10 (61.86)	2811.82 (53.03)
VII							425.88 (20.64)	4768.74 (69.06)	4449.44 (66.70)
VIII								6149.94 (78.42)	4634.32 (68.08)
IX									4309.27 (65.65)

Cluster Mean

A wide range of variation was observed in cluster mean for all the ten characters studied. In E_1 normal environmental condition maximum cluster mean for grain yield per plant (45.13), number of grains per panicle (187.35), flag leaf breadth (1.37) it was observed in cluster VI, while for flag leaf length (35.69) and number of panicles per plant (15.17) it was observed in cluster IV and for number of tillers per plant (22.80) it was observed in cluster I (Table 9).

Table 8 : Inter (D^2) and intra (D) cluster values of various clusters in rice in the Pooled analysis

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	3406.76 (58.37)	2247.23 (47.41)	2231.31 (47.24)	2874.52 (53.62)	2198.77 (46.89)	1899.60 (43.58)	3285.11 (57.32)	2626.45 (51.25)	3286.87 (57.33)	6132.04 (78.31)	4178.97 (64.65)
II		354.80 (18.84)	1056.22 (32.50)	749.59 (27.38)	847.78 (29.12)	1724.55 (41.53)	821.75 (28.67)	1191.18 (34.51)	861.20 (29.35)	4831.82 (69.51)	3930.09 (62.69)
III			365.34 (19.11)	744.28 (27.28)	943.31 (30.71)	1300.78 (36.07)	1532.07 (39.14)	1932.57 (43.96)	1199.85 (34.64)	3773.69 (61.43)	3709.78 (60.91)
IV				380.09 (19.50)	1503.15 (38.77)	2461.19 (49.61)	1095.81 (33.10)	2005.56 (44.78)	562.07 (23.71)	3925.76 (62.66)	5153.84 (71.79)
V					390.11 (19.75)	1305.17 (36.13)	1417.54 (37.65)	1207.29 (34.75)	1864.71 (43.18)	5859.92 (76.55)	3276.24 (57.24)
VI						417.94 (20.44)	2965.30 (54.46)	1946.97 (44.12)	3204.88 (56.61)	5169.88 (71.90)	2576.54 (50.76)
VII							525.85 (22.93)	2954.01 (54.35)	1373.50 (37.06)	4408.60 (66.40)	3976.83 (63.06)
VIII								809.93 (28.46)	2037.61 (45.14)	7571.67 (87.02)	5337.11 (73.06)
IX									873.75 (29.56)	4635.98 (68.09)	5924.68 (76.97)
X										5188.77 (72.03)	6700.40 (81.86)
XI											3783.68 (61.51)

Table 9 : Cluster means of 33 rice genotypes for various characters in E1

Cluster	Days to first flowering	Plant height	Number of tillers per plant	Number of panicles per plant	Flag leaf length	Flag leaf breadth	Panicle length	Number of grains per panicle	100 seed weight	Grain yield per plant
I	80.67	89.64	22.80	14.72	29.57	1.34	23.91	153.86	2.24	42.850
II	79.76	93.04	17.65	8.07	30.16	1.21	22.62	139.12	2.59	22.27
III	86.47	101.40	20.17	12.95	27.86	1.29	25.03	141.09	2.80	29.61
IV	86.88	104.84	20.83	15.17	35.92	1.30	25.02	171.50	2.31	44.10
V	77.89	94.81	19.45	11.57	27.19	1.27	20.77	106.12	2.20	25.13
VI	78.83	104.55	22.67	14.43	35.69	1.37	25.62	187.35	2.21	45.13
General mean	81.75	98.05	20.60	12.82	31.07	1.30	23.83	149.84	2.39	39.73

Table 10 : Cluster means of 33 rice genotypes for various characters in E2

Cluster	Days to first flowering	Plant height	Number of tillers per plant	Number of panicles per plant	Flag leaf length	Flag leaf breadth	Panicle length	Number of grains per panicle	100 seed weight	Grain yield per plant
I	82.61	83.95	19.73	12.62	28.11	1.34	22.46	132.68	2.32	35.03
II	75.10	78.84	17.03	10.00	23.61	1.14	23.65	137.68	2.78	22.74
III	84.11	88.02	16.84	7.24	25.88	1.21	22.24	122.33	2.51	20.58
IV	76.05	96.04	17.51	11.84	31.70	1.32	24.35	152.13	2.57	29.02
V	76.76	85.61	20.76	15.77	25.15	1.11	24.69	138.81	1.99	35.65
VI	71.23	93.32	20.65	10.42	29.00	1.18	22.58	136.53	2.12	27.18
VII	80.15	72.08	16.31	8.74	23.80	0.99	20.65	99.29	2.52	18.05
VIII	89.08	95.02	18.48	13.72	31.64	1.34	24.70	168.75	2.23	44.37
IX	78.65	88.89	21.50	13.75	31.90	1.39	23.34	175.89	2.06	44.56
General mean	79.30	86.86	18.76	11.57	27.87	1.22	23.18	140.45	2.34	30.80

Table 11 : Cluster means of 33 rice genotypes for various characters in the Pooled analysis

Cluster	Days to first flowering	Plant height	Number of tillers per plant	Number of panicles per plant	Flag leaf length	Flag leaf breadth	Panicle length	Number of grains per panicle	100 seed weight	Grain yield per plant
I	81.44	83.15	20.06	12.38	29.08	1.33	23.04	146.03	2.43	37.56
II	77.31	93.99	19.63	9.18	27.87	1.23	22.34	136.88	2.31	25.84
III	84.19	93.83	17.94	13.89	26.35	1.15	24.30	150.91	2.41	36.71
IV	81.54	102.73	16.42	12.63	31.83	1.31	22.54	129.57	2.51	26.71
V	73.53	87.66	22.13	15.55	23.44	1.15	24.37	133.24	2.13	31.07
VI	82.24	79.26	21.20	13.95	26.36	1.29	21.12	164.78	1.95	41.06
VII	70.55	105.12	22.80	13.13	34.37	1.28	26.08	170.66	2.40	31.86
VIII	81.66	79.65	19.15	10.99	24.99	1.08	20.02	85.96	2.36	18.56
IX	84.23	103.56	18.54	10.42	29.70	1.31	24.58	122.41	2.53	24.25
X	87.11	109.25	19.03	13.62	40.16	1.51	26.04	208.46	1.98	50.05
XI	73.67	89.91	29.99	18.01	32.79	1.31	25.65	190.92	2.21	61.21
General Mean	79.77	93.47	20.63	13.07	29.72	1.27	23.64	149.07	2.29	34.99

Table 12 : Contribution of different characters to genetic divergence

S. No	Characters	E1	E2	Pooled analysis
1	Days to 50% flowering	22.16	11.74	21.40
2	Plant Height	5.30	7.96	11.36
3	Number of Tillers per plant	18.75	8.90	21.40
4	Number of Panicles per plant	5.87	3.22	5.87
5	Flag Leaf Length	1.71	4.92	6.63
6	Flag Leaf Breadth	5.11	3.41	4.17
7	Panicle Length	2.08	0.57	1.52
8	Grains Per Panicle	6.82	5.68	7.77
9	100 Seed Weight	22.16	26.52	2.08
10	Grain Yield per plant	10.04	27.08	17.80

In E_2, saline environment, maximum cluster mean for grain yield per plant (44.56), number of grains per panicle (175.89), flag leaf length (31.90), flag leaf breadth (1.39), number of tillers per plant (21.50) was observed in cluster IX, while for panicle length (24.70) it was observed in cluster VIII and number of panicles per plant (15.77) was maximum in cluster V (Table 10).

In pooled analysis cluster XI recorded maximum cluster mean values for the number of tillers per plant (29.99), number of panicles per plant (18.01) and maximum grain yield per plant (61.21). While cluster X for flag leaf length (40.16), flag leaf breadth (1.51) and the number of grains per panicle (208.46) and cluster VII for panicle length (26.08) (Table 11).

A comparison of cluster means revealed that there was a moderate shift of mean values because of the saline condition in E_2, which has reduced plant height, panicle length and the number of grains per panicle. These results were in agreement with the findings of Blum (2002).

Indirect selection for yield improvement in any crop depends upon the selection of yield attributing traits that have a direct positive effect on yield. Selection for these traits should be done in the clusters which show the highest cluster mean values for those characters.

The relative contribution of individual character towards the expression of genetic diversity estimated over character-wise D^2 value revealed that days to 50 per cent flowering (22.16 per cent) 100 seed weight (22.16) contribute on par towards genetic divergence. The number of tillers (18.5 per cent) grain yield per plant (10.04 per cent) were the next major contributing characters in E_1 (Table 12).

In E_2, grain yield per plant (27.08 per cent) and 100 seed weight (26.52 per cent) contribute higher towards the genetic diversity followed by days to 50 per cent flowering (11.74 per cent) (Table 12).

In pooled analysis, days to 50 per cent flowering (21.40 per cent). The number of tillers per plant (21.40 per cent) and grain yield per plant (17.80 per cent) were the major contributing characters towards genetic diversity (Table 12).

Similar findings were made by Mohan *et al.,* (2014) for 100 seed weight and days to 50 per cent flowering. Pandey *et al*. (2011) Kumari Priyanka *et al.* (2015) for days to 50 per cent flowering. Chamundeswari (2016) for grain yield/plant and 100 seed weight. Chandramohan *et al.* (2016) for days to 50 per cent flowering and 100 seed weight.

To study the field performance of the selected 33 rice genotypes, field screening from vegetative stage upto harvest was carried out during June 2019 (kuruvai season). The crop was raised simultaneously in two different environments E1 (normal field condition) and E2 (saline field environment).

Observations were recorded for ten yield contributing traits along with grain yield per plant. A comparison of the mean data from normal (E1) and (E2) conditions revealed a 1.03 per cent reduction in days to 50 per cent flowering (Table 13). Reduction in plant height under abiotic stress was reported by Folkard Asch (2004).

Table 13 : Character-wise comparison of mean values for various traits under normal (E1) and drought (E2) condition in rice.

Sl. No	Characters	E1	E2	Change in general mean	% reduction in general mean
1	Days to 50% flowering	81.20	80.36	0.84	1.03
2	Plant height	99.51	87.26	12.25	12.31
3	Number of tillers per plant	21.72	19.50	2.22	10.22
4	Number of panicles per plant	13.99	12.35	1.64	11.72
5	Flag leaf length	32.92	29.00	3.92	11.91
6	Flag leaf breadth	1.33	1.29	0.04	3.01
7	Panicle length	24.59	23.18	1.41	5.73
8	Number of grains per panicle	165.70	148.27	17.43	10.52
9	100 seed weight	2.30	2.27	0.03	1.30
10	Grain yield per plant	40.85	35.31	5.54	13.56

Generally, rice genotypes with increased plant stature are often larger in overall plant size, intercept more light quantities and use water more rapidly by transpiration, resulting in lower plant water status (Kamoshita *et al.,* 2004), higher dead leaf ratings, and more spikelet sterility, resulting in lower yields (Kato *et al.,* 2007). In our investigation, three genotypes G_7, G_{20}, G_{15} which recorded maximum plant height under saline recorded significant yield and saline score.

The number of tillers per plant was reduced to 10.22 per cent while the number of panicles per plant reduced to 11.72 per cent in the saline field environment (E2) when compare to normal field condition (E1).

Flag leaf length was reduced to 11.91 per cent while flag leaf breadth reduced to 3.01 per cent and panicle length reduced to 5.73 per cent in the saline field environment (E2) than normal field condition (E1). Yue *et al.* (2006) also observed that grain yield loss under abiotic stress condition was associated with the increase of spikelet sterility and reduction of fertile panicle rate and grain weight. Mitra (2001) also stated that the reduction of flag leaf area under an abiotic stress condition when compared to normal conditions. The change in grain characters including grain length, grain breadth and 100 seed weight were very negligible indicating the high heritability of these traits.

Grain yield was drastically affected by an increase in salinity. Blum (2002) reported a reduction in plant height and grain yield under abiotic conditions. He stated that under abiotic stress condition, plant development is reduced as a consequence of poor root development; reduced leaf-surface traits (form, shape, composition of cuticular and epicuticular wax, leaf pubescent and leaf color), which affect the

radiation load on leaf canopy; delay in or reduced rate of normal plant senescence as it approaches maturity; and inhibition of stem reserves. The negative effect of salinity on plant height and grain yield concurs with the results of previous studies of Tiwari *et al.,* 2016.

Comparison of mean of various characters over normal (E1) and saline field environment (E2) revealed the phenomena of decreased plant height along with the reduced number of tillers per plant, number of panicles per plant, flag leaf length, flag leaf breadth, panicle length, number of grains per panicle and grain yield per plant under saline field environment (E2). When compared to normal crop growth in (E1).

Subudhi *et al.,* (2008) opined that genetic drift and selection in different environments may cause greater diversity than geographical diversity. Genotypes belong to clusters separated by high genetic distance may be used in a hybridization programme to obtain a wide spectrum of variation among the segregants (Bhatt, 1970).

Therefore, selection of divergent genotypes from the clusters namely III and IV, II and VIII and II and X from E_1, E_2 and pooled analysis respectively would produce a broad spectrum of variability for different traits studied, which may enable further selection and improvement of grain yield along with saline tolerance. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce a high magnitude of heterosis or desirable segregants which would be rewarding in a rice breeding programme.

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