Original research articles

Genetic divergence analysis of rice genotypes under salt stress environment

ABSTRACT

The present investigations were conducted in randomized block design with three replications within the net house of the department of PMB&GE, A. N.D.U.A.T, Kumar Ganj, Ayodhya to estimate the genetic divergence under normal and salt stress conditions involving 20 rice genotypes during Kharif 2018-19, on the basis of relative parameters of D^2 values, the clustering pattern of 20 rice genotypes under normal and salt stress conditionswere grouped into five non-overlapped clusters. Under normal condition, Cluster III having highest 7 rice genotypes, Cluster II having 5 genotypes, cluster V having 4 genotypes and IV having highest 3 rice genotype. Cluster I having only one genotype. Under saline condition, Cluster I having highest rice 6 genotypes, cluster III having 5 genotypes and cluster II & IV having 4 genotypes respectively. Cluster V having only one genotype. It means the genetic similarity was found in the genotypes were expressed within the cluster and the pattern of distribution of genotypes in variousclusters exhibited that topographical diversity wasn't associated with ancestral diversity as genotypes of same countryside were grouped into different cluster and vice-versa. The highest inter cluster distance was recorded between cluster 2 and cluster 5 (26108.030) followed by between cluster 1 and cluster 5 (18550.010), cluster 3 and cluster 5 (15231.860), cluster 4 and cluster 5 (5335.860) in normal condition andin saline condition the maximum inter cluster distance was existed between cluster 4 and cluster 5 (2344.091) followed by between cluster 3 and cluster 5 (2067.610), cluster 2 and cluster 5 (1447.564), cluster 1 and cluster 5 (1238.095). The results showed extensive variation from one cluster to other in respect of cluster means for all parameters, which represented that genotypes having distinctly different mean performance for various characters were reported into different clusters.

Keywords: Rice, Genotypes, Clusters and D^2 analysis

Introduction

Rice (*Oryza sativa* L.) is one of the most important plants from poaceae. Rice is acost-effective important food crop with nourishment diversification and useful in poverty eradicationmore than three billion of world populations. Rice is ranked as the world's number one human food crop. In India, rice is grown in an area of 43.97 million hectares with the production and productivity levels of 104.32 million tonnes and 2372 kg/ha, respectively, (Indiastat, 2017-2018). Plant breeding programme with different genetic base could encourage a high level of crop yield. The narrow genetic base of semi-dwarf germplasm is likely to build

them vulnerable to various biotic and abiotic stresses. heterogeneity in rice has been contributed to breed high yielding varieties. Germplasmof rice are being assembledover past several decades to use them in crop improvement programmes to improve high yielding, resistant to biotic and abiotic stresses with good adaptability. The success of any breeding programme depends on the exploitation of existing diversity and therefore, it is desirable to assemble, examine and utilize the existed diversity for crop improvement to required a specific ecosystem. D^2 analysis among the ancestral is important because a cross involving genetic diversity of parents is likely to produce maximum heterogenetic effect and also more diversity could be expected in segregating generations. Therefore, a meaningful classification of genotypes will enable the breeder to identify the best ancestral with wide D^2 and to utilize some of the selected diverse parents in the hybridization programme.

Materials and Method

Rice germplasm a total twenty rice genotypes were used in this study, which were IR68144-2B-2-2-3-1-120, IR-68144-2B-2-2-3-1-127, IR-91167-99-1-1-1-3, IR-91167-133-1-1-2-3, NUD-3, NDR-359, IR-28, FL-478, NUD-2, CSR-13, AYYAR, NDRK-2008, IR-64, SWARNA, IR-92953-49-1-3, IR-91171-66-3-2-1-3, IR-83668-35-2-2-2, SAMBHA MANSURI, TARAMON and MTU-1010.

The experiments were conducted in Randomized Block Design with three replications in normal and salt stress conditions in the green house of the department of PMB&GE, A. N.D.U.A.T, Kumar Ganj, Ayodhya during Kharif 2018-19. The data were recorded on days to 50% flowering, plant height, panicle bearing tillers/plants, panicle length (cm), spikelets/panicle, grains/panicle, spikelet fertility (%), test weight (g), biological yield (g), harvest index (%), grain yield (g) Na^+ content, K^+ content (mg g^{-1}) and Na^+/K^+ ratio. Observations were recorded on randomly selected five plants from each variety in each replication at maturity except for days to 50% flowering which were recorded on the plot basis at flowering stage.

Estimation of genetic divergence (D^2)

The genetic divergenceanalysis of 20 genotypes of rice was worked out using Mahalanobis (1936) D^2 statistics (Rao, 1952).

The calculation of D^2 values involved following steps

1. A set of uncorrelated linear combinations (y's) was obtained by pivotal condensation of the common dispersion matrix (Rao, 1952) of a set of correlated variables (x's). The common dispersion matrix was arranged with the help of error mean sum of squares and mean sum of products.

2. the combination between y's and x's the mean values of various genotypes for different characters (X1 to X10) were transformed into the mean values of a set of uncorrelated linear combinations (Y1 to Y10).

3. The D^2 values between i^{th} and j^{th} genotypes for kth characters is calculated as:

$D^2ij = K (Yit-Yjt)2$ Where, t = 1

The K components were calculated separately and added to get D^2ij.

1. The 'K' components of 'D^2ij' for each combination were ranked in descending order of magnitude.

2. These ranks were added up for each component D^2ij over all combinations of i and j^{th} rank totals were obtained.

Group constellation

The D^2 values were arranged in an increasing order of magnitude. The grouping of the strains into variousclusters was done using Tocher's method (Rao, 1952). The two widely related groups were chosen and third groups were found which had the smaller average D^2 value from the first two. Similarly, the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 value did not fit in with the former group and was, therefore, taken as another cluster.

Intra and inter-cluster distance

The inter-cluster D^2 was calculated as the sum of n (n-1)/2 genotypes within a cluster divided by total number of combinations. All possible D^2 values between the groups of two clusters were added and then divided by n1 × n2 for computing inter-cluster distance. Where, n1 and n2 = the number of genotypes in two clusters.

Cluster mean

the cluster mean forthe distinct character is the summation of mean values of the genotypes included in a cluster classified by number of genotypes in the cluster.

Result and Discussion

The selection of appropriate various oldsters for sexual union is a vital feature of any crop breeding programmes as a result of parental diversity in optimum magnitude is needed to get superior genotypes in segregating generations (Moll et al., 1962). The importance of genetic divergence in crop improvement has been stressed by many scientists (Griffing and Lindstrom, 1954; felon et al., 1962 Arunachalam (1981) and Hawkas (1981).D^2 analysis has been used by many employees for the assessment of genetic divergence in many crops (Malhotra and Singh, 1971).

In the present study, the twenty genotypes of rice were grouped into five different non-overlapping clusters under normal and saline conditions (Table 1a and b), suggesting considerable amount of genetic diversity in the materials. under control condition Yadav, Pratibha, et al(2019) . Cluster III having highest rice genotypes (7) namely NDR-359, IR-29, CSR 13, AYYAR, NDRK2008, IR-92953-49-1-3 and IR-83668-35-2-2-2, Cluster II having five genotypes i.e. IR-68144-2B-2-2-3-1-120, FL-478,

NUD-2, TARAMON and MTU-1010, Cluster V having four genotypes i.e. IR-68144-2B-2-2-3-1-127, NUD-3, IR-64 and SWARNA, Cluster IV having three genotypes i.e. NDR-359, IR-91171-66-3-2-1-3 and SAMBA MASURI, Cluster I having only one genotype i.e. IR-91167-133-1-1-2-3. While in saline condition Cluster I having highest rice genotypes (6) namely, IR-68144-2B-2-2-3-1-120, IR-91167-133-1-1-2-3, NDR-359, IR-29, NUD-2 and CSR 13, Cluster III having five genotypes i.e. IR-68144-2B-2-2-3-1-127, NUD-3, NDRK-2008, SAMBA MASURI and TARAMON, Cluster II & IV having four genotypes i.e. FL-478 , AYYAR, IR64, SWARNA and IR-91167-99-1-1-1-3, IR-92953-49-1-3, IR-83668-35-2-2-2, IR-91171-66-3-2-1-3, respectively. Cluster V having one genotypes i.e. MTU-1010. It means the general genetic similarity was found within the genotypes were reported within the cluster and therefore the pattern of distribution of genotypes in various clusters exhibited that topographical diversity wasn't related with genetic diversity as genotypes of same countryside were grouped into various cluster and vice-versa, as supported by earlier finding of Devi et al. (2020); Devi M. et al. (2019); Devi Shashi and Dwivedi, (2016); Devi et al. (2006); Mall et al. (2011) and Ovung et al. (2012).

Table 1a: Clustering pattern of 20 rice genotype on the basis on D^2 analysis for 14 characters I controlled condition.

Cluster No.	No. of genotypes	Genotypes
I	1	IR-91167-133-1-1-2-3
II	5	IR-68144-2B-2-2-3-1-120, FL-478, NUD-2, TARAMON, MTU-1010
III	7	NDR-359, IR-29, CSR 13, AYYAR, NDRK-2008, IR-92953-49-1-3, IR-83668-35-2-2-2
IV	3	NDR-359, IR-91171-66-3-2-1-3, SAMBA MASURI
V	4	IR-68144-2B-2-2-3-1-127, NUD-3, IR-64, SWARNA

Table 1b: Clustering pattern of 20 rice genotype on the basis on D^2 analysis for 14 characters in saline condition

Cluster No.	No. of genotypes	Genotypes
I	6	IR-68144-2B-2-2-3-1-120, IR-91167-133-1-1-2-3, NDR-359, IR-29, NUD-2, CSR 13

II	4	FL-478, AYYAR, IR-64, SWARNA
III	5	IR-68144-2B-2-2-3-1-127, NUD-3, NDRK-2008, SAMBA MASURI, TARAMON
IV	4	IR-91167-99-1-1-1-3, IR-92953-49-1-3, IR-83668-35-2-2-2, IR-91171-66-3-2-1-3
V	1	MTU-1010

The estimates of average intra and inter cluster distances for presented in table 2a and table 2b revealed that the maximum intra cluster distance was exhibited by the genotypes of cluster 5 followed by cluster 4, cluster 3, cluster 2 and cluster 1.The highest inter cluster distance was recorded between cluster 2 and cluster 5 (26108.030) followed by between cluster 1 and cluster 5 (18550.010), cluster 3 and cluster 5 (15231.860), cluster 4 and cluster 5 (5335.860) under normal condition while, under saline condition the highest intra cluster distance was recorded by cluster 5 followed by cluster 4, cluster 3 and cluster 2. the highest inter cluster distance was recorded between cluster 4 and cluster 5 (2344.091) followed by between cluster 3 and cluster 5 (2067.610), cluster 2 and cluster 5 (1447.564), cluster 1 and cluster 5 (1238.095)reportedgood diversity between them and genotypes in these clusters could be used as ancestral in breeding programme to improve desirable line because crosses between genetically divergent lines will generate heterotic segregates. As heterosis can be best exploited and chances of getting transgressive segregates are high when generating divergent lines are hybridized (Zaman et al., 2005 and Saxesena et al., 2013). Many researchers in various crops have also reported that selection of ancestral for breeding should be done from two clusters having wide inter-cluster distance to get maximum diversity in segregating generations. Heterosis is generally attributed to genetic divergence among the ancestral lines involved in the cross. Nevertheless, the genetic divergence for the maximum expression of the heterotic effects has a limit Moll et al., (1965) and Arunachalam et al., (1984).

Table 2a: Estimation of average inter cluster D^2 value under control condition

Cluster no.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	710.163	2072.070	2170.370	4805.715	18550.010

Cluster 2		1276.286	2620.302	9190.650	26108.030
Cluster 3			867.018	3981.772	15231.860
Cluster 4				811.451	5335.071
Cluster 5					0.000

Table 2b: Estimation of average inter cluster D^2 value under saline condition

Cluster no.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	422.428	823.908	825.924	1072.397	1238.095
Cluster 2		361.387	927.603	1455.013	1447.564
Cluster 3			522.126	1195.375	2067.610
Cluster 4				837.769	2344.091
Cluster 5					597.118

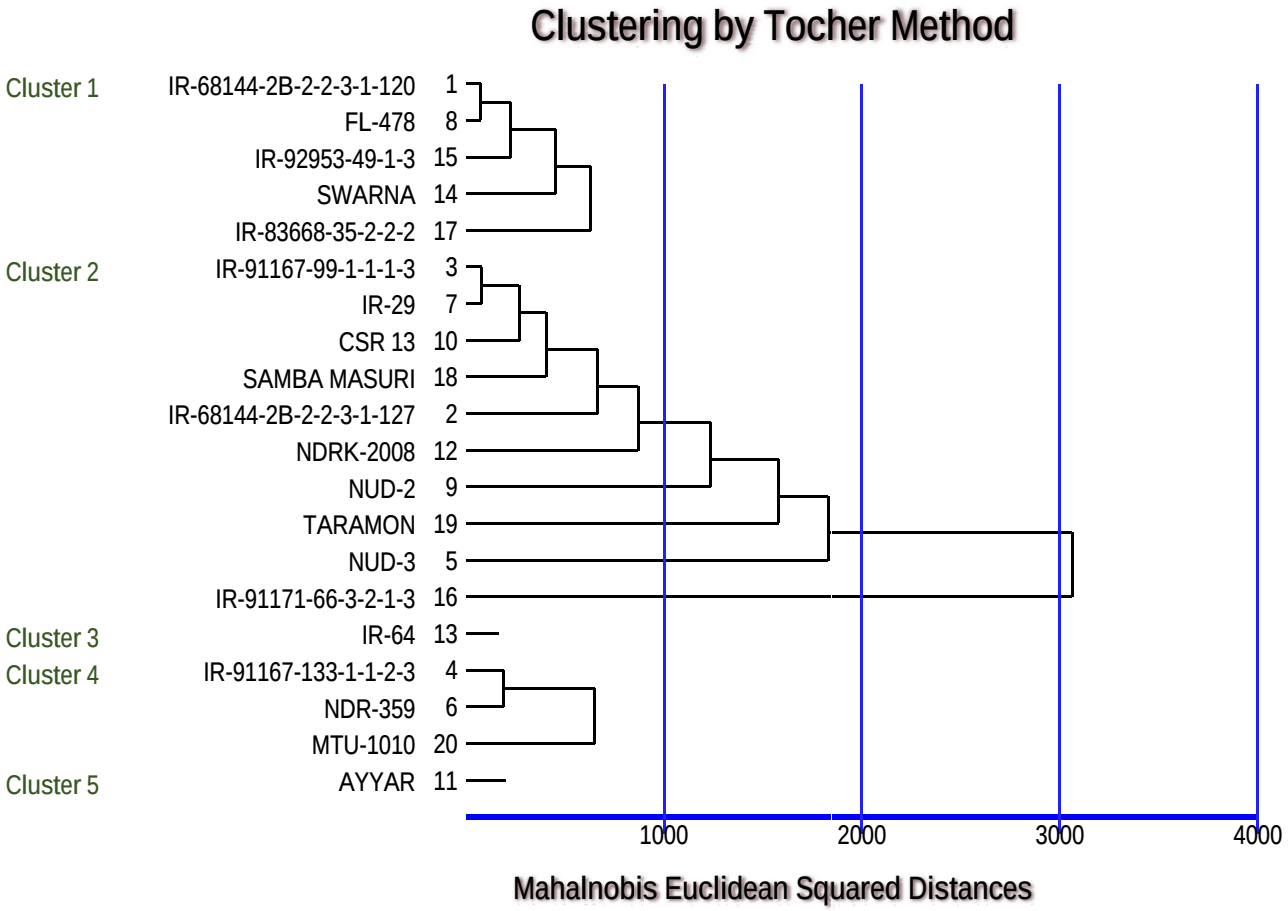
The comparison of cluster means revealed considerable differences among the clusters of various characters undercontrol and salty soil (Table 3a and 3b).Under control condition cluster mean for days to 50% flowering ranged from 90.74 (cluster 1) to 98.86 days (cluster 5). Early flowering genotypes were grouped in cluster 1 (90.74) followed by cluster 2 (95.67) and cluster 5 (98.86), while in salt stress cluster mean for days to 50% flowering ranged from 88.08 (cluster 1) to 102.37 days (cluster 3). Early flowering genotypes were grouped in cluster 1 (88.08) followed by cluster 5 (89.21), cluster 4 (91.65) and cluster 2 (95.87).The results showed wide diversity from one cluster to another in respect of cluster means for all characters, which representedthese varieties having distinctly different mean performance for different characters were reported into different clusters as supported by earlier finding of Singh M. et al. (2020); Devi Shashi and Dwivedi, (2016); Gaurav and Dwivedi, (2018).

Table 3a: Cluster mean of 20 rice genotypes under control condition

Characters	Days to 50% flowering	Plant height (cm)	Panicle bearing tillers/ plant	Panicle length (cm)	Spikelet / panicle	Grains /panicle	Spikelet fertility (%)	Test weight (g)	Biological yield/ plant (g)	Harvest index (%)	Na^+	K^+	Na^+/K^+	Grain yield/ plant (g)
Cluster 1	90.74	85.56	5.86	20.73	170.41	143.58	84.17	22.85	47.86	41.15	3.69	25.98	0.14	19.62
Cluster 2	95.63	105.90	6.81	20.93	138.16	114.93	82.81	23.16	49.85	42.70	3.71	23.58	0.15	21.29
Cluster 3	94.76	114.09	6.30	21.60	146.82	122.50	82.98	25.94	44.67	41.95	3.64	28.32	0.12	18.62
Cluster 4	94.77	86.00	6.61	21.80	140.38	121.20	86.19	23.24	41.90	40.86	3.23	32.95	0.09	17.03
Cluster 5	98.86	92.77	8.91	16.85	195.59	173.85	88.89	22.81	57.20	31.18	3.53	39.56	0.08	17.82

Table 3b: Cluster mean of 20 rice genotypes under saline condition

characters	Days to 50% flowering	Plant height (cm)	Panicle bearing tillers/ plant	Panicle length (cm)	Spikelet / panicle	Grains /panicle	Spikelet fertility (%)	Test weight (g)	Biological yield /plant (g)	Harvest index (%)	Na^+	K^+	Na^+/K^+	Grain yield/ plant (g)
Cluster 1	88.08	89.03	5.54	21.47	97.47	80.48	82.37	17.80	27.56	39.84	3.29	25.77	0.12	10.90
Cluster 2	95.87	90.94	5.11	22.70	165.10	143.43	86.91	20.51	30.82	39.79	3.01	26.32	0.11	12.26
Cluster 3	102.37	85.60	4.64	24.18	118.71	98.82	83.51	21.67	31.57	35.31	3.61	26.06	0.14	11.01
Cluster 4	91.65	88.87	5.94	19.17	122.33	98.29	80.78	18.63	29.29	39.69	3.02	34.69	0.08	11.60
Cluster 5	89.21	103.8	4.62	19.15	95.49	77.43	80.79	18.63	36.76	38.66	3.24	26.22	0.12	14.21


Clustering by Tocher Method
Cluster 1
IR-68144-2B-2-2-3-1-120 1
FL-478 8
IR-92953-49-1-3 15
SWARNA 14
IR-83668-35-2-2-2 17
Cluster 2
IR-91167-99-1-1-1-3 3
IR-29 7
CSR 13 10
SAMBA MASURI 18
IR-68144-2B-2-2-3-1-127 2
NDRK-2008 12
NUD-2 9
TARAMON 19
NUD-3 5
IR-91171-66-3-2-1-3 16
Cluster 3
IR-64 13
Cluster 4
IR-91167-133-1-1-2-3 4
NDR-359 6
MTU-1010 20
Cluster 5
AYYAR 11
1000
2000
3000
4000
Mahalnobis Euclidean Squared Distances

Conclusion

In the present study, the genetic divergence for fourteen characters of 20 genotypes of rice were grouped into five different non-overlapping clusters under normal and saline conditions, suggesting considerable amount of genetic diversity in the materials. under control condition, Cluster III having highest seven rice genotypes, while in saline condition Cluster I having highest six rice genotypes. It means the general genetic similarity was found within the germplasms were presented within the cluster the estimates of average intra and inter cluster distances for 20 rice genotypes. the maximum intra cluster distance was exhibited by the genotypes of cluster 5 followed by cluster 4, cluster 3, cluster 2 and cluster 1 under normal condition while, under saline condition the highest intra cluster distance was recorded by cluster 5 followed by cluster 4, cluster 3 and cluster 2. suggesting wide diversity between them and germplasm in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregates. The comparison of cluster means revealed considerable differences among the clusters of different characters, cluster mean of days to 50% flowering showed considerable difference Under both conditions. The results showed wide variation from one cluster to another in respect of cluster means for all characters, which indicated that varieties having distinctly different mean performance for various characters.

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