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Genetic Divergence Analysis in Rice (*Oryza sativa* L.) Germplasms under Sodic Soil

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ABSTRACT

Background: Salt affected areas have increased day by day because of excessive use of irrigation water with improper drainage coupled with the poor quality of irrigation water. The assessment of genetic divergence existing in the germplasm collections is very important for success of hybridization programme leading to development of high yielding varieties.

Methods: The experiment on 113 genotypes (aromatic and non-aromatic rice) including three checks *viz.,* Sarjoo 52, FL 478 and CSR 10 (salt tolerant) of rice (*Oryza sativa* L.) was conducted to work out the genetic divergence.

Result: The 113 genotypes were grouped in to eleven different non-overlapping clusters. Cluster II, having 20 genotypes, emerged with highest number of entries. The highest intra-cluster distance was found for cluster X. The maximum inter-cluster distance was recorded between cluster VII and XI. The highest cluster mean for grain yield per plant was observed in cluster III. Presence of substantial genetic diversity among the germplasm lines screened in the present study indicating that this material may serve as good source for selecting the diverse parents for further hybridization program aimed at isolating desirable segregants for grain yield and other important characters.

Key words: Cluster, Genetic divergence, Grain yield, Rice, Sodic soil.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important staple food crop (Wang *et al.* 2018). The demand for rice is expected to increase with continuous increase in global population. India has the largest area 43.78 million hectare constituting 28.26% of the land under rice in the world and rank second in total production 118.87 million tonnes next to China with an average productivity of 2705 Kg/hectare (DAC and FW, 2019-20).

The soil sodicity is a major factor that adversely affecting the growth and yield of crop plant (Wang, *et al.* 2012). Approximately one-third of the land area on which rice is grown is affected by salinity (He *et al.* 2019). Current scenario, approximately 10% of the world's total land area (950 million ha), 20% of the world's arable land (300 million ha) and 50% of the total irrigated land (230 million ha) are affected by soil salinization (Kashyap *et al.* 2020). Further, it is expected to influence 50% of total cultivated land in 2050 at a dis-quieting rate (Munns and Tester 2008 and Ruan *et al.* 2010). Every year almost 12 billion US$ are globally lost due to salt stress that significantly affects the agricultural production (Qadir *et al.* 2008 and Flowers *et al.* 2010).

Most varieties are having only few major desirable significance, that are the subjects of intensive breeding efforts. The assessment of genetic divergence existing in the germplasm collections is very important for success of hybridization and recombination breeding in an autogamous crop such as rice leading to development of high yielding, multiple resistance/tolerance coupled with high quality and wider adoptive superior hybrids varieties for commercial exploitation as well as recover transgressive segregants in segregating generations (Arunachalam, 1981). Thus, adoptions of high yielding rice varieties to various stress/underutilized land such as sodic soil would be an important strategy to meet this challenge.

MATERIALS AND METHODS

The study was designed to work out the genetic divergence and cluster analyses of their various attributes on grain yield per plant among 113 genotypes (aromatic and non-aromatic rice) including three check varieties *viz*., Sarjoo 52, FL 478 and CSR 10. The experiment was conducted during *Kharif,* 2018 at the Main Experimental Station of A.N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya under natural sodic soil with the pH, EC and ESP

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were 9.5, 3.2 dSm-1 and 45% respectively. Geographically, experimental site is located between 24° 47′ and 26° 56′N latitude, 82° 12′ and 83° 98′E longitude and at an altitude of 113 m above mean sea level. This area falls in sub-tropical climatic zone. The experiment was laid out in 11 blocks of augmented design suggested by Federer, W.T. (1961). An examination of the clustering pattern of the mean was adjusted after augmented RBD of 113 genotypes. The observations were recorded on sixteen different grain yield and its contributing traits. Chlorophyll content, leaf nitrogen and leaf temperature data were recorded by Soil Plant Analysis Development (SPAD value). The certain selected statistical approaches were used for data analysis *i.e.* non-hierarchical euclidean cluster analysis by following Beale, 1969 and Spark, 1973; Mahalanobis (1936) D^2 statistic. Tocher´s method as described by Rao (1952) was followed for cluster formation with the help of INDOSTAT and MS excel.

RESULTS AND DISCUSSION

Genetic divergence analysis

The study of genetic divergence among 113 rice genotypes including checks were grouped in to eleven different non-overlapping clusters as presented in Table 1 according to non-hierarchical euclidean cluster analysis by following

Table 1: Clustering pattern of 113 rice genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 16 characters.

Cluster number	No. of genotypes	Genotypes
I	10	CSR-30, CSR-36, Jaya, Sambha Mahsuri, IR 74095 AC 5, Narendra 6093, IR 12 T 195, Pusa 1121, Kashturi Chandauli, AT 401
II	20	NDRK 5026, FL 449, PNR 381, IR11T265, IR11T159, IR11T255, CSR 28, NDRK 50031, Narendra Usar 3, NDRK 50005, Narendra User 2, IR 12 T 193, IR 13 T 141, NDR 359, NDRK 5070, IR 64527-2B-2-1-1, NDRK 5003, IR 11 T 230, NDRK 5095, IR 11 T 205
III	15	CSR-27, Improved PB-1, NUD-2008, NUD-2009, IR 45427-2B-2-2B-1-1, NDRK 50052, IR 87856-1AJAY1-B, IR 71866-3 R -1-2-1-B, NDRK 50055, NDRK 50057, NDRK 50044, NDRK 50030, IR 12 T 210, IR 13 T145, IR 11 T 132
IV	7	Jallahri, Kalanamak, CSR-23, NDRK 50036, IR 12 T 147, FL 478 ©, CSR 10©
V	8	Deepak, Pusa Sugandha 4, Sugandha 3, NDRK 5027, NDRK 50032, NDRK 50053, NDRK 5017, NDRK 50046
VI	12	NDRK 50035, NDRK 5092, NDRK 50047, NDRK 5036, NDRK 50028, NDRK 5083, NDRK 5067, NDRK 5087, CST 7-1, IR 86731-1-1-1-3-3-2-1, IR 85921-9-2-1AJAY1-1-B, IR 55179-3B-11-3
VII	7	NDRK 5007, NDRK 5014, NDRK 50033, NDRK 5011, IR 85920-11-2-1AJAY1-2-B, Kalanamak 3, Sundari
VIII	8	NDR 510, NDRK 5019, NDRK 5089, NDRK 50019, IR 45427-2B-2-2B-1-1, IR 65427-2B-2-2, NDRK 50029, NDRK 5093
IX	10	NDRK 50039, NDRK 50045, NDRK 50050, NDRK 5034, IR 86341-B-AJAY1-B, IR 11 T 171, IR 86376-47-3-1-B, IR 11T 208, IR 11 T 213, IR 13 T 144
X	4	USAR 1, NDRK 5049, NDRK 50056, Pokkali (Acc 108921)
XI	12	NDRK 5062, NDRK 5099, NDR 2064, NDRK 5038, NDRK 5047, NDRK 5042, CSR 28, Pusa Basmati 1, Moti Gold, IR 11 T 183, CSR 43, Sarjoo 52©

Table 2: Estimates of average intra- and inter-cluster distances for 11 clusters in rice.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	**22.451**	37.916	37.911	34.891	38.734	37.731	71.065	42.845	32.368	41.655	44.385
Cluster II		**22.604**	26.179	25.955	26.732	26.349	46.384	31.698	28.921	40.129	46.673
Cluster III			**18.657**	25.790	26.436	28.068	54.139	28.986	26.252	37.486	41.639
Cluster IV				**7.859**	20.358	25.934	52.302	26.607	24.095	43.425	32.485
Cluster V					**11.787**	21.673	38.650	31.577	31.068	46.151	50.554
Cluster VI						**16.431**	40.023	37.218	35.225	44.182	61.996
Cluster VII							**19.536**	58.872	58.307	63.163	82.207
Cluster VIII								**16.016**	20.362	28.173	23.365
Cluster IX									**15.933**	28.611	22.702
Cluster X										**23.302**	32.400
Cluster XI											**9.124**

Bold figures represent intra-cluster distances.

Beale 1969, Spark 1973 and by tocher method. Cluster II, having 20 genotypes, emerged with highest number of entries followed by cluster III with 15 genotypes, cluster VI and cluster XI with 12 genotypes, cluster I and cluster IX with 10 genotype, cluster V and VIII with 8 genotypes, cluster IV and VII with 7 genotypes and cluster X with only 4 genotypes. Cheema *et al.* (2004) advocated that the number of clusters formed, number of genotypes in the clusters and superposition of the genotypes within the clusters indicated the possibility of genetic improvement for yield and yield components.

The estimates of intra and inter-cluster distances for eleven clusters are presented in Table 2 according to non-hierarchical euclidean cluster analysis by following Beale 1969, Spark 1973 and clustering and their interrelationships by Mahalnobis euclidean distance. The highest intra-cluster distance was found for cluster X (23.302) followed by cluster II (22.604), cluster I (22.451), cluster VII (19.536), cluster III (18.657), cluster VI (16.431), cluster VIII (16.016), cluster IX (15.933), cluster V (11.787), cluster XI (9.124) and cluster IV (7.859). The maximum inter-cluster distance was recorded between cluster VII and XI (82.207) followed by cluster I and VII (71.065), cluster VII and X (63.163), cluster VI and XI (61.996), cluster VII and VIII (58.872), cluster VII and IX (58.307), cluster III and VII (54.139), cluster IV and VII (52.302), cluster V and XI (50.554), cluster II and XI (46.673), cluster II and VII (46.384), cluster V and X (46.151), cluster I and XI (44.385), cluster VI and X (44.182), cluster IV and X (43.425), cluster I and VIII (42.845), cluster I and X (41.655), cluster II and X (40.129) and cluster VI and VII (40.023). The discrimination of germplasm lines into so many discrete clusters indicating presence of high degree of genetic diversity in the evaluated materials. Earlier workers have also reported substantial genetic divergence in the rice materials (Nayak *et al.*, 2004; Suman *et al.*, 2005; Gahalain, 2006; Chandra *et al.*, 2007; Singh *et al.*, 2008; Dushyantha and Kantti 2010; Seetharaman *et al.* 2013; Supriya *et al.* 2017; Sarif *et al.* 2020).

The highest intra-cluster distance was found for cluster X (23.302) has symmetrical genetic dissimilarity matrix depicting pairwise comparisons between the tested genotypes indicates closer genetic similarity within USAR 1, NDRK 5049 NDRK 50056 and Pokkali, suggesting their common origin and geographical occurrence (Table 3). Moreover, the maximum inter-cluster distance was recorded between cluster VII (NDRK 5007, NDRK 5014, NDRK 50033, NDRK 5011, IR 85920-11-2-1AJAY1-2-B, Kalanamak 3, Sundari) and XI (NDRK 5062, NDRK 5099, NDR 2064, NDRK 5038, NDRK 5047, NDRK 5042, CSR 28, Pusa Basmati 1, Moti Gold, IR 11 T 183, CSR 43, Sarjoo 52). These genetically highly dissimilar genotypes belonged to different climatic situations and may act as prospective parents for transgressive breeding and exploitation of heterosis in hybrid breeding programs.

Table 3: Clusters means for 16 characters in rice.

Clusters	Days to 50% flowering	Chloro phyll content	Leaf nitrogen	Leaf temper--ature	Flag leaf area (cm^2)	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield/plant (g)	Harvest index (%)	L/B ratio	1000-grain weight (g)	Grain yield/ plant (g)
Cluster I	105.552	8.944	0.94	36.175	34.766	90.238	7.988	24.407	135.883	105.394	78.600	42.789	35.458	2.668	21.722	15.455
Cluster II	99.805	13.632	0.542	35.635	24.888	97.620	9.677	22.958	162.696	140.787	86.393	51.527	37.857	3.162	21.754	19.247
Cluster III	100.171	14.098	0.622	36.417	27.675	86.277	8.354	22.451	133.733	109.665	82.073	48.485	44.685	2.958	22.365	21.634
Cluster IV	90.422	12.616	0.611	32.819	23.410	100.487	6.999	23.748	172.876	142.334	82.218	43.532	40.494	2.485	24.236	17.595
Cluster V	95.509	13.825	0.711	36.097	33.298	102.061	7.156	22.809	150.161	130.472	86.692	55.054	34.461	2.866	25.874	19.033
Cluster VI	101.647	13.843	0.672	36.325	34.668	99.281	9.899	27.620	178.375	149.753	83.839	49.581	38.154	2.887	23.837	18.715
Cluster VII	97.812	12.977	0.729	35.792	27.570	102.118	9.934	26.485	182.216	156.377	85.939	53.640	35.807	3.105	28.314	19.062
Cluster VIII	90.997	14.083	0.600	36.100	21.648	109.410	9.265	21.960	103.751	88.127	85.096	33.692	42.005	3.010	22.730	14.090
Cluster IX	94.759	13.580	0.545	35.388	22.082	92.228	9.124	21.642	117.228	91.112	77.512	37.638	38.152	2.998	22.637	14.254
Cluster X	107.972	13.804	0.500	36.905	24.815	120.117	8.742	23.684	101.224	78.741	77.032	33.447	42.209	3.530	22.032	13.921
Cluster XI	93.283	12.262	0.501	33.195	16.401	100.255	6.448	19.407	80.855	65.949	81.145	24.572	42.693	3.164	21.802	10.484

Table 4: Contribution of 16 traits of rice towards divergence.

Source	Times ranked 1st	Contribution %
Days to 50% flowering	151	2.39
Chlorophyll content	0	0.00
Leaf nitrogen	0	0.00
Leaf temperature	0	0.00
Flag leaf area (cm^2)	150	2.37 %
Plant height (cm)	714	11.28
Panicle bearing tillers/plant	0	0.00
Panicle length (cm)	1	0.02
Spikelets/panicle	3500	55.31
Grains/panicle	1462	23.10
Spikelet fertility (%)	23	0.36
Biological yield/plant (g)	297	4.69
Harvest index (%)	29	0.46
L/B ratio	0	0.00
1000-grain weight (g)	1	0.02
Grain yield/plant (g)	0	0.00

The intra-cluster group means for sixteen characters (Table 3) revealed marked differences between the clusters in respects of cluster means for different characters. The highest cluster mean for grain yield per plant was observed in cluster III (21.634 g) followed by cluster II (19.247 g), cluster VII (19.062 g) and cluster V (19.033 g), while XI possessed low cluster mean for grain yield per plant *i.e.,* 10.484 g.

Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that this material may serve as good source for selecting the cluster VII (NDRK 5007, NDRK 5014, NDRK 50033, NDRK 5011, IR 85920-11-2-1AJAY1-2-B, Kalanamak 3, Sundari) and XI (NDRK 5062, NDRK 5099, NDR 2064, NDRK 5038, NDRK 5047, NDRK 5042, CSR 28, Pusa Basmati 1, Moti Gold, IR 11 T 183, CSR 43, Sarjoo 52) diverse parents for hybridization programme aimed at isolating desirable segregants for grain yield and other important characters.

The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in rice (Nayak *et al.*, 2004; Suman *et al.*, 2005; Gahalain, 2006; Chandra *et al.*, 2007; Singh *et al.*, 2008; Dushyantha and Kantti 2010; Seetharaman *et al.* 2013; Supriya *et al.* 2017; Sarif *et al.* 2020)

Contribution of sixteen traits of rice toward divergence

The contribution of sixteen characters towards divergence in Table 4 showed the highest contribution by spikelets per panicle (55.31%) followed by grains per panicle (23.10%), while the grain yield per plant (0.00%) showed lowest contribution towards divergence.

CONCLUSION

The eleven clusters formed in divergence analysis contained genotypes of heterogeneous origin, thereby indicating non-parallelism between genetic and geographic diversity. Therefore, crosses between the members of diverse clusters separated by high inter-cluster distances are likely to throw desirable segregants. The highest intra-cluster distance was found for cluster X which has symmetrical genetic dissimilarity matrix depicting pairwise comparisons between the tested genotypes indicating closer genetic similarity within cluster X genotypes *i.e.,* USAR 1, NDRK 5049, NDRK 50056 and Pokkali, suggesting their common origin and geographical occurrence. Moreover, the maximum inter-cluster distance was recorded between cluster VII (NDRK 5007, NDRK 5014, NDRK 50033, NDRK 5011, IR 85920-11-2-1AJAY1-2-B, Kalanamak 3, Sundari) and XI (NDRK 5062, NDRK 5099, NDR 2064, NDRK 5038, NDRK 5047, NDRK 5042, CSR 28, Pusa Basmati 1, Moti Gold, IR 11 T 183, CSR 43, Sarjoo 52). It is suggested that cluster VII and XI have highly genetically dissimilar genotypes belonged to different climatic conditions and therefore, these tested materials expected to act as prospective parents for transgressive breeding and exploitation of heterosis in hybrid breeding programs.

Conflict of interest: None.

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