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Genetic divergence analysis in rice (*Oryza sativa* L.) under sodic soil condition

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Abstract
Genetic divergence and variability was assessed among eighty eight (88) diverse rice genotypes including three checks (Narendra Usar Dhan 3, Jaya and CSR-36) which were evaluated in augmented deign under sodic soil using non-hierarchical Euclidean cluster analysis. The genotypes were grouped into ten clusters which indicate presence of high degree of genetic diversity in germplasm collections. Among the different clusters, cluster V with eighteen (18) entries got the highest number of genotypes followed by thirteen (13) entries in both cluster I and II. Although the least number of genotypes was observed in Cluster X but the highest intra-cluster distance was identified in cluster X (25.00), followed by cluster VIII (14.62) and VII (13.76). In case of inter-cluster distance maximum value was found between cluster X and III (46.19). So the genotypes present in the diverse clusters may serve as parental materials for hybridization programme which will leads to isolation of desirable segregants for developing high yielding rice varieties in sodic soil.

Keywords: Rice, sodic soil, divergence, high yield

Introduction

Rice (*Oryza sativa* L.) is one of the most staple food crops which belong to family poaceae (Graminae) with an annual production of 759.6 million tonnes (FAOSTAT, 2018) [4]. It is grown in more than 114 countries occupying wide range of ecosystems under different temperatures and water regimes (Rukmini Devi *et al*., 2020) [10]. The world rice production for the year 2019-20 was estimated as 496.67 million metric tons (USDA, 2020) [13]. However to meet the demands of rapidly increasing population along with food security in the country, rice production need to be increased in a rapid manner. According to Economics of Salt-Induced Land Degradation and Restoration Forum (2014) about 6.73 million hectares of land is affected by salt in our country (Sharma and Chaudhari, 2012) [11]. Uttar Pradesh has a share of 1.37 million hectares salt affected soil out of total 2.348 million hectares area in Indo-gangetic plains of our country (Maurya *et al*., 2017) [6]. Thus, to mitigate the loss due to various abiotic stresses such as sodic soil, adoption of high yielding varieties would be an effective alternative. In this context, the amount of variability and genetic diversity present in the population plays a key role in the development of high yielding rice varieties superior to the already existing varieties. For the development of varieties the parents should be divergent in nature and for that germplasm provides an immense opportunity for wide range of variability (Zafer *et al*., 2020) [14]. The nature and magnitude of genetic divergence and variability would help plant breeders to identify better parents in hybridization programmes with an object to get higher amount of heterotic value in F_1 and wide variability in segregating generations (Rukmini Devi *et al*., 2020) [10].

After acknowledging the importance of variability and genetic diversity in plant breeding programme, the present study was conducted with an aim to understand the nature and magnitude of genetic diversity and also to identify better accessions with regards to various yield contributing traits in rice under sodic soil condition.

Materials and Methods

The study was conducted at the research farm of department of genetics and plant breeding, A.N.D.U.A.T, Kumarganj, Ayodhya under sodic soil condition with a soil pH of 9.3 with ECe = 2.24 (dS^{m-1}). A total of eighty eight (88) diverse genotypes were screened with three checks

(CSR 36, Jaya and Narendra Usar Dhan 3) for divergence analysis. In augmented experimental design, the field was divided into 8 blocks consisting of 14 plots each. Seedlings were transplanted into the main field after attaining a maturity of twenty eight (28) days old with a spacing of 20 cm x 15 cm. A composite of five plants of each genotype were used randomly for recording observations on the plants for different yield components such as days to 50% flowering (DTF), plant height in centimeter (PH), panicle length in centimeter (PL), flag leaf area in cm^2 (FLA), panicle bearing tillers per plant (TPP), spikelets per panicle (SPP), spikelet fertility (SF%), 1000-grain weight in gram (GW), biological yield per plant (BYPP), harvest-index (HI) and grain yield per plant (GYPP). The mean values of genotypes in each replication were subjected to analysis of variance and to examine the genetic divergence present in rice genotypes, Non-hierarchical Euclidean Cluster analysis (Beale, 1969; Spark 1973) [1, 12] was used.

Result and Discussion
Analysis of variance
Analysis of variance revealed that for all the characters under study (Table 1), variation due to blocks was significant or highly significant for majority of the characters except for spikelet fertility where non-significant means square was observed. In case of check varieties, the differences were also found to be highly significant for most of the characters except panicle bearing tillers per plant (TPP), 1000-grain weight (GW), biological yield per plant (BYPP), harvest index (HI) and spikelet fertility (SF %).

Table 1: Analysis of variance for grain yield and yield related characters in rice under sodic soil condition

Characters	Source of variation		
	Blocks	**Checks**	**Error**
	d.f. (7)	**d.f. (2)**	**Error (14)**
Panicle bearing tillers/plant	24.80*	0.62	8.43
Plant height (cm)	307.54**	294.30**	29.07
Days to 50% flowering	43.95 **	17.54**	1.02
Flag leaf area (cm²)	153.05**	197.87**	14.98
Panicle length (cm)	16.37**	19.00**	2.39
Spikelet fertility %	78.92	18.03	29.98
Spikelets/ panicle	5311.96**	7131.29**	782.10
1000-grain weight (g)	3.90*	0.97	0.92
Grain yield/ plant (g)	180.46**	22.77	21.86
Biological yield/ plant (g)	1116.69**	39.94	121.57
Harvest index (%)	13.37*	29.10**	4.24

* Significant at 5% probability level.
** Significant at 1% probability level.

Genetic divergence analysis
To study the genetic diversity based on eleven (11) quantitative characters, the Non-hierarchical Euclidean cluster analysis was conducted among ninety one (91) rice germplasm. With the help of pseudo F-test, all the genotypes were grouped into ten (10) non-over lapping cluster arrangements (Table 2). A total of eighteen (18) numbers of genotypes were present in cluster V which represent the maximum entries followed by thirteen (13) entries each in cluster I and II. Among the other clusters, Cluster IX, VII, VI and III constitute twelve (12), eleven (11), eight (8) and five (5) genotypes respectively whereas Cluster VIII and X consist of four (4) genotypes each. With only three (3) genotypes Cluster X has the lowest entry. Therefore the ninety one (91) genotypes categorized into ten (10) clusters is an indication of

presence of high amount of genetic diversity in the germplasm. Here clustering was not based on any specific pattern of the crop with respect to origin, similar observation was also recorded in previous reports on rice (Mohanty *et al*., 2010; Devi *et al*., 2020) [8, 10]. In the present study a considerable amount of genetic diversity was found among the germplasm lines which suggested that these diverse lines may serve as good source for selecting parents in hybridization programmes with an object to identify desirable segregants with respect to grain yield and other yield related traits. Similar study was conducted to isolate desirable segregants (Chandramohan *et al*., 2016; Devi *et al*., 2019) [2, 10]. Reports (Murthy and Arunachalam., 1966; Devi *et al*., 2020) [7, 10] has found out that as compare with geographic distance, genetic drift and selection in environment leads to more diversity. Genetic diversity plays a crucial role by producing distant hybrids and more recombinants. Therefore the choice of the diverse parental lines depending on genetic divergence analysis would be more high-yielding as compare with the selected parents based on geographical distances

The genotypes present in different clusters exhibit wider variability, whereas present within a cluster indicate narrow range of genetic variability. The estimates of average intra and inter cluster distances are presented in Table 3. Highest value of intra-cluster distance was found in cluster X (25.00) followed by cluster VIII (14.62) and VII (13.76) whereas, the minimum value was observed in cluster IV (5.71), followed by cluster V (9.96) and VI (10.76). In case of inter-cluster distances, the maximum value was recorded between cluster X and III (46.19) followed by cluster X with clusters II (45.50), VI (45.09), V (42.67), IV (42.10), VIII (37.95) and I (35.52). High order inter cluster distances were also observed by cluster IV from cluster VIII (40.28) and VII (37.49) and also cluster II with cluster VII (35.46). The least value of inter-cluster distance was observed between cluster V and VI (15.06). So it is not rewarding to hybridize the genotypes having low inter-cluster distances (Kumar and Verma 2015). The intra-cluster group means (Table 4) disclosed distinct differences between the clusters in respect of cluster means for different characters. In cluster I all the thirteen (13) genotypes resulted into low cluster means for spikelets per panicle (SPP) (101.22), spikelet fertility (SF %) (80.12%), panicle length (PL) (21.20 cm) and plant height (PH) (85.24 cm) besides having moderate cluster means for remaining characters. Cluster II resulted in low cluster means for most of the characters such as spikelets per panicle (SPP), panicle length (PL), biological yield per plant (BYPP) and plant height (PH), grain yield per plant (GYPP) and panicle bearing tillers per plant (TPP) but it had moderate means value for remaining five characters. The three genotypes of cluster III were responsible for low cluster means for 1000-grain weight (GW) (19.74 g), days to 50% flowering (DTF) (89.24 days), flag leaf area (FLA) (21.86 cm²) and biological yield per plant (BYPP) (37.92 g) but it showed high cluster mean values for harvest index (HI) (41.50%) and spikelet fertility (SF %) (88.44%) along with moderate means for remaining characters. Cluster IV having least number of three genotypes recorded low cluster means for majority of the characters whereas cluster IV had second highest mean for days to 50% flowering (DTF) (102.49) besides having moderate means for remaining characters. The highest number of eighteen (18) genotypes of cluster V emerged with high cluster mean value for 1000-grain weight (GW) (25.20 g) along with high means for panicle length (PL) (25.04 cm) and flag leaf area (FLA)

(30.35 cm²). For remaining most of the characters, moderate mean value was observed. In case of cluster VI which is constituted by eight germplasm lines, showed highest cluster mean for spikelet fertility (SF %) (91.87%) and low mean values for remaining most of the characters whereas the eleven entries of cluster VII exhibited highest cluster means for flag leaf area (FLA) (37.70 cm²), panicle length (PL) (25.38 cm) and grain yield per plant (GYPP) (28.23 g) and second highest cluster means for harvest index (HI) (40.03%), biological yield per plant (BYPP) (69.55 g) and panicle bearing tillers per plant (TPP) (13.07). In cluster VIII which has four genotypes, produced highest cluster means for panicle bearing tillers per plant (TPP) (16.63) and spikelets per panicle (SPP) (185.79) and second highest means for spikelet fertility (SF %) (89.72%) and grain yield per plant (GYPP) (25.64g) whereas the eleven entries of cluster IX showed moderate means for almost all the eleven characters

under study. The four genotypes present in cluster X resulted in highest cluster mean values for days to 50% flowering (DTF) (108.88 days), plant height (PH) (123.06 cm) and biological yield per plant (BYPP) (72.48 g) along with high cluster means for flag leaf area (FLA) (29.96 cm²), panicle bearing tillers per plant (TPP) (12.70), spikelets per panicle (SPP) (180.88) and grain yield per plant (GYPP) (24.02 g), whereas low mean values for harvest index (HI) (33.27%) and moderate values for remaining characters. Similar study was also conducted by different rice breeders (Rukmini Devi *et al*., 2017) [9]. Based on cluster mean values, it is always advisable to go for genotypes belonging to different clusters but having more than one desirable trait (Rukmini Devi *et al*., 2020) [10]. The present investigation shows that selection of genotypes having higher cluster mean could be used for the improvement of characters in rice breeding programme under sodic soil.

Table 2: Clustering pattern with distribution of ninety one (91) rice genotypes in sodic soil by Non-hierarchical Euclidean cluster analysis.

Cluster No.	Number of genotypes	No. of genotypes
I	IR 29, NDRK 5013, NDRK 5071, CSR 423, NDRK 5036, NDRK 50011, MTU 20-1, IR 77664-B-25-1-23-1-1, NDRK 5027, CSR 13, A 691-1, NDRK 5018, IR 55179-3B-11,	13
II	IR 9418-7B-2-1, NDRK 5039, IR 74095AC64, NDRK 50028, HP 3319-2-2, NDRK 5015, NDRK 5099, IR 76346-3B-10-1-1-1, NDRK 5012, Usar 1, IR-28, NDRK 5025, NDRK-5016	13
III	IR77664-B-25-1-23-1-1, AT 401, IR 72579-B-2R, NDRK 50004, NDRK 5005-2-2	5
IV	CSR 43, IR 64 Sub 1, NDRK 5026,	3
V	NDRK 5043, IR 71829-3R-10-3, IR 45427-2B-2-2B-1-1, IR 8806-B-B-1-1-2, NDRK 50040, IR 76397-2-2-B-6, NDRK 5050, NDRK 5059, NDRK 5074, CSR 28, NDRK 50001, NDRK 5040, CSR 901-R-2, NDRK 5064, NDRK 50006, IR 72593-B-B-33-1, IR 51499-2B-29-2B-1-1	18
VI	N16, Panvel 1, TCCP 261-3-3-B-10-2-1, NDRK 5047, IR 59443-B-7-3-2, IR 72579-B-2R-1-3-2, IR64527-2B-2-1-1, N2	8
VII	Narendra Usar Dhan 2008,NDRK 5083, NDRK 50023, Narendra Usar-3, CSR 23, NDRK 5005-2-2, Jaya, NDRK 5082, NDRK 5018, NDRK 5014, NDRK 50025	11
VIII	NDRK 5070, NDRK 5035, NDRK 5029, NDRK 5023	4
IX	IR-5099 2B-29-2B-1-1, NDRK 5049, NVSR 6029, NDRK 5004, Sundari, CSR (CS)-52-1, Getu, IR 76397-2-2-B-6, NDRK 5042, NDRK 50005, CSR 36, NDRK 5075	12
X	NDRK 5048, CSR (CS) 22-5, Nona Bokra, Pokkali (AC 10892)	4

Table 3: Estimates of average intra and inter-cluster distances under sodic soil for 10 clusters in ninety one (91) rice germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**12.92**	18.12	23.18	20.90	19.60	25.31	22.68	21.24	18.39	35.52
II		**11.66**	17.98	17.15	17.95	15.87	35.46	31.88	19.73	45.50
III			**12.65**	19.66	18.71	19.94	32.60	27.78	21.25	46.19
IV				**5.71**	25.10	28.78	37.49	40.28	21.88	42.10
V					**9.96**	15.06	23.62	27.18	16.48	42.67
VI						**10.76**	32.71	32.38	17.96	45.09
VII							**13.76**	21.41	20.35	31.85
VIII								**14.62**	24.39	37.95
IX									**11.95**	24.68
X										**25.00**

Bold figures indicate intra-cluster distances.

Table 4: Cluster means for different characters in rice germplasm under sodic soil condition

Cluster	DTF	PH (cm)	TPP	FLA (cm²)	PL (cm)	SPP	SF (%)	GW(g)	BYPP(g)	HI (%)	GYPP(g)
I	96.81	85.24	12.29	27.61	21.20	101.22	80.12	23.58	54.93	38.18	23.98
II	93.40	83.92	8.99	25.65	20.87	97.03	83.16	22.09	37.76	34.36	14.77
III	89.24	94.91	9.78	21.86	21.82	140.18	88.44	19.74	37.92	41.50	15.47
IV	102.49	86.88	6.32	21.57	22.13	128.38	70.96	20.12	43.63	39.89	14.77
V	89.67	89.77	9.62	30.35	25.04	118.99	87.99	25.20	42.73	39.33	15.93
VI	86.13	90.66	8.12	26.86	23.93	120.83	91.87	23.02	44.86	32.00	13.64
VII	93.22	93.06	13.07	37.70	25.38	166.09	84.62	23.28	69.55	40.03	28.23
VIII	91.46	84.61	16.63	25.76	20.79	185.79	89.72	23.81	63.61	39.08	25.64
IX	97.49	100.82	10.97	27.99	24.90	145.69	84.16	22.85	55.06	34.82	18.83
X	108.88	123.06	12.70	29.96	23.48	180.88	81.66	22.98	72.48	33.27	24.02

Conclusion

The present investigation indicate that the selection of parents should be done based on values of inter cluster distance, high mean performance for yield and its components and also by considering contribution of different traits with regard to total genetic divergence. Non-parallelism between genetic and geographic diversity was observed in the present study as all the genotypes present in ten (10) clusters are of heterogeneous origin. Here, cluster X, had very high inter-cluster distance from cluster III, II, VI, V, IV, VIII and cluster I. In addition, very high inter-cluster distances were also observed by cluster IV from cluster VIII and VII, while cluster II exhibited high inter cluster distance from cluster VII. Therefore, crosses between the genotypes belonging to diverse clusters and showing high mean performance values in desirable direction for different yield contributing traits may be chosen as parents in rice improvement programme under sodic soil.

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