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Study of Genetic Diversity for Selected Genotypes in Rice

Ch Sai Nayan Raju[1*], Gabrial M. Lal[1] and Ch. Damodar Raju[2]

[1]Department of Genetics and Plant Breeding, Naini Agriculture Research Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India.
[2]Jayashankar Telangana State Agricultural University, India.

Authors' contributions

This work was carried out in collaboration among all authors. Author CHSNR designed the study, performed the field experiment, generated data and wrote the whole manuscript. Author GML edited, read and approved the final manuscript. Author CHDR read and approved the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was undertaken to study the 54 rice genotypes to estimate the diversity, among selected rice genotypes for yield and its component characters. The experiment was carried out during *Kharif*, 2020, in a randomized block design with three replications at the Indian Institute of Rice Research, Rajendranagar, Hyderabad voluntary center (Kampasagar), in Telangana State. The data was collected on characters viz and salt-tolerant score 0-9 scale. The 54 genotypes of rice were grouped into twelve clusters. Clusters with their genotypes are presented in. Cluster I had 15 genotypes, Cluster II had 13 genotypes, whereas Cluster III had 4 genotypes Cluster IV, V had 4 genotypes and cluster VI had 6 genotypes cluster VII had 1 genotype cluster VIII had three genotypes cluster Ⅸ, Ⅹ, Ⅺ had 1 genotypes cluster Ⅻ had 3 genotypes Highest inter-cluster distance was exhibited between clusters VIII and Ⅺ. and lowest cluster divergence found between the clusters Ⅳ and VII Greater the distance, wider the genetic diversity among the genotypes of those clusters. For high heterotic recombinants performing genotypes would be used as parents in the recombination breeding program.

**Corresponding author: E-mail: docternayan@gmail.com, docternayan49@gmail.com;*

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1. INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the genus *Oryza*, tribe Oryza, and the family Gramineae. It is an important crop, which supplies staple food for nearly 50% of the global population. It is the world's second most important cereal after wheat. In India, the area under rice is 43.79 million hectares with a production of 116.2 million tones and productivity of 2756 kg/ha during 2018-19 (Directorate of Economics and Statistics) Uttar Pradesh the area under rice 5.75 million hectares production of 15.4 MT and productivity 3037 kg/ha (Directorate of Economics and Statistics). The three largest rice-producing states in India are West Bengal (16.05MT) followed by Uttar Pradesh (15.4MT) and Punjab (12.82MT) during 2018-19 (Directorate of Economics and Statistics). with a yield of over 26.59 quintals/hectare 2018-19. the slogan of "Rice is life" is most appropriate for India as this crop plays a vital role in our national food security and is a means of livelihood for millions of rural households. Asia accounts for 90 percent of the world's rice area and 92 percent of the world's rice production [1]. In most Asian countries, agriculture and rice play an important role in economic development, and in most parts of Asia, rice plays a vital role in society, culture, and politics, employing more people, directly and indirectly, more than any other industry.

Rice has been cultivated in India across ages under a wide range of latitudes. Rice covers an area of 149.15 m ha with 550.19 million tons. In India cultivated across an area of 44.6 million ha with 23 percent of total world rice production and 45 percent of the total Indian food grain production. India ranks first in area and second in production following China, the largest producer of rice. In Karnataka, rice is cultivated in an area of 1.39 m ha with 4.05 million tons of production annually and productivity of 2.92 t / ha [2]. It is the staple food for two-thirds of the world's population.

Rice germplasm has genetic variability, allowing for a wide range of crop improvement opportunities. For rational use of genetic resources, information on genetic diversity within and among closely related crop varieties is required. It aids in the monitoring of germplasm and can be used to predict potential genetic gains. Similarly, quantification of genetic diversity within and between groups of germplasm is important, and crosses between parents with the greatest genetic divergence are generally the most responsive to genetic improvement [3] for achieving higher heterosis and superior recombinants. Given the above background, an investigation was carried out with 54 rice genotypes to study genetic divergence of 12 yields and yield traits using Mahalanobis D^2 analysis.

The knowledge of genetic diversity has a significant impact on the improvement of crop plants and this information has been successfully used for efficient germplasm management, fingerprinting, and genotype selection [4].

Mahalanobis's D^2 statistics [5] is a powerful tool in quantifying the degree of genetic divergence between the genotypes and relate clustering patterns with the geographic origin. The genetic distance had a definite role to play in the efficient choice of parents for hybridization programs [6]. Several workers studied the genetic diversity, clustering pattern, and relative contribution of different characters toward divergence and effectiveness of selection [7]; Ekka et al. (2013); Beevi et al. (2014)). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the rice genotypes for selection of suitable parents for utilizing in hybridization program and to study the genetic parameters attributing to yield.

2. MATERIALS AND METHODS

The experiment was carried out during *Kharif* 2020 with 54 selected genotypes at the Indian Institute of rice (IIRR) voluntary center (kampasagar) in randomized block design (RBD) with three replications in a single plot with three rows 5 meters in length and with a spacing of row to row distance 20 cm and plant to plant distance 15cm data was recorded for 12 quantitative characters viz days to 50 % flowering (DFF), plant height (cm), panicle length (cm), panicle weight (g), number of effective tillers per plant, the total number of filled grains per panicle, 1000- seed weight (g), seed yield per plant, sterility percentage (%), grain length, grain width, l:b ratio observations were recorded from randomly selected three competitive plants of each genotype of each replication for most of the yield and yield-related components

The genotypes are CSR MAGIC 157,JGL 24423,CSRM1-45,CSR-36(CHECK),CSRM1-

7,KR 15066 (224-4-3-1-1),CSR 23,CSR-RIL-06-178,RNR 11718,CSR 89-IR 15,CSR 10,CSR 449S-13,FL 478,CSR MAGIC 167,Pusa 44 (check),MTU-1001,GNV 18-64,CSR YET 59,CSAR-7-9-2020,RP 6112-MS-M-8-2-9-3-4-6-8,Narendra usar-2CSR YET 55,GNV 1801-9,CSR-27,CSAR 12-10-2020,CSR CPB 69,USAR-1,RP 6112- MS-M-98-2-5-7-23-6-1IIRRH-147,CSR TPB 159,SATYA,CSR YET 8,KPS- 2874,R-56,RRHP-MI30,R-RHZ-IB-80,CGZR-1,Kalanamak,IET 24780,R-RHZ-SM-14,MI 156,Samba Mahsuri,Zinco rice MS,DRR Dhan 45,R-RHZLI 23,MI 127,IR 64,IET 2638,CGZR-2,R-RHZ-IH-82,DRR Dhan 49,Chandra Hasini,R RHZ-SD-94,CR Dhan 311.

The mean values of all recorded attributes from all genotypes in all replications were compiled, and Mahalanobis D2 analysis was performed on fifty-four selected genotypes for all 12 characters. Tocher's optimization method, as described by Rao [8], was used to group genotypes into different clusters. In the form of a table, the D^2 values of all combinations were sorted in ascending order. as outlined by Singh and Choudhary [9]. Each character was ranked based on their contribution to the divergence between two entries. Each of the characters was ranked from rank '1' (a character with the greatest mean difference) to rank 'p' for all combinations of entries (the character with the lowest mean difference).

3. RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among genotypes for all the characters studied, indicating existence of a good amount of genetic variability. On the basis of D^2 cluster analysis all the 54 genotypes (including checks) were grouped into 12 distinct non-overlapping clusters). The composition of different clusters varied from 1 to 16 genotypes. The maximum number of genotypes (16) was grouped into cluster I while, cluster IX, X, XI had single genotype. The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported existence of substantial genetic divergence in rice materials by Devi et al. [10], Parimalan et al. [11] and Rouf et al. [12]. The distribution of genotypes from different eco-geographical regions into these clusters was apparently random. Genotypes of similar origin were grouped into different clusters and vice versa, thereby indicating non-relationship between geographical and genetic diversity. This also suggests that the genotypes within cluster may have some degree of ancestral relationship. Therefore, Presence of substantial genetic diversity among the lines screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed as isolating desirable segregates for developing high yielding varieties of rice suitable for saline soil. The selection of parental materials for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographic distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in rice by Deepsankar et al. [13], Chandra et al. [14], Kumar [15], Raut et al. (2009).

The relative contribution of different characters included in the study towards diversity is presented in Table 1. relative contribution of characters towards genetic divergence number of times that each of the 4 characters appeared in first rank and its respective per cent contribution towards genetic divergence The results showed that the contribution of Days to 50% flowering towards genetic divergence was highest (65.61%%) by taking 938 times ranking first, followed by Seed yield per plant (g) (34.17%) by ranking 489 times first, 1000 seed weight (g) (0.13%) by 2 times ranking first, (0.06%) by Sterile percentage ranking 1 times first, to the total genetic divergence.

3.1 Composition of Clusters

Based on D^2 values, fifty-four genotypes were grouped into twelve clusters using Tocher method [9]. Clusters with their genotypes . Cluster I had fifteen genotypes, Cluster II had thirteen genotypes, whereas Cluster III had 4 genotypes cluster IV, V had 4 genotypes and cluster VI had six genotypes cluster VII had single genotype cluster VIII had three genotypes cluster IX, X, XI had single genotype XII had three genotypes.

The clustering pattern indicated that the genetic diversity was not fully associated with geographical diversity, hence there was no formal relationship between geographical diversity and genetic diversity. This could be because, there were other forces than

geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation responsible for genetic diversity

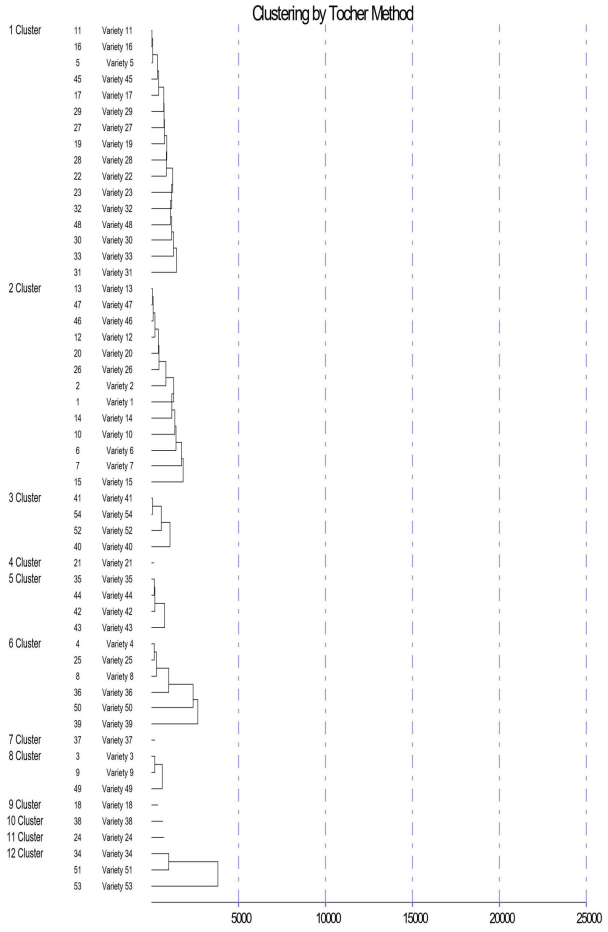
Intra cluster D^2 values are minimum (0.00) in cluster Ⅳ, VII, Ⅸ, Ⅹ and Ⅺ as these were monogenotypic clusters and genotypes in these clusters were more divergent and they could be utilized as parents for hybridization. Maximum intra cluster distance was observed in cluster Ⅻ (**11037.94**), followed by cluster Ⅵ (**5829.01**) and Ⅱ (**3591.21**) revealing that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean value for the desirable characters. The intra cluster distance was lower than inter cluster distance (Table 1), indicating the existence of genetic diversity mong the genotypes under study.

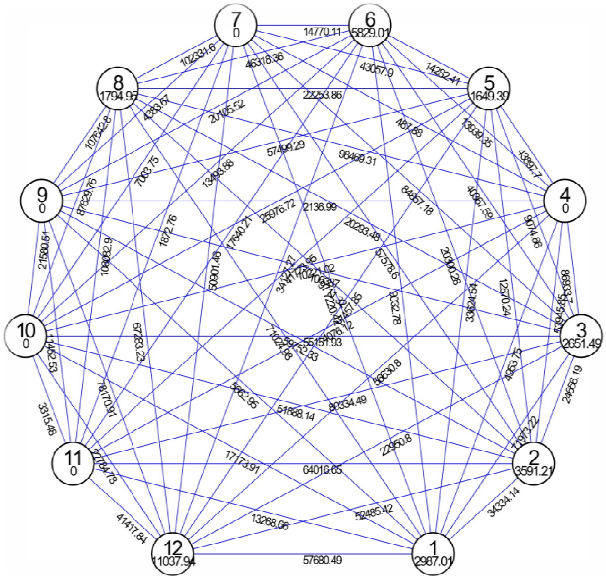
Table 1. Relative contribution of different characters to genetic diversity in 54 rice genotypes

Sl. No	Characters	Times ranked first	Contribution (%)
1	Das to 50% flowering	939	65.61%
2	Plant height (cm)	0	0.00 %
3	Panicle length (cm)	0	0.00 %
4	Effective tillers per plant	0	0.00 %
5	Panicle weight (g)	0	0.00 %
6	Total no. of filled grains per panicle	0	0.00 %
7	Sterile percentage	1	0.06 %
8	1000 seed weight (g)	2	0.13 %
9	Grain length	0	0.00 %
10	Grain width	0	0.00 %
11	Length Breadth Ratio	0	0.00 %
12	Seed yield per plant (g)	489	34.17%

Table 2. Clustering composition among 54 rice genotypes under study by Tocher method

S. No	Cluster number	No. of Genotypes	Genotypes
1	I	16	CSR 10, MTU-1001, R-RHZLI 23, GNV 18-64, IIRRH-147, CSR 23, CSAR-7-9-2020, CSR YET 55, RP 6112-MS-M-98-2-5-7-23-6-1, GNV 1801-9, CSR YET 8, IET 26383, CSRTPB 159, KPS-2874, SATYA
2	II	13	FL 478, IR 64, MI 127, CSR 449S-13, RP 6112-MS-M-8-2-9-3-4-6-8, CSR CPB 69, JGL 24423, CSR MAGIC 167, CSR 89-IR 15, CSR 23, KR 15066 (224-4-3-1-1), Pusa 44
3	III	4	MI 156, CR Dhan 311, R-RHZ-SM-14, R-RHZ-IH-82
4	IV	1	Narendra usar-2,
5	V	4	RRHP-MI30, DRR Dhan 45, Samba Mahsuri, Zinco rice MS
6	VI	6	CSR 36, CSAR 12-10-2020, R-RHZ-IB-80, CSR-RIL-06-178, R-RHZ-IH-82, IET 24780
7	VII	1	CGZR-1,
8	VIII	3	CSRM1-45, RNR 11718, CGZR-2
9	η	1	CSR YET 59
10	Ⅹ	1	Kalanamak
11	φ	1	CSR 27
12	κ	3	Rp-56, DRR Dhan 49, R RHZ-SD-94





Cluster diagram of 54 rice genotypes by Tocher method

Table 3. Intra (diagonal) and inter cluster distances of D2 values of 54 genotypes under study

	1	2	3	4	5	6	7	8	9	10	11	12
1	2987.01	34334.14	71973.22	4953.75	33624.54	9032.78	7220.42	71024.98	5662.95	17173.91	13268.66	57680.49
2		3591.21	24656.19	53945.85	12870.24	20300.28	57578.60	9711.32	59752.33	51888.14	64016.65	52485.42
3			2651.49	86933.70	9074.86	40367.59	84857.18	20293.48	106387.00	55151.93	80334.49	22950.80
4				0.00	43897.70	13939.35	487.88	98469.31	2136.99	10221.02	4076.12	56630.80
5					1649.39	14282.41	43057.90	22253.86	57499.29	25976.72	41723.95	17457.85
6						5829.01	14770.11	46318.36	20105.52	13493.88	17640.21	34127.27
7							0.00	102331.60	4383.67	7003.75	1872.76	50901.46
8								1794.95	107642.80	87629.76	108082.90	67283.23
9									0.00	21580.51	11452.53	78170.91
10										0.00	3315.48	22784.78
11											0.00	41417.84
12												11037.94

Table 4. Cluster means of 54 rice genotypes under study by Tocher method

Characters	I	II	III	IV	V	VI	VII	VIII	η	ι	φ	κ
Days to 50% flowering	91.41	107.21	111.28	87.00	104.58	96.50	86.70	114.87	85.70	90.70	86.70	100.67
Plant height (cm)	76.98	79.43	97.83	71.33	102.70	86.92	87.37	87.84	67.63	124.13	105.50	114.91
Panicle length (cm)	19.11	20.42	22.28	18.87	22.31	20.24	20.43	20.39	17.80	25.23	23.10	25.22
No. of effective tillers per plant	13.00	10.77	14.88	9.90	12.58	12.44	9.77	9.48	13.23	11.10	8.23	12.10
Panicle weight (g)	7.52	7.04	8.07	6.74	7.31	7.17	7.64	7.68	7.90	6.68	7.90	8.69
No. of filled grains per panicle	81.14	79.04	97.68	46.90	57.91	61.39	67.57	92.97	61.33	115.10	114.77	78.11
Sterile percentage	27.94	18.28	28.84	16.43	16.43	20.43	21.50	15.37	7.83	32.67	88.10	15.62
1000 grain weight (g)	17.07	22.30	18.19	20.73	20.76	21.99	22.69	18.57	25.51	23.28	9.21	20.51
Grain length	8.63	8.67	8.45	8.74	8.76	8.99	8.70	8.53	8.62	8.79	8.26	9.24
Grain width	1.92	1.86	1.82	2.27	1.80	1.99	1.85	1.87	1.76	2.05	2.27	1.94
L B Ratio	4.61	4.75	4.70	3.90	4.88	4.61	4.72	4.68	4.91	4.29	3.70	4.85
Seed yield per plant (g)	6.42	6.70	32.16	12.26	24.38	14.37	16.06	8.65	4.36	28.83	23.08	43.37

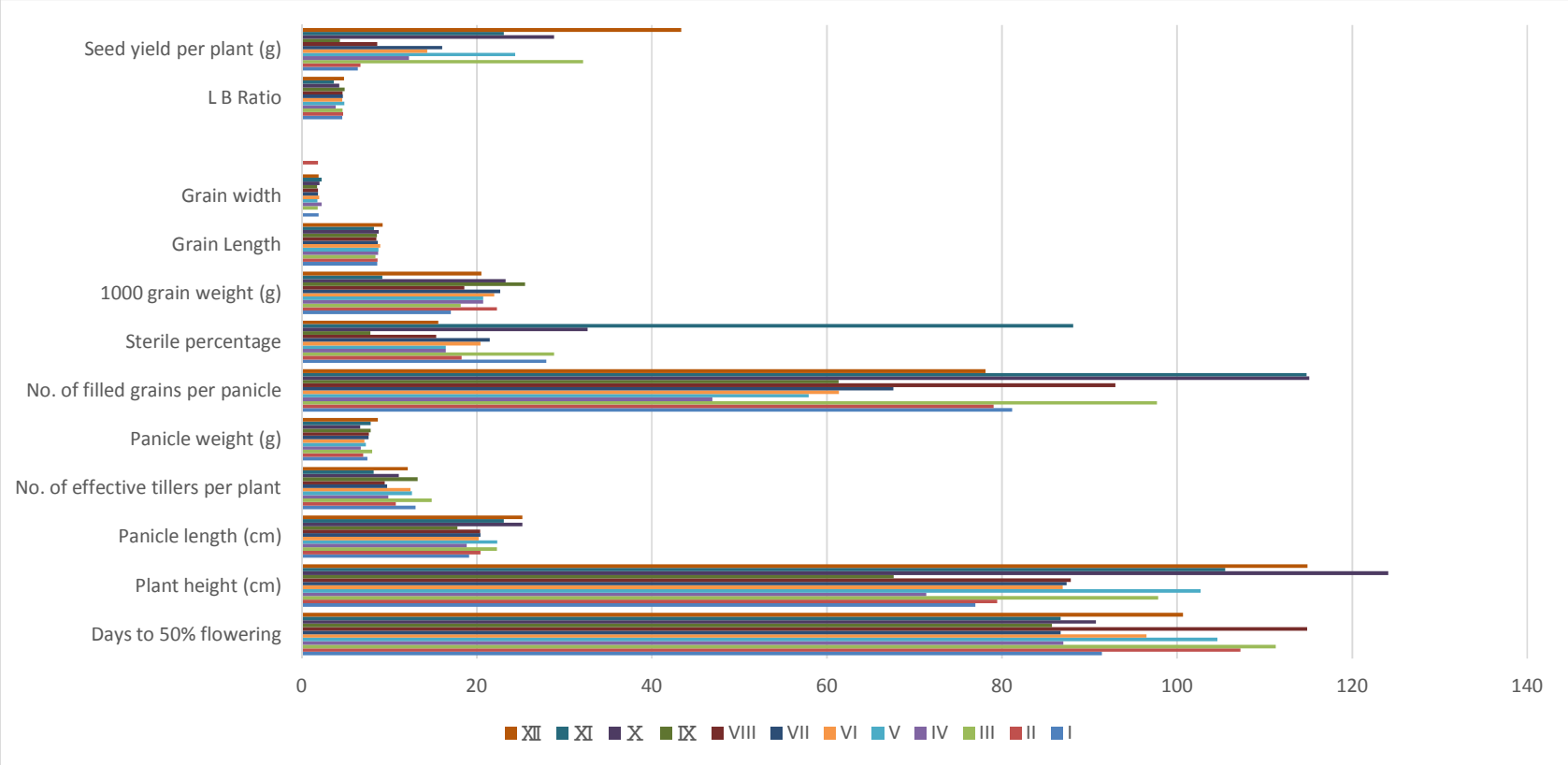


Fig. 1. Graph Representing Cluster means of 54 rice genotypes under study by Tocher method

Maximum inter cluster distance was exhibited between clusters VIII and XI (**108082.90**) followed by clusters IX and VIII (**107642.80**), These findings are in conformity with the findings of **Suresh *et al*. (2014)**. clusters IX and III (**106387.00)** clusters VII and VIII (**102331.60**), cluster IV and VIII (**98469.31**) and, clusters IX and XII (**78170.91**), cluster **Greater** the distance, wider the genetic diversity among the genotypes of those clusters. For high heterotic recombinants performing genotypes would be used as parents in recombination breeding programme. and lowest cluster divergence found between the clusters IV and VII **(487.88),** clusters XI and VII (**1872.76)**, clusters IX and IV (**2136.99),** clusters X and VII **(7003.75).**

It is observed that genotypes from cluster VIII (CSRM1-45, RNR 11718, CGZR-2) and clusters XI (CSR 27), from clusters IX (CSR YET 59) and VIII ((CSRM1-45, RNR 11718, CGZR-2) ,from clusters IX (CSR YET 59)and cluster III (MI 156, CR Dhan 311, R-RHZ-SM-14, R-RHZ-IH-82),From clusters VII (CGZR-1,) and VIII (CSRM1-45, RNR 11718, CGZR-2), From cluster IV (Narendra usar-2,) and VIII (CSRM1-45, RNR 11718, CGZR-2), From clusters IX (CSR YET 59) and XII (Rp-56, DRR Dhan 49, R RHZ-SD-94) can be used as parents in the hybridization programme to generate breeding material with high diversity to get encouraging results in case of D^2 analysis for both quantitative and qualitative characters.

3.1.1 Cluster means of the characters

The cluster means for of 12 characters are presented in Table 3. From the results of cluster means generated by Tocher method, it can be concluded that considerable differences existed for all the traits studied among the clusters. Cluster means data indicates days to 50% flowering was highest in cluster III (111.28) and lowest in cluster IX (85.70), plant height recorded highest in cluster X (124.13) and lowest in cluster IX (67.63), panicle length was observed highest in cluster X (25.23) and lowest in cluster IX (17.80), No. of effective tillers per plant was highest in cluster III (14.88) and lowest in cluster XI (8.23), Panicle weight (g) recorded highest in cluster XII (8.69) and lowest in cluster X (6.68), No. of filled grains per panicle was found to be highest in cluster X (115.10) and lowest in cluster V (57.91) . was found to be Sterile percentage highest in cluster XI (88.10) and lowest in cluster IX (7.83). 1000 grain weight (g) highest in cluster IX (25.51) and lowest in cluster XI (9.21). Grain Length highest in cluster XII (9.24) and lowest in cluster XI (8.26). Grain width highest in cluster IV (2.27) and lowest in cluster IX (1.76) L B Ratio highest in cluster (4.91) and lowest in cluster XI (3.70) L B Ratio highest in cluster (4.91) and lowest in cluster XI (3.70) Seed yield per plant (g) highest in cluster (43.37) and lowest in cluster IX (4.36).

Mahalanobis D2 statistic has been used by many researchers for multivariate analysis such as degree of divergence studies in crop germplasm collections. Kandhola and Panwar [16], Singh et al. [17], Kuchanur et al. [18], Vennela et al. (2017), Bhati et al. [19] and Behera et al. [20] has reported the success of this model for studying genetic divergence in rice genotypes.

4. CONCLUSION

In this Saline soil experiment, various clusters showed considerable differences in inter-cluster group means for 12 characters. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter-cluster distance between them are likely to be more rewarding and can be used in the breeding in crop improvement.

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COMPETING INTERESTS

Authors have declared that no competing interests exist

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