Genetic diversity analysis for yield and quality traits in rice cultivars of Manipur and Assam.

ABSTRACT

The present investigation was carried out with 41 diverse cultivars of rice to estimate the nature and magnitude of genetic divergence among the genotypes using Mahalanobis D^2 statistic. The genotypes were grouped under 12 different clusters and cluster IV was the largest comprising the maximum number of genotypes with 12 genotypes, followed by cluster V with eight genotypes, cluster X with five genotypes, clusters II and XII with four genotypes each, cluster I with two genotypes and clusters III, VI, VII, VIII, IX & XI with one genotype each. Among all the characters studied, grain length exhibited maximum contribution towards divergence. Clusters X and XII showed the maximum inter-cluster distance and the maximum intra cluster distance was exhibited by cluster XII, indicating the existence of a significant amount of variability within the cluster. Hybridization among the genotypes of these two clusters is expected to produce better heterotic combinations.

Keywords: Rice, diversity, D^2 statistic, hybridization.

INTRODUCTION

Rice (*Oryza sativa* L. 2n=24) is the most important staple food crop in the world particularly the South East Asia including India. About 90% of all rice in the world is grown and consumed in the Asian region which is also known as the 'Rice Bowl of the World'. Globally, India stands first in the area and second in production after China and contributing 25.1% of global rice production. Among the states, the North-Eastern region of India is endowed with rich biodiversity and is considered to be one of the hot pockets of rice genetic resources in the world with extremely diverse rice-growing conditions as compared to other parts of the country.

Rice grain quality breeding has become a major attraction in the past few years. With the increase in population, it is very important to analyze whether the production of rice can keep pace with population growth. Hence, to support the demand of the increasing population, emphasis should be given to the development of high-yielding rice with outstanding quality traits.

For a successful breeding program, the most essential prerequisite is the availability of genetic variability and the development of superior hybrids with good qualities mainly depends on the existence of diversity among the genotypes. The study of genetic diversity allows us to know about the magnitude of genetic variability that is available in the population and also gives information about the genetic distance among the group of genotypes. The knowledge of genetic diversity in terms of nature and degree of divergence for grain yield, yield components, and quality characters helps the breeders in the selection of parents for hybridization for developing potential high yielding rice varieties with good grain qualities [1]. Therefore, the present investigation was carried out to estimate the nature and magnitude of genetic divergence present in the 41 rice genotypes and to identify the diverse genotypes for a future breeding program.

MATERIALS AND METHODS

41 rice genotypes (**Table 1**) collected from the farmers' fields of Manipur and Assam were transplanted in a randomized block design with three replications during the *Kharif* season, 2020. In each replication, the plants were grown with a spacing of 20 cm between the plants and 25 cm between the rows. Five plants from each plot in each replication were randomly sampled for observation for days to 50 *per cent* flowering, days to maturity, plant height (cm), panicle length (cm), panicle number per plant, the total number of grains per panicle, number of filled grains per panicle, 100-grain weight (g), spikelet fertility, grain yield (g), biological yield (g), harvest index, panicle harvest index, grain length (mm), grain breadth (mm), grain length: breadth ratio, kernel length (mm), kernel breadth (mm), kernel length: breadth ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, kernel widening ratio and volume expansion ratio. The analysis of variance (ANOVA) was done using the RCBD design as suggested by Panse and Sukhatme (1961) [2]. Mahalanobis' (1936) D^2 statistic [3] was used for assessing the genetic divergence between the rice cultivars under study and the *per cent* contribution of each character was estimated following Tocher's method as suggested by Rao [4] and described by Singh and Choudhury [5]. The data analysis was carried out using INDOSTAT software.

RESULTS AND DISCUSSION

Analysis of variance for 24 characters revealed significant differences among the genotypes for all the characters under study at 1% level of significance indicating the presence of greater variability among the genotypes studied suggesting that there is ample scope for selection from these diverse sources for yield and its components and quality traits. The details pertaining to ANOVA are presented in **Table 2**. These results were in accordance with Ketan *et al.* [6] and Devi *et al.* [7].

The distribution of 41 genotypes in different clusters is presented in **Table 3**. The genotypes could be clustered into 12 clusters based on Mahalanobis D^2 values. Sabesan *et al.* [8] calculated a similar clustering pattern for 26 rice genotypes into 13 different clusters based on 12 morphological and quality characters. The maximum number of genotypes were grouped in cluster IV with 12 genotypes, followed by cluster V with eight genotypes, cluster X with five genotypes, clusters II and XII with four genotypes each, cluster I with two genotypes and clusters III, VI, VII, VIII, IX & XI maintained their separate identities by forming monogenetic groups with one genotype each. The distribution of the germplasm into many clusters showed the presence of genetic diversity among the germplasm taken in the experiment which further indicated that the materials considered may serve as a good source for selecting the diverse parents for hybridization programs for isolating desirable segregants for grain yield and quality traits. These results are in accordance with Chandramohan *et al*. [9] and Devi *et al.* [10].

The grouping of the clusters revealed that the genotypes did not follow their geographical distribution as the varieties from diverse sources can be seen to be grouped into the same cluster. For example, in clusters IV and XII, the genotypes originating from both Manipur and Assam were included. Whereas, clusters II and VI were observed to have only the Manipuri varieties and clusters I, III, V, VII, VIII, IX, X and XI consisted only of the genotypes from Assam. On the contrary, the genotypes originating from a common geographical location were also grouped into different clusters, which may be a result of differential adaptation to varied agro-ecosystems [11, 12]. This revealed that geographic diversity is not the sole factor in contribution to genetic diversity and that it may be due to different genetic backgrounds involved in the clustered genotypes.

The intra cluster distance was minimum (68.59) for cluster I, and zero for clusters III, VI, VII, VIII, IX and XI as they consist of a single genotype each. It was maximum (1146.89) for cluster XII. The inter cluster distance was also recorded minimum of 104.43 (between clusters I and III) which indicated a close relationship and presence of similarity for most of the characters and was maximum (2678.57) between clusters X and XII, which indicates the presence of high diversity among the genotypes. Clusters X with five genotypes and cluster XII with four genotypes were the most divergent groups with a maximum inter cluster distance of 2678.57 (**Table 3**). Therefore, it is expected that intercrossing between two genotypes of these clusters having high inter cluster distance can exhibit a high heterotic effect and would yield better recombinants. These findings corroborate well with Chandra *et al.* [13], Anjali *et al.* [14] and Shivani *et al.* [15] regarding the use of parents with wide inter cluster distances in hybridization programs since intercrossing between divergent parents is likely to produce wide variation and transgressive segregations. Rahaman *et al*. [16] also suggested the same.

Cluster means analysis with respect to 24 characters revealed a wide range of variation for all the traits under study and is presented in Table 5. Cluster II exhibited the maximum cluster means for grain length: breadth ratio, kernel length: breadth ratio and kernel widening ratio. Cluster III showed the maximum cluster means for kernel elongation ratio and volume expansion ratio and the highest cluster means for kernel length, grain yield per plant, biological yield and grain length were exhibited by cluster VI. Cluster VII showed maximum values for panicle length, the total number of grains per panicle, number of filled grains per panicle, 100-grain weight, spikelet fertility and panicle harvest index. The maximum cluster means for days to maturity, kernel breadth and kernel breadth after cooking were exhibited by cluster VIII. For panicle number per plant and harvest index, the maximum cluster mean values were shown by cluster IX; cluster XI genotypes exhibited the maximum cluster means for days to 50 *per cent* flowering, days to maturity, plant height and grain breadth. Cluster XII exhibited the maximum cluster mean value for kernel length after cooking. It was observed that all the clusters did not contain genotypes with all the desirable traits which could be directly selected. The minimum and maximum cluster means were found to be distributed in relatively distant clusters. However, it can be estimated that the genotypes belonging to cluster V are endowed with many important traits.

The *per cent* contribution of 24 characters to the total genetic divergence is presented in **Table 6**. Among all the characters studied, the maximum contribution towards divergence was found to be provided by grain length followed by kernel length after cooking, grain breadth, 100-grain weight, kernel breadth after cooking, days to 50 *per cent* flowering, volume expansion ratio, panicle harvest index, biological yield, days to maturity, plant height, panicle length, kernel elongation ratio, panicle number per plant, grain yield per plant and kernel length. While characters *viz*. total number of grains per panicle, number of filled grains per panicle, spikelet fertility, harvest index, grain length: breadth ratio, kernel breadth, kernel length: breadth ratio and kernel widening ratio showed no contribution towards divergence and hence, they were of less importance. Therefore, those characters having maximum contribution towards divergence should be given importance during hybridization programs as selection and choice for potential parents mainly depend on their contribution and selection for these characters may be rewarding.

Based on the mean performance of the genotypes for different traits, their genetic distance and their contribution to total divergence, genotypes with desirable characteristics can be selected for hybridization programs to produce a greater heterotic effect. Hence, it can be suggested that the earliness of Maizubiron from cluster XII concerning days to 50 *per cent* flowering and maturity can be utilized in crossing with diverse genotypes from different clusters to develop early maturing plant varieties and for enhancing the performance of the genotypes with respect to different desirable traits.

Table 1. List of 41 rice cultivars taken for the experiment

Sl. No.	Genotypes	Sl. No.	Genotypes
1.	Bhogali	22.	Kunkuni Joha
2.	Biriabhonga Bao	23.	Machuri
3.	Biyoi Sali	24.	Maguri Dhan
4.	Black Rice	25.	Maizubiron
5.	Boga Joha	26.	Maizubiron 1
6.	Bokul	27.	Manipur Joha
7.	Bonni	28.	Manohar Sali
8.	Bor Jahinga	29.	Navin Dhan
9.	Buthao Sticky Rice	30.	Nepali Sokowa
10.	Chaoren Phou	31.	Noinoi Phou
11.	Hacky Nagaland	32.	Nolbora
12.	Hemo Phou	33.	Rangali Sali
13.	Hindubor	34.	Ranjit
14.	Kaleja Phou	35.	Sekmai Phou
15.	Karbi Dhan	36.	Solpuna
16.	Kokua Bao	37.	Sulsuli Bao
17.	Kola Joha	38.	Swarna Joha
18.	Kola Manipuri	39.	Thoibi Phou
19.	Kolakon Joha	40.	Til Bora 1
20.	Konguti	41.	Xaru Jahinga
21.	Kumol Dhan 1		

Table 2: Analysis of variance for yield, yield components and quality traits in rice cultivars.

Sl no.	Character	Mean Sum of Squares			CV (%)	CD (5 %)
		Replication (d.f= 2)	Treatment (d.f= 40)	Error (d.f= 80)		
1.	Days to 50 *per cent* flowering	8.422	445.781**	2.872	1.41	2.75
2.	Days to maturity	2.203	487.536**	5.311	1.52	3.74
3.	Plant height (cm)	388.108	2818.96**	89.081	5.99	15.33
4.	Panicle length (cm)	10.847	27.021**	3.309	6.74	2.95
5.	Panicle number per plant	6.508	12.889**	0.761	8.32	1.41
6.	Total number of grains per panicle	222.038	5901.24**	194.070	10.29	22.63
7.	Number of filled grains per panicle	232.292	4979.98**	123.042	10.66	18.02
8.	100-grain weight (g)	0.0007	0.566**	0.002	2.13	0.07
9.	Spikelet fertility	29.934	206.215**	26.522	6.81	8.36
10.	Grain yield per plant (g)	52.416	183.088**	7.210	13.20	4.36
11.	Biological yield (g)	166.696	716.824**	19.546	8.62	7.18
12.	Harvest index	20.969	507.929**	9.972	7.73	5.13
13.	Panicle harvest index	4.019	57.445**	2.710	1.98	2.67
14.	Grain length (mm)	0.010	2.861**	0.003	0.71	0.09
15.	Grain breadth (mm)	0.014	0.412**	0.001	1.56	0.07
16.	Grain length: breadth ratio	0.022	0.517**	0.002	1.72	0.08
17.	Kernel length (mm)	0.037	1.934**	0.008	1.62	0.15
18.	Kernel breadth (mm)	0.024	0.284**	0.006	3.62	0.13
19.	Kernel length:breadth ratio	0.048	0.482**	0.006	3.06	0.13
20.	Kernel length after cooking (mm)	0.012	3.687**	0.006	0.95	0.12
21.	Kernel breadth after cooking (mm)	0.008	0.627**	0.001	1.15	0.07
22.	Kernel elongation ratio	0.0004	0.017**	0.0005	1.64	0.03
23.	Kernel widening ratio	0.004	0.070**	0.003	3.34	0.09
24.	Volume expansion ratio	0.009	1.269**	0.010	3.50	0.16

** Significant at 1 % level

Table 3: Clustering pattern of 41 rice genotypes.

Clusters	No. of Entries	Name of genotypes
I	2	Navin Dhan, Swarna Joha
II	4	Buthao Sticky Rice, Sekmai Phou, Thoibi Phou, Hemo Phou
III	1	Karbi Dhan
IV	12	Kokua Bao, Til Bora 1, Manohar Sali, Ranga Sali, Black Rice, Xoru Jahinga, Manipuri Joha, Maguri Dhan, Hacky Nagaland, Bokul, Bonni, Kaleja Phou
V	8	Solpuna,Sulsuli Bao, Machuri, Kumol Dhan 1, Ranjit, Nolbora, Nepali Sokowa, Bor Jahinga
VI	1	Chaoren Phou
VII	1	Biria Bhonga Bao
VIII	1	Biyoi Sali
IX	1	Maizubiron 1
X	5	Kola Joha, Kunkuni Joha, Boga Joha, Konguti, Kolakon Joha
XI	1	Hindubor
XII	4	Bhogali, Kola Manipuri, Noinoi Phou, Maizubiron.

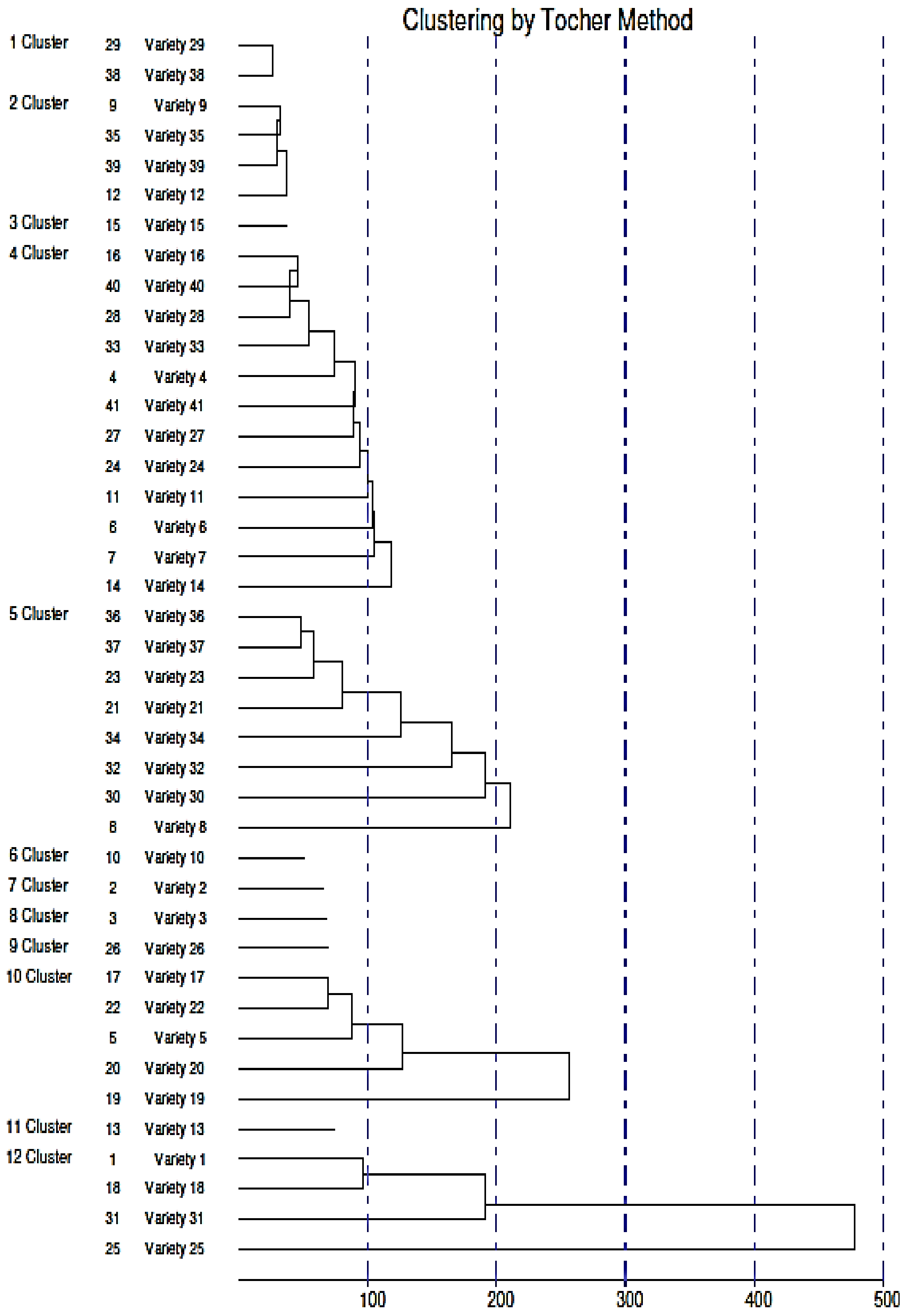

Fig. 1: Dendrogram based on Cluster analysis by Tocher's method

Table 4: Average inter and intra cluster distances for yield, yield components and quality traits in rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**68.59**											
II	221.38	**120.39**			`							
III	104.43	427.62	**0.00**									
IV	365.78	340.45	607.25	**289.77**								
V	454.73	583.02	626.10	425.82	**495.24**							
VI	418.41	192.33	661.17	375.63	728.20	**0.00**						
VII	702.99	532.05	998.52	465.54	734.54	510.24	**0.00**					
VIII	691.86	623.38	933.23	572.23	723.92	824.91	181.64	**0.00**				
IX	764.75	755.94	979.03	754.67	909.72	995.67	356.92	183.11	**0.00**			
X	1746.67	2050.57	1733.51	1836.43	1789.90	2374.78	1627.95	1378.13	915.10	**565.72**		
XI	777.31	706.64	946.57	581.34	692.75	792.25	350.13	196.34	435.94	1460.08	**0.00**	
XII	656.91	690.18	822.44	696.87	872.67	683.98	1113.77	1200.91	1459.37	2678.57	1136.15	**1146.89**

* Diagonal values indicate intra cluster distances * Above and below diagonal values indicate inter cluster distances

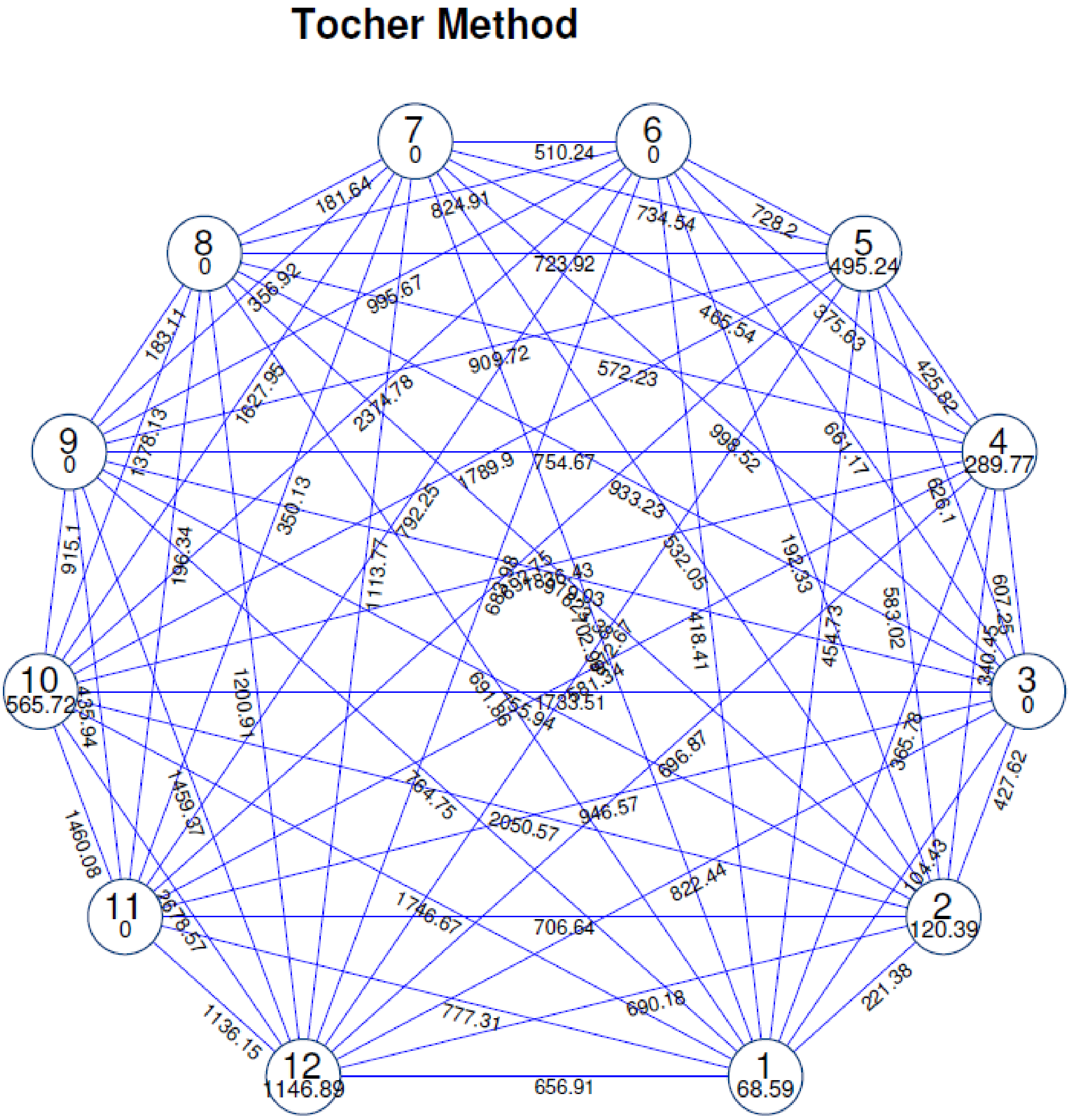

Fig 2: Mahalonobis' Euclidean distance

Table 5: Cluster means for yield, yield components and quality traits in rice genotypes

Clusters	DF	DM	PH	PL	PN	TG	FG	100 gw	SF	GYP	BY	HI
I	99.83	131.50	124.99	25.41	11.11	85.61	61.84	2.09	72.21	15.01	37.74	40.28
II	107.67	139.42	99.96	23.47	9.03	105.94	76	2.26	72.36	14.54	42.11	39.08
III	89.33	118.67	132.53	26.26	8.22	93.02	74.89	1.82	80.51	11.48	42.12	27.25
IV	123.17	155.03	171.06	27.44	11.13	149.32	116.02	2.32	77.18	22.66	52.59	44.34
V	127.42	159.17	167.44	26.65	10.90	145.48	113.23	1.96	75.28	23.23	49.77	44.84
VI	109.33	139.33	115.55	25.68	11.45	130.67	99.45	2.71	76.12	32.65	92.94	34.65
VII	126.33	155.33	190.29	33.28	7.67	201.45	174.44	2.92	86.62	28.23	73.76	38.28
VIII	129	166.33	162.64	29.22	9.44	107.89	84.22	2.29	78.07	19.77	45.33	43.63
IX	127.33	157.33	173.90	29.74	13.22	107.56	81.44	2.14	75.54	22.96	49.08	46.97
X	127.13	156.87	157.38	27.90	10.71	149.81	120.48	1.44	78.49	17.14	55.52	31.41
XI	133.33	166.33	193.45	28.51	9.33	82.89	52.78	1.88	63.98	9.35	68.50	13.52
XII	108.42	141.08	163.45	26.64	9.11	131.28	92.31	2.28	70.80	19.33	44.48	46.43

Table 5 Contd…

Clusters	PHI	GL	GB	GL: B	KL	KB	KL: B	KLC	KLI	KER	KWR	VER
I	81.95	8.31	2.54	3.28	5.83	2.13	2.74	8.46	3.87	1.45	1.82	3.37
II	79.40	8.91	2.71	3.29	6.24	2.22	2.82	8.16	4.10	1.31	1.85	3.04
III	82.91	8.14	2.51	3.25	5.60	2.21	2.53	8.47	3.72	1.51	1.69	3.79
IV	83.98	8.55	2.87	3.01	6.14	2.31	2.69	8.65	3.85	1.41	1.68	2.90
V	84.11	8.38	2.69	3.17	6.08	2.18	2.81	8.83	3.72	1.46	1.72	3.31
VI	82.51	8.99	3.05	2.95	6.36	2.46	2.59	8.81	4.10	1.38	1.67	2.59
VII	91.71	8.04	3.00	2.69	5.36	2.42	2.22	7.55	4.24	1.41	1.76	3.16
VIII	86.49	7.88	3.11	2.54	5.13	2.74	1.87	7.29	4.30	1.42	1.57	3.28
IX	85.23	7.29	2.89	2.52	4.87	2.32	2.10	6.54	4.14	1.34	1.78	1.97
X	78.73	6.09	2.39	2.57	4.23	1.81	2.37	6.13	2.91	1.44	1.62	1.77
XI	75.63	8.09	3.37	2.40	5.44	2.63	2.07	7.88	4.15	1.45	1.58	3.74
XII	83.88	8.90	3.16	2.88	6.33	2.46	2.68	9.28	3.85	1.47	1.59	2.94

Table 6. *Per cent* distribution of each character towards divergence in rice genotypes evaluated in field condition.

Sl no.	Character	Contribution (%)
1	Days to 50 *per cent* flowering	6.46
2	Days to maturity	0.37
3	Plant height	0.24
4	Panicle length	0.24
5	Panicle number per plant	0.12
6	Total number of grains per panicle	0.00
7	Number of filled grains per panicle	0.00
8	100- grain weight	9.51
9	Spikelet fertility	0.00
10	Grain yield per plant	0.12
11	Biological yield	2.44
12	Harvest index	0.00
13	Panicle harvest index	2.68
14	Grain length	40.73
15	Grain breadth	9.88
16	Grain length:breadth ratio	0.00
17	Kernel length	0.12
18	Kernel breadth	0.00
19	Kernel length:breadth ratio	0.00
20	Kernel length after cooking	17.44
21	Kernel breadth after cooking	6.59
22	Kernel elongation ratio	0.24
23	Kernel widening ratio	0.00
24	Volume expansion ratio	2.8

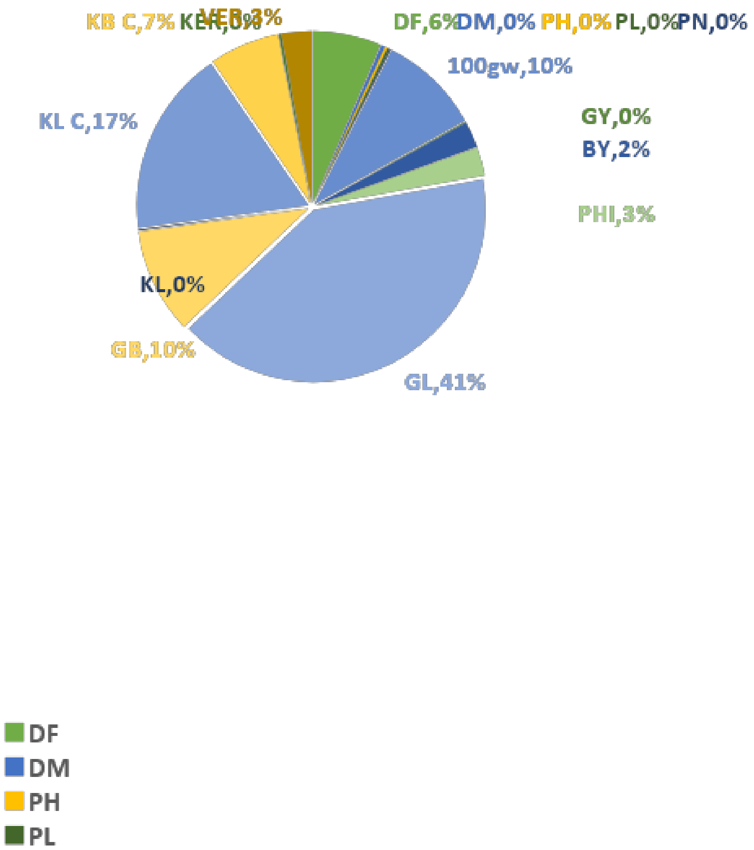

Fig 3: Percent contribution of different characters towards genetic divergence in genotypes

CONCLUSION

From the above findings, it can be concluded that substantial genetic diversity was observed in the materials studied for all the traits. It can be estimated that these germplasm lines can be taken as breeding material in future breeding programs in the region especially focusing on the rice grain quality. Recombination breeding can be suggested among the genotypes of cluster XII having maximum intra cluster distance to improve the yield potential. As the maximum inter cluster distance was observed between clusters X and XII, crosses involving the genotypes from these two clusters would give wider and desirable recombinations. Hence, an efficient hybridization program can be formulated for breeding better quality grains with higher yields by crossing two distantly related superior rice genotypes.

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