

Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method

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Abstract. The nature and magnitude of genetic divergence was estimated in one hundred and fourteen F_5 families of rice obtained from six different crosses along with their seven parents using ward's minimum divergence method by considering 10 characters. Results revealed existence of considerable amount of diversity in the material. The genotypes were grouped into twelve clusters. Cluster V constituted maximum number of genotypes (27). The genotypes falling in cluster XII had the maximum divergence (123.339), which was closely followed by cluster IX (112.928). The maximum inter cluster Euclidean² values was observed between cluster II and XII (1882.852) followed by cluster IX and XII (1488.520) suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Key words: Genetic divergence, cluster analysis, wards method.

INTRODUCTION

Rice is the staple food of more than half of the world's population – more than 3.5 billion people depend on rice for more than 20% of their daily calories. Rice provides 19% of global human per capita energy and 13% of per capita protein. The demand for rice production is increasing day by day because of expansion of rice consuming people. Globally, it is cultivated in an area of about 154 million hectares with an annual production of 600 million tonnes. India ranks first in area (43.85 million hectares) and second in the production (104.78 million tonnes) with a productivity of 2185 kg ha⁻¹.

The average productivity of rice in India, at present, is 2.2 tonnes/ha, which is far below the global average of 2.7 tonnes/ha. At the current rate of population growth of 1.58% in India, the requirement of rice by 2025 is estimated to be around 140.7 million tonnes

(<http://worldfood.apionet.or.jp>). To make India self-sufficient in rice, it is needed to improve the productivity to a greater extent (Hossain, 1996; Mishra, 2002). The task is quite challenging and the options available are very limited. Exploitation of hybrid vigour is one of the readily available alternatives to boost up the rice yield potential.

Demand for rice is increasing day by day and keeping in view of the future demand of rice as a food for human, there is a continuous need to evolve new varieties, which should surpass the yield of existing high yielding varieties. Variation present in the population is an important prerequisite for improvement of any crop species. For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable

Table 1. List of crosses studied and number of families studied under each cross

Cross	Number of families studied
MTU 7029/ MTU 1081	45
MTU 7029/ JGL 11118	5
MTU 7029/ NLR 34449	18
MTU 7029/ MTU 1121	3
MTU 7029/ PAU 3116-25-5-1	15
MTU 7029/ PAU 3140-126-1	28
Total - Six crosses	114

recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm. Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be useful for discrimination among the population occupying ecologically marginal habitats.

Chanbeni *et al.* (2012) reported that hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. The cluster analysis using Euclidean² distance provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. Singh and Chaudhary (1977) stated that selection of diverse parents for hybridization programme can be effective by the identification of characters responsible for the genetic diversity among the populations. Hence, in this study one hundred and fourteen F₅ families obtained from six crosses along with their seven parents of rice were evaluated to assess the nature and magnitude of genetic diversity among the genotypes and divide them into different clusters by using ward's minimum variance method for further utilization in breeding programmes.

MATERIAL AND METHODS

The experimental material consisted of one hundred and fourteen F₅ families belonging to six crosses of rice along with seven parents (Table 1 & 2) obtained from Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru were sown in randomized block design with two replications during *kharif*, 2015. Thirty days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and plants, respectively. Observations were recorded on five

randomly selected plants for eight characters *viz.*, plant height, number of panicles per plant, panicle length, grain yield per plant, test weight, kernel length, kernel breadth and Length/Breadth) ratio, while for other two characters *viz.*, days to 50 per-cent flowering, days to maturity, observations were recorded on plot basis. The mean values over two replications were used for statistical analysis and analysis was done using wards method to measure the genetic divergence.

RESULTS AND DISCUSSION

The quantitative assessment of genetic divergence was made by adopting ward's minimum divergence method for yield and its contributing characters. Genetic divergence was estimated for 10 characters of 121 lines (114 F₅ families along with their seven parents) of rice and the results obtained from the study are discussed below.

The 121 lines (114 F₅ families along with their seven parents) were grouped into 12 clusters. The distribution of families were presented in Table 3 and Figure 1. Among all the clusters, cluster V was largest containing 27 families followed by cluster XI with 14 families, cluster III and VIII each with 13 families, cluster I with 11 families, cluster IV with 10 families, cluster VII and IX with 9 families each, cluster VI and X with 5 lines each, cluster XII with 3 lines and cluster II with 2 families. The mutual relationship between clusters is represented diagrammatically in Figure 2 by taking average intra and inter cluster Euclidean distances.

Average intra and inter cluster Euclidean distance values

The average inter and intra cluster Euclidean² distances were estimated based on ward's minimum variance and were presented in Table 4 and Figure 3. By ward's method, the 121 lines were grouped into 12 clusters of which cluster XII had the maximum intra cluster distance (123.339), which was closely followed by cluster IX

Table 2. List of F₅ families studied

S. No.	Code	Entry	Cross combination
1	TSM-1	MTU 2462-1-1-1	MTU 7029/ MTU 1081
2	TSM-2	MTU 2462-1-1-2	MTU 7029/ MTU 1081
3	TSM-3	MTU 2462-1-2-1	MTU 7029/ MTU 1081
4	TSM-4	MTU 2462-1-5-1	MTU 7029/ MTU 1081
5	TSM-5	MTU 2462-1-5-2	MTU 7029/ MTU 1081
6	TSM-6	MTU 2462-1-8-1	MTU 7029/ MTU 1081
7	TSM-7	MTU 2462-1-8-2	MTU 7029/ MTU 1081
8	TSM-8	MTU 2462-1-9-1	MTU 7029/ MTU 1081
9	TSM-9	MTU 2462-1-9-2	MTU 7029/ MTU 1081
10	TSM-10	MTU 2462-2-1-1	MTU 7029/ MTU 1081
11	TSM-12	MTU 2462-4-1-1	MTU 7029/ MTU 1081
12	TSM-16	MTU 2462-6-2-1	MTU 7029/ MTU 1081
13	TSM-17	MTU 2462-8-1-1	MTU 7029/ MTU 1081
14	TSM-18	MTU 2462-8-2-1	MTU 7029/ MTU 1081
15	TSM-19	MTU 2462-8-2-2	MTU 7029/ MTU 1081
16	TSM-20	MTU 2462-12-1-1	MTU 7029/ MTU 1081
17	TSM-22	MTU 2462-12-2-1	MTU 7029/ MTU 1081
18	TSM-29	MTU 2462-15-1-1	MTU 7029/ MTU 1081
19	TSM-32	MTU 2462-15-3-1	MTU 7029/ MTU 1081
20	TSM-33	MTU 2462-15-3-2	MTU 7029/ MTU 1081
21	TSM-35	MTU 2462-17-2-1	MTU 7029/ MTU 1081
22	TSM-36	MTU 2462-17-3-1	MTU 7029/ MTU 1081
23	TSM-37	MTU 2462-18-1-1	MTU 7029/ MTU 1081
24	TSM-39	MTU 2462-21-1-1	MTU 7029/ MTU 1081
25	TSM-42	MTU 2462-22-2-1	MTU 7029/ MTU 1081
26	TSM-43	MTU 2462-22-3-1	MTU 7029/ MTU 1081
27	TSM-48	MTU 2462-23-3-1	MTU 7029/ MTU 1081
28	TSM-50	MTU 2462-26-3-1	MTU 7029/ MTU 1081
29	TSM-51	MTU 2462-26-3-2	MTU 7029/ MTU 1081
30	TSM-54	MTU 2462-27-3-1	MTU 7029/ MTU 1081
31	TSM-56	MTU 2462-29-2-1	MTU 7029/ MTU 1081
32	TSM-57	MTU 2462-30-1-1	MTU 7029/ MTU 1081
33	TSM-58	MTU 2462-31-2-1	MTU 7029/ MTU 1081
34	TSM-61	MTU 2462-34-1-1	MTU 7029/ MTU 1081
35	TSM-62	MTU 2462-34-4-1	MTU 7029/ MTU 1081
36	TSM-63	MTU 2462-35-2-1	MTU 7029/ MTU 1081
37	TSM-64	MTU 2462-35-2-2	MTU 7029/ MTU 1081

Table 2. Contd

38	TSM-65	MTU 2462-37-1-1	MTU 7029/ MTU 1081
39	TSM-66	MTU 2462-37-2-1	MTU 7029/ MTU 1081
40	TSM-67	MTU 2462-37-2-2	MTU 7029/ MTU 1081
41	TSM-68	MTU 2462-41-2-1	MTU 7029/ MTU 1081
42	TSM-69	MTU 2462-42-2-1	MTU 7029/ MTU 1081
43	TSM-72	MTU 2462-45-1-2	MTU 7029/ MTU 1081
44	TSM-73	MTU 2462-45-2-1	MTU 7029/ MTU 1081
45	TSM-74	MTU 2462-49-2-1	MTU 7029/ MTU 1081
46	TSM-76	MTU 2463-4-1-2	MTU 7029/ JGL 11118
47	TSM-77	MTU 2463-4-2-1	MTU 7029/ JGL 11118
48	TSM-79	MTU 2463-8-2-1	MTU 7029/ JGL 11118
49	TSM-82	MTU 2463-14-1-1	MTU 7029/ JGL 11118
50	TSM-83	MTU 2463-15-1-1	MTU 7029/ JGL 11118
51	TSM-85	MTU 2465-4-1-1	MTU 7029/ NLR 34449
52	TSM-86	MTU 2465-4-2-1	MTU 7029/ NLR 34449
53	TSM-87	MTU 2465-6-2-1	MTU 7029/ NLR 34449
54	TSM-88	MTU 2465-8-1-1	MTU 7029/ NLR 34449
55	TSM-90	MTU 2465-10-1-1	MTU 7029/ NLR 34449
56	TSM-92	MTU 2465-11-3-1	MTU 7029/ NLR 34449
57	TSM-93	MTU 2465-11-3-2	MTU 7029/ NLR 34449
58	TSM-94	MTU 2465-12-2-1	MTU 7029/ NLR 34449
59	TSM-95	MTU 2465-12-2-2	MTU 7029/ NLR 34449
60	TSM-96	MTU 2465-13-3-1	MTU 7029/ NLR 34449
61	TSM-97	MTU 2465-13-3-2	MTU 7029/ NLR 34449
62	TSM-99	MTU 2465-16-2-1	MTU 7029/ NLR 34449
63	TSM-101	MTU 2465-16-2-3	MTU 7029/ NLR 34449
64	TSM-102	MTU 2465-22-1-1	MTU 7029/ NLR 34449
65	TSM-103	MTU 2465-22-2-1	MTU 7029/ NLR 34449
66	TSM-104	MTU 2465-22-2-2	MTU 7029/ NLR 34449
67	TSM-108	MTU 2465-24-3-2	MTU 7029/ NLR 34449
68	TSM-110	MTU 2465-27-2-1	MTU 7029/ NLR 34449
69	TSM-114	MTU 2466-4-2-1	MTU 7029/ MTU 1121
70	TSM-115	MTU 2466-4-2-2	MTU 7029/ MTU 1121
71	TSM-116	MTU 2466-4-3-1	MTU 7029/ MTU 1121
72	TSM-118	MTU 2468-1-1-1	MTU 7029/ PAU 3116-25-5-1
73	TSM-120	MTU 2468-2-1-1	MTU 7029/ PAU 3116-25-5-1
74	TSM-128	MTU 2468-8-2-1	MTU 7029/ PAU 3116-25-5-1
75	TSM-132	MTU 2468-18-1-1	MTU 7029/ PAU 3116-25-5-1

Table 2. Contd

76	TSM-133	MTU 2468-18-1-2	MTU 7029/ PAU 3116-25-5-1
77	TSM-134	MTU 2468-20-1-1	MTU 7029/ PAU 3116-25-5-1
78	TSM-138	MTU 2468-21-4-1	MTU 7029/ PAU 3116-25-5-1
79	TSM-141	MTU 2468-25-2-1	MTU 7029/ PAU 3116-25-5-1
80	TSM-146	MTU 2468-27-2-1	MTU 7029/ PAU 3116-25-5-1
81	TSM-147	MTU 2468-28-1-1	MTU 7029/ PAU 3116-25-5-1
82	TSM-148	MTU 2468-29-2-1	MTU 7029/ PAU 3116-25-5-1
83	TSM-149	MTU 2468-29-3-1	MTU 7029/ PAU 3116-25-5-1
84	TSM-150	MTU 2468-29-4-1	MTU 7029/ PAU 3116-25-5-1
85	TSM-152	MTU 2468-30-2-2	MTU 7029/ PAU 3116-25-5-1
86	TSM-153	MTU 2468-31-1-1	MTU 7029/ PAU 3116-25-5-1
87	TSM-164	MTU 2469-6-1-2	MTU 7029/ PAU 3140-126-1
88	TSM-165	MTU 2469-6-2-1	MTU 7029/ PAU 3140-126-1
89	TSM-166	MTU 2469-6-3-1	MTU 7029/ PAU 3140-126-1
90	TSM-167	MTU 2469-6-3-2	MTU 7029/ PAU 3140-126-1
91	TSM-168	MTU 2469-6-5-1	MTU 7029/ PAU 3140-126-1
92	TSM-169	MTU 2469-7-1-1	MTU 7029/ PAU 3140-126-1
93	TSM-171	MTU 2469-8-1-1	MTU 7029/ PAU 3140-126-1
94	TSM-174	MTU 2469-10-2-1	MTU 7029/ PAU 3140-126-1
95	TSM-175	MTU 2469-11-1-1	MTU 7029/ PAU 3140-126-1
96	TSM-178	MTU 2469-14-1-1	MTU 7029/ PAU 3140-126-1
97	TSM-183	MTU 2469-23-2-1	MTU 7029/ PAU 3140-126-1
98	TSM-184	MTU 2469-23-2-2	MTU 7029/ PAU 3140-126-1
99	TSM-190	MTU 2469-32-1-1	MTU 7029/ PAU 3140-126-1
100	TSM-191	MTU 2469-32-2-1	MTU 7029/ PAU 3140-126-1
101	TSM-200	MTU 2469-36-1-1	MTU 7029/ PAU 3140-126-1
102	TSM-204	MTU 2469-38-4-1	MTU 7029/ PAU 3140-126-1
103	TSM-211	MTU 2469-41-2-2	MTU 7029/ PAU 3140-126-1
104	TSM-213	MTU 2469-42-1-1	MTU 7029/ PAU 3140-126-1
105	TSM-215	MTU 2469-42-3-1	MTU 7029/ PAU 3140-126-1
106	TSM-216	MTU 2469-42-4-1	MTU 7029/ PAU 3140-126-1
107	TSM-219	MTU 2469-55-1-1	MTU 7029/ PAU 3140-126-1
108	TSM-220	MTU 2469-55-2-1	MTU 7029/ PAU 3140-126-1
109	TSM-221	MTU 2469-55-2-2	MTU 7029/ PAU 3140-126-1
110	TSM-223	MTU 2469-57-1-2	MTU 7029/ PAU 3140-126-1
111	TSM-228	MTU 2469-68-1-1	MTU 7029/ PAU 3140-126-1
112	TSM-229	MTU 2469-68-1-2	MTU 7029/ PAU 3140-126-1
113	TSM-230	MTU 2469-68-2-1	MTU 7029/ PAU 3140-126-1

Table 2. Contd

114	TSM-235	MTU 2469-74-2-1	MTU 7029/ PAU 3140-126-1
		Parents	
115		MTU 7029	
116		MTU 1081	
117		MTU 1121	
118		JGL 11118	
119		NLR 34449	
120		PAU 3116-25-5-1	
121		PAU 3140-126-1	

Table 3. Clustering pattern of 121 lines (114 F₅ families and seven parents) of rice (*Oryza sativa* L.) by ward's minimum divergence method.

Cluster number	Number of genotypes	Name of the genotypes
Cluster I	11	TSM-1, TSM-147, TSM-7, TSM-87, TSM-32, TSM-35, TSM-43, TSM-4, TSM-6, TSM-5, TSM-29
Cluster II	2	TSM-8, TSM-9
Cluster III	13	TSM-3, TSM-88, TSM-36, TSM-96, TSM-97, TSM-69, TSM-85, TSM-72, TSM-87, TSM-42, TSM-86, TSM-90, TSM-99
Cluster IV	10	TSM-19, TSM-92, TSM-18, TSM-37, TSM-134, TSM-169, TSM-95, TSM-101, TSM-102, TSM-120
Cluster V	27	TSM-39, TSM-220, TSM-105, TSM-61, TSM-103, TSM-54, TSM-62, TSM-74, TSM-48, TSM-56, TSM-114, TSM-94, TSM-64, TSM-235, TSM-76, TSM-211, TSM-132, TSM-66, TSM-167, TSM-128, TSM-146, TSM-216, TSM-138, TSM-164, TSM-175, TSM-178, TSM-190
Cluster VI	5	TSM-58, TSM-18, TSM-219, TSM-65, TSM-141
Cluster VII	9	TSM-63, TSM-166, TSM-168, TSM-174, TSM-110, TSM-133, TSM-108, TSM-215, TSM-223
Cluster VIII	13	TSM-50, TSM-57, TSM-51, TSM-82, TSM-77, TSM-83, TSM-204, TSM-229, TSM-230, TSM-149, TSM-10, TSM-221, TSM-228
Cluster IX	9	TSM-152, TSM-183, TSM-153, TSM-213, TSM-191, TSM-148, TSM-68, TSM-165, TSM-200
Cluster X	5	TSM-10, MTU 7029, MTU 1121, PAU 3116-25-5-1, PAU 3140-126-1
Cluster XI	14	TSM-12, TSM-33, TSM-17, TSM-73, TSM-116, TSM-93, TSM-16, TSM-79, TSM-20, TSM-171, TSM-2, TSM-22, TSM-118, TSM-115
Cluster XII	3	MTU 1081, NLR 34449, JGL 11118

(112.928) and cluster VIII (107.172). The high intra cluster distance indicates the presence of wide genetic diversity among the genotypes. The inter cluster Euclidean² values varied between cluster III and cluster V (83.707) and cluster II and cluster XII (1882.852). All the remaining Euclidean² distances were lying between them.

Cluster I comprises of 11 families which was closest to cluster VI (153.593) but farthest from cluster XII (1374.224). Cluster II comprises of only two families which was farthest from cluster XII (1882.852) and closest to cluster I (220.368). Cluster III consists of 13

families which is far away from cluster XII (972.556) and closest to cluster V (83.707). Cluster IV consists of 10 families which is closest to cluster V (110.367) and farthest from cluster XII (938.274). Cluster V consists of 27 families (largest one) which is farthest from cluster XII (1065.466) and closest to cluster III (83.707) and cluster VII (85.793). Cluster VI consists of five families which is closest to cluster V (101.208) and far away from cluster XII (1418.118). Cluster VII consists of nine families which is farthest from cluster XII (1042.041) and closest to cluster V (85.793). Cluster VIII consists of 13 families and



Figure. 1. Number of lines in each cluster

it was closest to cluster V (138.872) followed by cluster III (147.151) while it was far away from cluster XII (1488.520) and was closest to cluster VII (151.717). Cluster X consists of five families which is closest to cluster XI (174.636) and farthest from

farthest from cluster XII (1488.520) and was closest to cluster VII (151.717). Cluster X consists of five families which is closest to cluster XI (174.636) and farthest from

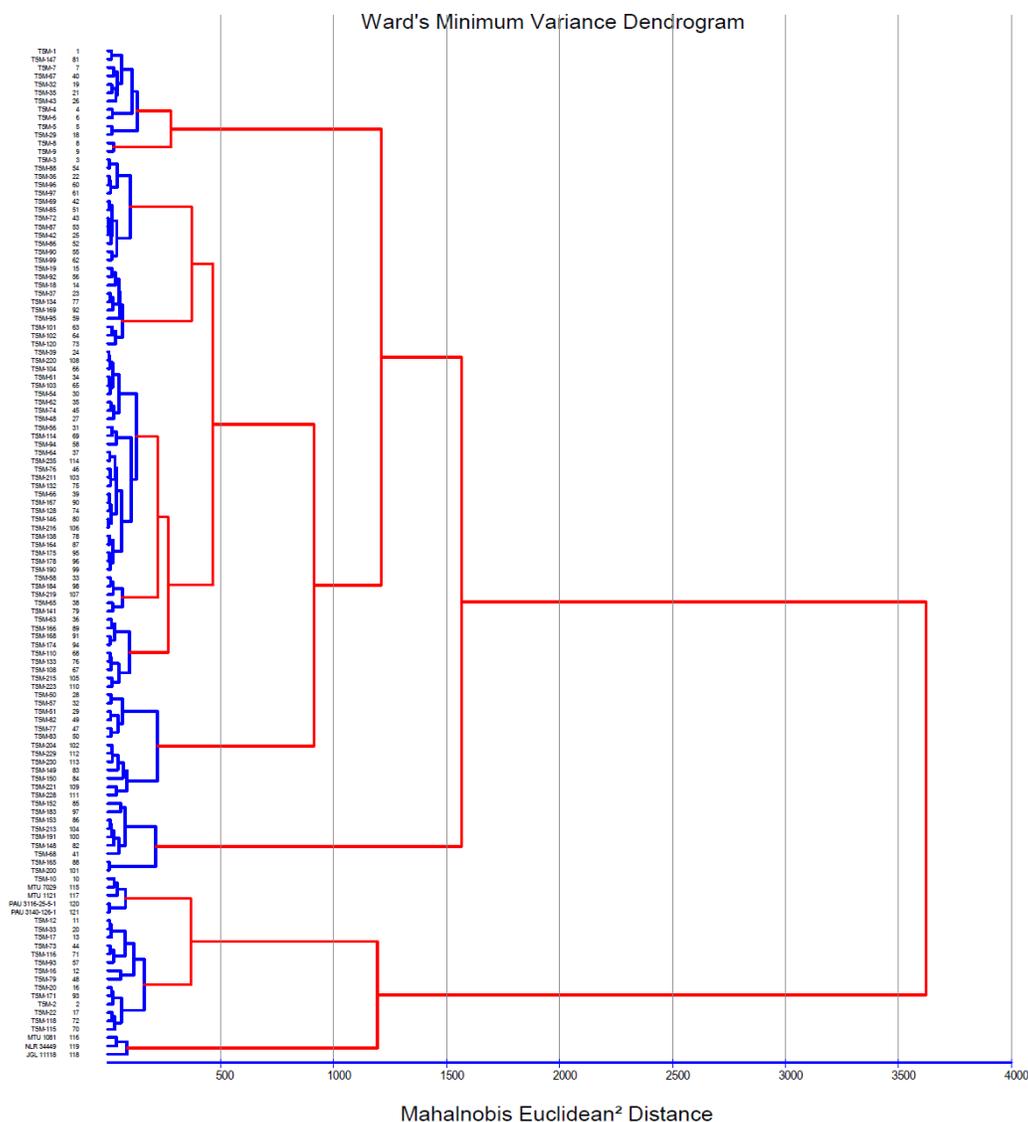


Figure. 2: Dendrogram showing relationship among 121 lines of rice (*Oryza sativa* L.) in twelve clusters based on Euclidean² values.

cluster II (591.884). Cluster XI consists of 14 families which is farthest from cluster II (716.216) and it was close to cluster V (163.163). Cluster XII consists of 3 lines which is closest to cluster X (496.599) and was far away from cluster IX (1488.520).

The intra cluster distance values reveals that maximum distance was found in cluster XII (123.339) indicating that the lines within this cluster were more divergent. Based on inter cluster distance values, it can be inferred that maximum distance was found between cluster II and cluster XII (1882.852) followed by cluster X and cluster XII (1488.520) and cluster VI and cluster XII (1418.118). Based on these studies, crosses may be made between genotypes of clusters II and cluster XII followed by genotypes of clusters X and XII; clusters VI

and XII to obtain new desirable recombinants in rice. Accessions falling in a particular cluster indicate their close relationship among themselves as compared to the other clusters. Therefore, it could be expected that accessions within a cluster were less genetically different with each other, and were diverse from the cultivars belonging to other clusters. These findings are in conformity with the results of Khare *et al.* (2014) and Singh *et al.* (2013).

Cluster mean values of characters

The cluster mean values for 10 characters are presented in Table 5. The data indicated that mean values exhibited

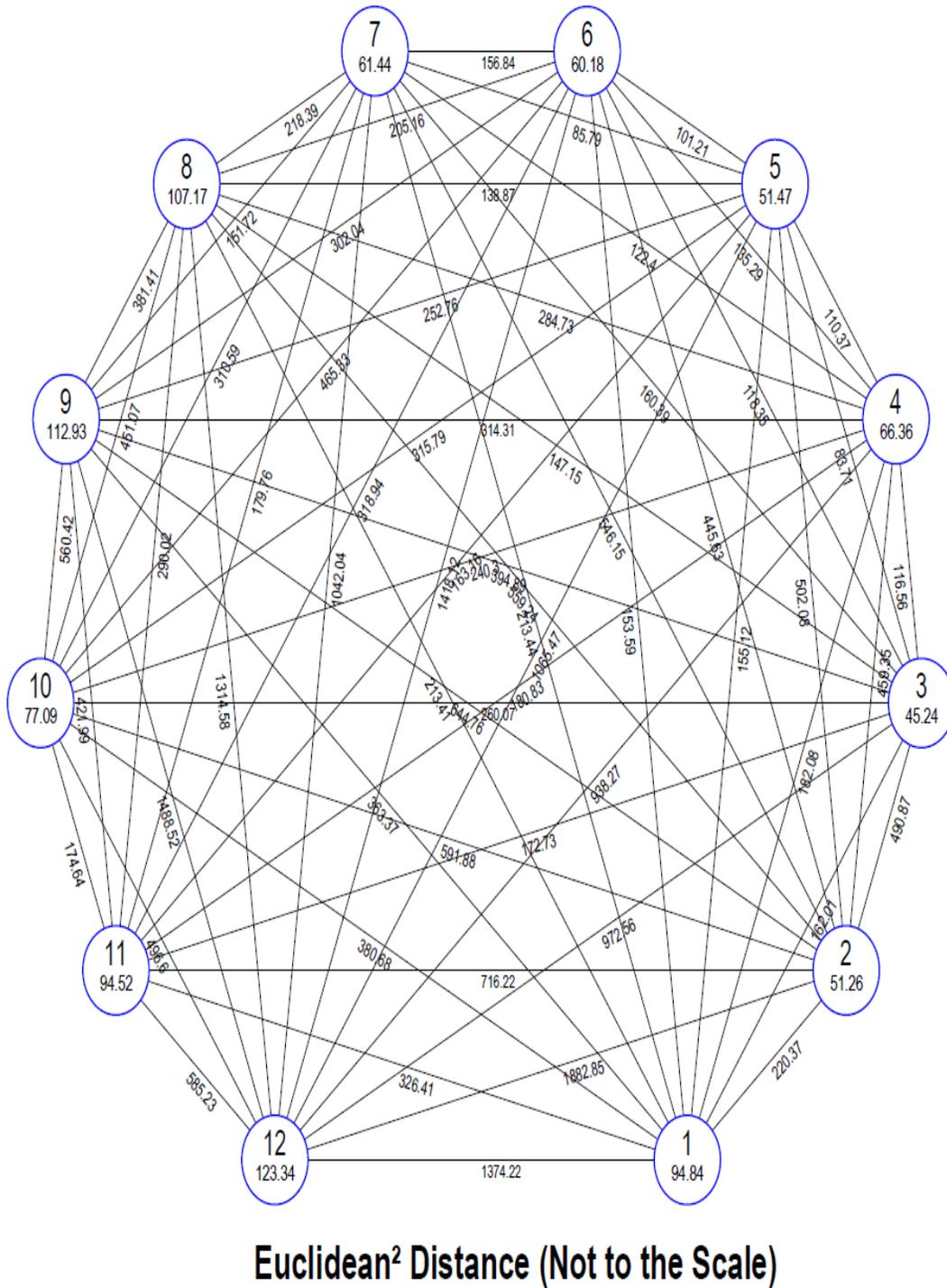


Figure. 3: Average intra and inter cluster distances among 121 lines of rice (*Oryza sativa* L.) in twelve clusters based on Euclidean² values.

wide range for almost all the traits studied. Days to 50% flowering had a range of 92 days for cluster XII to 124 days for cluster VI; days to maturity had a range of 118 days for cluster XII to 149 days for cluster VI; Plant height (cm) varied from 99.07 cm for cluster XII to 125.13 cm for

cluster VIII; Number of panicles per plant had a range of 9 for cluster XII to 12 for cluster VIII; Panicle length had a range of 22.80 cm for cluster IX to 26.25 cm for cluster II; Grain yield per plant had a range of 16.99 g for cluster V to 42.68 g for cluster II; Test weight (g)

Table 4. Average intra-and inter –cluster Euclidean² values among twelve clusters in 121 lines of rice (*Oryza sativa* L.) genotypes.

Euclidean ² : Cluster Distances : Ward												
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
Cluster I	94.844	220.368	162.015	182.084	155.122	153.593	213.442	213.406	363.372	380.678	326.415	1374.224
Cluster II		51.263	490.874	459.349	502.079	445.630	546.151	559.245	644.757	591.884	716.216	1882.852
Cluster III			45.237	116.564	83.707	118.352	160.388	147.151	394.887	260.068	172.732	972.556
Cluster IV				66.356	110.367	135.291	122.400	284.735	314.309	240.303	180.825	938.274
Cluster V					51.471	101.208	85.793	138.872	252.758	315.786	163.163	1065.466
Cluster VI						60.179	156.843	205.158	302.041	465.331	318.940	1418.118
Cluster VII							61.436	218.387	151.717	310.591	179.759	1042.041
Cluster VIII								107.172	381.406	451.069	290.017	1314.583
Cluster IX									112.928	560.415	421.990	1488.520
Cluster X										77.090	174.636	496.599
Cluster XI											94.520	585.234
Cluster XII												123.339

Diagonal bold values indicate intra cluster distances

recorded as high as 34.62 g in cluster IX to as low as 15.80 g in cluster XII; Kernel length had a range of 5.7 mm for cluster X to 6.6 mm for cluster II; Kernel breadth varied from 2.1 mm for cluster XII to 2.5 mm for cluster VII and cluster IX; L/B ratio had a range of 2.52 for cluster X to 3.01 for cluster I. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied. It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

CONCLUSION

The conclusion drawn from the cluster analysis is that in the studied population high variability was observed between the genotypes in different clusters for different traits. Recombination breeding among genotypes belonging to cluster XII having maximum intra cluster distance can improve the yield potential. As maximum inter cluster distance was noticed between Euclidean² values was observed between cluster II and cluster XII (1882.852) followed by cluster X and cluster XII (1488.520) and cluster VI and cluster XII (1418.118), crosses made between genotypes of cluster II and cluster XII followed by genotypes of clusters X and XII and clusters VI and XII would

give wider and desirable recombinants.

The cluster I is having highest mean value for L/B ratio while cluster II is having higher mean for panicle length, grain yield per plant and kernel length. Cluster VI is having higher mean value for days to 50% flowering and days to maturity while cluster VII for kernel breadth and cluster VIII is having higher mean value for plant height and number of panicles per plant. The genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme as for a successful breeding programme selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants.

Table 5. Mean values of twelve clusters by Ward's minimum variance method for 121 lines of rice (*Oryza sativa* L.).

CLUSTER MEANS										
	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of panicles per plant	Panicle Length (cm)	Grain Yield (g)	Test Weight (g)	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio
Cluster I	119	146	113.57	11	25.00	26.96	19.94	6.55	2.21	3.01
Cluster II	121	147	116.05	11	26.25	42.68	20.93	6.60	2.43	2.73
Cluster III	116	143	111.90	11	25.57	18.91	16.78	5.77	2.20	2.65
Cluster IV	116	143	100.14	9	22.83	20.33	19.72	5.91	2.43	2.47
Cluster V	117	144	110.33	11	23.15	16.99	20.89	6.31	2.37	2.69
Cluster VI	124	149	105.82	11	23.06	18.54	19.47	5.83	2.29	2.58
Cluster VII	116	143	107.61	11	22.70	17.18	26.18	6.30	2.48	2.56
Cluster VIII	118	144	125.13	12	26.00	17.31	20.72	6.38	2.28	2.85
Cluster IX	120	146	110.09	12	22.80	18.26	34.62	6.38	2.46	2.63
Cluster X	108	132	110.13	9	25.85	27.89	20.26	5.67	2.41	2.52
Cluster XI	110	135	108.54	10	23.18	17.89	20.12	6.34	2.30	2.79
Cluster XII	92	118	99.07	9	25.37	18.03	15.80	5.82	2.08	2.92

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