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**Genetic divergence and cluster analysis studies in rice
(*Oryzasativa L.*) using D^2 statistics**

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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 Mahalanobis D^2 -statistics. ANOVA revealed the presence of considerable amount of variability among the genotypes. High PCV and GCV were observed for grain yield per plant and test weight. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, grain yield per plant and test weight indicating the presence of additive gene action in governing the inheritance of these traits. Hence, direct phenotypic selection is useful with respect to these traits. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into twelve clusters. Cluster IX constituted maximum number of genotypes (26). The genotypes falling in cluster VII had the maximum divergence, which was closely followed by cluster VII and cluster XI. The maximum inter cluster D^2 values was observed between cluster X and XI (931.276) followed by cluster VII and XI (814.784) suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Keywords: Variability, heritability, genetic advance, genetic divergence, D^2 analysis, cluster analysis.

Introduction

Rice is the staple food of more than half of the world's population and more than 3.5 billion people depend on rice for more than 20% of their daily calories. Asia accounts for 90% of global rice consumption, and total rice demand there continues to rise. Global rice consumption remains strong, driven by both population and economic growth, especially in many Asian and African countries. The demand for rice production is increasing day by day because of increase of rice consuming people. Globally, it is planted on about 158 million hectares with an annual production of 478 million tons. 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} .

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 could break the yield plateau. Variation present in the population is an important prerequisite for improvement of any crop species. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) gives information on nature and magnitude of variation present in a population. Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and is used as a predictive role in selection procedures (Allard, 1960)^[2]. The estimate of heritability alone is not very much useful because it includes the effect of both additive and non-additive gene. Heritability estimates along with genetic advance are more helpful in predicting gain under selection than heritability estimate alone (Johnson *et al.*, 1955)^[7].

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 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

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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.

Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together geneconstellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents (Chanbeni *et al.*, 2012) [4]. The multivariate analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. Further selection of diverse parents for hybridization programme can be effective by the identification of characters responsible for the genetic diversity among the populations (Singh and Chaudhary, 1977) [16]. Hence, in this study one hundred and fourteen F_5 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 for further utilization in breeding programmes.

Material and Methods

The experimental material consisted of one hundred and fourteen F_5 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 and were sown in randomized block design with two replications during *khari*, 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 L/B 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 as per Panse and Sukhatme (1961), Burton and Devane (1953), Johnson *et al.* (1955) [7], Falconer (1964) and the data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

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

Table 2: List of F_5 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
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
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
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	

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability (Table 3). The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation but the difference is very less indicating that low environmental influence (Table 4). High PCV and GCV was observed for grain yield per plant and test weight indicating the presence of high variability among the lines studied while number of panicles per plant and L/B ratio exhibited moderate PCV and GCV indicating the presence of moderate amount of variability among these genotypes.

Table 3: Analysis of variance (mean sum of squares) for 10 characters for 121 genotypes of rice (*Oryza sativa* L.) during *kharif*, 2015.

Source of variations	d. f.	Days to 50% flowering	Days to maturity	Plant height	Number of panicles per plant	Panicle length	Grain yield per plant	Test weight	Kernel length	Kernel breadth	Kernel L/B ratio
Mean sum of squares											
Replications	1	0.04	0.264	0.051	0.810	3.499	3.380	0.001	0.013	0.000	0.051
Genotypes	120	65.833**	66.903**	122.849**	4.795**	8.045**	52.314**	52.299**	0.336**	0.098**	0.216**
Error	120	2.071	0.981	4.117	0.510	1.250	1.706	1.160	0.025	0.196	0.038

** Significance at 5% level

Days to 50% flowering, days to maturity, plant height and panicle length exhibited low PCV and GCV where as kernel breadth reported low GCV indicating the presence of low amount of variation in these genotypes pertaining to these traits (Fig 1). These results were in conformity with the findings of Sameera *et al.* (2015), Shrivastava *et al.* (2014), Patel *et al.* (2014), Paikhomba *et al.* (2014), Khare *et al.* (2014), Gangashetty *et al.* (2013) and Aditya and Bhartiya (2013).

High heritability coupled with high genetic advance as per cent of mean was observed for number of panicles per plant, grain yield per plant and test weight (table 4) which indicated the predominance of additive gene action in the inheritance of these traits and simple selection can be practiced for genetic improvement of these traits. The high estimates of heritability coupled with moderate genetic advance as per cent of mean for plant height, panicle length, kernel length, kernel breadth and L/B ratio indicating the presence of both additive and non-additive gene actions and heterosis breeding for such traits will be effective. High heritability coupled with low genetic advance was reported for days to 50% flowering and days to maturity indicating the presence of non-additive gene action and hence simple selection for these traits would not be effective. Similar results were reported by Sameera *et al.* (2015), Patel *et al.* (2014), Paikhomba *et al.* (2014) and Aditya and Bhartiya (2013).

The quantitative assessment of genetic divergence was made by adopting Mahalanobis' D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 10 characters of 121 lines (114 F_5 families along with their seven parents) of rice and the results obtained from the study are discussed below.

Test with Wilk's criterion

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by per cent (%) at 1200 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously. The significance of 121 lines (114 F_5 families along with their seven parents) in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied among different genotypes. Hence, further analysis was made to estimate D^2 analysis.

Mahalanobis' D^2 values

In order to assess the genetic diversity among 121 lines (114 F_5 families along with their seven parents), D^2 statistic was used following the procedure given by Rao (1952). Since the entire 10 yield component characters were correlated, they were transformed into uncorrelated linear combination

through pivotal condensation method. The statistical distance (D^2) between the pairs of genotypes were obtained as the sum of squares of the difference between the pairs of

corresponding uncorrelated values of any two genotypes considered at one time.

Table 4: Estimates of genetic variability parameters of yield and yield component attributes in rice (*Oryza sativa* L.) during kharif, 2015.

S.No	Character	Range		Mean	Variability parameters		h ² (bs)	GAM
		Min.	Max.		PCV	GCV		
1	Days to 50% flowering	89	126	116	5.03	4.87	94.00	9.73
2	Days to maturity	117	151	142	4.10	4.04	97.00	8.20
3	Plant height (cm)	95.3	136.9	110.73	7.20	6.96	94.00	13.86
4	Number of panicles per plant	7	16	11	15.03	13.51	81.00	25.01
5	Panicle length (cm)	17.4	29.2	24.02	8.98	7.68	73.00	13.52
6	Grain yield per plant (cm)	10	43.75	19.59	26.53	25.68	94.00	51.20
7	Test weight (g)	11.5	41.4	21.36	24.20	23.67	96.00	47.69
8	Kernel length (mm)	5.3	6.95	6.2	6.85	6.36	86.00	12.16
9	Kernel breadth (mm)	1.75	2.8	2.33	10.39	8.48	67.00	14.24
10	L/B ratio	2.15	3.95	2.71	13.17	11.04	70.00	19.06

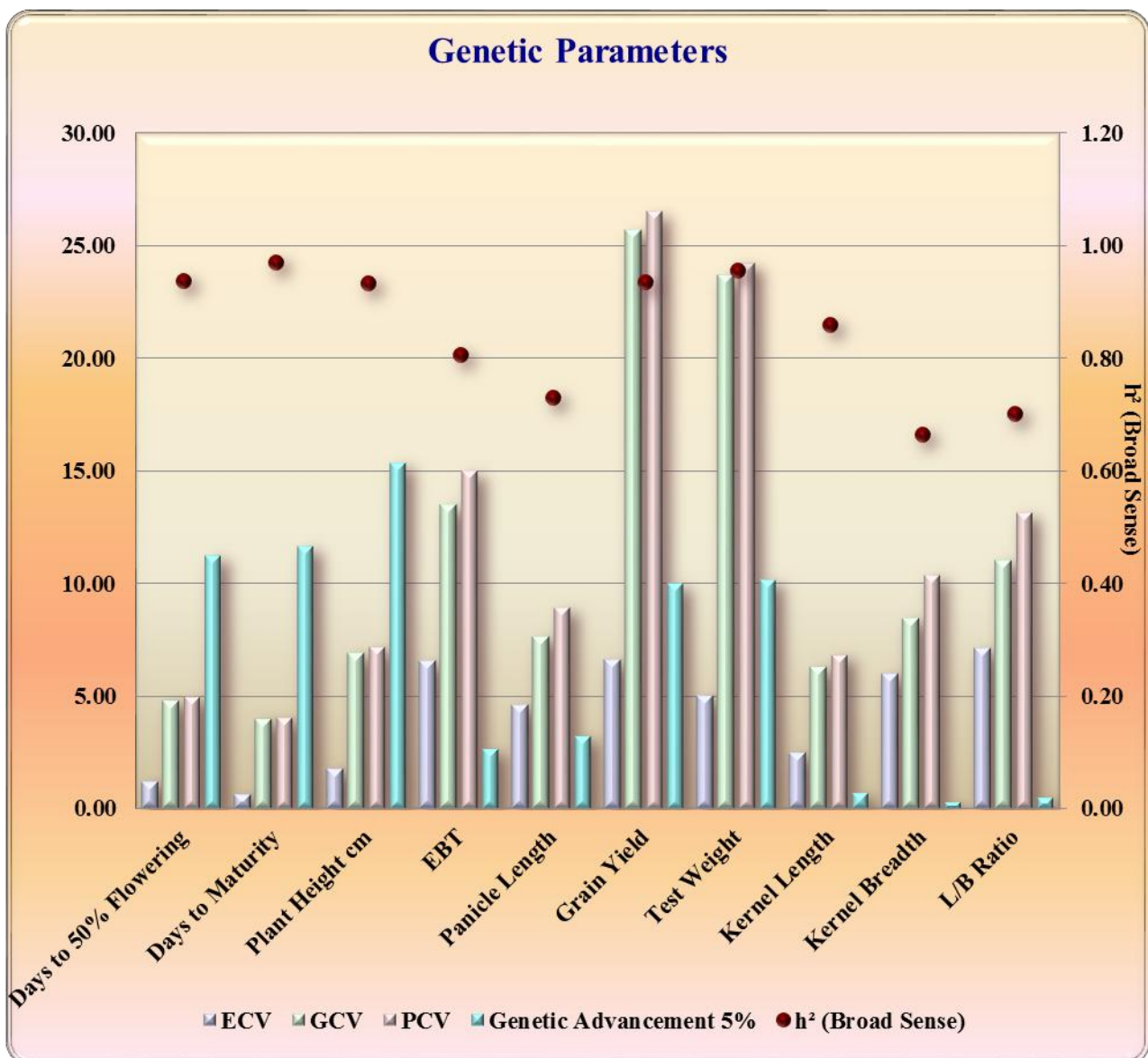


Fig 1: Estimates of genetic variability parameters of yield and yield component attributes of 121 lines of rice

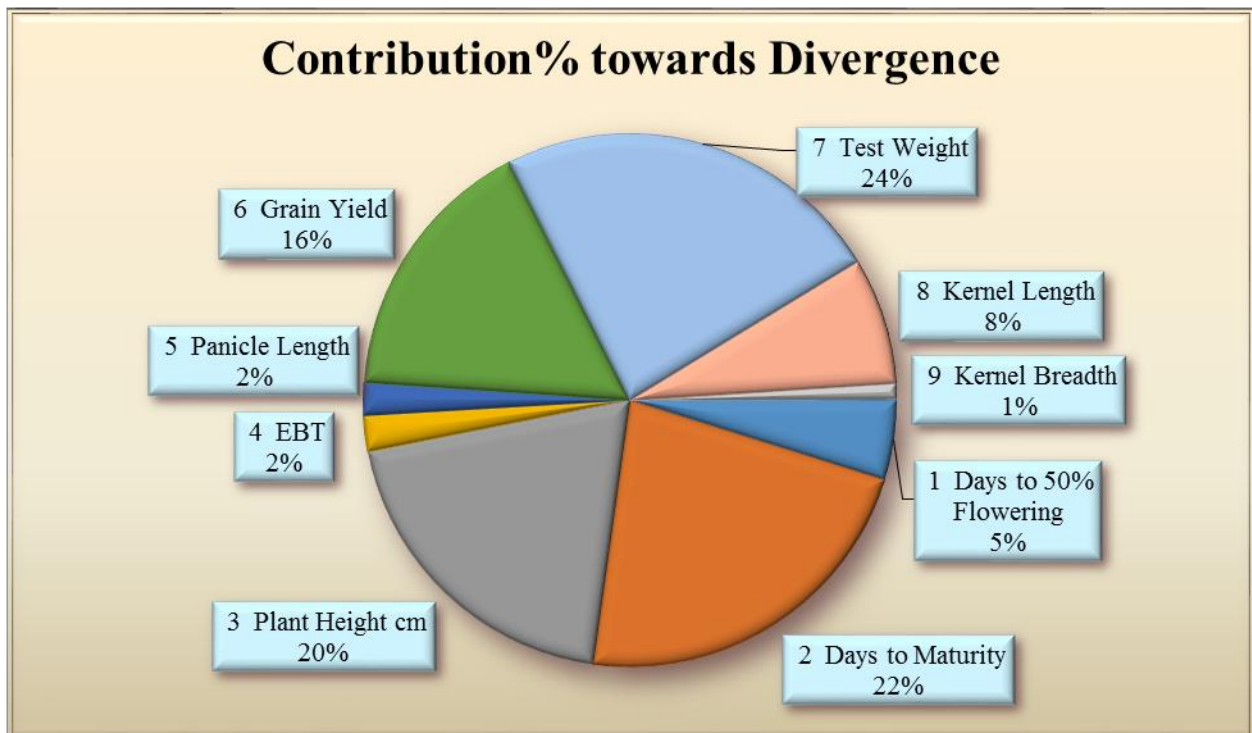
Relative contribution of individual characters towards divergence

The per cent contribution towards genetic divergence by all the 10 characters is presented in Table 5 and Fig 2. The trait test weight showed maximum contribution (23.79) towards genetic divergence followed by days to maturity (22.40), plant

height (19.68), grain yield per plant (16.46), kernel length (7.71), days to 50% flowering (4.82), number of panicles per plant (2.20), panicle length (1.96), kernel breadth (0.92) and L/B ratio (0.06). Senapati and Sarkar (2005) reported that test weight contributed mostly to genetic divergence.

Table 5: Contribution of different characters towards genetic divergence among 121 lines (114 F₅ families and seven parents) of rice (*Oryza sativa* L.).

	Source	Contribution %
1	Days to 50% Flowering	4.82
2	Days to Maturity	22.40
3	Plant Height	19.68
4	Number of panicles per plant (EBT)	2.20
5	Panicle Length	1.96
6	Grain Yield	16.46
7	Test Weight	23.79
8	Kernel Length	7.71
9	Kernel Breadth	0.92
10	L/B Ratio	0.06

**Fig 2:** Per cent contribution of different characters towards genetic divergence**Grouping of genotypes into various clusters**

The 121 lines were grouped into 12 clusters using the Tocher's method with the criterion that the intra-cluster average D^2 values should be less than the intercluster D^2 values. The distribution of 121 lines into 12 clusters is

presented in Table 6. The distribution of 121 lines into 12 clusters was at random with maximum number of 26 genotypes in cluster IX. Cluster VIII and cluster XI found to be the second largest with 13 families each followed by cluster VII with 12 genotypes.

Table 6: Clustering pattern of 121 lines (114 F₅ families and seven parents) of rice (*Oryza sativa* L.) by Tocher's method.

Cluster number	Number of genotypes	Genotypes
Cluster I	4	TSM-2, TSM-171, PAU-3116-25-5-1, PAU-3140-126-1
Cluster II	9	TSM-10, TSM-12, TSM-17, TSM-33, TSM-73, TSM-93, TSM-116, MTU 7029, MTU 1121
Cluster III	3	TSM-5, TSM-9, TSM-29
Cluster IV	11	TSM-4, TSM-54, TSM-58, TSM-67, TSM-141, TSM-147, TSM-149, TSM-184, TSM-204, TSM-219, TSM-230
Cluster V	11	TSM-1, TSM-8, TSM-32, TSM-50, TSM-51, TSM-57, TSM-77, TSM-82, TSM-83, TSM-97, TSM-221
Cluster VI	10	TSM-7, TSM-42, TSM-43, TSM-72, TSM-79, TSM-85, TSM-86, TSM-87, TSM-90, TSM-99
Cluster VII	12	TSM-3, TSM-16, TSM-69, TSM-74, TSM-88, TSM-92, TSM-94, TSM-95, TSM-101, TSM-115, TSM-120, TSM-228
Cluster VIII	13	TSM-63, TSM-68, TSM-108, TSM-138, TSM-148, TSM-150, TSM-164, TSM-166, TSM-168, TSM-174, TSM-175, TSM-183, TSM-190
Cluster IX	26	TSM-6, TSM-19, TSM-35, TSM-36, TSM-39, TSM-48, TSM-61, TSM-62, TSM-64, TSM-65, TSM-66, TSM-76, TSM-96, TSM-102, TSM-103, TSM-104, TSM-128, TSM-132, TSM-146, TSM-167, TSM-178, TSM-211, TSM-216, TSM-220, TSM-229, TSM-235
Cluster X	6	TSM-152, TSM-153, TSM-165, TSM-191, TSM-200, TSM-213
Cluster XI	13	TSM-18, TSM-20, TSM-22, TSM-37, TSM-56, TSM-110, TSM-114, TSM-118, TSM-133, TSM-134, TSM-169, TSM-215, TSM-223
Cluster XII	3	MTU 1081, JGL 11118, NLR 34449

Average intra and inter cluster D2 values

The average intra and inter cluster D2 values estimated as per the procedure given by Singh and Chaudhary (1977) ^[16] and were presented in Table 7. Intra- and inter -cluster distance of 121 lines of rice showed in Fig. 3. Dendrogram represented relationship among 121 lines in twelve clusters based on Mahalanobis's D2 values are presented in Fig. 4.

The maximum intra cluster D2 value was 72.356 for cluster VII followed by 64.619 for cluster VIII, 61.669 for cluster XI, 57.027 for cluster IV, 48.215 for cluster V, 43.698 for cluster II and 30.608 for cluster I while it was zero for clusters III, VI, IX, X and XII. The high intra cluster distance in cluster VII indicated the presence of wide genetic diversity among the genotypes viz., MTU 2462-1-2-1, MTU 2462-6-2-1, MTU 2462-42-2-1, MTU 2462-49-2-1, MTU 2465-8-1-1, MTU 2465-11-3-1, MTU 2465-12-2-1, MTU 2465-12-2-2, MTU 2465-16-2-3, MTU 2466-4-2-2, MTU 2468-2-1-1 and MTU 2469-68-1-1. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

Cluster I comprised of 4 families and was closest to cluster III (41.01) followed by cluster V (52.58) and it was farthest from cluster XI (536.701). Cluster II comprised of 9 families and

was closest to cluster X (65.107) and it was farthest from cluster XI (679.476). Cluster III comprised of 3 families and was closest to cluster I (41.018) and it was farthest from cluster XI (452.117). Cluster IV comprised of 11 families and was closest to cluster III (84.127) and it was farthest from cluster X (318.359). Cluster V comprised of 11 families and was closest to cluster I (52.586) and it was farthest from cluster XI (540.565). Cluster VI comprised of 10 families and was closest to cluster III (50.08) and it was farthest from cluster XI (451.248). Cluster VII comprised of 12 families and was closest to cluster I (75.122) and it was farthest from cluster XII (654.458). Cluster VIII comprised of 13 families and was closest to cluster I (136.941) and it was farthest from cluster XI (814.784). Cluster IX comprised of 26 families and was closest to cluster IX (56.339) and it was farthest from cluster XI (803.024). Cluster X comprised of 6 families and was closest to cluster IX (56.339) and it was farthest from cluster XI (931.276). Cluster XI comprised of 13 families and was closest to cluster IV (276.044) and it was farthest from cluster X (931.276). Cluster XII comprised of 3 families and was closest to cluster VI (63.771) and it was farthest from cluster X (451.742).

Table 7: Average intra-and inter -cluster D² values among twelve clusters in 121 lines of rice (*Oryza sativa* L.) genotypes.

Inter & Intra Cluster Distances : Tocher Method												
	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	30.608	137.36	41.018	103.582	52.586	68.121	75.122	136.941	71.94	178.791	536.701	117.145
Cluster II	137.36	43.698	171.401	200.015	144.139	303.303	193.106	265.297	73.57	65.107	679.476	345.638
Cluster III			0.000	84.127	54.125	50.08	102.476	150.798	115.175	256.925	452.117	120.639
Cluster IV				57.027	116.407	114.294	168.857	248.865	215.247	318.359	276.044	115.183
Cluster V					48.215	99.364	115.242	143.398	93.505	192.116	540.565	164.796
Cluster VI						0.0000	102.999	168.357	197.546	372.949	451.248	63.771
Cluster VII							72.356	180.408	113.984	227.211	654.458	125.238
Cluster VIII								64.619	172.828	274.49	814.784	287.62
Cluster IX									0.000	56.339	803.024	276.517
Cluster X										0.0000	931.276	451.742
Cluster XI											61.669	369.336
Cluster XII												0.0000

Diagonal bold values indicate intra cluster distances

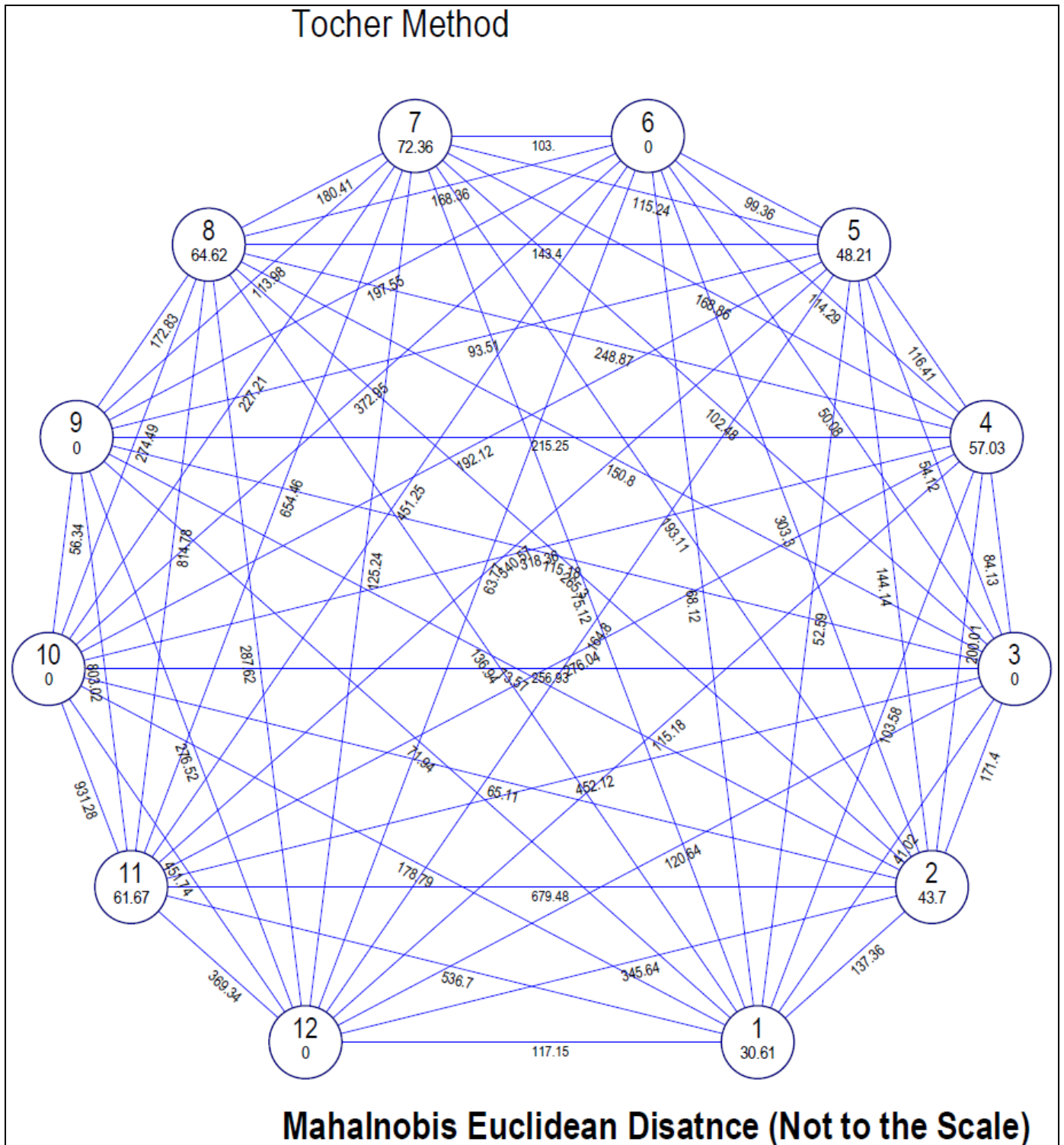


Fig 4: Intra-and Inter-cluster distances of 121 lines of rice (*Oryza sativa* L.) in twelve clusters based on Euclidean² distances

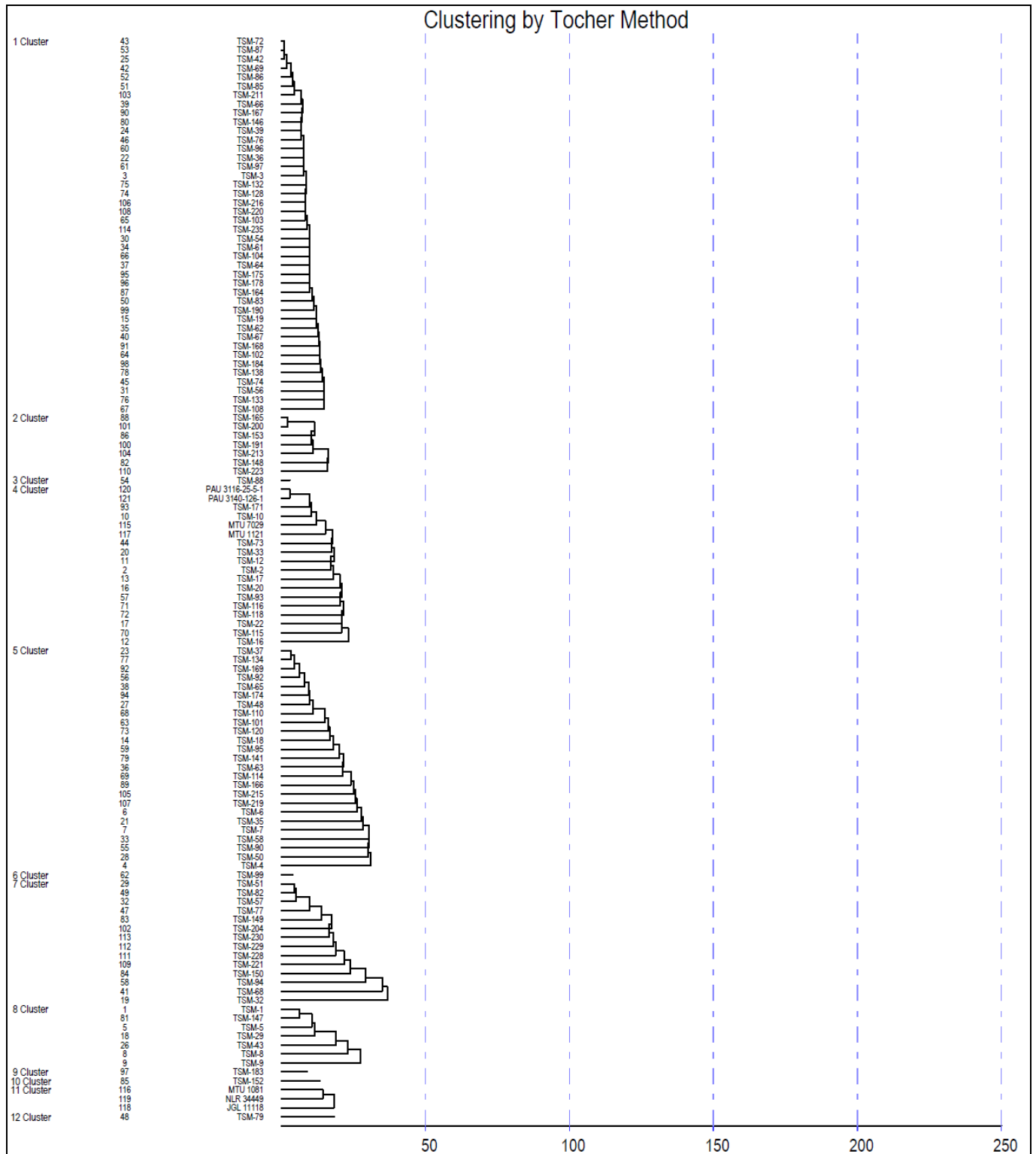


Fig 5: Dendrogram showing relationship among 121 lines of rice (*Oryza sativa* L.) genotypes in twelve clusters based on Mahalanobis's D^2 values.

The intra and inter cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between cluster X and XI (931.276) followed by cluster VIII and XI (814.784). Based on these studies crosses may be made between genotypes of clusters X and cluster XI followed by genotypes of clusters VIII and XI to obtain new desirable recombinants in rice.

Cluster mean values of characters

The cluster mean values for 10 characters are presented in Table 8. The data indicated a wide range of mean values

between the characters. Days to 50% flowering had a range of 126 days for cluster IX to 92 days for cluster XI; days to maturity had a range of 150 days for cluster IX and X to 118 days for cluster XI; Plant height (cm) varied from 124.29 cm for cluster VIII to 99.07 cm for cluster XI; Number of panicles per plant had a range of 16 for cluster X to 9 for cluster III and XI; Panicle length had a range of 27.05 cm for cluster III to 22.35 cm for cluster X; Grain yield per plant had a range of 33.12 g for cluster VIII to 15.40 g for cluster XII; Test weight (g) recorded as high as 36.70 g in cluster X to as low as 11.50 g in cluster VI; Kernel length had a range of 6.9 mm for cluster XII to 5.7 mm for cluster III; Kernel breadth

varied from 2.5 mm for cluster II, III and cluster X to 2.1 mm for cluster VI, IX and XI; L/B ratio had a range of 3.2 for cluster XII to 2.3 for cluster III. 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.

The cluster III is having highest mean value for panicle length and kernel breadth, Cluster VII for plant height, cluster VIII for grain yield per plant, cluster IX for days to 50% flowering and days to maturity, cluster X for ear bearing tillers per plant and test weight and cluster XII for kernel length and L/B ratio. 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 8: Mean values of twelve clusters by Tocher's method for 121 lines of rice (*Oryza sativa* L.).

Cluster Means : Tocher Method										
	Days to 50% Flowering	Days to Maturity	Plant Height	Number of panicles per plant	Panicle Length	Grain Yield per plant	Test Weight	Kernel Length	Kernel Breadth	L/B Ratio
Cluster I	118	144	110.45	11	23.82	18.02	20.41	6.2	2.3	2.7
Cluster II	118	144	108.86	11	22.59	17.64	35.24	6.4	2.5	2.6
Cluster III	117	144	105.80	9	27.05	18.80	18.25	5.7	2.5	2.3
Cluster IV	110	134	108.38	10	23.73	20.81	20.57	6.1	2.3	2.7
Cluster V	117	144	106.36	10	23.33	19.71	20.91	6.1	2.4	2.6
Cluster VI	113	142	115.20	12	25.25	19.40	11.50	5.7	2.1	2.8
Cluster VII	118	144	124.29	12	25.51	17.72	21.29	6.4	2.3	2.8
Cluster VIII	120	147	112.76	11	25.51	33.12	19.19	6.5	2.3	2.9
Cluster IX	126	150	110.00	12	23.80	16.40	28.90	6.2	2.1	3.0
Cluster X	125	150	111.30	16	22.35	18.60	36.70	6.3	2.5	2.6
Cluster XI	92	118	99.07	9	25.37	18.03	15.80	5.8	2.1	2.9
Cluster XII	110	135	119.30	12	26.75	15.40	12.80	6.9	2.2	3.2

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 VII having maximum intra cluster distance can improve the yield potential. The maximum inter cluster D2 values was observed between cluster X and XI (931.276) followed by cluster VII and X (814.784). Based on these studies crosses may be made between genotypes of cluster X and cluster XI followed by genotypes of clusters VI and XI, crosses involving genotypes from these clusters would give wider and desirable recombinants

References

- Aditya JP, Bhartiya A Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice in Uttarakhand hills. *Journal of Rice Research*. 2013; 6(2):24-34.
- Allard RW. Principles of Plant Breeding. John Wiley and Sons Inc., New York. 1960, 145-147.
- Burton GW, Devane EW. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clone material. *Agronomy Journal*. 1953; 45:478-481.
- Chanbeni Y, Ovung, Lal GM, Prashant Kumar Rai. Studies on genetic diversity in Rice (*Oryza sativa* L.). *Journal of Agricultural Technology*. 2012; 8(3):1059-1065.
- Falconer DS. An Introduction to Quantitative Genetics. Oliver and Boyd, Edinburgh, London. 1964, 312-324.
- Gangashetty PI, Salimath PM, Hanamaratti NG. Genetic variability studies in genetically diverse non-basmati local aromatic genotypes of rice (*Oryza sativa* L.). *Rice Genomics and Genetics*. 2013; 4(2):4-8.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean.

Agronomy Journal. 1955; 47:314-318.

- Khare R, Singh AK, Eram S, Singh PK. Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L.). *SAARC Journal of Agriculture*. 2014; 12(2):40-51.
- Paikhomba N, Arvind K, Chaurasia AK, Rai PK. Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *Journal of Rice Research*. 2014; 2:1-3.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. 1961, 242-246.
- Patel JR, Saiyad MR, Prajapati KN, Patel RA, Bhavani RT. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2014; 5(3):531-537.
- Rao CR. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc., New York, 1952, 236-272.
- Sameera SK, Prasanna Rajesh A, Jayalakshmi V, Nirmala PJ, Srinivas T. Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2015; 6(1):269-273.
- Senapati BK, Sarkar G. Genetic divergence in tall indica rice under rainfed saline soil of Sundarban. *Oryza*. 2005; 42(1):70-72.
- Shrivastava A, Mishra DK, Koutu GK, Singh SK. Heritability and genetic advance estimation from parental lines of hybrid rice. *International Journal of Scientific Research*. 2014; 3(7):11-13.
- Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, 1977, 215-218.