

## Genetic Diversity Studies for Yield and Quality Traits in Rice Genotypes (*Oryza sativa* L.)

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**Abstract** Genetic divergence was studied in 70 rice genotypes on the basis of yield and quality characteristics by utilizing Mahalanobis  $D^2$  statistics. Based on the genetic distance ( $D^2$  values), the rice genotypes were grouped into seven clusters. The pattern of distribution of genotypes into different clusters was at random. The maximum inter cluster distance was observed between cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VI (1282.97) and cluster III and VII (1268.29), cluster IV and V (1064.78). The genotypes from these clusters can be utilized in hybridization program for improvement of rice. Among different traits, kernel length, kernel breadth, days to 50% flowering, L/B ratio, 1000-grain weight and number of filled grains per panicle had maximum contribution towards total divergence, may be used as selection parameters in segregating generations.

**Keywords** Genetic divergence, Cluster,  $D^2$  statistics, Rice genotypes.

### Introduction

Rice (*Oryza sativa* L.) is a popular cereal crop commonly used as human food. It is actually a type of grass and belongs to a family of Poaceae that includes other cereals such as wheat and corn. Rice is rich in nutrients and contains a number of vitamins and minerals. It is an excellent source of complex carbohydrates the best source of energy. It is the most important staple food crop for more than 60% of the global population and forms the cheapest source of food energy and protein. It provides 43% of calorie of an average human diet in India and rice contributes 20-25% of agricultural income due to its intensive cultivation. In Asia as a whole, much of the population consumes rice in every meal. In many countries rice accounts for more than 70% of human caloric intake. In India, rice is one of the most important food crop in terms of area, production and consumer preference. India is the second largest producer and consumer of rice in the world. Rice is the premier food crop in India occupying nearly 43.97 million hectares area with annual production of 104.40 million tonnes and productivity of 2372 kg ha<sup>-1</sup> [1]. Genetic diversity among the parents is a pre-requisite for any breeding program. Study on genetic diversity helps and improves the chances of selecting better sergeants for various traits. Precise information on the nature and degree of genetic divergence would help for different breeding programs to exhibit higher amount of heterotic expression in segregating generations. Therefore the present investigation was undertaken to study the nature and magnitude of genetic divergence among 70 genotypes of rice to identify diversified genotypes.

### Materials and Methods

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**Table 1.** Analysis of variance for yield and quality traits in rice (*Oryza sativa* L.).

Sl. No.	Characters	Replications (df=2)	Mean sum of squares	
			Treatments (df=69)	Error (df=138)
1	Days to 50% flowering	0.23	188.06**	1.54
2	Days to maturity	0.13	164.39**	1.69
3	Plant height (cm)	15.36	234.64**	5.51
4	Number of productive tillers per plant	4.18**	4.59**	0.57
5	Panicle length (cm)	0.76	12.67**	0.27
6	Number of filled grains per panicle	3074.33**	7080.98**	123.73
7	Kernel length (mm)	0.00	1.36**	0.00
8	Kernel breadth (mm)	0.00	0.19**	0.00
9	L/B ratio	0.00	0.59**	0.00
10	Grain yield per plant (g)	8.75	138.85**	9.59
11	1000-grain weight (g)	0.04	53.18**	0.39
12	Hulling %	1.15	6.06**	0.46
13	Milling %	0.21	14.81**	1.15
14	Head rice recovery	7.69	35.63**	3.74

Seventy rice genotypes having different geographical origins were grown during *kharif*, 2014 at Regional Agricultural Research Station, Jagtial with three replications in a randomized block design with a spacing of 20 × 15 cm. Cultural practices were followed to raise the crop as per the standard recommendations. Five randomly selected plants were used for recording observations on fourteen characters viz., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percent-

age, head rice recovery, kernel length, kernel breadth and L/B ratio. The data were subjected to analysis of variance and multivariate analysis using statistics [2]. Based on genetic distances ( $D^2$  values), the genotypes were grouped into clusters of genetically closer related groups following the Tocher's method [3].

### Results and Discussion

The analysis of variance indicated high significant differences among the genotypes for all the traits under study (Table 1). Seventy genotypes were grouped into seven clusters based on  $D^2$  values. Clus-

**Table 2.** Grouping of 70 genotypes into different clusters by Tocher's method.

Cluster No.	No. of genotype	Genotype
I	40	JCL 20777, JGL 21078, JGL 23185, JGL 21883, JGL 23666, IR 05K 101, JGL 20122, MTU 1010, JGL 21005, JGL 21868, Shiva, JGL 21794, IR 60919-150-3-3-3-2R, IR 60819-34-2-1R, JGL 20171, JINMIBYEO, IR 69502-6-SRN-3-UBN, IR 10A234, IR 10K48, IRRI 142, IR 68888B, IR 68859B, IR 80151B, IR 68897B, IR 79128B, Varalu, IR 80559B, IR 11A208, JGL 21002, IR 65483-14-1-1-4-13R, GP247, HANGANGCHAL 1, IR 10K 153, MILYANG 240, JGL 17653, HANAREUM, JGL 18799, IRBL 9-W/RL, IRBL 3-CP4/RL IRBL 7-M/RL.
II	20	JGL 1798, JGL 3844, JGL 20779, JGL 19607, JGL 23183, JGL 18629, JGL 11470, JGL 18222, JGL 11118, JGL 21828, JGL 23710, JGL 23713, SAMGANG, GAYABYEO, JGL 21075, JGL 21820, JGL 20776, BPT 5204, JGL 11727, JGL 21851.
III	1	JGL 23745
IV	1	IR 58025B
V	6	MILYANG 23, IR 59624-34-2-2R, IR 50, IR 65514-5-2-19R, MTU-3626, HR 20654-39-3-5.
VI	1	IR 79156B
VII	1	IR 67684B

**Table 3.** Average intra (bold values) and inter cluster  $D^2$  values of seven clusters for 70 genotypes in rice.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	<b>12.47</b> <b>(155.53)</b>	25.38 (644.13)	19.55 (382.37)	16.96 (287.78)	23.57 (555.66)	18.74 (351.14)	29.08 (845.81)
Cluster II		<b>13.29</b> <b>(176.64)</b>	38.19 (1458.41)	29.75 (885.20)	30.31 (918.79)	32.38 (1048.31)	40.24 (1619.25)
Cluster III			<b>0.00</b> <b>(0.00)</b>	25.69 (659.79)	23.73 (563.23)	25.57 (653.94)	35.61 (1268.29)
Cluster IV				<b>0.00</b> <b>(0.00)</b>	32.63 (1064.78)	10.26 (105.32)	15.33 (234.88)
Cluster V					<b>16.81</b> <b>(282.73)</b>	35.82 (1282.97)	44.15 (1949.04)
Cluster VI						<b>0.00</b> <b>(0.00)</b>	14.95 (223.52)
Cluster VII							<b>0.00</b> <b>(0.00)</b>

tering of 70 genotypes into different clusters by Tocher's method are presented in Table 2. Average intra (bold values) and inter cluster  $D^2$  values of seven clusters for 70 genotypes in rice are presented in Table 3 and Figure 1. cluster mean values for different characters presented in Table 4 and contribution of different traits towards genetic divergence in 70 genotypes

of rice presented in Table 5 and Figure 2. The maximum inter cluster distance observed for between cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VI (1282.97) and cluster III and VII (1268.29). The genotypes from these clusters can be utilized in hybridization program for improvement of rice. Cluster V (282.7)

**Table 4.** Cluster means for yield components and quality traits ( $D^2$  analysis) for fourteen characters in 70 genotypes of rice (*Oryza sativa* L.).

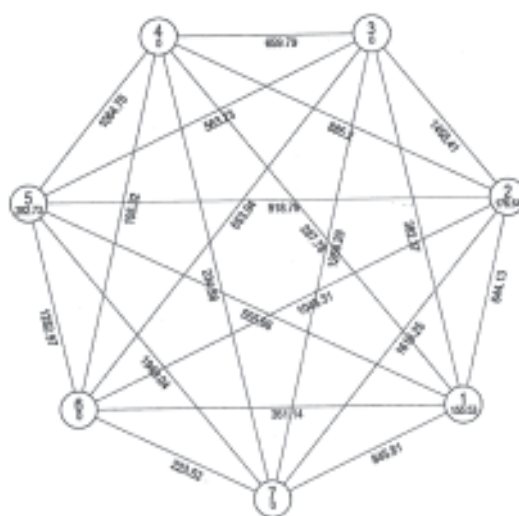
Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers / plant	Panicle length (cm)	Number of filled grains/ panicle	Kernel length (mm)
I	94.99	128.58	101.88	12.25	25.18	130.31	6.73
II	94.33	127.98	103.70	11.64	24.74	213.53	5.55
III	86.33	121.67	103.90	10.50	25.70	140.40	7.17
IV	92.67	125.67	85.30	13.00	24.20	100.80	7.08
V	93.72	127.67	89.75	11.13	21.98	129.64	5.74
VI	96.00	129.00	108.10	11.00	27.50	145.20	7.34
VII	97.67	131.67	92.60	11.90	24.40	91.20	7.17

**Table 4.** Continued.

Cluster No.	Kernel breadth (mm)	L/B ratio	Grain yield/ plant (g)	1000-grain/weight (g)	Hulling %	Milling %	Head rice recovery
I	1.98	3.41	32.79	22.27	81.06	71.95	59.42
II	1.65	3.38	31.36	14.65	81.98	72.85	62.55
III	2.44	2.94	30.42	28.87	81.80	73.60	56.55
IV	1.69	4.19	27.02	18.60	82.80	74.80	58.30
V	2.37	2.43	31.63	23.65	80.29	72.24	59.53
VI	1.71	4.31	31.94	20.79	80.20	70.55	61.50
VII	1.45	4.95	16.81	17.61	82.30	73.60	57.65

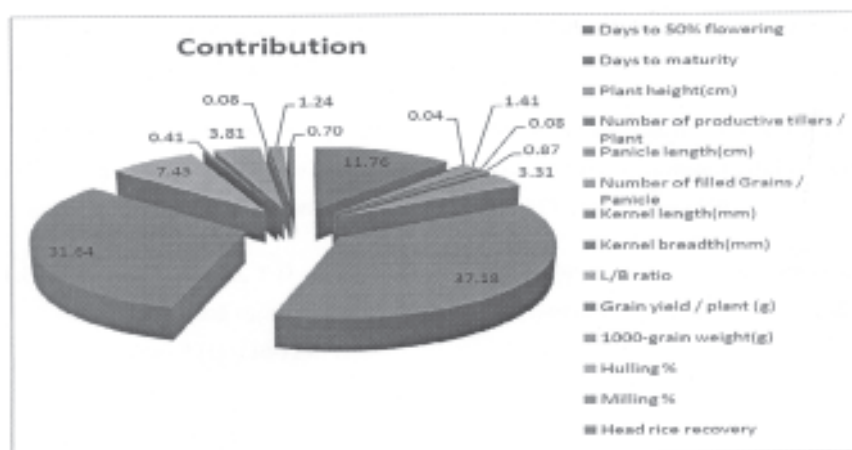
**Table 5.** Contribution of different traits towards genetic divergence in 70 genotypes of rice.

Sl. No.	Character	No. of times Contri- ranked first	Contri- bution (%)
1	Days to 50% flowering	284	11.76
2	Days to maturity	1	0.04
3	Plant height (cm)	34	1.41
4	Number of productives tillers/ Plant	2	0.08
5	Panicile length (cm)	21	0.87
6	Number of filled grains/panicle	80	3.31
7	Kernel length (mm)	898	37.18
8	Kernel breadth (mm)	764	31.64
9	L/B ratio	180	7.45
10	Grain yield / plant (g)	10	0.41
11	1000-grain weight (g)	92	3.81
12	Hulling %	2	0.08
13	Milling %	30	1.24
14	Head rice recovery	17	0.70

**Fig. 1.** Mahalanobis Euclidean Distance among 70 genotypes of rice.

had maximum intra cluster distance followed by cluster II (176.64), cluster I (155.53). Maximum genotypes (40) were grouped under cluster I followed by cluster II (20), cluster V (6) and cluster III, IV, VI and VII were represented by single genotype each. The clustering pattern of different genotypes from different geographical regions into different cluster was random. This suggests that geographical diversity does not necessarily relate to genetic diversity. The cluster I is having highest mean value for grain yield per plant, cluster II for number of filled grains per panicle, head

rice recovery percentage and cluster III for 1000-grain weight, kernel breadth, cluster IV for number of productive tillers per plant, hulling percentage, milling percentage, cluster VI for plant height, panicle length, kernel length and cluster VII for days to 50% flowering, days to maturity and L/B ratio. The promising genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization program. The

**Fig. 2.** Relative contribution of different characters to genetic diversity in 70 rice genotypes.

selection and choice of parents depends on contribution of characters towards genetic divergence [4]. In the present study kernel length [5, 6], kernel breadth followed by days to 50% flowering, L/B ratio, 1000-grain weight and number of filled grains per panicle had maximum contribution towards genetic divergence. The maximum inter cluster distance was observed between the cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VII (1282.97) and cluster III and VII (1268.29), suggesting that the genotypes in these clusters could be fully utilized in crossing programs to explore the wide range of heterosis for improvement of rice.

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