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**Lalita Kumari**  
Department of Plant Breeding  
and Genetics, OUAT,  
Bhubaneswar, Odisha, India

**DN Bastia**  
Department of Plant Breeding  
and Genetics, OUAT,  
Bhubaneswar, Odisha, India

**B Pradhan**  
Department of Plant Breeding  
and Genetics, OUAT,  
Bhubaneswar, Odisha, India

**KC Samal**  
Department of Agricultural  
Biotechnology, OUAT,  
Bhubaneswar, Odisha, India

**Sri Sai Subramanyam Das**  
Department of Plant Breeding  
and Genetics, BCKV, Mohanpur,  
West Bengal, India

**Ashish Rai**  
Laboratory Technician, RPCAU,  
Pusa, Bihar, India

## Multivariate analysis to study genetic diversity for yield improvement in advanced elite line of slender grain rice (*Oryza sativa* L.)

**Lalita Kumari, DN Bastia, B Pradhan, KC Samal, Sri Sai Subramanyam Das and Ashish Rai**

### Abstract

The increasing demand for superior rice in domestic and international market is directly defined by its appearance qualities. Thus, efforts to enhance rice productivity with keeping good grain quality are on the top priority in rice breeding. In the present experiment genetic divergence studies were conducted based on Mahalanobis  $D^2$  statistic and Anderson's canonical analysis based on variation present in 11 yield attributing traits. The present experiment was carried out with 52 advanced elite lines of slender grain rice including 6 checks, evaluated for eleven traits following RBD with two replication during *kharif*, 2019 at Rice Research station, O.U.A.T., Bhubaneswar.  $D^2$  values of all the fifty-two genotype combination based on 11 studied traits ranged from 6.61 (between OR 2674-14-4-4 and OR 2674-14-4-5) to 1762.45 (between OR 2762-1 and Samba mahsuri). L/B ratio and 1000 grains weight had maximum contribution to genetic divergence. Based on Mahalanobis  $D^2$  statistic 52 genotypes were grouped into 8 clusters. Cluster I was largest comprised of 13 lines, followed by cluster II with 11 lines, cluster III consisted of 10 lines, cluster IV accommodated 6 lines, cluster V comprised of 5 lines, cluster VI and cluster VII both composed of 3 lines and cluster VIII is monogenic. The intra cluster  $D^2$  value ranged from 00.00 (cluster VIII) to 926.511 (Cluster II). The inter cluster  $D^2$  value was found highest between cluster IV and Cluster VI (1398.889) and lowest between Cluster I and Cluster VIII (178.322). Therefore, the above information revealed that some lines were genetically very close to each other and rest possessed marked difference between them, accordingly they can be used for crossing programme. The genotypes OR 2762-35, OR2762-7, OR 2762-2 were found promising on the basis of yield and also revealed appreciable grain qualities and plant architecture.

**Keywords:** Multivariate, genetic, improvement, elite line, *Oryza sativa* L.

### Introduction

Rice (*Oryza sativa* L.,  $2n=24$ ) belongs to the order cyperales and family gramineae, is a self-pollinated cereal crop. Approximately three billion people (>60% population) around the world consume rice as a basic food which provides about 50 to 80% of their daily calories and 15% of protein (Das *et al.*, 2018) [7]. About 90% of the rice is produced and consumed in Asia only.

India is second largest producers of rice in the world, eastern and southern parts of the country are characterised by major rice growing region. Agronomic value of rice varieties are defined by several features; the most important features include high yielding ability, resistance to diseases and pests, resistance to undesirable environmental factors, and appearance quality of the products. Appearance quality (AQ) directly defines increasing demand for quality grain rice in domestic and international market. Grain shape (slender or bold) and grain length (short, medium or long) is one of the important appearance quality of rice grain, so the current challenge to rice improvement programs is to feed the ever-growing population and to meet the market demand with diminishing natural resources and environmental fluctuations by developing rice varieties with acceptable grain qualities along with high yield.

Consumer preferences for good quality rice varied from one geographical region to another (Juliano & Perez CM, 1984; Rathi *et al.*, 2010). People prefer a specific type of rice for a number of reasons. These traits included grain shape and appearance, aroma, texture and lack of chalk (ACIAR CSE-2009-005 Rice Market Survey). From the survey of rice consumers it has been found that in the large countries like China and India, although there are regional differences in preferences for grain length and shape, but rice varieties with medium to slender grained is most preferred one.

**Corresponding Author:**  
**Ashish Rai**  
Laboratory Technician, RPCAU,  
Pusa, Bihar, India

Odisha has been known as secondary centre of origin of rice and Jeypore tract (Koraput) is accepted as the home for a rich diversity of landraces (Ramiah and Ghose 1951, Ramiha and Rao 1953). About 3,000 rice germplasm accessions were collected by Dixit and Challam mainly from the six districts of Odisha; Balasore, Cuttack, Puri, Ganjam, Koraput, and Sambalpur. It has been shown that thousands of traditional rice varieties were cultivated in Odisha before the introduction of high-yielding rice varieties and still farmers cultivate hundreds of these indigenous types. A majority of these traditional cultivars are low yielders primarily due to their tall stature, weak culm, making them susceptible to lodging, low tillering ability, poor panicle features and low grain qualities. These cultivars were part of their culture due to the presence of specific traits for special purposes such as maturity duration, plant stature, tolerance to biotic and abiotic stress that safeguards against complete yield losses, special properties like aroma and cooking quality for special occasions.

It has been estimated that by 2050 Asia will be home to the largest proportion of middle classes and will represent half of the world's economic output, who will demand higher quality food, including higher quality rice. Thus to tackle food security in Asia by considering the geographic heterogeneity and specificity of consumer preferences, public rice breeding programs should incorporate widely preferred attributes for a particular part of the world, such as softness in Southeast Asia and slenderness in South Asia.

Genetic diversity studies occupy an important position in crop

breeding program as they ensure efficient utilization of germplasm resources and effective breeding system in the crop improvement programme. Genetic diversity is mainly measured based on the morphological differences of quantitative important traits. Therefore genetic diversity present in grain quality of the 52 advanced elite lines of slender grain rice used in this study can be used efficiently either for improvement of these traditional rice cultivar or as a parental line in varietal development.

In the present experiment an effort has been made to study 52 slendergrain rice genotypes including 6 checks with the objective to study the genetic divergence among advanced elite lines of slender grain rice to select parent materials for future crossing programme.

### Materials and Methods

The present investigation was carried out at rice research station EB1, Dept. Plant Breeding and Genetics, College of Agriculture, O.U.A.T Bhubaneswar, Odisha, during kharif 2019. Geographically, the place is located at about 24.00°N latitude and 90.25°E longitude with an elevation of 8.4 meters from the sea level and is characterized by subtropical climate. The soil of the experimental site was clay loam in texture.

The objectives of the study was to study the extent of genetic diversity existing in a set of fifty two advanced elite lines of slender grain rice including six released cultivar as checks. The detailed list of advanced elite lines of slender grain rice used in the present study is tabulated in Table-1.

**Table 1:** List of 52 advanced elite lines of slender grain rice and their parentage used in the study

Sl. No	Elite lines/Designation	Pedigree
1	OR 2762-1	Jyotirmayee/ 26P29
2	OR 2762-2	Jyotirmayee/ 26P29
3	OR 2762-4	Jyotirmayee/ 26P29
4	OR 2762-7	Jyotirmayee/ 26P29
5	OR 2762-12	Jyotirmayee/ 26P29
6	OR 2762-13	Jyotirmayee/ 26P29
7	OR 2762-14	Jyotirmayee/ 26P29
8	OR 2762-21	Jyotirmayee/ 26P29
9	OR 2762-22	Jyotirmayee/ 26P29
10	OR 2762-35	Jyotirmayee/ 26P29
11	OR 2762-45	Jyotirmayee/ 26P29
12	OR 2762-53	Jyotirmayee/ 26P29
13	OR 2762-55	Jyotirmayee/ 26P29
14	OR 2762-60	Jyotirmayee/ 26P29
15	OR 2762-61	Jyotirmayee/ 26P29
16	OR 2762-62	Jyotirmayee/ 26P29
17	OR 22674-14-2-2	CRMS 32A / OR 1889-5
Sl. No	Genotype/designation	Cross combination
18	OR 2674-14-2-4	CRMS 32A / OR 1889-5
19	OR 2674-14-2-6	CRMS 32A / OR 1889-5
20	OR 2674-14-3-2	CRMS 32A / OR 1889-5
21	OR 2674-14-3-7	CRMS 32A / OR 1889-5
22	OR 2674-14-4-3	CRMS 32A / OR 1889-5
23	OR 2674-14-4-4	CRMS 32A / OR 1889-5
24	OR 2674-14-4-5	CRMS 32A / OR 1889-5
25	OR 2674-14-4-6	CRMS 32A / OR 1889-5
26	OR 2674-14-5-1	CRMS 32A / OR 1889-5
27	OR 2674-14-5-3	CRMS 32A / OR 1889-5
28	OR 2674-14-7-1	CRMS 32A / OR 1889-5
29	OR 2674-14-8-1	CRMS 32A / OR 1889-5
30	OR 2674-14-8-2	CRMS 32A / OR 1889-5
31	OR 2674-14-8-3	CRMS 32A / OR 1889-5
32	OR 2674-14-8-4	CRMS 32A / OR 1889-5

33	OR 2674-14-8-5	CRMS 32A / OR 1889-5
34	OR 2674-14-8-6	CRMS 32A / OR 1889-5
35	OR 2674-17-1	CRMS 32A / OR 1889-5
36	OR 2675-3-1	CRMS 32A / OR 2324-18
37	OR 2675-6-4	CRMS 32A / OR 2324-18
38	OR 2676-1-1	CRMS 32A / OR 2345-19
39	OR 2676-2-2	CRMS 32A / OR 2345-19
40	OR 2676-2-3	CRMS 32A / OR 2345-19
41	OR 2676-2-5	CRMS 32A / OR 2345-19
42	OR 2676-2-6	CRMS 32A / OR 2345-19
43	OR 2676-3-1	CRMS 32A / OR 2345-19
44	OR 2676-4-2	CRMS 32A / OR 2345-19
45	OR 2676-5-1	CRMS 32A / OR 2345-19
46	OR 2676-5-3	CRMS 32A / OR 2345-19
47	CR 1014	—
48	Jajati	Rajeswari/ T 141
49	Gitanjali	—
50	Samba mahsuri	GEB24 /TN1
51	Khandagiri	—
52	Prativa	—

The field trial containing 52 advanced elite lines of slender grain rice were sown in an individual plot under suitable nursery condition at Rice Research Station, O.U.A.T. on 31<sup>th</sup> July 2019 and healthy seedlings were transplanted into the main plot on 28<sup>th</sup> August 2019.

The plot size was 3.705 m<sup>2</sup> with spacing 20 x 15 cm (19 plants x 6 lines) with 30cm varietal spacing following randomized block design and replicated twice in four rank each rank comprising 13 genotypes. All standard agronomic practices including need based irrigation, split dose of fertilizer and plant protection measures were adopted from sowing to the harvesting stage for raising a vigorous crop. Observations were recorded by sampling five competitive plants randomly in each plot from both the replication for eleven yield attributing characters. The test materials were analysed with respect to following yield and yield contributing traits:

1. Day's to 50% flowering
2. Plant height(cm)
3. No. of effective tillers per plant
4. Panicle length(cm)
5. Flag leaf area(cm<sup>2</sup>)
6. No. of filled grains
7. Fertility %
8. 1000 grain weight (gm.)
9. Whole grain length (mm)
10. L/B ratio (whole)
11. Yield (q/ha)

The data were recorded with respect to following characters for all 52 advanced elite lines from both the replication.

### Multivariate analysis

After testing of differences among genotypes for each of the 11 characters, a simultaneous test of significance of differences in mean values of the 11 correlated variables for 52 genotypes using Wilk's lambda ( $\Delta$ ) criterion (Wilks, 1932) and V-statistics (Rao, 1952).

### D<sup>2</sup> analysis

Rao (1952) suggested the application of D<sup>2</sup> technique by P.C. Mahalanobis (1928) for the assessment of genetic diversity. The original measurement was transferred to standardized,

un-correlated variables by pivotal condensation (Rao, 1952). The divergence between any two variables was obtained as the sum of the squares of differences in the values of corresponding transformed values.

$D^{2ij} = \sum (Y_{ij} - Y_{ji})^2$  gives the D<sup>2</sup> between i<sup>th</sup> and j<sup>th</sup> varieties for K characters i-k

The possible pairs of D<sup>2</sup> values are calculated from the 52 genotypes. The statistical significance of each D<sup>2</sup> value was tested by X<sup>2</sup> with p degrees of freedom, "p" being the no of characters considered for D<sup>2</sup> estimation. Following Torcher's method as described by Rao (1952), the genotypes were grouped into cluster.

### Canonical analysis

Canonical analysis was done according to Anderson (1958). The divergences of 34 aromatic rice genotypes were represented in two dimensional graph using first two canonical vectors (Z1 and Z2) as coordinates.

### Results

The present experiment was carried out for genetic divergence study among 52 advanced elite lines of slender grain rice genotypes including 6 checks (CR 1014, Jajati, Gitanjali, Samba Mahsuri, Khandagiri, Prativa). The 52 advanced elite lines of slender grain rice were evaluated under suitable field conditions to study the genetic basis of yield variations. The results obtained after analysis are discussed below for better comprehension.

Following Mahalanobis D<sup>2</sup> statistic and Anderson's canonical analysis, simultaneous variation in all 11 characters were estimated to assess nature and magnitude of divergence among 52 slender grain rice genotypes.

The D<sup>2</sup> values of all the genotype combination between 52 slender grain rice estimated on the basis of 11 characters studied (Table-2) to assess the degree of diversity among test materials. Highly significant differences were observed among the test lines; the D<sup>2</sup> values ranged from 6.61 (between OR 2674-14-4-4 and OR 2674-14-4-5) to 1762.45 (between OR 2762-1 and Samba mahsure). Therefore, the above information revealed that some lines were genetically very close to each other and rest possessed marked difference

between them. The analysed data were further used for grouping the test materials into different clusters. So inference could be drawn that present set of test material possess substantial quantity of genetic diversity among them.

**Table 2:** D<sup>2</sup> value (lowest and highest) among 52 advanced elite lines of slender grain rice for possible comparison.

Between lines/ genotypes		Lowest D <sup>2</sup> value	Highest D <sup>2</sup> value
1 and rest	52.79	(1 and 11)	<b>1762.45</b> (1 and 50)
2 and rest	53.26	(2 and 52)	1077.41 (2 and 50)
3 and rest	76.27	(3 and 14)	1737.73 (3 and 50)
4 and rest	61.95	(4 and 12)	988.81 (4 and 50)
5 and rest	24.29	(5 and 6)	1360.24 (5 and 50)
6 and rest	30.40	(6 and 12)	1295.47 (6 and 50)
7 and rest	32.48	(7 and 28)	1077.44 (7 and 47)
8 and rest	51.87	(8 and 10)	1529.11 (8 and 50)
9 and rest	52.10	(9 and 11)	1199.24 (9 and 50)
10 and rest	32.06	(10 and 12)	1429.64 (10 and 50)
11 and rest	46.75	(11 and 13)	1510.61 (11 and 50)
12 and rest	49.70	(12 and 13)	1159.60 (12 and 50)
13 and rest	55.31	(13 and 27)	1361.62 (13 and 50)
14 and rest	132.96	(14 and 16)	1570.75 (14 and 50)
15 and rest	62.19	(15 and 16)	988.10 (15 and 50)
16 and rest	48.83	(16 and 19)	1294.84 (16 and 50)
17 and rest	23.89	(17 and 19)	1357.84 (17 and 50)
18 and rest	20.62	(18 and 25)	1597.54 (18 and 50)
19 and rest	22.48	(19 and 26)	1279.34 (19 and 50)
20 and rest	14.11	(20 and 25)	1726.14 (20 and 50)
21 and rest	18.41	(21 and 24)	1421.02 (21 and 50)
22 and rest	20.46	(22 and 23)	1671.27 (22 and 50)
23 and rest	6.61	(23 and 24)	1642.54 (23 and 50)
24 and rest	38.05	(24 and 25)	1591.67 (24 and 50)
25 and rest	98.94	(25 and 26)	1721.50 (25 and 50)
26 and rest	90.26	(26 and 29)	1355.78 (26 and 50)
27 and rest	36.70	(27 and 29)	1202.61 (27 and 50)
28 and rest	59.42	(28 and 31)	1674.99 (28 and 50)
29 and rest	31.50	(29 and 30)	1300.53 (29 and 50)
30 and rest	24.55	(30 and 33)	1444.58 (30 and 50)
31 and rest	13.75	(31 and 34)	1633.34 (31 and 50)
32 and rest	12.70	(32 and 34)	1696.70 (32 and 50)
33 and rest	29.39	(33 and 34)	1368.33 (33 and 50)
34 and rest	202.59	(34 and 49)	1694.7 (34 and 50)
Between lines/ genotypes		Lowest D <sup>2</sup> value	Highest D <sup>2</sup> value
35 and rest	87.98	(35 and 36)	672.46 (35 and 50)
36 and rest	117.86	(36 and 40)	485.00 (36 and 50)
37 and rest	9.83	(37 and 42)	749.02 (37 and 50)
38 and rest	26.19	(38 and 44)	941.57 (38 and 50)
39 and rest	15.04	(39 and 46)	782.90 (39 and 50)
40 and rest	24.50	(40 and 46)	754.44 (40 and 50)
41 and rest	13.01	(41 and 45)	853.36 (41 and 50)
42 and rest	15.71	(42 and 43)	807.39 (42 and 50)
43 and rest	30.81	(43 and 46)	692.69 (43 and 50)
44 and rest	35.61	(44 and 45)	955.26 (44 and 50)
45 and rest	17.88	(45 and 46)	909.69 (45 and 50)
46 and rest	66.00	(46 and 48)	831.46 (46 and 50)
47 and rest	235.95	(47 and 50)	963.24 (47 and 49)
48 and rest	181.98	(48 and 49)	708.05 (48 and 50)
49 and rest	257.42	(49 and 52)	1470.00 (49 and 50)
50 and rest	484.40	(50 and 51)	1020.66 (50 and 52)

**Relative contribution of the characters**

The relative contribution of different characters to the total divergence was assessed by rank total and average D<sup>2</sup> as presented in Table-3. Among different characters, the order of

contribution to the total genetic divergence were high for L/B ratio (36.75%) moderate for 1000 grains weight (11.40%) and low (0.45% - 9.36%) for rest of the characters.

**Table 3:** Relative contribution of different characters to the total genetic divergence

S.no.	Characters	Rank total	Percentage of total divergence
1	Day's to 50% flowering	56	4.23
2	plant height (cm)	6	0.45
3	No. of effective tillers	110	8.30
4	Flag leaf area in cm <sup>2</sup>	69	5.21
5	Panicle length (cm)	107	8.07
6	No. of filled grain per panicle	81	6.11
7	Fertility %	19	1.43
8	1000 grain weight (gm)	151	11.40
9	Grain length (mm)	115	8.68
10	L/B ratio	487	36.75
11	yield (q/ha)	124	9.36

**Clustering pattern**

The 52 slender grains elite lines under study were classified into 8 clusters based on the relative magnitude of P.C. Mahalanobis D<sup>2</sup> values, following Tocher's method and different genotypes included in each cluster are presented in Table-4. Cluster I was the largest among all comprising of 13 lines, followed by Cluster II consisting of 11 lines, Cluster III accommodated 10 lines, Cluster IV consisting of 6 lines, Cluster V comprised of 5 lines, and Cluster VI and Cluster VII both composed of 3 lines and Cluster VIII consisting of only one line. The pattern of grouping demonstrates presence of remarkable variability among the 52 test lines.

**Table 4:** Clustering pattern of 52 advanced elite lines of slender grain rice

Clusters	No of Genotypes	Name of Genotypes
		OR 2674-17-1, OR 2675-6-4, OR 2676-1-1, OR 2676-2-2, OR 2676-2-3, OR 2676-2-5, OR 2676-2-6, OR 2676-3-1, OR 2676-4-2, OR 2676-5-1, OR 2676-5-3, Jajati, Prativa
I	13	
II	11	OR 2762-4, OR 2762-14, OR 2762-21, OR 2762-60, OR 2762-61, OR 2762-62, OR 2674-14-2-2, OR 2674-14-2-6, OR 2674-14-3-7, OR 2674-14-5-1, OR 2674-14-7-1,
III	10	OR 2762-1, OR 2762-35, OR 2762-45, OR 2762-55, OR 2674-14-5-3, OR 2674-14-8-1, OR 2674-14-8-2, OR 2674-14-8-3, OR 2674-14-8-4, OR 2674-14-8-6
IV	6	OR 2674-14-2-4, OR 2674-14-3-2, OR 2674-14-4-3, OR 2674-14-4-4, OR 2674-14-4-5, OR 2674-14-4-6
V	5	OR 2762-1, OR 2762-13, OR 2762-22, OR 2762-53, OR 2674-14-8-5
VI	3	CR 1014, Samba mahsuri, Khandagiri,
VII	3	OR 2762-7, OR 2762-2, Gitanjali
VIII	1	OR 2675-3-1

Average intra and inter-cluster D<sup>2</sup> value among 8 clusters were computed and have been presented in Table-5 and figure 1. The intra cluster D<sup>2</sup> value ranged from 00.00

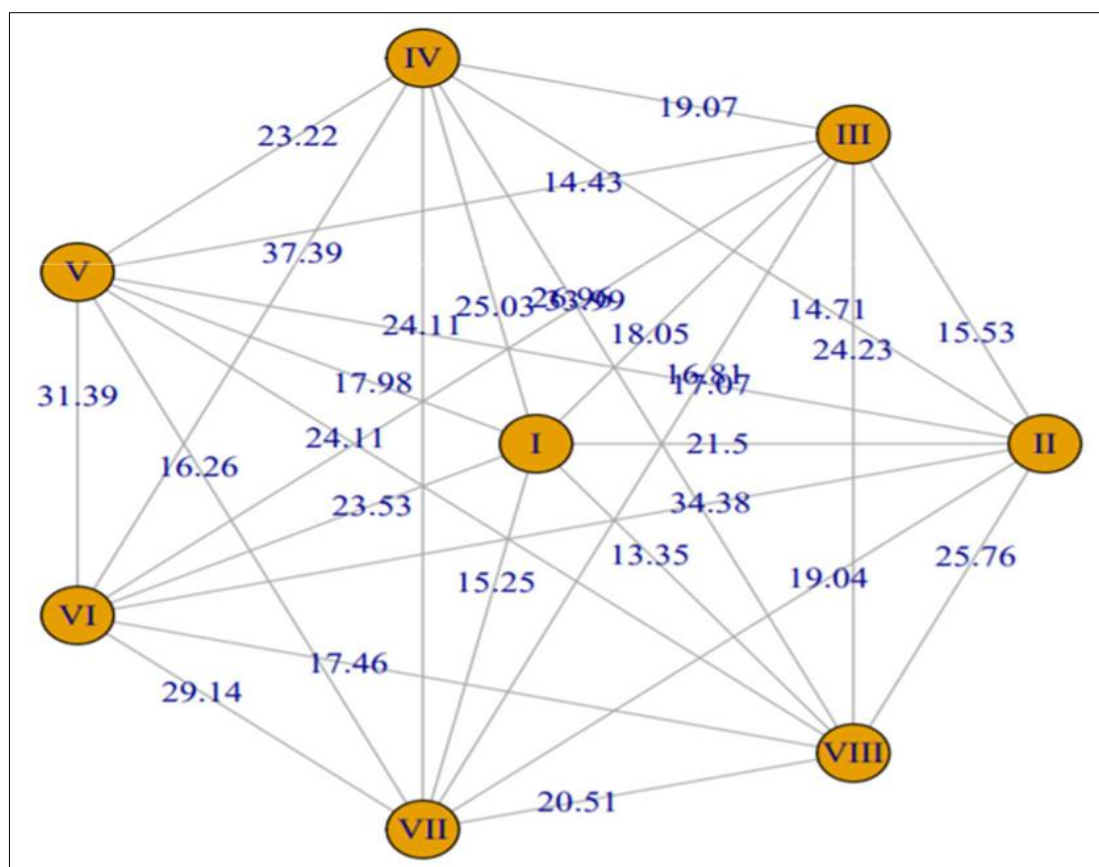


(cluster VIII) to 926.511 (Cluster II). The inter cluster D<sup>2</sup> value was found highest between cluster IV and Cluster VI (1398.889) indicated they were more divergent as they differ for more number of characters and lowest inter cluster

distance was recorded between Cluster I and Cluster VIII (178.322) suggesting relatedness between themselves due to similarity between them for majority of the traits under study.

**Table 5:** Average Intra and inter cluster D2 value of 52 advanced elite lines, grouped into 8 clusters (Intra cluster D2 value in diagonal

Clusters	I	II	III	IV	V	VI	VII	VIII
I	531.764	462.451	325.642	626.640	323.317	553.593	232.529	178.322
II		926.511	241.138	216.361	291.266	1181.889	362.645	663.771
III			791.583	363.807	208.095	1155.566	282.440	587.205
IV				79.221	539.249	1398.021	581.120	726.821
V					375.144	985.224	264.425	581.349
VI						390.578	848.939	305.001
VII							278.598	420.721
VIII								0.000



**Fig 1:** Average inter-cluster distance between 52 slender grain elite lines of rice, grouped into 8 clusters from D2 analysis

**Characteristic features of the clusters**

The mean values of the clusters revealed an extensive variation for all the traits under study which is presented in Table-6.

It is clear from the observation that genotypes included under cluster I are distinguished for medium maturity type, taller than all clusters except VIII with moderate tillering habit, longest panicle length and largest flag leaf area among all the groups, medium numbers of filled grains, medium fertility % along with high 1000 grains weight, long slender grained and intermediate yielders.

Cluster II had lines with intermediate stature plant and early maturing type plants having moderate no. of tillers/plant, large flag leaf area with intermediate filled grains per panicle with medium fertility %, high grain weight, long slender grained and good yielders. Cluster III was characterised by tall group plant with earliest maturing plants but having

lowest no. of filled grains among all the clusters with high tillering habit, longer panicle length, medium fertility %, and high grain weight, long slender grained and intermediate yielders.

Cluster IV described as tall stature medium maturity plant with intermediate tillering habit, long panicle length with intermediate numbers of filled grains/panicle, higher fertility % among all clusters except VI and VIII having higher test weight and longest slender grained among all groups and intermediate yielders.

The genotypes in Cluster V are indicated as intermediate height, early maturity plant types having highest no. of tillers per plant among all groups, intermediate no. of filled grains/panicle and fertility %, long grained and high yielders.

Cluster VI was distinguished as lowest grain weight and flag area, shortest panicle length and grain length, highest no. of filled grains/panicle among all the clusters, high fertility %, and

intermediate height and good yielding plant types. Cluster VII characterised by intermediate height intermediate maturity plant having higher numbers of tillers per plant, large flag leaf area, longer panicle length, intermediate no. of filled grains/ panicle and fertility%, long grained, highest grain

weight with highest yielding ability among all groups. Cluster VIII distinguished for tallest plant groups with longest maturity duration, highest fertility% among all the groups, large flag leaf area, long panicle length, high test weight, long slender grained and high yielding plant type.

**Table 6:** Average mean performance of different clusters for 11 traits in 52 advanced elite lines of slender grain rice

Sl. No.	Characters/ Clusters	I	II	III	IV	V	VI	VII	VIII
1	Day's to 50% flowering	94.65	84.09	84.20	86.25	84.80	105.00	88.17	100.00
2	plant height(cm)	119.62	103.48	116.44	117.42	102.22	102.37	108.15	131.10
3	No. of effective tillers	9.32	10.70	10.81	9.88	11.26	10.73	10.63	10.20
4	Flag leaf area in cm <sup>2</sup>	31.49	24.44	31.25	27.08	30.58	19.74	29.68	31.45
5	Panicle length(cm)	26.46	24.23	25.89	24.91	23.58	21.66	24.95	23.00
6	No. of filled grain per Panicle	118.65	117.03	109.78	113.28	112.18	129.40	111.91	115.00
7	Fertility%	70.00	78.94	75.58	79.89	78.80	82.24	79.50	87.09
8	1000 grain weight(gm)	22.06	22.26	22.10	22.88	19.86	17.76	23.64	21.45
9	Grain length (mm)	9.88	10.38	10.80	11.49	9.61	8.48	9.51	10.36
10	L/B ratio	4.19	5.10	4.64	6.13	4.10	3.72	4.15	4.38
11	yield (q/ha)	24.98	30.83	29.52	29.17	31.48	30.91	35.36	32.33

### Canonical analysis

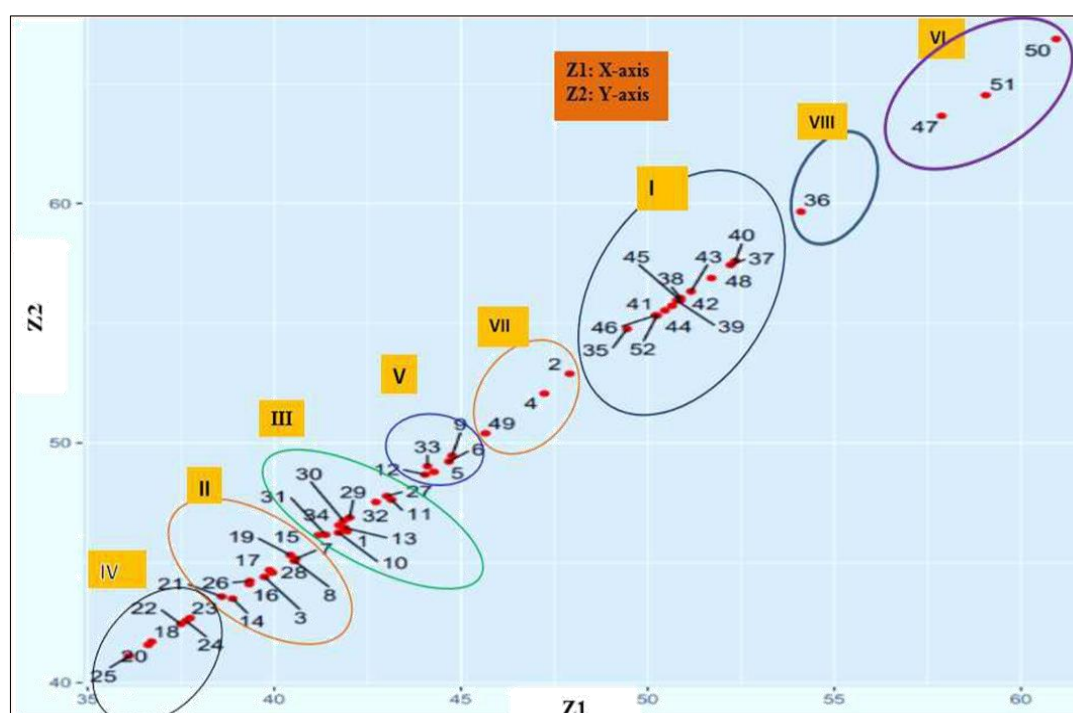
In the present set of test material we can conclude that two canonical roots are good enough to account for  $\geq 80\%$  of the total variability, therefor qualifying for the graphical presentation. Two dimensional dispersion complex (Fig.2) has been obtained by plotting two coordinates from the mean values of two canonical vectors Z1 and Z2 (Table-7). The

grouping obtained through D<sup>2</sup> analysis has been found to be superimposed on the two dimensional representation of the advanced elite lines of slender grain rice by pivotal condensation. The scattered points on the Z1-Z2 graph were generally in accordance with the magnitude of divergence measured by D<sup>2</sup> statistics, therefor well validating the grouping by Tocher's optimization method (Rao, 1952).

**Table 7:** The mean values of two canonical vectors Z1 and Z2 for 52 advanced elite lines of slender grain rice.

S.no.	Genotypes /Elite lines	z1	z2	Mean
1	OR 2762-1	41.95	46.32	44.13
2	OR 2762-2	47.91	52.89	50.40
3	OR 2762-4	39.74	44.41	42.08
4	OR 2762-7	47.24	52.07	49.65
5	OR 2762-12	44.28	48.80	46.54
6	OR 2762-13	44.68	49.23	46.95
7	OR 2762-14	40.58	45.16	42.87
8	OR 2762-21	40.54	45.08	42.81
9	OR 2762-22	44.76	49.47	47.12
10	OR 2762-35	41.72	46.26	43.99
11	OR 2762-45	43.14	47.64	45.39
12	OR 2762-53	44.04	48.68	46.36
13	OR 2762-55	41.89	46.46	44.18
14	OR 2762-60	38.88	43.50	41.19
15	OR 2762-61	41.18	46.16	43.67
16	OR 2762-62	39.33	44.11	41.72
17	OR 2674-14-2-2	39.87	44.70	42.28
18	OR 2674-14-2-4	36.71	41.71	39.21
19	OR 2674-14-2-6	40.43	45.33	42.88
20	OR 2674-14-3-2	36.62	41.58	39.10
21	OR 2674-14-3-7	38.59	43.59	41.09
22	OR 2674-14-4-3	37.49	42.45	39.97
23	OR 2674-14-4-4	37.75	42.70	40.22
24	OR 2674-14-4-5	37.64	42.58	40.11
25	OR 2674-14-4-6	36.10	41.10	38.60
26	OR 2674-14-5-1	39.35	44.24	41.80
27	OR 2674-14-5-3	43.02	47.79	45.40
28	OR 2674-14-7-1	39.95	44.59	42.27
29	OR 2674-14-8-1	42.017	46.89	44.45
30	OR 2674-14-8-2	41.85	46.76	44.30
31	OR 2674-14-8-3	41.37	46.17	43.77
32	OR 2674-14-8-4	42.72	47.54	45.13
33	OR 2674-14-8-5	44.10	49.03	46.57
34	OR 2674-14-8-6	41.74	46.57	44.15
35	OR 2674-17-1	49.45	54.76	52.11

36	OR 2675-3-1	54.11	59.65	56.88
37	OR 2675-6-4	52.22	57.43	54.83
38	OR 2676-1-1	50.88	56.05	53.47
39	OR 2676-2-2	50.78	55.94	53.36
40	OR 2676-2-3	52.35	57.61	54.98
41	OR 2676-2-5	50.65	55.73	53.19
42	OR 2676-2-6	50.87	55.98	53.43
43	OR 2676-3-1	51.16	56.33	53.75
44	OR 2676-4-2	50.46	55.53	53.00
45	OR 2676-5-1	50.88	55.95	53.42
46	OR 2676-5-3	50.21	55.33	52.77
47	CR 1014	57.87	63.65	60.76
48	Jajati	51.71	56.89	54.30
49	Gitanjali	45.66	50.41	48.03
50	Samba Mahsuri	60.95	66.86	63.90
51	Khandagiri	59.06	64.52	61.79
52	Prativa	50.25	55.32	52.79



**Fig 2:** Two dimensional representation of divergence among 52 advanced elite lines of slender grain rice, using the first two canonical vectors (Z1 and Z2) as coordinates, the grouping by  $D^2$  super imposed

## Discussion

Rice is one of the most important cereal crop around the world. It meets the daily nutritional requirements of half of the world's population. As the living standards of the country slowly improving, consumer demand for quality grain rice is continuously on high demand. Thus, in recent decades improving the grain quality of rice has been the foremost important breeding objective to enable farmers to capture market surplus by considering consumer preference for quality rice.

In the present investigation, an effort has been made to evaluate fifty-two advanced elite lines of slender grain rice including six checks to short out lines with superior grain quality along with high yield on the basis of multivariate analysis.

The  $D^2$  values of all the genotype combination between 52 slender grain rice estimated on the basis of 11 characters studied (Table-2) to estimate the degree of diversity among test materials for the studied characters. Highly significant differences were observed among the test lines; the  $D^2$  values

ranged from 6.61 (between OR 2674-14-4-4 and OR 2674-14-4-5) to 1762.45 (between OR 2762-1 and Samba mahsuri).

The 52 slender grains elite lines under study were classified into 8 clusters as presented in Table-4. Cluster I was the largest cluster comprising of 13 lines, followed by Cluster II with 11, Cluster III accommodated 10 lines, Cluster IV consisting of 6 lines, Cluster V comprised of 5 lines, and Cluster VI and Cluster VII both composed of 3 lines and Cluster VIII consisting of only one lines.

The intra cluster  $D^2$  value ranged from 00.00 (cluster VIII) to 926.511 (Cluster II). The inter cluster  $D^2$  value was found highest between cluster IV and Cluster VI (1398.889) indicated they were more divergent as it was seen they differ for more number of characters and lowest inter cluster distance was recorded between Cluster I and Cluster VIII (178.322) suggesting relatedness between themselves due to similarity between them for majority of the traits under study. The presence of high inter-cluster distanced genotypes permits the selection of divergent parents. This avoids the selection of parents from genetically homogeneous clusters

and thus reducing the crossing of population with narrow genetic base. Higher genetic distance between the clusters suggested a wide diversity among the genotypes. The crosses made between the genotypes from the above clusters might give useful transgressive segregants (Sharma and Bhuyan, 2004) [23].

The relative contribution of different characters to the total divergence was assessed by rank total and average  $D^2$  in Table-3. Among different characters, the order of contribution to the total genetic divergence were high for L/B ratio (36.75%) moderate for 1000 grains weight (11.40%) and low (0.45% - 9.36%) for rest of the characters. More or less similar study has been also done by many researchers like Biswaranjan *et al.* (2017) [3], Govintharaj *et al.* (2018) [8], Putra and Saptisingrum (2019) [17], Majumder *et al.* (2020) [16].

The mean values of the clusters revealed an extensive variation for all the traits under study which is presented in Table-6. In a concrete way we may conclude that cluster I could be distinguished for longest panicle length and largest flag leaf area among all, Cluster II for with highest L/B ratio, Cluster III for earliest maturing genotypes. Cluster IV had higher test weight and longest slender grained type genotypes and genotypes in Cluster V have been indicated by highest tillering plant type. Cluster VI possessed highest number of filled grains/panicle. Cluster VII had highest yielding genotypes with highest mean grain weight and Cluster VIII distinguished by tallest and longest maturing genotypes exhibiting highest fertility % among all the groups.

### Summary and Conclusion

Rice being most important staple food is very much affected by these variations, with slowly improving economy and changing life standards, rice consumers are looking for quality grain rice. Quality rice is an important commodity to earn foreign exchange due to its increasing demand in domestic as well as export market. It is also important to notice that improvement of grain quality should not be compromised with the yield potential so that farmers can be equally benefited by producing this type of quality grain rice. Therefore, consumer oriented rice breeding incorporating productivity plus grain quality (Dhurai *et al.*, 2014) is need of time to improve the economy of country.

A prime requirement for any crop improvement programme is presence of genetic diversity. Genetic divergence studies were conducted based on Mahalanobis  $D^2$  statistic and Anderson's canonical analysis based on variation present in 11 yield attributing traits.

The  $D^2$  values of all the genotype combination between 52 slender grain rice ranged from as low as 6.61 (between OR 2674-14-4-4 and OR 2674-14-4-5) to 1762.45 (between OR 2762-1 and Samba mahsuri). L/B ration and 1000 grains weight had maximum contribution to genetic divergence. All the test entries were grouped into eight clusters. Cluster I was largest among all, comprising of 13 lines, followed by Cluster II with 11 lines, Cluster III accommodated 10 lines, Cluster IV consisting of 6 lines, Cluster V comprised of 5 lines, Cluster VI and Cluster VII both composed of 3 lines and Cluster VIII is monogenic line. Cluster VII comprised of highest yielding genotypes. The intra cluster  $D^2$  value ranged from 00.00 (cluster VIII) to 926.511 (Cluster II). The inter cluster  $D^2$  value was found highest between cluster IV and Cluster VI (1398.889) and lowest between Cluster I and

Cluster VIII (178.322). Accordingly, test genotypes can be further used for crop improvement programme by crossing most diverse genotypes. It was also found that among 52 advanced elite lines of slender grain rice studied; the most promising lines with high yield performance along with appreciable grain qualities and plant architecture were OR 2762-35, OR 2762-7 and OR 2762-2.

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