

## Multivariate Analysis in Upland Rice Genotypes

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**Abstract:** Fifty-seven upland rice genotypes including 32 local rice germplasm were assessed for the nature and magnitude of genetic divergence among them based on 14 agro-morphological traits following Mahalanobis'  $D^2$ -statistic and Anderson's canonical analysis. On the basis of  $D^2$  values, the 57 genotypes were grouped into five clusters following Tocher's method. The grouping by Tocher's method showed three multi-genotypic and two mono-genotypic clusters along with close resemblance to the two dimensional representation of entries by first two canonical vectors. The most divergent clusters were III and IV ( $D^2 = 3387.9$ ) followed by III and V ( $D^2 = 2808.2$ ) and clusters II and III ( $D^2 = 1908.7$ ). Highest intra-cluster distance was observed in cluster I followed by cluster II. Cluster I was largest one containing 50 genotypes from different origin. The clustering patterns of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were grain L/B ratio, 1000-grain weight, grain length, grain yield and biological yield.

**Key words:** Multivariate analysis · Canonical analysis · genetic distance · upland rice

### INTRODUCTION

Orissa State, India, particularly Jeypore tract, is considered as one of the centers of origin of rice. This area is rich in genetic diversity of rice owing to its ecological diversity offered by dense forest and hilly tracts/terrains. The age-old traditional cultivars grown in this area are in isolation more particularly by the tribals residing in the foothills and in the forest. These traditional cultivars are under cultivation for long period over generations and expected to possess gene(s) responsible for their adaptability to such environmental conditions. Hence, their role in developing improved varieties suitable for that environment cannot be ruled out. Earlier development of short-duration varieties when envisaged at different rice breeding centers in India, more particularly in Orissa state have utilized the pure-line varieties selected earlier but have ignored the importance of these primitive cultivars/land races still in vogue in hilly tracts. The study of genetic variability and magnitude of genetic divergence present in the available early rice germplasm is therefore highly essential for further improvement of upland rice varieties. The estimation of genetic divergence in the available germplasm is important for successful selection of parents for hybridization purpose. The divergent lines belonging to different and distantly located clusters have higher probabilities of

giving heterotic hybrids or superior progenies than those parental lines belonging to the same cluster or group possessing low genetic distance. Several workers have emphasized the importance of genetic divergence for selection of desirable parents [1-3].

Keeping in view on the importance of varietal improvement in upland rice, the present investigation was undertaken to assess the nature and magnitude of genetic divergence among fifty-seven upland rice genotypes.

### MATERIALS AND METHODS

The experimental material comprised of 57 early rice genotypes, which included (i) 32 local rice germplasm collections, (ii) 23 high yielding short duration varieties and (iii) two mutant collections (Table 1). The field layout was done in Randomized Block Design with 3 replications in each year of sowing. The experiment was conducted at Central Research Station, O.U.A.T., Bhubaneswar during wet season, 2002 and 2003. The seed materials were direct seeded in 3 rows of 3-metre length with row-to-row 20 cm and plant-to-plant 10 cm spacing. Recommended agronomic practices and need based plant protection measures were followed to raised a healthy crop. Observations were recorded on days to heading, plant height, flag leaf length, flag leaf area, panicle length, panicles/meter square, no. of filled grains/panicle, spikelet

Table 1: Description of upland rice genotypes/lines

Sl No.	Genotype	IC No.	Parentage	Plant height	Place of origin / adaptation
1	KCM 73	298382	Local collection	Tall	Dugudi, G.Udyagiri, Kandhamal, Orissa
2	KCM 74	298383	Local collection	Tall	Dugudi, G.Udyagiri, Kandhamal, Orissa
3	KCM 75	298384	Local collection	Tall	Dugudi, G.Udyagiri, Kandhamal, Orissa
4	KCM 76	298385	Local collection	Tall	Gamuli, G.Udayagri, Kandhamal, Orissa
5	KCM 93	298402	Local collection	Tall	Gamuli, G.Udayagri, Kandhamal, Orissa
6	KCM 104	298413	Local collection	Tall	Badabandha,Tumudibandha,Kandhamal, Orissa
7	KCM 105	298414	Local collection	Tall	Badabandha,Tumudibandha,Kandhamal, Orissa
8	KCM 106	298415	Local collection	Tall	Badabandha,Tumudibandha,Kandhamal, Orissa
9	KCM 107	298416	Local collection	Tall	Badabandha,Tumudibandha,Kandhamal, Orissa
10	KCM 129	298438	Local collection	Tall	Sikharpadu, Rayagada, Rayagada, Orissa
11	KCM 130	298439	Local collection	Tall	Sikharpadu, Rayagada, Rayagada, Orissa
12	KCM 143	298452	Local collection	Tall	Madanpur, Kolhnara, Rayagada, Orissa
13	KCM 158	298467	Local collection	Tall	Rupakana, Rayagada, Rayagada, Orissa
14	KCM 170	298479	Local collection	Tall	Mahantaput, Baipariguda, Koraput, Orissa
15	KCM 176	298485	Local collection	Tall	Utakapadu, Rayagada, Rayagada, Orissa
16	KCM 186	298495	Local collection	Tall	Sunabahal, Malkanagiri, Malkanagiri, Orissa
17	KCM 187	298496	Local collection	Tall	Pandripani, Malkanagiri, Malkanagiri, Orissa
18	KCM 188	298497	Local collection	Tall	Pandripani, Malkanagiri, Malkanagiri, Orissa
19	KCM 327	321742	Local collection	Tall	Biswanathpur, Lanjiguda, Kalahandi, Orissa
20	KCM 338	321753	Local collection	Tall	Phulajhari, Umarmkot, Nawarangpur, Orissa
21	KCM 378	321793	Local collection	Tall	Kesharibida, Umarmkot, Nawarangpur, Orissa
22	KM 2	-	Mutant from Kalakeri	Tall	OUAT, Bhubaneswar, Orissa
23	KM 6	-	Mutant from Kalakeri	Short	OUAT, Bhubaneswar, Orissa
24	PB 16	256528	Local collection	Tall	Deogarh, Orissa
25	PB 21	256533	Local collection	Tall	Deogarh, Orissa
26	PB 25	256537	Local collection	Tall	Deogarh, Orissa
27	PB 66	256578	Local collection	Tall	Sundargarh, Orissa
28	PB 73	256585	Local collection	Tall	Sundargarh, Orissa
29	PB 102	256614	Local collection	Tall	Sundargarh, Orissa
30	PB 138	256650	Local collection	Tall	Sundargarh, Orissa
31	PB 140	256652	Local collection	Tall	Sundargarh, Orissa
32	PB 141	256653	Local collection	Tall	Sundargarh, Orissa
33	PB 148	256660	Local collection	Tall	Sundargarh, Orissa
34	PB 160	256672	Local collection	Tall	Sundargarh, Orissa
35	JD 6	-	Mutant from (Dular x N 22)	Short	IARI, New Delhi
36	JD 13	-	Mutant from (Dular x N 22)	Short	IARI, New Delhi
37	N 22	-	Pure line selection	Tall	Uttarpradesh
38	Blackgora	-	Pure line selection	Tall	Bihar
39	Kalakeri	-	Pure line selection	Tall	Orissa
40	Dular	-	Pure line selection	Tall	West Bengal
41	Annapurna	-	PTB 10/T(N) 1	Short	Kerala
42	Rudra	-	Parijat/IET 3225	Short	OUAT, Bhubaneswar, Orissa
43	Shankar	-	Parijat/IET 3225	Short	OUAT, Bhubaneswar, Orissa
44	Parijat	-	TKM 6/T (N) 1	Short	OUAT, Bhubaneswar, Orissa
45	Subhadra	-	T (N) 1/SR 26 B	Short	OUAT, Bhubaneswar, Orissa
46	Pathara	-	CO 18/Hema	Short	OUAT, Bhubaneswar, Orissa
47	Ghanteswari	-	IR 2061-628/N 22	Short	OUAT, Bhubaneswar, Orissa
48	Lalitgiri	-	Badami/IR 1996-364	Short	OUAT, Bhubaneswar, Orissa
49	Udayagir	-	IRAT 138/TR 13543-66	Short	OUAT, Bhubaneswar, Orissa
50	Bhatta Sel. 2	-	Pureline selection	Tall	Orissa
51	Kalinga 3	-	AC 540/Ratna	Tall	CRRRI, Cuttack, Orissa
52	Annada	-	MTU 15/Yai Kyaku Kantoku	Short	CRRRI, Cuttack, Orissa
53	Heera	-	CR 404-48/CR 289-1208	Short	CRRRI, Cuttack, Orissa
54	Neela	-	CR 94-1512-6/Pusa 2-21	Short	CRRRI, Cuttack, Orissa
55	Sneha	-	Annada/CR 143-2-2	Short	CRRRI,Cuttack, Orissa
56	Vandana	-	C 22/Kalakeri	Tall	CRRRI, Cuttack, Orissa
57	Vanaprava	-	ARC 12422/ARC 12751	Tall	CRRRI,Cuttack, Orissa

fertility, 1000-grain weight, grain length, grain length/breadth ratio, biological yield and harvest index.

Simultaneous variation in all the 14 characters of 57 rice genotypes were subjected for assessing nature of divergence among them following Mahalanobis'  $D^2$  statistic [17] and Anderson's [18] canonical analysis following the procedure Rao [4].

## RESULTS AND DISCUSSION

The aggregate effect of all the 14 characters tested by Wilks' criterion indicated highly significant differences among the genotypes in the present study. The principal component analysis showed that the first two canonical roots accounted for 61.1% of the total variation. Based on cluster; the 57 genotypes were grouped into five clusters (Table 2), three multi-genotypic and two mono-genotypic clusters. Cluster I was the largest accommodating 50 genotypes.

The average intra and inter-cluster distance ( $D^2$  value) presented in Table 3, revealed that the highest intra- cluster distance of 488.8 was observed in Cluster I

followed by cluster II ( $D^2= 465.9$ ). It is evident from inter-cluster distance that the most divergent clusters were III and IV ( $D^2 = 3387.9$ ) followed by clusters III and V ( $D^2 = 2808.2$ ) and clusters II and III ( $D^2 = 1908.7$ ) suggesting wide diversity between them and the genotypes in these clusters could be used as parents in hybridization program. Highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. The hybrids developed from these genotypes within the limit of compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding for successful breeding program for upland rice. On the other hand, the minimum inter-cluster distance was found between clusters I and V ( $D^2 = 811.4$ ) followed by clusters I and II ( $D^2 = 954.2$ ) and clusters I and III ( $D^2 = 1424.6$ ), indicating that the genotypes of these clusters were genetically similar. [3, 5, 6] have also reported that selection of parents for hybridization should be done from two clusters having wider inter-cluster distances to get maximum variability in the segregating generations.

Table 2: Clustering of 57 upland rice genotypes pooled over years

Cluster	No. of genotypes	Name of genotypes	Place of origin
I	50	KCM 73, KCM 74, KCM 75	Dugudi, G.Udayagiri, Kandhamal, Orissa
		KCM 104, KCM 105, KCM 106, KCM 107	Badabandha, Tumudibandha, Kandhamal, Orissa
		KCM 130	Sikharpadu, Rayagada, Orissa
		KCM 158	Rupakana, Rayagada, Orissa
		KCM 170	Mahantput, Baipariguda, Koraput, Orissa
		KCM 176	Utkapadu, Rayagada, Orissa
		KCM 186	Sunabahal, Malkangiri, Orissa
		KCM 187, KCM 188	Pandripani, Malkangiri, Orissa
		KM 2, KM 6, Kalakeri, Rudra, Sankar, Parijat, Subhadra, Pathara, Ghanteswari, Lalitgiri, Udayagiri, Bhatta Selection 2	OUAT, Bhubaneswar, Orissa
		PB 16, PB 21, PB 25	Deogarh, Orissa
		PB 66, PB 73, PB 102, PB 138, PB 140, PB 141, PB 148, PB 160	Sundargarh, Orissa
		JD 6, JD 13	IARI, New Delhi
		Kalinga 3, Annada, Heera, Neela, Sneha, Vandana, Vanaprabha	CRRI, Cuttack, Orissa
		N 22	Uttar Pradesh
		Blackgora	Bihar
		Dular	West Bengal
Annapurna	Kerala		
II	3	KCM 76, KCM 93	Gamuli, G.Udayagiri, Kalahandi, Orissa
		KCM 129	Sikharpadu, Rayagada, Orissa
III	2	KCM 338	Phulajhari, Umakot, Nawarangpur, Orissa
		KCM 378	Kesharibeda, Umakot, Nawarangpur, Orissa
IV	1	KCM 143	Madanpur, Kolhnara, Rayagada, Orissa
V	1	KCM 327	Biswanathpur, Lanjigada, Kalahandi, Orissa

Table 3: Average intra- and inter-cluster distance ( $D^2$  value) in 57 rice genotypes pooled over years

Cluster	I (50*)	II (3)	III (2)	IV (1)	V (1)
I	488.8	954.2	1424.6	1511.9	811.40
II		465.9	1908.7	1576.1	1594.9
III			398.5	3387.9	2808.2
IV				0.0	1617.9
V					0.0

\* Figures in parentheses indicate number of genotypes in the respective clusters

Table 4: Cluster mean of 57 rice genotypes for 14 characters pooled over years

Character	Cluster (number of genotypes in the cluster)				
	I (50)*	II (3)	III (2)	IV (1)	V (1)
Day to heading	65.70	70.80	72.30	77.00	49.80
Plant height (cm)	91.50	114.20	100.10	119.80	79.40
Flag leaf length (cm)	28.90	33.50	33.10	30.40	27.90
Flag leaf area (cm <sup>2</sup> )	24.90	39.50	34.50	43.70	21.00
Panicle length (cm)	21.10	24.80	23.50	24.10	17.40
Panicles/meter square	65.70	52.00	59.00	47.70	54.00
Number of grains/panicle	58.60	78.70	84.20	96.70	51.80
Spikelet fertility (%)	73.00	77.90	80.90	72.60	83.80
1000-grain weight (g)	21.10	23.50	15.60	12.80	22.30
Grain length (mm)	8.90	8.50	9.90	6.50	7.80
Grain L/B ratio	2.75	2.68	3.56	2.05	2.44
Biological yield/meter (g)	134.70	175.40	141.50	130.10	101.00
Harvest index (%)	41.70	53.90	41.70	39.00	49.40
Grain yield/meter (g)	55.90	93.90	56.80	49.50	49.70

\* Figures in parentheses indicate number genotypes included in the cluster  
Underline bold figures indicate maximum (double line) and minimum (single line) values

The cluster means for each of 14 characters are presented in Table 4. It is evident from the Table that the cluster I was characterized for its highest panicle number and second highest values for grain length and grain L/B ratio. The cluster II was distinguished for its longest flag leaf, longest panicle, highest value of 1000-grain weight, biological yield, grain yield and harvest index. The cluster III had the highest values for grain length and grain L/B ratio and ranked second for panicle number and grain number. The cluster IV was distinguished for its longest flowering duration, tallest plant height, highest leaf area and grain numbers and the lowest values for number of panicles/meter square, spikelet fertility, 1000-grain weight, grain length, grain L/B ratio, harvest index and grain yield. The cluster V had the earliest genotypes possessing the shortest plant height and panicle length, the lowest flag leaf length and area, grain number, biological yield and highest spikelet fertility. Therefore, hybridization among members of the distant clusters is suggested to get desirable progenies.

Table 5: Coefficient of first two canonical vectors ( $Z_1, Z_2$ ) for 14 characters of 57 rice genotypes

Character	Canonical vectors	
	$Z_1$	$Z_2$
Days to heading (DH)	0.2120	0.0862
Plant height (PH)	-0.0475	0.2010
Flag leaf length (FLL)	-0.0270	0.1080
Flag leaf area (FLA)	-0.0291	0.1294
Panicle length (PL)	0.0530	0.1328
Panicle/metre square (PN)	-0.0130	-0.0579
Grains/Panicle (GN)	0.0049	0.2065
Spikelet fertility (SF)	-0.1468	0.1225
1000-grain weight (GW)	-0.3343	0.1857
Grain length (GL)	0.4923	0.1227
Grain L/B ratio (GL/B)	0.6981	0.2761
Biological yield (BY)	-0.0290	0.5052
Harvest index (HI)	-0.2107	0.1791
Grain yield (GY)	-0.2002	0.6573
Variation accounted for (per cent)	$\lambda_1 = 37.1$	$\lambda_2 = 24.0$

A two-dimensional scatter diagram was constructed using the values of the first two canonical vectors,  $Z_1$  and  $Z_2$  as coordinates ( $Z_1$  as X axis and  $Z_2$  as Y axis) for graphic presentation (Fig. 1). As per scatter diagram, the groupings obtained by  $D^2$  analysis are super imposed on two-dimensional representations of the entries by canonical analysis. The scattered points on  $Z_1 - Z_2$  graph were broadly in agreement with the magnitude of divergence, measured by  $D^2$  statistic, thus very well corroborating the groupings by Tocher's method. This result is in agreement with the earlier reports of [7-9].

The relative importance of the characters contributing towards divergence is reflected in the coefficients of the first two canonical vectors ( $Z_1$  and  $Z_2$ ) presented in Table 5. It is evident from the Table that the characters contributing more towards genetic divergence were grain L/B ratio, 1000-grain weight, grain length, grain yield and biological yield. Relative importance of some of these characters in inter-varietal divergence in rice was reported by number of workers [10-12].

Clustering pattern in the present study indicated that the genotypes collected from different places did not correspond to their geographical origin. The traditional tall varieties like N 22 (Uttar Pradesh), Blackgora (Bihar), Dular (West Bengal), Kalakeri (Orissa) and modern varieties like Annada, Heera, Neela, Sneha, Vandana, Vanaprabha and Kalinga-III of CRRI, Cuttack, Orissa; Rudra, Pathara, Shankar, Parijat, Subhadra, Ghanteswari, Udayagiri, Lalitgiri of OUAT, Bhubaneswar, Orissa; JD-6 and JD-13 of IARI, New Delhi; Annapurna of Kerala were in cluster I along with local collections from Phulbani,

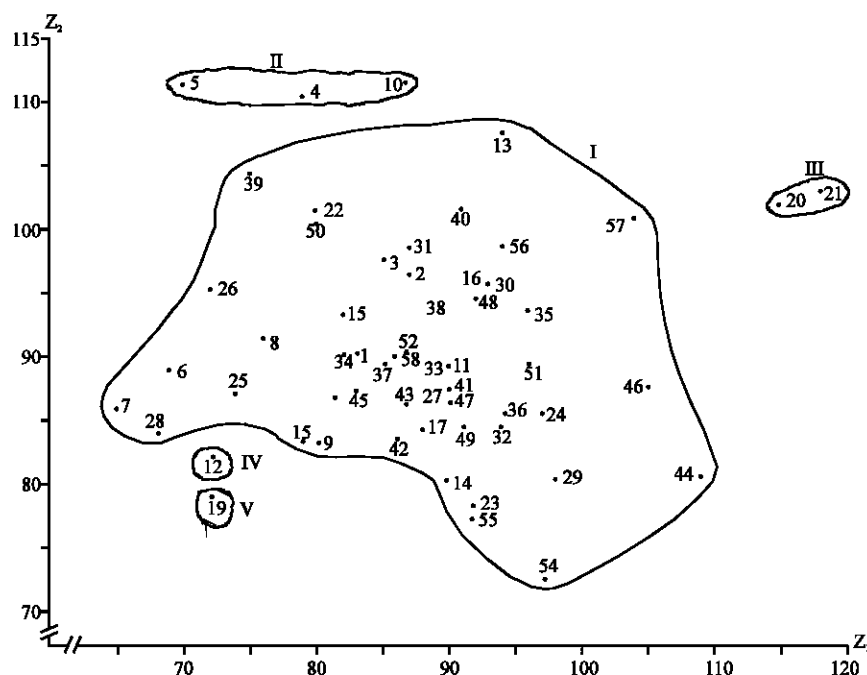


Fig. 1: Two dimensional representation of divergence of 57 rice genotypes pooled over years

Rayagada, Koraput, Malkangiri, Deogarh and Sundergarh districts of Orissa, indicating that no correspondence between clustering pattern and geographical origin. Similar results were also reported in rice by many workers such as [2, 13, 14].

The results obtained in the present study have great relevance to the future-breeding program of early duration rice varieties. In the present study, out of 32 local collections, 27 genotypes included in cluster I, 3 in cluster II and 2 in cluster III. It is apparently clear that the genotypes included in cluster I and II are having high intra- cluster distance. Member of the cluster having high genetic distance would produce superior segregants. Beside, inter crossing between members of clusters having high genetic distance is suggested for improvement of upland breeding program. Characters contributing maximum towards genetic divergence were observed to be L/B ratio, 1000 grain weight, grain length, grain yield and biological yield and would be useful as selection parameters for improvement of upland rice breeding program.

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