

## Genetic Divergence Analysis in Rice under Irrigated Conditions

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The nature and magnitude of genetic divergence were estimated in 134 rice germplasm accessions during *kharif* 2013 using Mahalanobis D<sup>2</sup> statistics. The genotypes were grouped into five clusters based on Euclidean cluster analysis. The pattern of distribution of genotypes into various clusters was random and independent of geographical origin or region of adoption indicating geographical diversity and genetic diversity were not related. Cluster means indicated considerable differences in the mean values of different traits. The genotypes of cluster II and cluster III exhibited high seed yield. The highest intra-cluster distance was observed among the genotypes, in cluster IV (12.19) followed by cluster III (11.03) and cluster V (10.90) indicating existence of wide genetic divergence among genotypes. Number of filled grains/panicle contributed highest towards divergence. The relative divergence of each cluster from other clusters displaced higher order of divergence between cluster IV and V followed by clusters II and V. The hybridization involving genotypes belong to these clusters is expected to give desirable segregants in rice breeding programmes.

**Key Words:** Clusters, Genetic divergence, Germplasm, Hybridization, Rice

### Introduction

Rice is the most important staple food grain and stands next to wheat in the global food grain production. India has the largest area under rice, about 44.6 million hectare area with a production of about 106.19 million tonnes (MoA, 2014). The germplasms found in Asia, America and Europe belong to *Oryza sativa*, while *O. glaberrima* in West Africa. *O. sativa* is a cultivated diploid species with 24 chromosomes of AA genome (Brar and Khush, 1986). The nature and magnitude of genetic improvement generally depend on the amount of genetic variability present in a population. The major thrust area for such genetic improvement depends on selecting efficient breeding system and identifying desirable parents in hybridization programmes. Genetic diversity plays an important role in plant breeding since progeny originating from diverse parents exhibit greater heterosis and provide broad spectrum of variability in segregating generations (Khush, 1974). Therefore, a meaningful classification of genotypes will enable the breeder to identify the best parents with wide genetic divergence and to utilize some of the selected diverse parents in the hybridization programme. In the present study, an attempt was made to classify and understand the nature and magnitude of genetic diversity.

### Materials and Methods

The experiment was carried out during *kharif* 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental seed material comprised 134 rice genotypes collected from International Rice Research Institute, the Philippines; National Bureau of Plant Genetic Research, New Delhi; Central Rice Research Institute, Cuttack; Narendra Dev University of Agriculture and Technology, Faizabad and National Research Centre on Plant Biotechnology, New Delhi (Table 1). The nursery was sown on June 9, 2013, and 21-day-old seedlings were transplanted in a randomized block design (RBD) with three replications. Each plot consisted of five rows of 1.5 m length with spacing 15 × 20 cm. The recommended package of practices were followed for raising good and healthy crop. Observations were recorded on, days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers/plant, panicle weight, total number of grains/panicle, filled grains/panicle, spikelet fertility percentage, test weight (g), kernel length (mm), kernel breadth (mm), kernel length/breadth ratio, kernel length after cooking (mm), grain elongation ratio and grain yield/plant. The analysis of variance was carried out for all the traits and the data were

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Table 1. List of 134 rice germplasm accessions and their collection site

Accession No.	Variety	Source	Accession No.	Variety	Source
1	HSUNG TIENG	IRRI, Philippines	68	IR 64	IRRI, Philippines
2	DULAR	IRRI, Philippines	69	SWARNA	IRRI, Philippines
3	FR13A	IRRI, Philippines	70	KASALATH	IRRI, Philippines
4	FR13B	IRRI, Philippines	71	IR 42	IRRI, Philippines
5	DHOLAMON 64-3	IRRI, Philippines	72	IR-73707-45-3-23	IRRI, Philippines
6	KARKATI 87	IRRI, Philippines	73	BARA SALI	NBPGR, New Delhi
7	JC 1	IRRI, Philippines	74	IR-36	NBPGR, New Delhi
8	JP 5	IRRI, Philippines	75	HUR-W-1	BHU, Varanasi
9	VANAN VELLAI	IRRI, Philippines	76	CHANGMAKA	NBPGR, New Delhi
10	NAALUMOLI KARUPPAN	IRRI, Philippines	77	CHOW HALA	NBPGR, New Delhi
11	ARC 614	IRRI, Philippines	78	BAGI BARDHANA	NBPGR, New Delhi
12	BIRPALA	IRRI, Philippines	79	CHANGMAN	NBPGR, New Delhi
13	BINULAWAN	IRRI, Philippines	80	BABARAKSHA KARA	NBPGR, New Delhi
14	MAPOI	IRRI, Philippines	81	JOHAINANG (WET)	NBPGR, New Delhi
15	MENYARHUNEI	IRRI, Philippines	82	BARACHIRAMARA	NBPGR, New Delhi
16	MUYAMBA	IRRI, Philippines	83	HUKKANNA KUMBALOA	NBPGR, New Delhi
17	PAIAM	IRRI, Philippines	84	HULTA BALUNGA (WILD)	NBPGR, New Delhi
18	PALENEMA	IRRI, Philippines	85	MEGHI	NBPGR, New Delhi
19	PATAIM	IRRI, Philippines	86	JOKHRU	NBPGR, New Delhi
20	PECALO	IRRI, Philippines	87	PANIKAKUA	NBPGR, New Delhi
21	TAGBA	IRRI, Philippines	88	CHUMANSAL-39	NBPGR, New Delhi
22	TIEBIMAH	IRRI, Philippines	89	JAHABHOG	NBPGR, New Delhi
23	GODA HEENATE	IRRI, Philippines	90	CHANG MUI	NBPGR, New Delhi
24	TEPEP	IRRI, Philippines	91	PANI DUBI	NBPGR, New Delhi
25	HEEN SULAI	IRRI, Philippines	92	MEGHRAJ	NBPGR, New Delhi
26	JAYMIS	IRRI, Philippines	93	ASAMIA	NBPGR, New Delhi
27	KALUWEE	IRRI, Philippines	94	CHARETSUK	NBPGR, New Delhi
28	MADAL	IRRI, Philippines	95	BAGA GOHA	NBPGR, New Delhi
29	MAHA DIKWEE	IRRI, Philippines	96	BARA RANGA	NBPGR, New Delhi
30	NCHEL PARAGAHAKALE	IRRI, Philippines	97	JAGANATHA BALLAVA	NBPGR, New Delhi
31	USA BATAPOLAAL	IRRI, Philippines	98	JALKANTHI	NBPGR, New Delhi
32	KOSHIHIKARI	IRRI, Philippines	99	CHUDI	CRRI, Cuttack
33	AUSBORO	IRRI, Philippines	100	MANOHAR SALI	CRRI, Cuttack
34	JALDUNGI	IRRI, Philippines	101	BABAI LACHHA	CRRI, Cuttack
35	NIRBOI	IRRI, Philippines	102	LUNISHREE	CRRI, Cuttack
36	PAKRIBUNA	IRRI, Philippines	103	MANDIRA	CRRI, Cuttack
37	VADAI	IRRI, Philippines	104	ASANA	CRRI, Cuttack
38	MARS	IRRI, Philippines	105	PANI DHAN-2	CRRI, Cuttack
39	CR 1009	IRRI, Philippines	106	SWARNA SUB-1	BHU, Varanasi
40	BUNTOK	IRRI, Philippines	107	BAD DHANA	CRRI, Cuttack
41	RITEK SIRENDAN MERA	IRRI, Philippines	108	ASHU BHAJNA	CRRI, Cuttack
42	AZUCENA	IRRI, Philippines	109	BAD GEDE	CRRI, Cuttack
43	HOURA KANI	IRRI, Philippines	110	PANIKEKEUA	CRRI, Cuttack
44	NALDAK	IRRI, Philippines	111	PANKEI	CRRI, Cuttack
45	BR 11	IRRI, Philippines	112	BAD JHARLI	CRRI, Cuttack
46	ZOGBUI	IRRI, Philippines	113	S-183	CRRI, Cuttack
47	SOSSON HONDON	IRRI, Philippines	114	SAMBHA SUB-1	NDUAT, Faizabad
48	VAN	IRRI, Philippines	115	JALNIDHI	NDUAT, Faizabad
49	KHAIYAN	IRRI, Philippines	116	GOTHAWA	NRCPB, New Delhi
50	LIU-TIAO-NU	IRRI, Philippines	117	KAJARAHAWA	NRCPB, New Delhi
51	MA-ZHAN(RAD)	IRRI, Philippines	118	RAJBHOG	NRCPB, New Delhi
52	MOUSSAYA	IRRI, Philippines	119	SINGHARA	NRCPB, New Delhi
53	KAOLACK	IRRI, Philippines	120	SATHI	NRCPB, New Delhi
54	NCS 348	IRRI, Philippines	121	KARIYWA	NRCPB, New Delhi
55	ZECHUM	IRRI, Philippines	122	MOTI	NRCPB, New Delhi
56	KARABONKA	IRRI, Philippines	123	SUGAPANKH	NRCPB, New Delhi
57	EMPING ARA	IRRI, Philippines	124	SARJOO-52	NRCPB, New Delhi
58	ROM RUNTIK	IRRI, Philippines	125	LALKA DHAN	NRCPB, New Delhi
59	LATSIKA	IRRI, Philippines	126	DUDHA LADU	NRCPB, New Delhi
60	SANG KHLA	IRRI, Philippines	127	S-148	CRRI, Cuttack
61	SANTI BAHN	IRRI, Philippines	128	S-177	CRRI, Cuttack
62	TAH TONE	IRRI, Philippines	129	S-138	CRRI, Cuttack
63	WAHNG	IRRI, Philippines	130	S-169	CRRI, Cuttack
64	SIPULUT PANDAN	IRRI, Philippines	131	S-141	CRRI, Cuttack
65	NANHI	IRRI, Philippines	132	S-155	CRRI, Cuttack
66	KARNAL LOCAL	IRRI, Philippines	133	KALA BUNDE	NBPGR, New Delhi
67	KHAO HLANON	IRRI, Philippines	134	KALA JOHA	NBPGR, New Delhi

subjected multivariate analysis following Mahalanobis's  $D^2$ -statistics (Mahalanobis, 1936) to measure the genetic divergence followed by the clustering of genotypes based on 16 characters following Tocher's method as described by Rao (1952).

## Results and Discussion

Analysis of variance revealed highly significant differences for all the characters studied, indicating a wide range of variation for all the 16 traits (Table 2). Based on the relative magnitude of  $D^2$  values of 134 genotypes, these were grouped into five different clusters. Cluster I consist of 68 genotypes forming the largest cluster followed by cluster II comprised 22 genotypes and cluster III had 21 genotypes, cluster IV contained 10 genotypes, cluster V comprising of 2 genotypes while 11 genotypes (Rom Runtik, Ncs 348, Ritek Sirendan Mera, Kaluwee, Manohar Sali, Jalkanathi, Chang Mui, Azucena, Muyamba, Meghi and Khaiyan) were ungrouped (Table 3). The genotypes included in a particular cluster indicated their close relationship among themselves as compared to genotype in other clusters. Therefore, it could be expected that genotype within a cluster were less

genetically different with each other, and were diverse from the genotype belonging to other clusters.

The highest intra-cluster distance was observed in cluster IV (12.19) followed by cluster III (11.03) and cluster V (10.90) while cluster I had lowest intra-cluster distance (Table 4). The highest inter-cluster distance was observed between cluster IV and cluster V (22.36) followed by cluster II and cluster V (21.85) and cluster I and cluster V (20.16) indicated that the hybridization between the most diverse genotypes would yield desirable segregates with the accumulation of favourable genes in the segregating generations. The lowest inter-cluster distance was recorded between cluster I and cluster IV (12.82) indicating close relationship and similarity for most of the characters of genotypes falling in these clusters. Such analysis was meant to avoid selection of parents from genetically homogenous clusters and to maintain a relatively broad genetic base. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents. Similar results of inter and intra cluster distances in rice were reported by Senapati and Sarkar (2005), Kuchanur *et al.* (2009) and Roy (2013).

**Table 2. Analysis of variance for 16 traits in 134 rice germplasm accessions**

Source of variation	Df	Mean sum of squares															
		DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	GER	GYP
Replicate	2	48.60	257.63	2391.04	246.13	37.78	1.88	2582.41	3094.59	1.6105	0.22	144.7	0.26	0.03	3.32	0.004	587.45
Treatments	133	2191.52**	2329.73**	1729.01**	23.65**	19.91**	1.12**	2981.16**	3501.09**	1.39**	0.196**	76.29**	15.26**	0.58**	2.19**	0.03**	128.71**
Error	266	34.39	40.07	60.05	1.89	0.43	0.02	16.60	19.69	0.03	0.01	0.67	2.717	0.02	0.1	0.0007	2.82

\*\*Significant at 1% level of significance.

DF= Days to 50% flowering; DM= Days to maturity; ET= Number of Effective tillers/plant; FG= Filled grains/panicle; GER= Grain elongation ratio; GYP= Grain yield /plant; KB= Kernel breadth; KL= Kernel length; KLAC= Kernel lenth after cooking; LB= Kernel length/breadth ratio;PH= Plant height; PL= Panicle length; PW= panicle weight; SF= Spikelet fertility percentage; TG= Total no. of grains/panicle; TW= Test Weight

**Table 3. Grouping of 134 rice germplasm accessions into five clusters by Tocher's method**

Cluster number	Name of germplasm	No. of accessions
I	Asamia, Ashu Bhajna, Babai Lachha, Bad Gede, Bad Jharli, Baga Goha, Bagi Bardhana, Bara Ranga, Bara Sali, Br 11, Buntok, Changmaka, Charetsuk, Chumansal-39, Cr 1009, Emping Ara, Fr13a, Goda Heenate, Houra Kani, Hukkana KumbAloa, Hultra Balunga(Wild), Ir-36, Ir-7307-45-3-23, Jaganatha Ballava, Jahabhog, Jaldungi, Jalnidhi, Jaymis, Jc-1, Johaineang(Wet), Kala Joha, Kaolack, Karabonka, Kasalth, Koshihikari, Latsika, Lunishree, Madal, Maha Dikwee, Mandira, Mapoi, Meghraj, Menyarhunei, Naldak, Nanhi, Nchel Paragahakale, Nirboi, Paiam, Pakribuna, Palenema, Pani Dubi, Panikakua, Panikekeua, Pankei, Pecalo, Santi Bahn, Sipulut Pandan, Sossion Hondon, Swarna Sub-1, Swarna, Tagba, Tah Tone, Tiebimah, Vadai, Van, Wahang, Zobgui	68
II	Babarakshakara, Chow Hala, Chudi, Dholamon 64-3, Dudha Ladu, Gothawa, Heen Sulai, Kajarahawa, Kala BuNde, Kariywa, Karkati 87, Lalka Dhan, Mars, Moti, Naalumoli Karuppan, Pani Dhan-2, S-141, S-148, Sarjoo-52, Singhara, Sugapankh, Usa Batapolaal,	22
III	Ausboro, Barachiramara, Binulawan, Dular, Hsung Tieng, Ir-64, Jokhru, Karnal Local, Khao Hlan On, Liu-Tiao-Nu, Ma-Zhan (Rad), Moussaya, S-138, S-155, S-169, S-177, S-183, Sang Khla, Sathi, Tetep, Zechum	21
IV	Arc614, Asana, Bad Dhana, Birpala, Changman, Fr 13b, Jp5, Rajbhog, Sambha Sub-1, Vanen Vellai,	10
V	Hur-W-1, Ir-42	2
Ungrouped	Azucena, Chang Mui, Jalkanathi, Kaluwee, Khaiyan, Manohar Sali, Meghi, Muyamba, Ncs 348, Ritek Sirendan Mera, Rom Runtik	11

**Table 4. Average intra and inter-cluster D2 values among five clusters of 134 rice germplasm accessions**

Cluster	I	II	III	IV	V
I	9.47	13.36	13.27	12.82	20.16
II		10.71	16.04	15.00	21.85
III			11.03	17.49	19.90
IV				12.19	22.36
V					10.90

(Figures in diagonal indicates intra cluster D value)

The cluster mean values showing a wide range of variation for all the characters were taken in the study (Table 5). Cluster II exhibited highest mean values for plant height, panicle length, panicle weight, filled grains/panicle, total number of grains/panicle, test weight and grain yield/ plant and lowest for number of effective tillers/ plant while Cluster I had the highest mean values for days to 50% flowering, days to maturity and kernel length after cooking. Similarly, cluster V exhibited highest mean values for number of effective tillers per plant, kernel length and length-breadth ratio while cluster III exhibited highest mean value for kernel breadth and lowest for filled grains/panicle. The cluster IV had highest mean value for spikelet fertility percentage and grain elongation ratio while lowest for kernel length after cooking. Thus, the accessions in cluster II, V, I and III seem to be quite promising for many of the traits which were studied. Distribution of highest and lowest mean values for different traits in distinct cluster indicated the traits contributing to the total divergence.

The contribution of characters towards the total genetic divergence is important in deciding the characters for selection. The present findings revealed that the filled grain/panicle, test weight, kernel length after cooking, days to 50% flowering and kernel length were the major

**Table 6. Relative contribution of 16 characters to genetic diversity**

Character	Times ranked 1 <sup>st</sup>	Contribution %
50% DF	803	9.01%
Days to maturity	320	3.59%
Plant height (cm)	227	2.55%
Panicle length (cm)	15	0.17%
Effective tiller	591	6.63%
Panicle weight (g)	414	4.65%
Filled grain	2665	29.91%
Total grain	9	0.10%
Kernel length (mm)	532	5.97%
Kernel breadth (mm)	74	0.83%
Test weight (g)	1907	21.40%
Yield /plant (g)	162	1.82%
Spikelet fertility%	5	0.06%
lb ratio	6	0.07%
KLAC (mm)	952	10.68%
Elongation ratio	229	2.57%

KLAC= Kernel length after cooking

contributing factors towards total divergence. Therefore, selection of genotypes would be more effective if it is based on the above said traits. Kole (2000) also reported that the traits such as kernel length, number of panicles/ plant, test weight and days to 50% flowering were the major contributors towards divergence. Similar results were obtained by Singh *et al.* (2011), Ovung *et al.* (2012) and Kumar *et al.* (2014). Clusters IV and V and Clusters II and V were diverse to each other therefore, selection of diverse accessions with desirable traits, and utilizing them in multiple crossing programmes, is expected to be effective in accumulation of favourable genes in segregating generations.

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**Table 5. Cluster mean values for 16 different traits**

Traits \ Cluster	50% DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	GER	GYP
I	145.43	180.77	125.99	22.00	7.91	2.11	87.83	98.47	6.20	2.32	20.67	89.06	2.70	8.28	1.34	15.05
II	122.80	162.50	143.60	24.64	7.38	3.10	137.43	154.07	6.23	2.43	23.25	89.04	2.59	8.07	1.29	20.99
III	97.05	128.73	126.02	23.06	10.32	2.33	71.71	80.38	6.30	2.47	23.73	89.07	2.62	8.19	1.30	18.04
IV	140.40	173.67	119.80	20.11	8.18	2.33	119.39	131.19	5.50	2.11	15.21	90.59	2.67	7.97	1.45	16.35
V	93.50	128.83	111.18	24.51	10.62	1.75	81.99	92.00	8.05	2.44	14.46	88.82	3.32	8.22	1.02	12.57
Mean	140.59	178.11	125.85	22.07	7.73	2.20	95.10	106.79	6.25	2.23	21.34	88.43	2.84	8.10	1.31	15.35

DF= Days to 50% flowering; DM= Days to maturity; ET= Effective tillers/plant; FG= Filled grains/panicle; GER= Grain elongation ratio; GYP= Grain yield /plant; KB= Kernel breadth; KL= Kernel length; KLAC= Kernel length after cooking; LB= Kernel length/breadth ratio; PH= Plant height; PL= Panicle length; PW= panicle weight; SF= Spikelet fertility percentage; TG= Total no. of grains/panicle; TW= Test Weight

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