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Assessment of genetic diversity among rice (*Oryza sativa* L.) genotypes for growth and yield characters

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Abstract
The present study was with aim to know genetic diversity among the rice genotypes for agronomical and yield traits. The present study comprising 60 germplasm (indigenous and exotic) of rice The results indicated that the sixty germplasm both indigenous and exotic were grouped into eight clusters based on the relative of D^2 values following Tocher's method of cluster formation. In Y_1 Cluster III is the largest cluster consisting of 21 genotypes while Cluster V & VI was the smallest with only a single genotype. In Y_2 Cluster II is the largest cluster consisting of 23 genotypes while Cluster III was the smallest with only a 10 genotype. And in Pooled Cluster II is the largest cluster consisting of 23 genotypes while Cluster IV was the smallest with only a 8 genotype. The maximum intra cluster distance (D = 510.68) was found in cluster VII and VIII consisting of 6 and 2 genotype in Y_1. The maximum intra cluster distance (D = 222.07) was found in cluster V and VIII consisting of 1 and 2 genotype in Y_2. The maximum intra cluster distance (D = 120.55) was found in cluster VI and VIII consisting of 1 and 1 genotype in Pooled. In the present study, maximum inter cluster distance was estimated between cluster VII and VIII ($\sqrt{D2}$ = 510.68) which was followed by clusters VII and VIII ($\sqrt{D2}$ =1941). Based on the rank totals, the characters which contributed maximum towards genetic divergence in the present studies were by number of seedling dry weight (g) (54.58) followed by root length (cm) (18.59), and shoot length (cm) (8.59) in Y_1. Reported in Y_2 seedling dry weight (g) (60.00) followed by root length (cm) (24.01), and shoot length (cm) (9.04). maximum contributed genetic divergence in the present field studies in Y_1 were by 100 –seed weight (52.43g) followed by plant height (24.18), grain / panicle (9.38), biological yield (7.80g), days to 50% flowering (2.77%), harvest index (2.15), panicle length (0.68 cm), tillers/plant (0.51), panicle bearing/ plant (0.11). Hence these traits could be focused for selection while improving seed yield and seed quality. On the basis of their greater inter cluster distance, high value of cluster mean and performance of the individual germplasms for the character, the germplasm could be used in improving seed yield and seed quality programme for improvement of different plant characters of the rice.

Keywords: Rice, genetic divergence, yield and seed traits

Introduction

Rice (*Oryza sativa* L., 2n= 24) belongs to the genus *Oryza*, tribe *Oryzeae* and family Gramineae, is one of the staple food and the most important cereal crop which contributes more to our food requirements annually. It is the second largest principal food crop in the world after wheat in India. It accounts for about 46 percent of total food grain production in the country. At the current rate of population growth (1.8 percent), rice requirement by 2020 would be around 125 million tons. The understanding of genetic architecture and direct and indirect selection parameters of agronomic ally important traits helps in deciding the type of variety to be developed and the breeding methodology to be followed in a particular situation. Although, the information on above aspects in rice is a available, but most of these studies are based on irrigated rice ecosystem and literature in context of upland, salinity and aromatic rices is meager. Therefore, further studies aimed at generating and comparing information on above aspects in rice are warranted to facilitate development of high yielding rice cultivars for above ecosystems. The cultivated rice belongs to genus *Oryza* and there are about 25 species of rice distributed in tropical, sub- tropical and warm temperate regions of the worlds. The *Oryza sativa* is divided in-to three sub-species, viz., indica, japonica and javonica. The importance of genetic diversity in selecting parents to recover transgressive segregates has been repeatedly emphasized by many workers (Arunachalam, 1981; Jatasara and Paroda, 1983). Information on the nature and degree of divergence provides a rational basis and helps the plant breeders in choosing suitable parents for realizing superior segregates in breeding programmes. Non-hierarchical Euclidean cluster analysis and Mahalanobis'D^2 analysis, serve

as a most potential tools for classification, are a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, are derived to represent the varieties in the graphical from and gives measurement of genetic divergence in terms of special distance.

Several literatures in respect of genetic variability, correlation, path analysis and genetic divergence in rice is available. However, the result of the earlier studies on such aspect are relevant only for materials and environment involved in the particular study due to their non-consistent nature and cannot be generalized. Therefore, studies on above aspect on the available germplasm are essential for successful utilization of germplasm resources for the development of superior rice variety.

Materials and Methods

The materials for the present experiment consisted of 60 rice genotypes along with four standard (check) variety viz., Type-3, Lalmati, NDR-2064, NDR-359 received from the genetic resource pool and different part of the through Crop Research Station (CRS) Masodha, Faizabad,. The details of genotype are given in Table 1.

These germplasms were grown in the The present investigation was carried out at the Crop Research Station (CRS) Masodha, Faizabad, and Student Instructional Farm of N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad and seed quality parameters will be tested in Seed Testing Laboratory of the Seed Technology Section, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.). during *Kharif* season of 2016 and *Kharif* 2017. The experiment was laid out in the Randomized Block Design with three replications. The inter and intra row spacing were maintained at 20×15cm. The recommended plant protection measures and agronomical practices were followed. The experimental data on various quantitative characters were recorded. Five plants from middle three rows of each plot were randomly sampled and the quantitative characters were recorded following actual measurement on each of the sampled plants and then averaged it out. The variables measured for quantitative characters were days to 50% flowering, days to maturity, plant height (cm), number of tillers/plant, number of panicles bearing tillers/plant, panicle length (cm), number of grains/panicle, biological yield (g), harvest Index, 1000-seed weight (g), seed yield/plant (g), seed moisture content (%), speed of germination (%), standard germination (%), shoot length (cm), root length (cm), seedling length (cm), seedling dry weight (g) and vigour index (VI-1). Mahalanobis (1928) D2 statistics was used to estimate genetic divergence among the 41 germplasms. The germplasms were grouped into clusters according to Tocher's methods by Rao (1952).

Results and Discussion

The result of D^2 analysis is presented in table. The study of genetic divergence among sixty genotypes of rice were carried out by using Manalanobis D^2 statistics'. In present investigation sixty genotypes of garden pea were grouped in seven distinct non- over lapping clusters. This indicated presence of considerable diversity in the genotypes. The major clusters in the above mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instances of grouping of genotypes of different origin or geographically of same region in same clusters were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity.

The clustering pattern of 64 genotypes under field condition showed that genotypes were grouped into eight different non-overlapping clusters. In Y_1, cluster III (21) highest number of genotypes followed by cluster-I (19), cluster-II (9) and cluster V&VI had only one genotype. In Y_2, cluster –II (23) had highest number of genotypes followed by cluster –I (21), cluster-III (10) and in pooled analysis cluster –II (23) had maximum number of genotypes followed by cluster-I (20) and cluster IV (8). However, minimum genotype (1) was counted in cluster V and VI during both the years and in pooled analysis.

The clustering pattern of 64 genotypes under laboratory condition showed that genotypes were grouped into eight different non-overlapping clusters. In Y_1, the cluster II containing maximum (35) genotypes followed by cluster I (10) and cluster III (8). In Y_2, cluster I & II had maximum genotypes (16) followed by cluster III (13) and cluster V (9). In pooled analysis cluster III had maximum (19) followed by cluster IV (15) and cluster I (8). However, minimum number of genotype was cluster VI and VIII containing only one genotype during both the years and in pooled analysis.

The intra and inter cluster distance under field condition, the cluster-V and VI showed minimum (0.00) intra cluster distance each during both the years and in pooled analysis. However, maximum intra cluster distance showed by cluster VII (49.41) in Y_1, cluster III (53.33) in Y_2 and cluster VII (33.75) in pooled analysis. Maximum inter cluster distance (510.68) was found between cluster VII and cluster VIII in Y_1, cluster V and cluster VIII (222.07) in Y_2 and between cluster VI and cluster VIII (120.55) in pooled analysis. While minimum inter cluster distance between cluster IV and cluster VI (26.56) in Y_1, between cluster IV and cluster VII (33.11) in Y_2 and between cluster I and cluster II (12.58) in pooled analysis under field condition. The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters while, lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. Similar finding were also recorded by Shiv-Datt and Mani (2003) and Chandra *et al.* (2007) [4].

The intra and inter cluster distance laboratory condition, the cluster-VI and VIII showed minimum (0.00) intra cluster distance each during both the years and in pooled analysis. However, maximum intra cluster distance showed by cluster III (12.09) in Y_1, cluster III (8.99) in Y_2 and cluster IV (3.47) in pooled analysis.

Maximum inter cluster distance (57.98, 61.98 and 120.55) was found between cluster III and cluster VIII in Y_1, Y_2 and in pooled analysis, respectively. While minimum inter cluster distance between cluster I and cluster VI (6.22) in Y_1, between cluster I and cluster IV (6.45) in Y_2 and between cluster V and cluster VI (1.66) in pooled analysis under field condition.

The cluster mean for different character are presented in table- 2. the highest cluster mean for speed of germination (%) was found in case of cluster VIII (19.74) followed by cluster III (19.65), cluster I (19.35), cluster IV (19.34), cluster II (19.26), cluster V (19.25), cluster VI (19.24), cluster VII (19.03) and lowest intra cluster mean for speed of germination (%) was recorded in case of cluster VII (19.03)

The cluster mean for different characters are presented in table-3. The highest cluster mean for standard germination (%) was found in case of cluster III (84.89) followed by cluster VI (84.33), cluster I (84.25), cluster IV (83.78), cluster II (83.51), cluster VII (83.67), cluster VIII (83.67), cluster V (82.83) and lowest intra cluster mean for standard germination (%) was recorded in case of cluster V (82.83).

The cluster mean for different characters are presented in table-4. the highest cluster mean for shoot length (cm) was found in case of cluster IV (13.75) followed by cluster VI (13.26), cluster II (12.91), cluster VIII (12.84), cluster VII (12.18), cluster I (11.91), cluster III (11.59), cluster V (10.91) and lowest intra cluster mean for shoot length (cm) was recorded in case of cluster V (10.91).

The cluster mean for different characters are presented in table-5. The highest cluster mean for root length (cm) was found in case of cluster VI (17.22) followed by cluster V (16.04), cluster VII (15.46), cluster VIII (15.03), cluster II (13.89), cluster III (12.08), cluster I (11.95), cluster III (10.92) and lowest intra cluster mean for root length (cm) was recorded in case of cluster III (10.92).

The cluster mean for different characters are presented in table-6. The highest cluster mean for seedling length (cm) was found in case of cluster VI (30.43) followed by cluster VII (28.01), cluster VIII (28.00), cluster VI (26.85), cluster V (26.81), cluster IV (25.21), cluster I (23.95), cluster III (23.72) and lowest intra cluster mean for seedling length (cm) was recorded in case of cluster III (23.72).

The cluster mean for different characters are presented in table-7. The highest cluster mean for seedling dry weight (g) was found in case of cluster VIII (0.33) followed by cluster VII (0.28), cluster IV (0.26), cluster II (0.21), cluster I (0.17), cluster VI (0.16), cluster V (0.15), cluster III (0.14) and lowest intra cluster mean for seedling dry weight was recorded in case of cluster III (0.14).

The cluster mean for different characters are presented in table-7. The highest cluster mean for seedling vigour index-1 was found in case of cluster VI (2567.46) followed by cluster VII (2343.36), cluster VIII (2342.66), cluster V (2233.40), cluster II (2242.41), cluster III (2013.38), cluster IV (2113.39), cluster I (2016.10) and lowest intra cluster mean for seedling vigour index-1 was recorded in case of cluster I (2016.10).

Percent contribution in genetic divergence in rice is presented in table – 7. The highest percent contribution in genetic divergence of rice was reported by seedling dry weight (g) (60.00) followed by root length (cm) (24.01), and shoot length (cm) (9.04).

The other four contribution were by seed moisture content (%) (4.46) followed by days to speed of germination (%), seedling length (cm) (0.68), standard germination (%). Based on estimates of percent contribution g), and seed moisture content (%), speed of germination (%), seedling length (cm) and standard germination (%), were found to contribute negligible. There were no contribution were by seedling vigour index-1.

Table 1: Details of genotypes included in experiment

S.N.	Germplasm		S.N.	Germplasm
1	Type -3		31	Badshah bhog
2	Lalmati	Checks varieties	32	Hazaar dana
3	NDR-359		33	Heera
4	NDR-2064		34	Tinpakani
5	Kalamadan		35	Dudhi
6	Naina		36	Binni
7	Ram gandha		37	Bakain
8	Son – kharcha		38	Nankawa
9	Karangi		39	Padhani
10	Joginiya		40	Mutra
11	Gujraj		41	Mazeera
12	Bazaar bang		42	Aguwari
13	Parson		43	Ghee bhat
14	Pahariya		44	Bee
15	Akatahawa –BBK		45	Raj muniya
16	Moti farm		46	Singul
17	Karahani white		47	Chingari
18	Sona chur		48	Ketaki
19	Ram bilas		49	Sukhawan
20	Ram bhog-1		50	Basahwa
21	Sakkar chinni		51	Mangla
22	Madhuri		52	Hari krishana
23	Rasi		53	Norin
24	Lal surya		54	TCA-52
25	Kabira		55	TCA-151
26	Sapana		56	IET-16719
27	Bagari Gorakhpur		57	IET-16717
28	Bhadhi black		58	IET-16724
29	Karahni		59	IET-16735
30	Ram kajara		60	IET-4673

Table 2: Clustering pattern of sixty genotypes of Rice on the basis of Mahalanobis 'D^2' statistics over two years and Pooled

Cluster number	Years	No. of genotypes	Genotypes
I	Y$_1$	19	Son- kharcha, Hari Krishna, Chingari, Rasi, Norin, Madhuri, Basahwa, Hazar dana, Bhadhi black, Kabira, Ghee bhat, Nankawa, Mazeera, Akatahaw- BBK, Lal surya, Joginiya, Gujraj, Bee, TCA-151.
	Y$_2$	21	Ram bilas, Ram bhog-1, NDR-2064, Sona chur, Moti farm, Akatahaw- BBK, Gujraj, Padhani, Hazar dana, Lal surya, Nankawa, Basahwa, Chingari, Ghee bhat, Heera, Son-kharcha, Madhuri, rasi, Jogininiya, Bazaar bang, Bhadhi black
	Pooled	20	Ram bilas, Ram bhog 1, NDR-2064,Moti farm, Sona chur, Aguwari, Gujraj, Joginiya, Padhani, Nankawa, Akatahaw-bbk, Son-kharcha, Hazar dana, Heera, Basahwa, Ghee bhat, Chingari, Lal surya, Rasi, Bazaar bang
II	Y$_1$	9	NDR-2064, Ram bilas, Ram bhog-1, Aguwari, Sona chur, Moti farm, Raj muniya, Dudhi, Kalamadan.
	Y$_2$	23	Tinpakani, IET-16735, IET-4673, Mazeera, Ketaki, IET-16719, Kabira, Mutra, TCA-151, Bee, Hari krishana, Binni, Bagari Gorakhpur, Sukhawan, Parson, Mangla, Naina, Ram ghandha, NDR-359, Norin, Karangi, Type-3, Aguwari
	Pooled	23	Tinpakani, IET-16735,IET-4673,Mazeera, Ketaki, Hari krishana,TCA-151, Bee, Mutra, Kabira, Norin, Madhuri, Bhadhi black Sukhawan, Bagari Gorakhpur, Binni, Parson, Naina, NDR-359, Ram ghandha, Mangla, Type-3, Karangi
III	Y$_1$	21	Tinpakan, IET-16735, IET- 4673, Ketaki, Heera, Bazeer bang, Bakin, IET-16719, Padhani, NDR-359, Mutra, Ram ghandh, Naina, Sukhawan, Mangla, Parson, Bagari Gorakhpur, Binni, IET-16717, Karangi, Type-3.
	Y$_2$	10	Lalmati, Karahni, Badshah bhog, Sapana, IET-16724, IET-16717, Singul, Pahariya, Kalamadan, Ram kajara
	Pooled	1	Badshah bhog
IV	Y$_1$	1	Badshah Bhog.

	Y₂	1	Dudhi
	Pooled	8	Lalmati, karahni, Sapana, IET-16724, Pahariya, Singul, IET-16717, TCA-52
V	Y₁	1	TCA-52.
	Y₂	1	TCA-52
	Pooled	1	Dudhi
VI	Y₁	1	IET-16724.
	Y₂	1	Bakain
	Pooled	1	Bakain
VII	Y₁	6	Lalmati, Karahni, Pahariya, Sapana, Singul, Ram kajara,
	Y₂	1	Raj muniya
	Pooled	5	Karahani white, Sakker chini, Raj muniya, Kalamadan, IET-16719
VIII	Y₁	2	Karahani – white, Sakkar chini
	Y₂	2	Karahani –white, Sakkar chini
	Pooled	1	Ram kajara

Table 3: Clustering pattern of sixty genotypes of Rice on the basis of Mahalnobis 'D²' statistics over two years and Pooled

Cluster number	Years	No. of genotypes	Genotypes
I	Y₁	10	Sapana, Basahwa, Tinpakani, NDR-359, Badshah bhog, chingari, IET-4673, Ketaki, Joginiya, Parson,
	Y₂	16	Rasi, Norin, Hari krishana, Ghee bhat, Mutra, Mangla, IET-16724, Bagari Gorakhpur, Bee, Padhani, Raj muniya Ram ghandha, IET-16735, Mazeera, Kabira, NDR-2064
	Pooled	8	Bakain, Mazeera, IET-16735, Ghee bhat, NDR-2064, Ram ghandha, Singul, Bee
II	Y₁	35	Bazaar bang, Moti farm, Bee, Padhani, Mazeera, Mutra, Ghee bhat, IET-16735, Ram ghandha, Singul, Karahani white, Hazar dana, Son kharcha, Nankawa, Ram bilas, Bhadhi black, NDR-2064, Ram bhog-1, Gujraj, Karangi, Sona chur, IET-16719, Dudhi, Akatahaw-bbk, TCA-52, Bakain, Sukhawan, IET-16724, Sakker chini, Mangla, Rasi, Pahariya, Kabira, Norin, Bagari Gorakhpur
	Y₂	16	Akatahaw-bbk, IET-16719, Sakkar chini, Bhadhi black, Dudhi, Karangi, Sona chur, Gujraj, Nankawa, Karahani-white, Hazar dana, Son-kharcha, Ram bilas, Ram bhog 1, Madhuri, Singul
	Pooled	14	Karahani- white, Dudhi, Bhadhi black, Ram bhog 1, Nankawa, Sona chur, Gujraj, Son-kharcha, Hazar dana, Ram bilas karangi, IET-16719, Akatahaw-bbk, Sakker chini
III	Y₁	8	Hari krisana, TCA-151, Ram kajra, Raj muniya, Karahni, Type-3, IET-16717, Binni
	Y₂	13	Parson, Ketaki, Badshah bhog, Heera, IET-4673, Joginiya, Tinpakani, Sapana, Basahwa, Chingari, NDR-359, Lalmati, Lal surya
	Pooled	19	Rasi, Norin, IET-16724, Mutra, Mangla, Padhani, Bagari Gorakhpur, Kabira, TCA-52, Ram kajara, IET-16717, Hari krishana, Moti farm, Raj muniya, Karahni, Sukhawan, Bazaar bang, TCA-15,1, Type-3
IV	Y₁	1	Lal surya
	Y₂	1	TCA-52
	Pooled	15	Sapana, Basahwa, Tinpakani, IET-4673, Badshah bhog, Joginiya, Chingari, Ketaki, Parson, NDR-359, Lalmati, Heera, Lal surya, Madhuri, Naina
V	Y₁	1	Madhuri
	Y₂	9	Bakain, TCA-151, Sukhawan, IET-16717, Moti farm, Bazaar bang, Karahni, Ram kajara, Type-3
	Pooled	1	Binni
VI	Y₁	1	Lalmati
	Y₂	1	Binni
	Pooled	1	Pahariya
VII	Y₁	3	Naina, Aguwari, Kalamadan
	Y₂	3	Kalamadan, Naina, Aguwari
	Pooled	1	Aguwari
VIII	Y₁	1	Heera
	Y₂	1	Pahariya
	Pooled	1	Kal;amadan

Y₁=2016 and Y₂=2017

Table 4: Intra-cluster group mean for 8 clusters in Rice over two years and pooled

Cluster number	Years	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers/ plant	panicles bearing tillers/ plant	Panicle length (cm	grains/ panicle	Biological yield (g)	Harvest Index	1000-seed weight (g)	Seed yield/plant (g)
I	Y₁	91.23	120.05	107.45	14.23	9.07	23.67	118.63	70.62	39.36	23.34	27.70
	Y₂	91.62	120.84	112.51	13.37	8.35	23.41	121.10	65.50	38.20	24.30	24.86
	Pooled	91.16	120.28	114.96	13.25	8.59	23.68	120.82	68.63	38.12	24.74	25.99
II	Y₁	95.81	124.96	135.44	12.47	8.85	24.08	125.76	78.63	36.31	25.53	28.46
	Y₂	91.83	120.94	106.48	14.26	9.04	23.52	117.89	87.41	39.74	23.15	34.72
	Pooled	92.32	121.10	106.33	14.05	9.33	23.56	122.64	80.59	40.02	22.53	32.26
III	Y₁	92.59	121.21	105.43	13.57	9.86	23.62	126.09	73.79	40.23	23.54	29.77
	Y₂	91.03	120.20	112.47	13.34	8.65	21.70	121.68	63.68	38.36	17.06	24.21
	Pooled	85.50	115.00	92.40	15.75	9.33	21.97	110.15	64.75	41.64	17.37	27.04
IV	Y₁	86.33	115.33	93.23	15.07	9.47	22.37	113.87	76.79	42.33	17.50	32.50
	Y₂	97.00	126.33	151.89	9.60	8.20	24.09	128.67	83.17	35.61	26.40	29.70
	Pooled	89.60	118.81	107.79	14.40	9.45	22.10	124.85	67.62	39.81	17.65	27.11

V	Y₁	95.33	125.33	90.42	17.83	12.63	24.39	173.73	89.85	41.95	20.97	37.67
	Y₂	93.33	122.00	88.60	19.53	9.53	23.62	181.20	94.98	42.78	20.77	40.63
	Pooled	97.67	127.17	153.00	9.90	8.03	24.10	132.43	83.53	35.17	26.32	29.40
VI	Y₁	84.67	113.00	107.90	10.67	9.87	21.01	80.53	46.59	38.94	18.57	18.10
	Y₂	99.00	127.00	94.86	11.93	7.93	22.85	84.03	49.76	42.04	27.67	20.96
	Pooled	98.67	127.17	96.41	12.17	8.92	23.39	86.65	49.44	41.65	27.72	20.62
VII	Y₁	89.94	119.94	119.36	12.64	8.54	22.27	137.94	70.38	39.20	15.69	28.11
	Y₂	105.67	134.67	137.05	17.80	8.67	23.13	168.17	96.96	36.13	28.03	35.06
	Pooled	97.23	126.67	126.28	14.10	9.10	22.08	132.28	84.18	36.71	31.05	31.01
VIII	Y₁	93.00	121.67	138.00	13.43	8.90	20.75	119.87	86.71	35.74	38.48	31.11
	Y₂	91.83	120.33	135.14	13.63	8.80	20.97	134.68	79.36	35.95	36.85	28.50
	Pooled	97.17	125.83	138.45	9.63	7.15	23.24	159.43	71.42	35.57	11.90	25.46

Table 5: Intra-cluster group mean for 8 clusters in Rice over two years and pooled

Cluster number	Years	Seed Moisture Content (%)	Speed of Germination (%)	Standard Germination (%)	Shoot Length (cm)	Root Length (cm	Seedling Length (cm	Seedling Dry Weight (g)	Seedling Vigour Index
I	Y₁	11.77	18.93	83.07	13.59	11.25	24.93	0.26	2069.78
	Y₂	12.14	19.71	84.48	11.55	11.90	23.51	0.14	1985.84
	Pooled	11.86	19.35	84.25	11.91	11.95	23.95	0.17	2016.10
II	Y₁	11.78	19.29	83.65	12.35	12.91	25.29	0.17	2115.27
	Y₂	11.86	19.32	83.90	12.89	13.83	26.80	0.21	2249.17
	Pooled	11.81	19.26	83.51	12.91	13.89	26.85	0.21	2242.41
III	Y₁	11.38	19.80	86.08	10.75	12.46	23.19	0.13	1995.56
	Y₂	11.71	19.51	84.26	14.29	10.92	25.24	0.27	2129.68
	Pooled	11.79	19.65	84.89	11.59	12.08	23.72	0.14	2013.38
IV	Y₁	12.87	19.69	85.00	12.77	9.05	21.85	0.21	1862.63
	Y₂	13.15	18.34	82.00	11.52	12.90	24.57	0.13	2015.24
	Pooled	11.84	19.34	83.78	13.75	11.45	25.21	0.26	2113.39
V	Y₁	12.63	19.53	84.33	11.53	12.70	24.35	0.24	2053.52
	Y₂	11.37	19.63	85.33	12.02	12.06	24.13	0.14	2059.41
	Pooled	11.11	19.25	82.83	10.91	16.04	26.81	0.15	2233.40
VI	Y₁	11.23	19.12	84.00	14.41	12.89	27.33	0.31	2296.65
	Y₂	11.41	19.04	83.00	10.39	16.34	26.75	0.15	2219.10
	Pooled	11.29	19.24	84.33	13.26	17.22	30.43	0.16	2567.46
VII	Y₁	11.66	19.30	83.67	12.64	15.00	27.75	0.30	2321.43
	Y₂	11.57	19.76	84.22	12.81	15.42	28.49	0.30	2399.38
	Pooled	11.13	19.03	83.67	12.18	15.46	28.01	0.28	2343.36
VIII	Y₁	11.42	19.74	82.67	14.27	11.12	23.73	0.29	1961.84
	Y₂	11.37	20.22	85.67	13.42	17.78	31.29	0.15	2680.09
	Pooled	11.27	19.74	83.67	12.84	15.03	28.00	0.33	2342.66

Table 6: Percent contribution of 11 characters towards total genetic divergence in Rice over two years and pooled

S.N.	Characters	Contribution (%)		
		Y₁	Y₂	Pooled
1	Days to 50% Flowering	2.77%	4.07%	4.69 %
2	Days to Maturity	0.00%	0.00%	0.00%
3	Plant Height cm	24.18%	24.46%	25.85%
4	Tillers/ Plant	0.51%	0.40%	0.73%
5	Panicle Bearing/ Plant	0.11%	0.23%	0.23%
6	Panicle Length cm	0.68%	0.68%	1.53%
7	Grains/ Panicle	9.38%	18.31%	11.30%
8	Biological Yield/ Plant	7.80%	16.38%	7.06%
9	Harvest Index	2.15%	1.58%	1.07%
10	1000 Seed Weight	52.43%	33.90%	47.57%
11	Seed Yield / Plant	0.00%	0.00%	0.00%

Y₁=2016 and Y₂=2017

Table 7: Percent contribution of 8 characters towards total genetic divergence in Rice over two years and pooled

S.N.	Characters	Contribution (%)		
		Y₁	Y₂	Pooled
1	Seed Moisture Content (%)	7.91%	3.73%	4.46%
2	Speed of Germination (%)	1.86%	2.49%	1.19%
3	Standard Germination (%)	4.01%	0.34%	0.62%
4	Shoot Length (cm)	8.59%	11.47%	9.04%
5	Root Length(cm)	18.59%	31.53%	24.01%
6	Seedling Length (cm)	1.64%	0.73%	0.68%
7	Seedling Dry Weight (g)	54.58%	49.27%	60.00%
8	Seedling Vigour Index	2.82%	0.45%	0.00%

Y₁=2016 and Y₂=2017

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