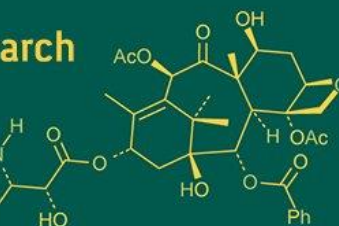
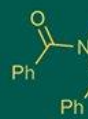


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Vikrant, Soyal Kumar
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

LK Gangwar
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Anant
Department of Genetics and Plant
Breeding, Rani Lakshmi Bai Central
Agricultural University, Jhansi, Uttar
Pradesh, India

J Lokesh
Department of Genetics and Plant
Breeding, Agriculture College,
Acharya N G Ranga Agricultural
University, Mahanandi, Andhra
Pradesh, India

Mukesh Kumar
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Lavi Dabas
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Kosh Mahajan
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Kushagra Yadav
Department of Agricultural
Biotechnology, Sardar Vallabhbhai
Patel University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Monu
Department of Vegetable Science,
Sardar Vallabhbhai Patel University
of Agriculture & Technology, Meerut,
Uttar Pradesh, India

Corresponding Author:
Vikrant, Soyal Kumar
Department of Genetics and Plant
Breeding, Sardar Vallabhbhai Patel
University of Agriculture &
Technology, Meerut, Uttar Pradesh,
India

Study of divergence in non-basmati rice (*Oryza sativa* L.) for grain yield during reproductive stages under drought condition

Vikrant, Soyal Kumar, LK Gangwar, Anant, J Lokesh, Mukesh Kumar, Lavi Dabas, Kosh Mahajan, Kushagra Yadav and Monu

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Abstract

Genetic diversity among 53 rice genotypes was assessed under control and reproductive-stage heat stress conditions using Mahalanobis D² statistics. Significant variation was observed for all traits, indicating the presence of substantial genetic variability. Tocher's clustering grouped the genotypes into six clusters under both environments, with Cluster V comprising the highest number of genotypes. Greater inter-cluster than intra-cluster distances indicated wide genetic divergence, with the maximum divergence observed between Clusters III and VI under both conditions, suggesting their potential use in hybridization programmes. Cluster mean analysis identified Cluster VI as superior for biological and grain yield under control conditions, whereas Cluster V recorded the highest grain yield under drought stress. Flag leaf dimensions, panicle length, effective tillers, fertility percentage, and total grains per panicle were the major contributors to genetic divergence. These findings provide valuable information for selecting genetically diverse parents for developing high-yielding and drought-tolerant rice cultivars.

Keywords: Genetic diversity, Mahalanobis D² statistics, rice

Introduction

Rice is a monocotyledon plant, chromosome number 2n = 24, with ~ 430 MB genome size. Rice belongs to the Gramineae (Poaceae) grass family in cereals. In tropical, subtropical and warm temperate temperatures all across the world, there are 22 wild and 2 cultivated species in the genus *Oryza*. The two cultivars are *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* originated in South East Asia (Vaughan, 1994) [11] while *Oryza glaberrima* is indigenous to West Africa (Niger River delta). *Oryza glaberrima* is only grown in a few locations such as West Africa, whereas *Oryza sativa* is produced all over the world. The *Oryza sativa* is further divided into the indica, japonica, and javanica subspecies. Short-grained, sticky Japonica rice is generally farmed in dry regions. A non-sticky, long-grained kind of rice called indica is frequently grown in fields that are submerged. Both varieties are available in a broad variety (RABBANI 2010) [9]. Rice is a starchy cereal grain and highly self-pollinating crop with Southeast Asian origins. More over half of the world's population relies on rice as a staple diet, making up more than 20% of all calories consumed. Rice is the second most extensively grown cereal grain in the world. The world's most important food crop is rice (*Oryza sativa*).

The amount of genetic variability present in the population is the primary requirement for developing high yielding rice varieties outperforming present day cultivated varieties. Thus, studies on genetic diversity to know the nature and degree of divergence for yield traits will help in designing efficient breeding programme by facilitating the selection of elite parental lines which can be further used in hybridization programme to develop superior and high yielding varieties. Also cluster analysis offers a best method for selecting parents to realize high heterosis to strengthen hybrid breeding programme in rice. With this background the present study was carried out to understand and classify the magnitude and nature of genetic diversity among the studied germplasm lines.

2. Materials and Methods

2.1 Experimental materials: The experimental material consists of 49 non-basmati rice lines with broad genetics base along with 4 non-basmati lines as check varieties were used for the study the name of 53 genotypes is given in the table 1.

2.2 Formula to calculate Genetic Divergence

The genetic divergence in fifty-three genotypes of rice was estimated using Mahalanobis D² statistic (1936) following Rao (1952) ^[10].

$$D^2 = \lambda^{ij} \delta I \delta J$$

Where,

λ^{ij} = reciprocal matrix to the common dispersion matrix.

δI = Difference between the mean values of the two populations for Ith character δJ = Difference between the mean values of the two populations for Jth character. The parameter D² can be estimated as D² static (Rao, 1952) ^[10]

$$D^2 = \sum \sum \delta IJ, di dJ = \text{Sample estimate of } XIJ$$

Where,

δIJ = Sample estimates of X^{ij} Sample estimates of δI

$di dJ$ = Sample estimates of δJ

Unstandardized and correlated variables (mean value of character) are transformed into standardized uncorrelated variables. After transformation X₁, X₂, ...X_p variable (unstandardized and correlated) becomes Y₁, Y₂.....Y_p variable (standardized and uncorrelated variables). This transformation was done according to the square root of Dwyer, described by Rao (1952) ^[10]. The variable transformations is done because this formula requires the inversion of n order of determinants and then evaluation of (n + 1)/2 term whose sum is D².

Inter and intra-cluster distances were calculated by Tocher's method as suggested by Rao (1952) ^[10] to form the clusters. This criterion was based on the concept that populations belonging to the same cluster should, on average, have lower D² value than populations from separate clusters.

3. Results

3.1 Genetic Divergence

D² statistics which is the most important and potent biometrical tool in quantifying the degree of divergence in various crop plants was used in the present investigation. D² statistics utilizes multivariate distribution of natural variation to construct the dispersion matrix.

The analysis of variance revealed significant differences among genotypes for all the characters studied and thereby, indicating existence of a good amount of genetic variability. All the genotypes differed from each other with respect to these characters (Table 2&5). Cluster analysis of genotypes was performed based on all characters using Tocher method and then groups were compared.

3.2 Clustering Pattern

Cluster analysis, based on all the studied traits, divided the genotypes into six clusters in control condition and six clusters in stress conditions (Table 4&7). Among the six clusters, cluster V consisted maximum number of genotypes

(16) followed by cluster I consist 12 genotypes and cluster II, III, IV all consisted 7 genotypes and VI cluster consist 4 genotypes. whereas in stress condition, among the six clusters, cluster V consisted maximum number of genotypes (14) followed by cluster I consist 12 genotypes and III consist 8 genotypes, cluster II and IV each consist 7 genotypes and cluster VI consist 5 genotypes.

3.3 Clustering Distance

In control condition the intra and inter cluster average distances among six clusters were variable according to the result represented in (Table 3).

Intra cluster distance ranged from 3.731 to 3.085 and 3.805 to 3.097 in control and stress conditions, respectively. (Table 3 & 6) whereas the highest intra-cluster distance was recorded for cluster III (3.731) followed by cluster VI (3.704), cluster V (3.221), cluster II (3.163), cluster IV (3.092), and cluster I (3.025) in control condition. Maximum intra cluster distance was observed in cluster III (3.805) followed by cluster VI (3.463), cluster I (3.427), cluster V (3.214), cluster IV (3.113), cluster II (3.097) in stress condition (Table) indicating wide genetic variability within the genotypes of these clusters. The highest inter-cluster distance was observed between cluster III and VI (5.392), followed by cluster I and VI (5.267), cluster II and III (4.671), cluster II and V (4.514), cluster II and VI (4.444), cluster III and IV (4.204), cluster V and VI (3.868), cluster III and V (3.79), cluster II and IV (3.77), cluster I and IV (3.737), cluster I and II (3.674), cluster I and III (3.632), cluster I and V (3.282) cluster IV and V (3.053) in control condition, while in stress condition the highest inter-cluster distance was observed between cluster III and VI (6.856), followed by cluster I and VI (6.597), cluster IV and VI (5.186), cluster II and VI (5.087), cluster II and III (4.834), cluster V and VI (4.775), cluster III and IV (4.301), cluster III and V (3.946), cluster I and V (3.816), cluster I and III (3.722), cluster I and II (3.533), cluster I and V (3.435), cluster IV and V (2.798) indicating wider genetic diversity among the genotypes between these groups.

3.4 Cluster Mean

A comparison of the mean values of different clusters for nineteen traits has been presented in (Table 2&5). Considerable differences in cluster mean values were evident for all the characters studied. The present study revealed that cluster I had highest mean value for 1000-seed weight (19.90), hulling percentage (77.66), milling percentage (64.91) and grain length (6.89) in control condition indicating directly towards better yield potential while, Cluster II had noticed highest mean value for days to 50 percent flowering, harvest index (28.94). Cluster III had highest mean value for number of effective tillers per plant (7.98), grain width (2.44) in control condition indicating directly towards better yield potential in control condition while, cluster IV had noticed highest mean value for plant height (96.58), fertility percentage (87.15). Cluster V noticed highest mean value for panicle length (21.65) and cluster VI had noticed highest mean value for flag leaf width (1.19), number of unfilled grains per panicle (31.06), number of filled grains per panicle (173.68), total number of grains per panicle (204.64), grain width (2.44), biological yield per plot (2630.27), grain yield per plot (625.17) under control condition.

Under stress condition, cluster I had highest mean value for flag leaf width (1.15), fertility percentage (90.03), 1000 seed weight (19.96), hulling percentage (73.86) and grain length (6.68) while, cluster II had high mean value for days to 50% flowering (134.52), number of effective tillers per plant (7.14), harvest index (26.37). Cluster IV had noticed highest mean value for plant height (88.60), grain width (2.83). Cluster V had highest mean value for panicle length (18.16), flag leaf length (25.09), grain yield per plot (424.44) while, cluster VI had exhibited high mean value for number of unfilled grains per panicle (18.41), number of filled grains per panicle (112.96), total number of grains per panicle (134.04), milling percentage (60.61), biological yield per plot (2119.66).

4. Discussion

The importance of identifying and selecting genetically diverse plant materials using discriminant functions was first emphasized by Fisher (1936) [4]. Among various multivariate techniques, Mahalanobis D² analysis has been recognized as a reliable and accurate method for estimating genetic divergence based on multiple quantitative traits. However, its effectiveness depends on the stability of the D² measure under different environmental conditions. Earlier studies suggested that genetic diversity has often been associated with geographical or ecological variation (Joshi and Dhawan, 1966) [6], although genetic drift, natural selection, and human-mediated selection across different agroecological regions can generate greater diversity than geographical separation alone. Arunachalam (1977) [2] highlighted that genetic divergence is an effective criterion for identifying well-defined populations and selecting diverse parents in crop improvement programmes. Murty and Arunachalam (1966) [8] demonstrated several advantages of D² analysis. The method utilizes a dispersion matrix that reflects the natural variation among traits, distinguishes genotypic and environmental variability through replicated observations, and assigns self-weighted importance to each character based on its contribution to total variation, thereby minimizing selection bias. Furthermore, D² analysis enables simultaneous evaluation of a large number of genotypes and traits with computational efficiency.

In the present investigation, 53 rice genotypes were evaluated using Mahalanobis D² statistics based on 16 quantitative traits under both control and reproductive-stage drought stress conditions. The genotypes were grouped into six clusters in each environment, indicating substantial genetic divergence. The clustering pattern confirmed that geographical origin alone is not a reliable indicator of genetic diversity, supporting the usefulness of Mahalanobis D² analysis for identifying genetically diverse parents irrespective of their origin.

Under control conditions, Cluster V contained the highest number of genotypes (16), followed by Cluster I (12), Clusters II, III and IV (7 each), and Cluster VI (4). In stress conditions, Cluster V again contained the maximum number of genotypes (14), followed by Cluster I (12), Cluster III (8), Clusters II and IV (7 each), and Cluster VI (5). In both environments, inter-cluster distances were greater than intra-cluster distances, indicating broad genetic diversity among clusters. The highest intra-cluster distance was recorded in Cluster III (D² = 3.731) under control conditions and Cluster III (D² = 3.805) under stress conditions, indicating greater variability within these clusters.

Cluster mean analysis further revealed substantial variation among clusters for yield and yield-related traits. Under control conditions, Cluster VI recorded the highest biological yield per plot (2630.27) and grain yield per plot (625.17), Cluster III exhibited the highest number of effective tillers per plant (7.98) and grain width (2.44), whereas Cluster V recorded the highest panicle length (21.65) and flag leaf length (25.96). Under Drought stress, Cluster VI showed the highest biological yield per plot (2119.66) and total number of grains per panicle (134.04), Cluster II recorded the highest number of effective tillers per plant (7.14) and days to 50% flowering (134.52), while Cluster V exhibited the highest panicle length (18.16) and flag leaf length (25.09). These findings are consistent with earlier reports by Banumathy *et al.* (2010) [3], Arivoli *et al.* (2009) [1], and Hosan *et al.* (2010) [5].

Table 1: List of Germplasms

S. No.	Germplasms
1	Daftri-621
2	CR Dhan 300
3	CRR 759-11-B-1
4	Anjali
5	Til Kormel Mutant-1
6	NVSR 781
7	Bhata Mahsuri Mutant-1
8	RYT 3844
9	Ad 18006
10	MTU 1363
11	CSR 189-11-80
12	Gontra Bidhan 3
13	RYT 3936
14	Narendra 57
15	Luchai Mutant-1
16	CRAC 3998-128-1
17	RDR 1934
18	DRR Dhan 45
19	KPS 6251
20	JR 12
21	JGL37180
22	NVSR 2842
23	NDR 359
24	CRR 635-254
25	BPT 3059
26	CRR 668-20
27	Lalat
28	Co-51
29	Vandana
30	Sahabnagi Dhan
31	Savitri Sub-1
32	BRRI Dhan-45
33	Tatep
34	BRRI Dhan-356
35	Anang
36	Kimad
37	Pat GS-70
38	Kamboka
39	SR-26B
40	B. kesar
41	Tilcol-43 (Til 43)
42	Kaley
43	Pycol-20 (Py-20)
44	Yellow Basmati
45	Pat GS-28
46	Putige
47	Tilcol-661
48	Bina Dhan-8
49	Chirang Sub-1
50	Burma-B
51	Gomti Than
52	Solumphiki
53	BL-4 CL05
	Total = 53

Table 2: Cluster mean MAHALANOBIS D² analysis under normal condition

Cluster		Days to 50% Flowering	Plant Height (cm)	Panicle length	Number of effective tillers/hills	Flag leaf length (cm)	Flag leaf width (cm)	No. of unfilled grain per panicle	Number of filled grain per panicle	Total number of grains per panicle	Fertility percentage (%)	1000-seed weight (g)	Hulling percent (%)	Milling percent (%)	Grain length (cm)	Grain width (cm)	Biological yield/plot	Harvest index (%)	Grain yield/plot (g)
I	Mean	103.81	77.72	19.30	7.89	19.60	0.97	12.71	78.83	91.71	86.83	19.90	77.66	64.91	6.89	2.33	2153.76	23.94	507.02
	±SE	14.24	8.62	1.48	0.93	2.14	0.10	3.64	10.86	11.09	2.12	3.22	3.22	4.88	0.64	0.31	516.94	6.10	132.04
II	Mean	130.16	73.07	17.55	7.91	19.13	1.02	16.76	116.09	132.53	86.29	15.67	76.88	61.25	5.41	2.39	2015.19	28.94	554.80
	±SE	13.63	11.39	0.99	0.70	1.88	0.12	4.98	21.46	19.23	1.93	2.61	3.81	4.25	0.43	0.42	531.28	8.67	105.82
III	Mean	91.18	89.52	19.91	7.98	22.58	0.96	16.55	65.37	83.06	80.45	17.67	76.57	59.78	5.36	2.44	1837.09	16.07	293.45
	±SE	13.22	9.97	1.70	1.57	2.20	0.05	7.90	14.36	11.11	6.77	4.71	2.86	6.79	0.62	0.48	456.17	3.97	105.45
IV	Mean	120.98	96.58	20.13	6.25	23.54	1.15	12.70	100.33	113.42	87.15	17.47	74.48	60.34	5.83	2.90	2073.85	25.39	515.10
	±SE	15.83	12.95	1.98	0.80	1.71	0.13	1.74	19.87	19.99	2.91	3.38	3.23	5.12	0.83	0.19	229.26	6.95	93.03
V	Mean	100.76	89.37	21.65	6.61	25.96	1.10	18.94	94.18	112.77	82.49	18.82	76.28	60.27	6.37	2.43	2310.25	26.41	595.36
	±SE	9.84	11.17	1.40	0.95	3.55	0.11	3.49	10.77	11.50	3.11	2.54	4.45	5.53	0.61	0.35	447.77	5.00	98.48
VI	Mean	113.85	92.81	20.74	6.80	24.36	1.19	31.06	173.68	204.64	83.30	14.13	75.86	63.95	5.38	2.44	2630.27	24.39	625.17
	±SE	15.79	6.48	1.63	1.16	1.45	0.31	9.94	37.19	30.77	5.34	2.65	3.47	3.48	0.36	0.44	428.40	5.20	62.73

Table 3: Inter and intra distances under normal condition

Clusters	I	II	III	IV	V	VI
I	3.085					
II	3.533	3.163				
III	3.722	4.834	3.731			
IV	3.816	3.683	4.301	3.092		
V	3.435	4.271	3.946	2.798	3.221	
VI	6.597	5.087	6.856	5.186	4.775	3.704

Table 4: Number of genotypes in each cluster under normal condition

Clusters	No of genotypes	Genotypes
I	12	CRR-759-11-B-1, RYT-3844, CSR-189-11-80, RYT-3936, Narendra-57, Luchai mutant-1, BRRI Dhan-45, Tatep, B. kesar, Pat GS-28, Bina dhan-8, Chirang Sub-1,
II	7	Gontra Bidhan-3, CRAC-3998-128-1, BPT-3059, Savitri Sub-1, Tilcol-43, Yellow Basmati, Burma-B
III	7	Daftri-621, Anjali, AD-18006, CRR-635-254, Vandana, Kamboka, Kaley
IV	7	JGL-37180, Pat GS-70, SR-26-B, Putige, tilcol-661, Solumphiki, BL-4 CL-05
V	16	Til Kormel Mutant-1, CRR Dhan-300, NVSR-781, MTU-1363, RDR-1934, DRR Dhan-45, NVSR-2842, NDR-359, CRR-668-20, Lalat, CO-51, Sahabhangi Ddan, BRRI Dhan-356, Anang, Pycol-20, BL-4 CL-05
VI	4	Bhata Mahsuri Mutant-1, KPS-6251, JR-12, Kiamd

Table 5: Cluster mean MAHALANOBIS D² analysis under drought condition

Cluster		Days to 50% Flowering	Plant Height (cm)	Panicle length	Number of effective tillers/hills	Flag leaf length (cm)	Flag leaf width (cm)	No. of unfilled grain per panicle	Number of filled grain per panicle	Total number of grains per panicle	Fertility percentage (%)	1000-seed weight (g)	Hulling percent (%)	Milling percent (%)	Grain length (cm)	Grain width (cm)	Biological yield/plot	Harvest index (%)	Grain yield/plot (g)
I	Mean	109.26	71.92	16.24	6.58	18.67	1.15	7.77	66.83	74.26	90.03	19.96	73.86	58.47	6.68	2.28	1849.81	20.23	370.91
	±SE	13.21	6.72	1.17	0.78	2.32	0.86	1.89	10.05	10.27	1.90	2.64	2.49	4.48	0.51	0.30	361.15	3.24	78.99
II	Mean	134.52	66.85	14.96	7.14	17.82	0.97	9.59	95.39	104.01	89.27	15.18	72.40	58.39	5.30	2.33	1558.23	26.37	399.02
	±SE	14.38	10.51	0.83	0.65	1.71	0.12	1.85	20.58	20.92	1.91	2.58	2.87	2.42	0.43	0.42	332.33	7.49	93.93
III	Mean	95.47	79.10	16.55	6.64	20.91	0.88	10.53	56.68	67.79	84.47	16.73	72.19	56.36	5.47	2.36	1343.96	15.96	209.31
	±SE	12.12	11.59	1.12	0.93	2.33	0.08	6.06	16.03	14.49	6.48	4.37	2.15	5.90	0.87	0.45	304.35	3.19	45.13
IV	Mean	125.38	88.60	16.92	5.62	21.66	1.11	8.26	84.34	94.54	89.39	16.90	69.65	54.77	5.74	2.83	1669.06	23.36	381.86
	±SE	15.82	12.97	1.49	0.62	1.59	0.16	1.45	21.86	22.72	2.50	3.32	2.61	3.93	0.75	0.18	179.70	6.10	66.19
V	Mean	103.73	82.83	18.16	5.88	25.09	1.00	12.42	73.87	86.78	85.40	18.49	72.20	58.23	6.27	2.40	1768.40	24.66	424.44
	±SE	8.79	11.09	1.39	0.62	4.37	0.11	2.16	10.99	13.05	2.46	2.46	2.36	5.32	0.58	0.35	364.60	5.12	77.47
VI	Mean	118.54	84.23	17.50	6.01	22.89	1.10	18.41	112.96	134.04	86.55	13.77	71.69	60.61	5.16	2.30	2119.66	19.65	406.70
	±SE	14.63	5.42	1.04	0.68	1.54	0.25	4.03	41.04	42.28	4.17	2.38	2.48	4.05	0.35	0.41	390.38	3.62	37.52

Table 6: Inter and intra distances under drought condition

Clusters	I	II	III	IV	V	VI
I	3.427					
II	3.674	3.097				
III	3.632	4.671	3.805			
IV	3.737	3.77	4.204	3.113		
V	3.282	4.514	3.79	3.053	3.214	
VI	5.267	4.444	5.392	4.225	3.868	3.463

Table 7: Number of genotypes in each cluster under drought condition

Clusters	No of genotypes	Genotypes
I	12	Til Kormel Mutant-1, RYT 3844, MTU 1363, CSR 189-11-80, RYT 3936, RYT 3936, BRRI Dhan-45, Tatep, B. Kesar, Pat GS-28, Bina Dhan-8,
II	7	Gontra Bidhan-3, CRAC-3998-128-1, BPT-3059, Savitri Sub-1, Tilcol-43, Yellow Basmati, Burma-B
III	8	Daftri-621, Anjali, AD-18006, Narendra-57, CRR-635-254, Vandana, Kamboka, Kaley
IV	7	JGL-37180, Pat GS-70, SR-26B, Putige, Tilcol-661, Gomati Than, Solumphiki21
V	14	Anjali, NVSR-781, RDR-1934, DRR Dhan-45, NVSR-2842, NDR-359, CRR-668-20, Lalat, CO-51, Sahabhagi Dhan, BRRI Dhan-356, Anang, Pycol-20, BL-4 CL-05
VI	5	CR Dhan-300, Bhata Mahsuri Mutant-1, KPS-6251, JR-12, Kimad

5. Conclusion

The genotypes were divided into six clusters under control conditions and stress conditions using Mahalanobis D^2 statistics and the Tocher technique. The highest inter-cluster distance was observed between cluster III and VI, followed by cluster I and VI, cluster II and III, cluster II and V, cluster II and VI, cluster III and IV, cluster V and VI, cluster III and V, cluster II and IV, cluster I and IV, cluster I and II, cluster I and III, cluster I and V, Cluster IV and V in control condition, while in stress condition the highest inter-cluster distance was observed between cluster III and VI, followed by cluster I and VI, cluster IV and VI, cluster II and VI, cluster II and III, cluster V and VI, cluster III and IV, cluster III and V, cluster I and V, cluster I and III, cluster I and II, cluster I and V, cluster IV and V indicating wider genetic diversity among the genotypes between these groups.

References

1. Arivoli V, Saravanan K, Prakash M. A study on D^2 analysis in rice. International Journal of Plant Sciences, Muzaffarnagar. 2009;4(1):157-160.
2. Arunachalam V. Heterosis for characters governed by two genes. Journal of Genetics. 1977;63(1):15-24.
3. Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D, *et al.* Genetic diversity analysis of rice germplasm lines for yield attributing traits. Electronic Journal of Plant Breeding. 2010;1(4):500-504.
4. Fisher RA. Statistical methods for research workers. 1936.
5. Hosan SM, Sultana N, Iftakharudduala KM, Ahmed MNU, Mia S. Genetic divergence in landraces of Bangladesh rice (*Oryza sativa* L.). The Agriculturists. 2010;8(2):28-34.
6. Joshi AB, Dhawan NL. Genetic improvement in yield with special reference to self-fertilizing crops. 1966.
7. Mahalanobis PC. A note on the statistical and biometric writings of Karl Pearson. Sankhyā: The Indian Journal of Statistics (1933-1960). 1936;2(4):411-422.
8. Murty BR, Arunachalam V. The nature of divergence in relation to breeding systems in some crop plants. Indian Journal of Genetics and Plant Breeding. 1966;26:188-198.
9. Rabbani MA, Masood MS, Shinwari ZK, Shinozaki KY. Genetic analysis of basmati and non-basmati Pakistani rice (*Oryza sativa* L.) cultivars using microsatellite markers. Pak J Bot. 2010;42(4):2551-2564.
10. Rao CR. Advanced statistical methods in biometric research. 1952.
11. Vaughan DA. The wild relatives of rice: a genetic resources handbook. 1994.