

Assessment of Morphometric Diversity for Yield and Yield Attributing Traits in Rice (*Oryza sativa* L.) for Tolerance to Heat Stress

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation entitled "Assessment of morphometric diversity for yield and yield attributing traits in rice (*Oryza sativa* L.) for tolerance to heat stress" was carried out with objective of assessing genetic divergence in 200 germplasm of rice for eleven characters at ICRIAT, Patancheru, Hyderabad. The genotypes were grouped into fifteen clusters in Tocher's method, cluster analysis and principal component analysis, out of the 11 characters studied, number of grains per panicle, plant height, pollen viability and spikelet fertility contributed 96.73 per cent of the total divergence and these traits were found to be important potent factors for genetic differentiation in genotypes. Principal component analysis identified five principal components, which contributed for 78.66 percent % of cumulative variance. The overall results of the study revealed that crossing using the genotypes under cluster V and XI and cluster XI and XIII could be exploited by hybridization programme to yield good recombinants because they had maximum inter cluster distance and possessing high genetic diversity for the characters viz. panicle length, number of

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grains per panicle and single plant yield. The genotypes of cluster I, II, IV, VI, VII, VIII, XI, XII and XIII showed high spikelet fertility percentage. Hence the genotypes of these clusters can be used in breeding programmes for development of heat tolerant varieties. Euclidean² method indicated that genotypes of cluster III and IX exhibited high spikelet fertility percentage which can be utilized in development of heat tolerant cultivars. The results of principal component analysis revealed that genotypes of cluster I, cluster IV, cluster V, cluster VIII, cluster IX, cluster XI, cluster XII and cluster XV exhibited highest spikelet fertility percentage. Hence, the genotypes of the clusters can be used in breeding programmes for the development of heat tolerant varieties.

Keywords: Genetic diversity; clusters; D^2 statistic; rice.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most important staple food crop for more than 60 per cent of the global population and forms the cheapest source of food energy and protein. By origin, the crop is native to South East Asia with two cultivated (*Oryza sativa* and *Oryza glaberrima*) and 22 wild species. It belongs to the genus *Oryza* of grass family *poaceae*. The crop is cultivated under a wide range of agro-ecological situations. Although it is widely adoptable the crop is sensitive to high temperatures. Globally, it is grown in an area of 162.71 m ha with an annual production of 741.47 m t and productivity of 4556 kg ha⁻¹. It is the most important food crop of India with world ranking first in area (43.85 m ha), second to China in production. In India, rice is cultivated in an area of 43.49 m ha with an annual production of 104.40 m t and average productivity of 2400 kg ha⁻¹. In Telangana, it covers an area of 1.04 m ha with a production of 3.04 m t tonnes and average productivity of 2913 kg ha⁻¹ [1]. Heat waves are expected to be more intense and frequent in the future, which could jeopardize more rice areas. Therefore, any further increases in mean temperatures or of short episodes of high temperatures during sensitive stages, may be supra optimal and reduce grain yield. Genetic diversity is the basis for any crop improvement programme. The hybrids involving the parents with more diversity among them are expected to exhibit higher amount of heterotic expression and broad spectrum of variability in segregating generations. Mahalanobis D^2 analysis is useful tool to assess the genetic divergence among population. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distances [2]. It is a useful tool in studying the nature and cause of diversity prevalent in the available germplasm. It provides a measure of magnitude of divergence between biological population and

relative contribution of each component character to the total divergence.

2. MATERIALS AND METHODS

The experimental material comprised of two hundred germplasm of rice (*Oryza sativa* L.) grown in Augmented RBD at IIRR Farm, ICRISAT, Patancheru, Hyderabad, Telangana, India, during *Rabi* 2014-2015. The recommended agronomic and plant protection measures were followed in order to raise a normal crop. Observations on eleven different quantitative characters viz., days to 50% flowering, days to maturity, plant height, panicle length, number of tillers per hill, number of productive tillers per hill, number of grains per panicle, spikelet fertility, 1000 grain weight, pollen viability and single plant yield were recorded on five randomly selected competitive plants for each genotype except for days to 50% flowering and days to maturity where data is recorded on plot basis during various phenophases of the crop. Mean values from the five randomly selected plants for each genotype were averaged and expressed as the mean of the respective character and considered for statistical analysis. Genetic diversity was estimated as per Mahalanobis D^2 statistics and the grouping of genotypes into different clusters was done using the Tocher's method [3]. The criterion used in clustering by this method is that any two varieties belonging to the same cluster should at least on an average show a similar D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form [4]. Canonical variate analysis was used to compare the clustering pattern obtained by Mahalanobis D^2 statistic. The canonical roots vectors were calculated to present the genotypes in the graphical form The Inter cluster and intra cluster distances and contribution of each character to the

total divergence were also estimated. For statistical analysis, Windostat Version 9.2 software package was used.

3. RESULTS AND DISCUSSION

Analysis of variance for the experiment involving a set of 200 germplasm lines of rice for all the characters revealed highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement. Similar results were also reported by [5]. Based on D^2 values, the genotypes were grouped into fifteen clusters using Tocher's method. The dendrogram of the 200 genotypes presented in Fig. 1. Out of the fifteen clusters obtained, cluster IX was the largest with 46 genotypes followed by cluster II (38), cluster IV (34), cluster XIV (28), cluster III (17), cluster I and V (9), cluster XI (7), cluster V (6) and the remaining clusters (VI, VII, VIII, X, XII and XIII) are solitary. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural or human selection for diverse adaptive complexes. These genotypes may be very unique and useful in breeding point of view. The clusters IX, II, IV and XIV together included 146 genotypes reflecting narrow genetic diversity among them. The narrow genetic diversity may be attributed to similarity in the base material from which they have been evolved. The numbers of genotypes in each cluster with the genotypes were presented in the Table 1. The clustering pattern observed in the present study revealed that, genetic diversity was not necessarily parallel to geographic diversity. Genotypes evolved in the same area were grouped into different clusters [6].

3.1 Intra and Inter Relation of Clusters

The average D^2 values within (intra) and between (inter) clusters are given in Table 2 and Fig. 2. The inter cluster distances were higher than the average intra cluster distances, which indicated wide diversity among the genotypes of different groups than those of the same cluster. Similar results were reported in the studies of Hoque et al. [7]. Maximum differences among the genotypes within the same cluster were shown by cluster XV (4555.49) followed by cluster I (377.09), cluster XI (2433.02), cluster XIV (2395.25), cluster V (1604.39), cluster IV (1234.22), cluster IX (1209.23), cluster III

(916.36), cluster II (661.30) and cluster I (377.09). Solitary clusters (VI, VII, VIII, X, XII and XIII) showed zero intra cluster distances. Lowest intra cluster value for cluster I indicated that the genotypes included in the group showed closeness between them as compared to the genotypes included in cluster XV which showed maximum divergence within the group. It was reported that genotypes with in a cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance with regard to yield *per se*, provided that there is an adequate complementation [8]. The inter cluster D^2 values ranged from 212.13 to 18118.28. Minimum inter cluster D^2 values were observed between cluster VI and VII (212.13) followed by cluster VI and cluster VIII (392.67) indicating the close relationship among genotypes included in these clusters. Maximum inter cluster D^2 values were observed between cluster V and XI (18118.28) and cluster XI and XIII (16896.00). Thus, it can be inferred that genotypes in these clusters are genetically diverse and may give rise to high heterotic response. Similar results were reported by Jagadish et al. [9], Sabesan et al. [10], Baradhan et al. [11], Karthikeyan et al. [12], Venkanna et al. [13], Bhati et al. [14]., Devi et al. [15], Abhinav Sao and Preeti Singh [16] and Priya et al. [17]. Hence the crosses between the genotypes falling in cluster V (DOM SOFID, CPAU -12, NERICA-L-49, NERICA 14, MRC 603-383, WAB96-1-1, AZUCENA, DOMZARD, IR 50.) and cluster XI (BALILLA, HHZ 17 Y16 Y3 Y1, HHZ 12 SALB Y1 SAL1, HHZ 5 Y3 SAL2 SUBI, HHZ 5 DT 1 DT 1, ARC 15210, HHZ 12 SAL 8 Y1 Y2), cluster XI (BALILLA, HHZ 17 Y16 Y3 Y1, HHZ 12 SALB Y1 SAL1, HHZ 5 Y3 SAL2 SUBI, HHZ 5 DT 1 DT 1, ARC 15210, HHZ 12 SAL 8 Y1 Y2.) and cluster XIII (NAN-GUANG-ZHAN) could be exploited by hybridization programme for obtaining the desirable segregants with high potential. Based on cluster means, the important clusters are cluster VII for days to 50% flowering, days to maturity and number of productive tillers per hill. Cluster XIII for panicle length. Cluster III for number of tillers per hill. Cluster VI for spikelet fertility, cluster VIII for pollen viability, cluster X for 1000 grain weight, cluster XI for number of grains per panicle and single plant yield Thus, involving the genotypes of outstanding mean performance from these clusters in the crosses will be useful in the development of varieties with high yield and other desirable traits. Their segregating generations are also likely to yield good recombinants for economic traits.

3.2 Contribution of Different Characters towards Divergence

The contribution of different characters towards the genetic diversity is presented in Table 4 and Fig. 4. Number of grains per panicle (ranked first 11325 times out of 19900 total numbers of combinations) contributed 56.91 percent to the divergence of genotypes. This was followed by plant height (15.57%) by 3099 times, pollen viability (14.11%) by 2807 times, spikelet fertility (10.14%) by 2018 times, days to maturity (1.38%) by 275 times, days to 50% flowering (0.91%) by 181 times, single plant yield (0.65%) by 129 times, number of tillers per hill (0.24%) by 48 times, 1000 grain weight (0.05%) by 10 times, number of productive tillers per hill (0.03%) by 5 times, panicle length (0.02%) by 3 times ranked least, contributed very less towards divergence. The characters contributing maximum to the divergence were given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization. The results revealed that number of grains per panicle, plant height, pollen viability and spikelet fertility have contributed more towards divergence, so the direct selection for these traits would be helpful as evident from the number of times these traits appeared or ranked first during contribution to diversity. These results are in conformity with the reports given by earlier workers [18-25].

3.3 Principal Component Analysis or Canonical Variate Analysis

Group constellations were also independently developed by using Principal Component Analysis (PCA) to verify grouping obtained through D^2 statistics in two and three-dimensional graph forms. The eigene values, percent variance, per cent cumulative variance and factor loading of different characters studied are given in Table 5. In canonical variate analysis, the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variation produced by these characters. The five vectors accounted for 78.66 per cent of the total variability produced by all the characters under study. The first canonical vector (PC I) accounted for 25.62 percent of the total variability followed by second vector (PC II) accounted 17.89 percent, vector III (PC III) which accounted for 13.79 percent total variance, vector IV (PC IV) which accounted for 12.66 percent total variance and vector V (PC V) accounted for 8.68 percent total variance.

3.4 Canonical Graph

The principal factor scores of the canonical vectors for the five roots PC I (Z_1), PC II (Z_2), PC III (Z_3), PC IV (Z_4) and PC V (Z_5) are presented in Table 6. The mean scores of the first two canonical vectors were used to obtain graphical depiction of the genetic distance of the 200 genotypes. Using these scores, all the genotypes (numbers assigned to them) were plotted for PC I and PC II which cumulatively explained 43.52 percent variability and accounted for the most important yield contributing characters. The scatter plot of PC scores of the first two PC axes is presented in Figs. 5 & 6. The canonical root analysis in the present study accounted for 78.66 percent. For getting clear association of two-dimensional representation of variation, the first three canonical roots should be more than 95 percent [26]. On the contrary, the three canonical vectors as a whole contributed only for 57.31 percent towards genetic diversity because of which discernible overlapping which was observed in group constellations of canonical vectors. Most of the entries accumulated towards the left side of the PC II axis. Along the PC I axis, most of the entries accumulated towards the middle of the axis which accounts for the traits viz., single plant yield, number of grains per panicle and spikelet fertility with positive contribution towards divergence.

3.5 Distribution Pattern of Genotypes on Canonical Graph

The plot of PC I - PC II accounting for 43.52 per cent variation showed clear differentiation of genotypes according to their cluster membership. Genotypes belonging to common clusters have fallen nearer to each other and vice versa. Cluster VIII was largest comprising of 20 genotypes followed by cluster V, XI and XIII (18), cluster X and XII (17), cluster II and III (16), cluster I (12), cluster IX (11), cluster IV and XV (9), cluster VI (8), cluster XIV (7) and cluster VII (4). The clustering pattern of genotypes by PCA was shown in Table 7.

3.6 Mean Performance of the Clusters

Mean values of clusters for yield contributing characters were presented in Table 8. From the data, it can be concluded that considerable differences existed for all the characters studied. The data indicated that days to 50% flowering was lowest in cluster I (94.70 days) and

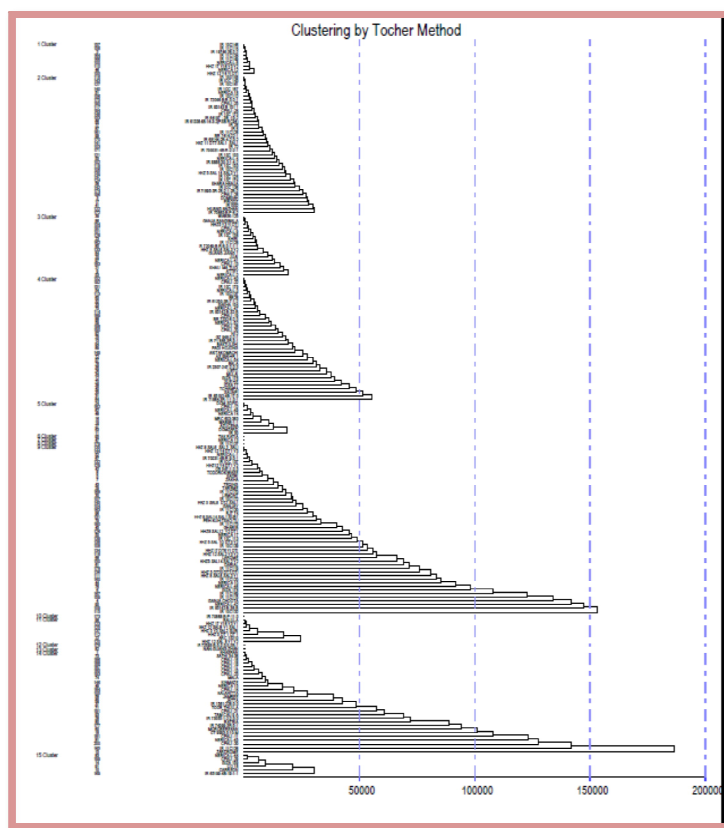


Fig. 1. Clustering of two hundred genotypes of rice employing Tocher’s method

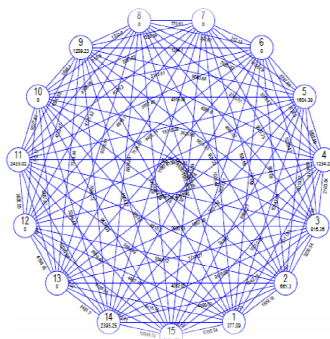


Fig. 2. Statistical distances among two hundred genotypes of rice by Tocher’s method (Not to the scale)

highest in cluster VIII (111.40 days). Days to maturity was lowest in cluster I (124.42 days) and highest in cluster VIII (141.45 days). Plant height was lowest in cluster XI (86.66 cm) and highest in cluster III (100.38 cm). Panicle length was highest in cluster VIII (23.84 cm) and the lowest in cluster I (19.64 cm). Highest number of tillers per hill were observed in cluster IX (18.27) whereas lowest in cluster VII (13.50). Number of

productive tillers per hill was recorded highest in cluster IX (14.67) and lowest in cluster VII (10.17). Highest number of grains per panicle were recorded in cluster IV (167.97) and lowest in cluster VI (55.83). Spikelet fertility was recorded highest in cluster IX (88.14 %) and lowest in cluster XIV (26.52%). 1000 grain weight was highest in cluster V (21.04 g) and lowest in cluster IX (16.86 g). Pollen viability was highest

Table 1. Clustering pattern among two hundred genotypes of rice (*Oryza sativa* L.) by Tocher's method

Cluster	Number of Genotypes	Genotypes
I	9	IR 10C146, IR 11C114, IR 19746-28-2-2, IR 11C134, IR 11C149, NERICA-L-8, HHZ 17 Y16 Y3 Y2, NERICA 12, HHZ 12 Y4 YI DTI.
II	38	IR 10C108, IR IOC 143, IR 10C161, IR 10C 167, NERICA 18, IR 10C112, IR 72046-B-R-3-2-1, CPAU -25, IR 83143 B 151 1, CPAU -24, IR 10C 173, IR 64197 - 3B -15-2, IR 61336-4B-14-3-2(PSB RC94), IR 28, IR 6, IR 11C126, BR 7414-22-1, IR 68144-2B-4-2-3-2, HHZ 11 DT7 SAL1 SAL1, IR 72, IR 700031-4B-R-2-2-1, IR 10C 103, NERICA-L-4, IR 8866-30-3-1-4-2, IR 10C 153, IR 10C110, HHZ 5 SAL 14 SAL2 Y1, IR 10C 126, IR 10C 174, KHARA HANJA, IR IOC 136, IR 71895-3R-26-2-1-2B-2, CPAU -26, DOMSIAH, FIROOZ, IR1552, HUANG ANZHAN, IR 70865-B-P-6-2.
III	17	WAB56-125, GANJA RANGWALA, HHZ5 Y3 YI DTI, CPAU -27, NERICA-L-9, IR 10C 138, KHIRI, IR 11C128, IR 72049-B-R-8-3-1-1-1, HHZ 8 SAL6 SAL3 Y2, GUANG JIANG 1, JIJAI, ARC 15210, CPAU -13, KHAU MA TUOI, ATTEY, NERICA-L-2.
IV	34	IR 10C 103, CPAU -22, IR 10C 179, NERICA-L-3, IR 10C137, BR26, IR 61250-3B-7-1-2, SAKHA 104, NERICA-L-47, IR 83142-B-32-B, CPAU -19, BR 7232-6-2-3, NERICA-L-52, CPAU -28, CPAU -20, N12, GZ 948-2-2-1, IR 71 866-3R-3-1, BAKTULSHI, PADI HOJONG, AKITAKOMACHI,, AS 996-HR 1, NERICA-L-54, BALA, IR 2307-247-2-2-3, LIETO, MULAI, GIZA 176, XUE HE, IDSA 77, TCHAMPA, SAUNFI, IR 65192-4B-17-3, IR 71864-3R-1-1-3-1.
V	9	DOM SOFID, CPAU -12, NERICA-L-49, NERICA 14, MRC 603-383, WAB96-1-1, AZUCENA, DOMZARD, IR 50.
VI	1	TAK RATIA
VII	1	NERICA 13
VIII	1	IR 11C127
IX	46	HHZ 8 SAL6 SAL3 SALI, HHZ 12 Y4 DT1 Y3, NERICA-L-1, IR 70031-4B-R-9-3-1, IR IOC 157, HHZ12 Y4 DT1 Y2, CR 547-1-2-3, TODOROKIWASE, SADRI, ZAKHA, TEQING, TAREME, IR 11C170, LEMONT, IR 10C172, HHZ 5 SAL8 DTZ SAL1, GANJAY, IR 11C130, RJT 74, HHZ 8 SAL14 SAL1 SUB1, PEH-KUH-TSAO-TU, IR 11C173, GHARIB, HHZ8 SAL12 Y2 DT1, NERICA 17, IR 10C 113, HHZ 5 SAL 10 DT3 Y2, IR 10C139, HHZ I7 DT6 YI DTI, HHZ 12 SAL2 Y3 Y2, LAROME, HHZ5 SAL14 SAL2 Y2, DARIAL, IR 11C119, HHZ 5 DT20 DT2 DTI, HHZ 8 SAL6 SAL3 Y1, IR 11C120, NERICA 10, NERICA-L-46, GIZA 178, IR 11C169, IR 11C115, GANJA CHOOTA, NERICA-L-42, IR 83142-B-36-B, IR 10C132. IR 70868-B-P-11-3
X	1	IR 70868-B-P-11-3
XI	7	BALILLA, HHZ 17 Y16 Y3 Y1, HHZ 12 SALB Y1 SAL1, HHZ 5 Y3 SAL2 SUBI, HHZ 5 DT 1 DT 1, ARC 15210, HHZ 12 SAL 8 Y1 Y2.
XII	1	IR 72593-B-3-2-3-3-2B-1
XIII	1	NAN-GUANG-ZHAN
XIV	28	KHASRAN, SATHI 34-36, CPAU -16, CPAU -18, CPAU -17, CPAU -15, CPAU -23, MALA, KINMAZE, NERICA 15, CPAU -14, KALAHITTA, JAMREE, JATTA, IR 1561-228-3-3, TOOR THULLA, CPAU -21, TAM CAU 9 A, IR 73055-1-2-2-3-3, RATRIA, IR 74099-3R-5-1, MOROBEREKAN, CT 9993-5-10-M, CPAU -11, NERICA-L-45, CPAU -30, IR 11C138, ZARDROME.
XV	6	NERICA-L-44, CPAU -29, GIZA 159, CO 18, CARREON, IR 65199-4B-19-1-1.

Table 2. Average intra (bold) and inter cluster D² and D values for fifteen clusters in two hundred genotypes of rice (*Oryza sativa* L.)

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV
Cluster I	377.09 (19.42)	1979.16 (44.49)	6651.81 (81.56)	5011.81 (70.79)	10543.06 (102.68)	665.71 (25.80)	1003.44 (31.68)	1055.76 (32.49)	1578.96 (39.74)	3768.20 (61.39)	2464.49 (49.64)	4467.15 (66.84)	9115.74 (95.48)	9017.57 (94.96)	6365.54 (79.78)
Cluster II		661.30 (25.72)	3250.54 (57.01)	1879.92 (43.36)	6219.07 (78.86)	881.08 (29.68)	926.09 (30.43)	908.23 (30.14)	2033.94 (45.10)	1846.55 (42.97)	6510.20 (80.69)	3362.12 (57.98)	4282.02 (65.44)	4989.00 (70.63)	8227.71 (90.71)
Cluster III			916.36 (30.27)	2103.54 (45.86)	1994.76 (44.66)	5239.46 (72.38)	5673.76 (75.32)	4682.02 (68.43)	5615.33 (74.94)	1616.22 (40.20)	13675.29 (116.94)	2920.53 (54.04)	1717.01 (41.44)	2478.56 (49.79)	8342.78 (91.34)
Cluster IV				1234.22 (35.13)	3805.99 (61.69)	3122.30 (55.88)	3313.43 (57.56)	2763.57 (52.57)	4086.80 (63.93)	2420.96 (49.20)	11076.83 (105.25)	4169.46 (64.57)	1857.48 (43.10)	3425.10 (58.52)	10010.35 (100.05)
Cluster V					1604.39 (40.05)	8747.66 (93.53)	9156.79 (95.69)	7920.92 (89.00)	8680.68 (93.17)	4315.06 (65.69)	18118.28 (134.60)	6132.15 (78.31)	2588.38 (50.88)	3532.82 (59.44)	9868.27 (99.34)
Cluster VI						0.00 (0.00)	212.13 (14.56)	392.67 (19.82)	1294.10 (35.97)	3113.61 (55.80)	3657.43 (60.48)	4405.74 (66.38)	6736.14 (82.07)	7191.14 (84.80)	7623.31 (87.31)
Cluster VII							0.00 (0.00)	770.61 (27.76)	1539.64 (39.24)	3293.62 (57.39)	4029.20 (63.48)	4848.11 (69.63)	7124.09 (84.40)	7567.97 (86.99)	8293.88 (91.07)
Cluster VIII								0.00 (0.00)	1532.60 (39.15)	3155.90 (56.18)	4566.38 (67.57)	4721.92 (68.72)	6058.61 (77.84)	6674.89 (81.70)	8122.29 (90.12)
Cluster IX									1209.23 (34.77)	3648.70 (60.40)	4500.88 (67.09)	4732.47 (68.79)	7376.04 (85.88)	7696.72 (87.73)	6964.27 (83.45)
Cluster X										0.00 (0.00)	9527.83 (97.61)	512.77 (22.64)	2887.67 (53.74)	3299.48 (57.44)	6473.09 (80.46)
Cluster XI											2433.02 (49.33)	9838.54 (99.19)	16896.00 (129.98)	16380.98 (127.99)	8659.49 (93.06)
Cluster XII												0.00 (0.00)	4198.16 (64.79)	4608.22 (67.88)	6185.55 (78.65)
Cluster XIII													0.00 (0.00)	2481.30 (49.81)	12032.91 (109.69)
Cluster XIV														2395.25 (48.94)	10999.74 (104.88)
Cluster XV															4555.49 (67.49)

Figures in parenthesis indicate D values

Table 3. Cluster mean values (Tocher's method) for eleven characters in two hundred genotypes of rice (*Oryza sativa* L.)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Tillers per hill	Productive tillers per hill	Grains per panicle	Spikelet fertility (%)	1000-grain weight (g)	Pollen viability (%)	Single plant yield (g)
ClusterI	110.222	140.089	87.743	23.920	17.112	12.028	142.786	83.826	20.354	71.111	29.154
ClusterII	102.461	132.904	84.458	22.219	15.815	12.478	107.959	84.672	21.146	82.421	24.683
ClusterIII	105.294	136.229	91.329	21.000	17.979	13.015	70.615	62.818	19.976	62.000	13.106
ClusterIV	102.147	132.171	99.765	22.020	17.295	12.560	81.997	80.808	20.395	83.985	19.218
ClusterV	101.722	130.839	105.895	22.325	16.151	12.017	59.333	42.364	19.200	65.889	7.719
ClusterVI	103.500	135.700	88.790	21.951	17.140	14.895	129.288	88.161	14.063	84.250	26.458
ClusterVII	99.000	126.450	84.625	24.808	16.590	16.245	129.154	87.401	20.603	88.250	30.853
ClusterVIII	110.500	143.200	88.995	20.961	14.090	4.720	123.686	85.061	20.915	89.250	18.673
ClusterIX	105.239	134.825	93.680	23.503	16.579	12.175	129.588	79.727	19.927	76.212	24.126
ClusterX	100.500	130.200	77.695	24.160	12.690	10.720	90.986	79.151	23.395	49.250	19.472
ClusterXI	107.214	138.950	96.401	22.619	16.554	13.209	176.801	84.626	19.624	70.071	31.639
ClusterXII	103.500	131.200	81.595	22.521	12.690	10.520	94.986	87.151	22.105	29.250	21.253
ClusterXIII	99.500	129.700	109.350	25.150	10.340	8.895	54.289	84.351	19.962	69.250	10.038
ClusterXIV	101.607	130.977	94.854	20.843	15.360	11.729	64.195	70.206	17.862	63.634	11.063
ClusterXV	101.000	130.867	104.353	21.782	13.723	11.662	135.635	42.016	17.994	28.667	13.947

Table 4. Percent contribution of different characters towards divergence in two hundred genotypes of rice (*Oryza sativa* L.)

S. no.	Characters	Times ranked first	Contribution (%)
1	Days to 50% flowering	181	0.91
2	Days to maturity	275	1.38
3.	Plant height (cm)	3099	15.57
4	Panicle length (cm)	3	0.02
5	Number of tillers per hill	48	0.24
6	Number of productive tillers per hill	5	0.03
7	Number of grains per panicle	11325	56.91
8	Spikelet fertility (%)	2018	10.14
9	1000-grain weight (g)	10	0.05
10	Pollen viability (%)	2807	14.11
11	Single plant yield (g)	129	0.65

Table 5. The eigene values, per cent variance and per cent cumulative variance for three principal components (PC's) and factor loading between PCs and traits studied in rice (*Oryza sativa* L.)

	PC1	PC 2	PC 3	PC 4	PC 5
Eigene Value (Root)	2.819	1.969	1.517	1.393	0.955
% Var. Exp.	25.623	17.898	13.793	12.664	8.686
Cum. Var. Exp.	25.623	43.522	57.315	69.979	78.665
Traits	Factor loading				
Days to 50% Flowering	0.323	0.538	0.128	0.143	0.228
Days to Maturity	0.320	0.541	0.119	0.169	0.215
Plant Height (cm)	-0.064	0.019	0.086	-0.666	0.280
Panicle Length (cm)	0.256	0.141	0.142	-0.517	-0.026
Number of Tillers per Hill	0.126	-0.244	0.632	0.134	0.060
Number of Productive Tillers per Hill	0.169	-0.322	0.582	0.052	0.033
Number of Grains per Panicle	0.404	0.064	-0.094	-0.068	-0.608
Spikelet Fertility (%)	0.360	-0.270	-0.337	0.221	0.156
1000-Grain Weight (g)	0.213	-0.117	-0.163	-0.391	0.137
Pollen Viability (%)	0.261	-0.296	-0.223	0.099	0.590
Single Plant Yield (g)	0.522	-0.237	-0.071	-0.059	-0.238

Table 6. The PCA scores for two hundred genotypes of rice (*Oryza sativa* L.)

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
1.	KHASRAN	171.967	74.399	-10.174	-0.003	90.828
2.	IR 19746-28-2-2	207.703	78.956	-6.288	-22.722	43.991
3.	DOMSIAH	196.761	78.852	2.522	-32.177	66.045
4.	GANJA CHOOTA	201.585	62.497	-8.468	-55.179	69.734
5.	SADRI	194.835	69.379	-5.582	-42.377	77.937
6.	GIZA 178	185.995	71.247	-6.979	-53.796	66.712
7.	ZAKHA	191.969	73.413	-4.833	-45.180	91.940
8.	TODOROKIWASE	194.536	88.197	0.310	-40.522	83.217
9.	ATTEY	172.048	79.793	15.099	-27.202	66.761
10.	CARREON	176.282	100.422	12.704	-72.603	19.098
11.	IR 50	146.225	89.131	22.267	-52.430	90.553
12.	GIZA 176	168.138	76.083	11.511	-35.385	76.837
13.	IR 71 866-3R-3-1	166.851	72.262	4.539	-26.322	74.353

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
14.	GIZA 159	140.443	105.085	30.619	-64.195	33.576
15.	ZARDROME	110.092	101.442	36.565	-45.885	75.662
16.	MRC 603-383	127.432	91.829	28.298	-37.910	84.848
17.	FIROOZ	203.108	72.017	-2.690	-25.210	64.909
18.	CT 9993-5-10-M	155.126	81.387	6.106	-57.045	81.154
19.	WAB96-1-1	136.697	89.704	25.393	-52.673	69.041
20.	JIJAI	165.843	90.211	19.148	-21.180	96.627
21.	KHAU MA TUOI	155.940	67.966	11.081	-23.926	90.642
22.	ARC 15210	211.586	68.905	-5.217	-59.439	43.064
23.	KHIRI	158.593	91.412	19.892	-28.358	74.239
24.	DOM SOFID	144.812	91.693	24.399	-30.935	96.114
25.	GZ 948-2-2-1	174.636	69.654	0.889	-31.685	98.816
26.	LIETO	170.856	72.362	7.642	-42.138	98.066
27.	AZUCENA	151.157	87.736	12.832	-42.377	114.122
28.	IR 73055-1-2-2-3-3	175.770	82.131	4.981	-47.554	81.453
29.	TAREME	194.546	95.191	6.961	-30.996	55.968
30.	LEMONT	174.181	74.626	-1.684	-27.694	62.479
31.	IR 65192-4B-17-3	183.847	58.870	-0.594	-33.655	66.190
32.	IR 61250-3B-7-1-2	183.230	68.854	-8.585	-25.370	97.511
33.	SAKHA 104	181.178	73.192	4.601	-30.806	93.255
34.	MULAI	159.944	61.493	1.983	-27.780	99.171
35.	SAUNFI	174.356	62.640	-9.937	-7.093	92.743
36.	IR 2307-247-2-2-3	159.452	63.245	-2.523	-24.943	79.892
37.	IR 1561-228-3-3	165.548	72.924	3.446	-40.764	114.048
38.	IDSA 77	194.853	64.539	2.154	-37.775	93.375
39.	WAB56-125	158.526	95.690	19.361	-31.322	78.215
40.	TCHAMPA	165.865	59.653	-5.445	-28.396	107.120
41.	IR1552	200.496	73.755	-0.338	-28.670	81.446
42.	CR 547-1-2-3	188.460	68.771	-0.765	-31.035	63.516
43.	TEQING	180.378	67.640	-7.606	-31.257	60.831
44.	NERICA 10	222.703	83.662	-13.883	-34.132	42.575
45.	G HARIB	214.361	70.040	-14.281	-21.375	47.577
46.	NERICA 12	214.583	87.125	-8.239	-29.798	50.133
47.	NERICA 13	205.346	66.499	-8.354	-21.256	56.980

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
48.	NERICA 14	140.041	80.296	16.024	-39.566	94.156
49.	NERICA 15	143.929	89.687	5.710	-9.373	82.036
50.	NERICA 17	205.696	59.184	-8.423	-28.097	45.841
51.	NERICA 18	193.210	86.966	-3.257	-5.894	72.345
52.	NERICA-L-1	204.759	70.360	-2.850	-25.408	75.084
53.	NERICA-L-2	163.198	86.836	16.332	-4.598	76.066
54.	NERICA-L-3	184.085	81.624	-3.229	-20.256	92.937
55.	NERICA-L-4	191.943	72.237	-6.911	-25.746	67.775
56.	KHARA HANJA	180.452	70.379	-4.211	-21.154	84.855
57.	NERICA-L-54	187.399	66.021	-1.312	-10.281	82.013
58.	JAMREE	155.442	64.678	2.050	-27.014	118.394
59.	NERICA-L-52	204.815	83.740	-2.261	-26.261	85.892
60.	MOROBEREKAN	151.721	91.789	11.623	-29.517	53.060
61.	DARIAL	195.940	89.298	-1.443	-35.939	40.026
62.	NERICA-L-49	136.640	104.897	21.989	-35.664	79.647
63.	DOMZARD	151.868	91.144	2.967	-22.998	107.133
64.	IR 71864-3R-1-1-3-1	182.001	92.776	5.319	-9.922	84.191
65.	BR26	185.556	74.080	-6.744	-20.378	92.400
66.	IR 61336-4B-14-3-2(PSB RC94)	199.733	73.205	-4.838	-22.345	81.002
67.	IR 70031-4B-R-9-3-1	207.756	73.526	-8.682	-36.602	75.466
68.	LAROME	210.374	95.297	6.282	-35.936	54.639
69.	JATTA	159.360	69.407	0.968	-35.326	122.465
70.	XUE HE	165.192	78.839	9.154	-47.100	88.902
71.	TOOR THULLA	159.021	74.612	-1.626	-37.445	117.674
72.	AS 996-HR 1	166.860	63.478	-12.192	-21.874	100.717
73.	SATHI 34-36	172.273	74.174	-4.587	-1.753	86.003
74.	MALA	152.332	72.749	3.362	-12.544	103.029
75.	NERICA-L-47	182.996	71.677	-0.879	-29.576	102.547
76.	NERICA-L-46	186.688	95.232	0.364	-41.647	39.376
77.	IR 28	196.104	62.322	-8.271	-19.652	75.999
78.	BALA	166.062	75.067	-3.105	-30.560	108.224
79.	PEH-KUH-TSAO-TU	189.265	87.329	6.489	-17.329	50.979
80.	RATRIA	170.701	96.499	13.080	-40.745	71.303
81.	NERICA-L-45	153.187	107.316	26.809	-53.784	71.198

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
82.	NAN-GUANG-ZHAN	155.731	79.571	-0.039	-34.462	102.806
83.	NERICA-L-44	162.823	122.597	19.468	-31.492	3.408
84.	GUANG JIANG 1	147.231	92.029	6.648	-21.449	88.098
85.	IR 72049-B-R-8-3-1-1-1	169.306	95.680	9.477	-22.817	71.331
86.	GANJA RANGWALA	155.732	98.954	17.723	-27.860	83.344
87.	IR 6	188.225	67.311	-11.113	-21.664	73.057
88.	BR 7232-6-2-3	189.885	90.301	10.694	-27.239	82.207
89.	PADI HOJONG	172.332	74.326	2.218	-14.283	88.472
90.	NERICA-L-42	179.217	63.153	-9.915	-9.180	65.467
91.	CO 18	175.179	103.927	19.896	-56.839	47.961
92.	N12	175.710	78.326	4.148	-38.149	104.699
93.	TAM CAU 9 A	138.394	85.316	6.283	-26.465	75.963
94.	BAKTULSHI	164.385	78.909	-0.083	-13.683	93.032
95.	TAK RATIA	204.200	76.698	-5.163	-17.763	59.049
96.	RJT 74	200.149	77.983	-12.418	-14.010	55.543
97.	NERICA-L-41	147.268	93.263	16.477	-23.458	94.287
98.	BALILLA	229.150	95.303	-11.281	-27.845	23.289
99.	BR 7414-22-1	199.506	64.433	-9.755	-10.011	66.810
100.	NERICA-L-8	209.801	86.263	-1.373	-19.753	54.146
101.	NERICA-L-9	157.879	97.888	15.421	-20.952	92.936
102.	IR 8866-30-3-1-4-2	199.106	84.105	-13.550	-21.239	74.865
103.	IR 72	200.615	73.500	-5.024	-16.768	65.491
104.	GANJAY	192.627	98.830	16.910	-29.448	61.151
105.	KALAHITTA	157.433	72.514	-13.038	-15.385	109.204
106.	IR 10C110	183.949	65.092	0.443	-19.477	65.259
107.	IR 10C172	203.278	84.226	4.831	-16.200	52.137
108.	IR 10C139	199.257	76.144	0.450	-18.574	33.523
109.	IR 83142-B-36-B	183.083	85.318	3.077	-16.088	54.397
110.	HHZ 17 Y16 Y3 Y2	212.972	95.486	-7.862	-27.164	50.147
111.	HHZ 8 SAL6 SAL3 Y1	212.124	86.128	-10.098	-26.559	25.763
112.	HHZ 5 DT 1 DT 1	219.452	98.816	-2.601	-34.330	10.727
113.	IR 10C137	182.525	81.387	7.263	-16.718	86.702
114.	IR 83142-B-32-B	185.373	72.063	-1.696	-32.517	86.423
115.	IR 10C132	175.612	95.431	1.481	-22.611	48.716

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
116.	IR 10C108	190.978	77.916	-7.810	-9.221	68.497
117.	IR 83143 B 151 1	194.068	70.442	-3.098	-20.639	76.115
118.	HHZ 12 SAL2 Y3 Y2	222.089	88.736	-2.900	-25.257	46.553
119.	IR 10C 153	183.112	69.970	-5.008	-23.189	82.684
120.	HHZ 12 SAL 8 Y1 Y2	207.067	100.408	2.743	-20.433	10.776
121.	IR 10C 103	187.474	76.952	0.540	-18.338	64.339
122.	HUANG ANZHAN	197.409	80.577	-1.452	-18.333	52.958
123.	HHZ 17 Y16 Y3 Y1	232.007	83.771	-10.955	-34.484	21.015
124.	IR 10C 174	195.521	79.052	-5.843	-27.459	58.157
125.	HHZ 12 SALB Y1 SAL1	237.246	82.277	-8.208	-22.015	33.384
126.	HHZ8 SAL12 Y2 DT1	224.724	83.280	-6.493	-22.659	56.028
127.	IR 10C161	192.780	74.075	-2.968	-9.836	61.795
128.	IR 10C 138	162.651	87.157	10.923	-28.771	79.367
129.	HHZ12 Y4 DT1 Y2	209.139	81.080	-6.655	-17.352	85.165
130.	HHZ 5 SAL 14 SAL2 Y1	187.988	77.868	6.656	-20.592	60.303
131.	HHZ 8 SAL14 SAL1 SUB1	205.095	77.778	-0.318	-13.057	49.992
132.	IR IOC 157	201.038	89.457	-2.693	-15.603	81.368
133.	HHZ 8 SAL6 SAL3 Y2	173.583	96.097	9.527	-20.799	88.857
134.	HHZ I7 DT6 Y1 DT1	198.617	91.953	-7.364	-32.136	35.785
135.	HHZ 8 SAL6 SAL3 SAL1	212.248	86.037	-3.888	-26.716	73.210
136.	HHZ 5 DT20 DT2 DT1	212.764	66.640	-18.008	-20.338	37.924
137.	HHZ 5 Y3 SAL2 SUB1	230.605	84.515	-8.643	-12.610	28.047
138.	HHZ 5 SAL 10 DT3 Y2	220.655	92.442	-9.589	-26.837	54.649
139.	IR 10C 113	223.306	77.991	-6.342	-18.737	51.060
140.	IR IOC 167	192.054	79.717	-9.598	-7.277	72.216
141.	HHZ 11 DT7 SAL1 SAL1	208.451	75.353	-12.996	-16.957	68.142
142.	IR IOC 136	188.143	89.361	-2.641	-18.198	80.242
143.	IR IOC 143	191.793	76.917	-5.780	-10.970	63.604
144.	HHZ 12 Y4 DT1 Y3	204.578	86.185	-6.268	-25.974	65.448
145.	HHZ 5 SAL8 DTZ SAL1	198.246	99.183	1.050	-19.994	53.160
146.	KINMAZE	142.972	78.504	0.194	2.861	93.338
147.	IR 10C 126	178.409	79.332	-2.515	-21.438	79.075
148.	IR 10C 173	190.923	79.223	-9.869	-17.677	71.960
149.	AKITAKOMACHI	160.394	66.113	-1.425	-28.883	96.274

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
150.	HHZ5 SAL14 SAL2 Y2	202.966	99.663	-1.174	-22.384	36.358
151.	IR 10C 179	182.321	89.985	-2.932	-20.549	91.727
152.	NERICA-L-40	191.520	88.668	-5.855	-21.157	92.107
153.	IR 64197 - 3B -15-2	195.249	84.388	-10.819	-13.050	79.053
154.	HHZ5 Y3 YI DTI	156.578	109.737	18.698	-34.744	72.268
155.	HHZ 12 Y4 YI DTI	213.638	99.592	2.971	-25.414	39.415
156.	IR 10C112	196.589	74.732	-3.762	-4.042	72.668
157.	IR 10C146	213.696	83.590	-4.284	-18.414	37.648
158.	IR 11C114	213.385	85.678	-2.860	-16.613	40.363
159.	IR 11C115	166.550	85.990	13.656	-33.542	62.818
160.	IR 11C120	209.448	96.891	1.400	-27.197	29.000
161.	IR 11C126	184.383	74.953	-2.700	-21.435	63.059
162.	IR 11C128	161.867	82.258	6.630	-25.550	83.515
163.	IR 11C130	191.991	79.117	-4.484	-15.725	45.675
164.	IR 11C134	208.196	92.862	-0.614	-25.271	36.360
165.	IR 11C138	126.505	107.003	29.050	-23.021	72.234
166.	IR 11C149	205.694	86.320	-1.841	-15.750	49.733
167.	IR 11C169	187.072	90.167	2.116	-15.878	39.900
168.	IR 11C170	192.866	88.749	3.331	-36.226	48.364
169.	IR 65199-4B-19-1-1	169.982	85.569	8.751	-21.741	6.169
170.	IR 68144-2B-4-2-3-2	195.968	69.479	-12.623	-16.841	56.957
171.	IR 700031-4B-R-2-2-1	192.897	76.962	-6.642	-18.643	61.344
172.	IR 70865-B-P-6-2	203.014	73.291	-10.174	-16.644	57.168
173.	IR 70868-B-P-11-3	171.987	85.514	1.348	-19.749	57.778
174.	IR 71895-3R-26-2-1-2B-2	202.430	86.876	-7.616	-15.932	60.557
175.	IR 72046-B-R-3-2-1	191.092	72.257	-12.747	-13.972	78.176
176.	IR 72593-B-3-2-3-3-2B-1	172.514	91.325	3.311	-20.993	46.215
177.	IR 74099-3R-5-1	143.464	106.083	28.503	-27.334	61.053
178.	IR 11C119	183.160	102.984	11.609	-24.404	45.815
179.	IR 11C127	201.801	88.445	-11.457	-18.078	70.485
180.	IR 11C173	200.641	92.738	-2.478	-4.117	57.800
181.	CPAU -11	157.931	85.449	11.070	-55.865	87.547
182.	CPAU -12	145.365	99.607	24.619	-34.292	92.000
183.	CPAU -13	147.813	74.751	5.812	-22.212	89.600

S.NO	Genotypes	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5
184.	CPAU -14	159.460	71.177	0.220	-1.789	63.641
185.	CPAU -15	157.085	90.698	13.743	8.373	83.639
186.	CPAU -16	163.045	69.567	6.426	6.695	96.442
187.	CPAU -17	150.690	73.271	13.001	-6.078	93.554
188.	CPAU -18	169.525	87.077	9.330	4.691	92.102
189.	CPAU -19	177.632	90.195	6.519	-30.055	88.175
190.	CPAU -20	167.015	92.944	2.678	-34.430	90.679
191.	CPAU -21	165.988	101.731	14.113	-42.044	85.287
192.	CPAU -22	192.045	83.844	-3.910	-20.806	95.549
193.	CPAU -23	170.595	85.585	7.571	-15.526	105.326
194.	CPAU -24	199.042	65.100	-6.727	-14.606	74.111
195.	CPAU -25	184.155	78.539	-9.760	-19.103	71.628
196.	CPAU -26	175.886	76.983	-1.325	-23.296	68.955
197.	CPAU -27	166.022	96.719	14.103	-21.296	82.763
198.	CPAU -28	179.829	72.355	5.688	-33.929	84.058
199.	CPAU -29	168.887	122.557	21.321	-33.639	16.654
200.	CPAU -30	148.657	98.573	18.552	-65.750	74.180

Table 7. Clustering pattern of rice (*Oryza sativa* L.) genotypes by principal component analysis

Cluster No	No. of genotypes	Names of the genotypes
I	12	KHAU MA TUOI, MULAI, IR 2307-247-2-2-3, TCHAMPA, JAMREE, JATTA, TOOR THULLA, AS 996-HR 1, KALAHITTA, AKITAKOMACHI, CPAU -14, CPAU -16.
II	16	KHASRAN, ATTEY, GIZA 176, IR 71 866-3R-3-1, GZ 948-2-2-1, LIETO, LEMONT, IR 1561-228-3-3, XUE HE, SATHI 34-36, BALA, PADI HOJONG, N12, BAKTULSHI, IR 11C128, CPAU -26.
III	16	IR 50, KHIRI, DOM SOFID, AZUCENA, WAB56-125, NERICA 15, MOROBEREKAN, DOMZARD, GUANG JIANG 1, GANJA RANGWALA, NERICA-L-41, NERICA-L-9, CPAU -11, CPAU -12, CPAU -15, CPAU -30.
IV	9	NERICA 10, BALILLA, HHZ 12 SAL2 Y3 Y, HHZ 17 Y16 Y3 Y1, HHZ 12 SALB Y1 SAL1, HHZ8 SAL12 Y2 DT1, HHZ 5 Y3 SAL2 SUBI, HHZ 5 SAL 10 DT3 Y2, IR 10C 113.
V	18	GIZA 178, IR 65192-4B-17-3, IR 61250-3B-7-1-2, SAKHA 104, SAUNFI, CR 547-1-2-3, TEQING, KHARA HANJA, NERICA-L-54, BR26, NERICA-L-47, IR 6, NERICA-L-42, IR 10C110, IR 83142-B-32-B, IR 10C 153, IR 11C126, CPAU -28.
VI	8	CT 9993-5-10-M, NERICA 14, MALA, NAN-GUANG-ZHAN, TAM CAU 9 A, KINMAZE, CPAU -13, CPAU -17,
VII	4	NERICA-L-45, NERICA-L-44, HHZ5 Y3 YI DTI, CPAU -29.

Cluster No	No. of genotypes	Names of the genotypes
VIII	20	NERICA 12, LAROME, NERICA-L-8, HHZ 17 Y16 Y3 Y2, HHZ 8 SAL6 SAL3 Y1, HHZ 5 DT 1 DT 1, HHZ 12 SAL 8 Y1 Y2, IR IOC 157, HHZ 8 SAL6 SAL3 SALI, HHZ 12 Y4 DT1 Y3, HHZ5 SAL14 SAL2 Y2, HHZ 12 Y4 YIDTI, IR 10C146, IR 11C114, IR 11C120, IR 11C134, IR 11C149, IR 71895-3R-26-2-1-2B-2, IR 11C127, IR 11C173.
IX	11	GANJA CHOOTA, ARC15210, IDSA77, GHARIB, NERICA13, NERICA17, NERICA-L-1, IR28, BR 7414-22-1, HHZ 5 DT20 DT2 DTI, CPAU -24.
X	17	TODOROKIWASE, TAREME, NERICA18, DARIAL, NERICA-L-46, PEH-KUH-TSAO-TU, BR 7232-6-2-3, GANJAY, HHZ I7 DT6 YI DTI, IR IOC 136, HHZ 5 SAL8 DTZ SAL1, NERICA-L-40, IR 64197 - 3B -15-2, IR 11C169, IR 11C170, IR 11C119, CPAU -22.
XI	18	DOMSIAH, SADRI, AKHA, NERICA-L-4, IR 10C108, IR 83143 B 151 1, IR 10C 103, IR 10C 174, IR 10C161, HHZ 5 SAL 14 SAL2 Y1, IR 10C 167, IR IOC 143, IR 10C 173, IR 10C112, IR 11C130, IR 68144-2B-4-2-3-2, 2, IR 700031-4B-R-2-2-1, IR 72046-B-R-3-2-1.
XII	17	IR 19746-28-2-2, FIROOZ, IR1552, NERICA-L-52, IR 61336-4B-14-3-2(PSB RC94, IR 70031-4B-R-9-3-1, TAKRATIA, RJT 74, IR 8866-30-3-1-4-2, IR72, IR 10C172, IR 10C139, HUANGANZHAN, HHZ12 Y4 DT1 Y2, HHZ 8 SAL14 SAL1 SUB1, HHZ 11 DT7 SAL1 SAL1, IR 70865-B-P-6-2.
XIII	18	CARREON, JIJAI, NERICA-L-2, RATRIA, IR 72049-B-R-8-3-1-1-1, CO18, IR 10C132, IR 10C 138, HHZ 8 SAL6 SAL3 Y2, IR 11C115, IR 65199-4B-19-1-1, IR 70868-B-P-11-3, IR 72593-B-3-2-3-3-2B-1, CPAU -18, CPAU -20, CPAU -21, CPAU -23, CPAU -27.
XIV	7	GIZA 159, ZARDROME, MRC 603-383, WAB96-1-1, NERICA-L-49, IR 11C138, IR 74099-3R-5-1.
XV	9	IR 73055-1-2-2-3-3, NERICA-L-3, IR 71864-3R-1-1-3-1, IR 83142-B-36-B, IR 10C137, IR 10C 126, IR 10C 179, CPAU -19, CPAU -25.

Table 8. Cluster mean values for eleven characters in two hundred genotypes of rice (*Oryza sativa* L.) (Principal component analysis)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Number of tillers per Hill	Number of productive tillers per hill	Number of grains per panicle	Spikelet fertility (%)	1000-grain weight (g)	Pollen viability (%)	Single plant yield (g)
Cluster I	94.708	124.429	95.196	19.645	15.907	11.992	60.933	82.641	19.091	82.917	12.955
Cluster II	99.844	129.841	98.293	20.819	16.481	12.997	78.729	76.078	19.469	78.188	17.315
Cluster III	104.375	134.747	100.389	20.931	15.799	11.768	65.940	57.001	17.671	61.484	9.194
Cluster IV	110.556	141.950	92.535	23.041	17.234	12.684	167.974	85.305	20.943	85.583	31.018
Cluster V	97.639	127.033	94.562	21.943	17.335	12.705	96.228	82.907	21.045	85.014	22.552
Cluster VI	96.125	125.669	94.386	20.367	14.478	10.933	55.835	72.491	16.868	64.594	8.992
Cluster VII	109.125	140.513	99.268	21.078	13.503	10.173	114.815	38.432	17.269	35.500	8.708
Cluster VIII	111.400	141.450	88.984	23.849	16.178	11.426	140.647	83.499	19.920	70.050	26.444
Cluster IX	97.636	127.291	97.759	22.838	18.276	14.670	128.340	88.144	20.575	90.182	30.728
Cluster X	109.941	139.215	91.581	23.795	15.075	11.652	116.958	73.765	20.798	71.985	20.733
Cluster XI	101.667	132.603	86.661	22.108	16.021	12.546	109.596	85.139	20.940	79.931	24.722
Cluster XII	105.324	135.553	88.827	23.245	17.790	12.992	122.685	85.806	19.730	84.809	27.353
Cluster XIII	106.306	135.742	93.784	22.884	16.527	12.320	88.972	69.298	20.235	54.444	16.080
Cluster XIV	98.857	128.236	97.596	23.244	16.390	11.958	66.876	26.526	19.732	42.393	5.800
Cluster XV	107.111	137.311	92.489	22.862	15.584	11.609	89.504	80.564	20.901	74.556	18.517

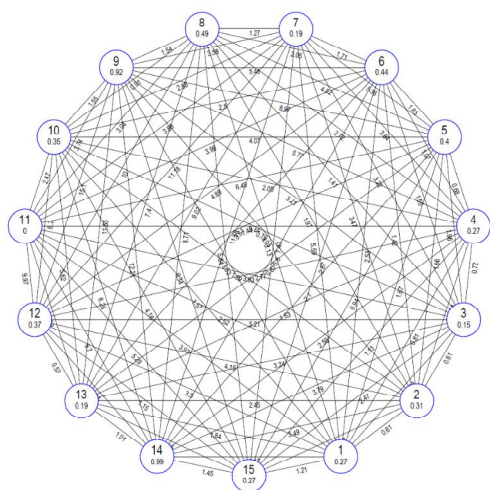


Fig. 3. Statistical distances among two hundred genotypes of rice (Cluster analysis) (Not to the scale)

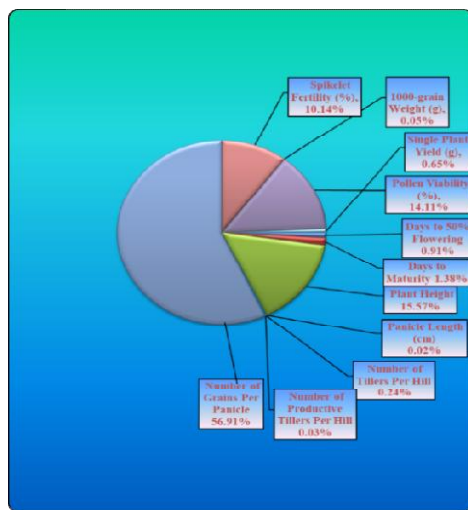


Fig. 4. Relative contribution of different characters towards genetic diversity

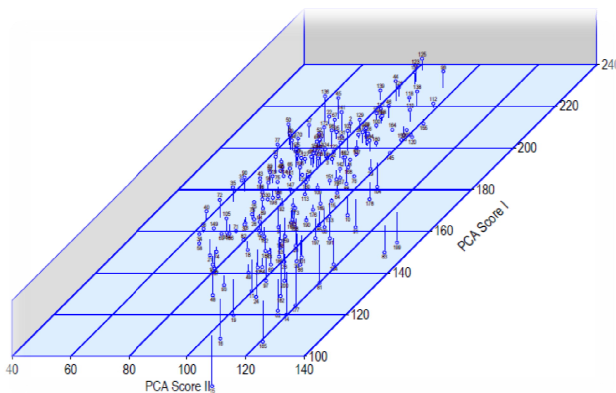


Fig. 5. Three-dimensional principal component scatter plot

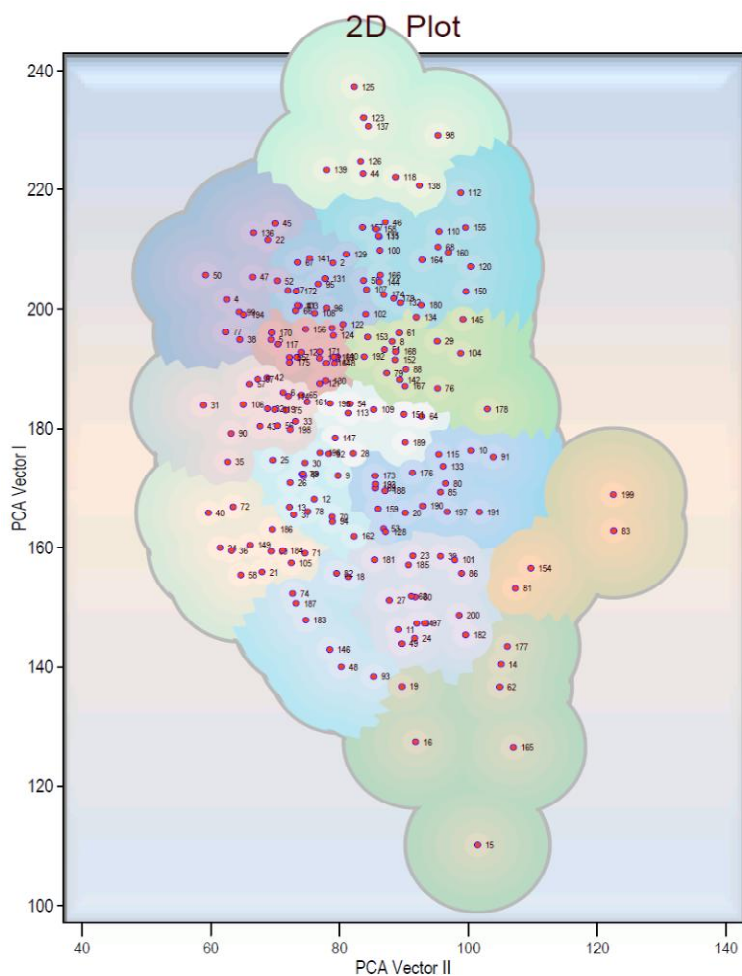


Fig. 6. Two-dimensional scatter plot of principal component analysis showing positions of two hundred genotypes of rice

in cluster IX (90.18%) and lowest in cluster VII (35.50%). Highest single plant yield was recorded in cluster III (31.01 g) and the lowest was observed in cluster XIV (5.80 g). The genotypes of cluster I, cluster IV, cluster V, cluster VIII, cluster IX, cluster XI, cluster XII and cluster XV exhibited highest spikelet fertility percentage. Hence, the genotypes of the cluster I, cluster IV, cluster V, cluster VIII, cluster IX, cluster XI, cluster XII and cluster XV can be used in breeding programmes for the development of heat tolerant varieties.

3.7 Comparison between D^2 Statistic and Principal Component Analysis

The pattern of distribution of genotypes into different clusters was at random (or independent from their geographic origin). Furthermore, the

two clustering methods grouped differently and clustering pattern for genotypes is not same. The Principal Component Analysis sorted out the total characters into five main principal components. The contribution of the main characters for variance easily identified by the characters loaded on the PC_1 as it explained maximum variance. By PCA, the in-depth analysis for genetic diversity can be made. In D^2 analysis, the characters viz., number of grains per panicle, plant height, pollen viability and spikelet fertility contributed more for the divergence. In PCA, the characters viz., single plant yield, number of grains per panicle and spikelet fertility in PC_1 and days to 50% flowering and maturity were loaded in PC_2 , and number of tillers per hill and number of productive tillers per hill in PC_3 , spikelet fertility, days to maturity and days to 50% flowering in PC_4 and pollen viability

and plant height in PC₅ towards variability. In the present study, D² cluster analysis and principal factor analysis revealed that number of grains per panicle and spikelet fertility as major contributors to the total divergence. The results of both D² cluster analysis and principal components analysis corroborated with each other.

4. CONCLUSION

Genetic diversity was the outcome of several factors along with a factor geographic diversity. Hence, the selection for hybridization should be more based on genetic diversity than geographic diversity. In the present study, D² cluster analysis and principal factor analysis revealed that number of grains per panicle and spikelet fertility as major contributors to the total divergence. The results of both D² cluster analysis and principal components analysis corroborated with each other.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Indiastat. 2015-16. Area, production and productivity of rice in India and Telangana. Available:www.indiastat.com
2. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Institute of Sciences, India. 1936; 12:49-55.
3. Rao CR. Advanced statistical methods in biometric research. Wiley, Oxford, England. 1952;17:390.
4. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi; 1979.
5. Sangeetha R, Saraswathi R, Amudha K, Senthil Kumar G. Genetic divergence studies in subspecies of *Oryza sativa* L. International Journal of Current Microbiology and Applied Sciences. 2019; 8(7):834-845.
6. Gautam AS. Genetic divergence in maize. International Journal of Agricultural Sciences. 2008;4(2):466-468.
7. Hoque A, Begum SN, Robin AHK, Hasan L. Partitioning of rice (*Oryza sativa* L.) genotypes based on morphometric diversity. American Journal of Experimental Agriculture. 2015;7(4):242-250.
8. Mundhe BS, Jambhale ND, Bendale VW. Genetic divergence in midlate genotypes of rice. Journal-of-Maharashtra-Agricultural-Universities. 2006;31(1):21-23.
9. Jagadish SVK, Craufurd PQ, Wheeler TR. High temperature stress and spikelet fertility in rice (*Oryza sativa* L.). Journal of Experimental Botany. 2007;58:1627-1635.
10. Sabesan T, Suresh R, Saravanan K. Genetic variability and correlation for yield and grain quality characters of rice grown in costal saline low land of Tamilnadu. Elect. J. Plant Breed. 2009;1:56-59.
11. Baradhan G, Thangavel P. D2 analysis in rice (*Oryza sativa* L.). Plant Archives. 2011;11(1):373-375.
12. Karthikeyan P, Anbuselvam Y, Elangaimannan R, Venkatesan M. Variability and heritability studies in rice (*Oryza sativa* L.) under coastal salinity. Electronic Journal of Plant Breeding. 2010;1(2):196-198.
13. Venkanna V, Rao MVB, Raju CHS, Rao VT, Lingaiah N. Association analysis of F2 generation in rice (*Oryza sativa* L.). International Journal of Pure Applied Bioscience. 2014;2(2):278-283.
14. Bhati PK, Singh SK, Dhurai SY, Sharma A. Genetic divergence for quantitative traits in rice germplasm. Electronic Journal of Plant Breeding. 2015;6(2):528-534.
15. Devi KR, Cheralu C, Parimala K. Study of genetic diversity in rice (*Oryza sativa* L.). Journal of Research, PJ TSAU. 2015;43 (1/2):83-86.
16. Abhinav Sao, Preeti Singh. Genetic divergence study in traditional local landraces of rice (*Oryza sativa* L.) predominant in Bastar Plateau Zone of Chhattisgarh. Advance Research Journal of Crop Improvement. 2016;7(2):192-196.
17. Priya CHS, Suneetha Y, Babu DR, Rao VS. Assessment of genetic divergence in rice for grain yield and quality traits.

- Environment and Ecology. 2017;35(3B): 2007-2011.
18. Ramya K, Kumar S. Genetic divergence in rice. *Crop Improvement*. 2008;35(2):119-121.
 19. Banumathy S., Manimaran R, Sheeba N, Manivannan Ramya B, Kumar D, Rama sabramanian GV. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic Journal of Plant Breeding*. 2010;1(4):500-504.
 20. Hosan SM, Sultana N, Iftekaruddaula KM, Ahmed Md. NU, Mia S. Genetic divergence in landraces of Bangladesh rice (*Oryza sativa* L.). *The Agriculturists*. 2010;8(2): 28-34.
 21. Vennila S., Anbuselvam Y. and Palaniraja K. D2 analysis of rice germplasm for some quantitative and quality traits. *Electronic Journal of Plant Breeding*. 2011;2(3):392-403.
 22. Anandan A, Eswaran R, Prakash M. Diversity in rice genotypes under salt affected soil based on multivariate analysis. *Pertanika Journal of Tropical Agriculture Science*. 2011;34(1):33-40.
 23. Sandhya GR, Lavanya G, Suresh Babu, Ravi Kumar, Satish Kumar Rai, Bandana Devi. Study of genetic variability and D² analysis in elite rice genotypes. *International Journal of Food, Agriculture and Veterinary Sciences*. 2014;4(2):12-16.
 24. Praveen SKC, Mahesh Naik B, Ebenezer BRR, Suji DB. Studies on genetic divergence among rice genotypes (*Oryza sativa* L.) under coastal saline condition. *Plant Archives*. 2019;19(2): 2825-2828.
 25. Ujjval IS, Mahesh BP, Lalji NG. Assessment of genetic divergence in rice genotypes under middle Gujarat condition. *International Journal of Chemical Studies*. 2019;7(3):2825-2828.
 26. Patel MZ, Reddi MV, Rana BS, Reddy BJ. Genetic divergence in safflower (*Carthamus tinctorius* L.). *Indian Journal of Genetics and Plant Breeding*. 1989;49: 113-118.

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