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 ICRISAT, Patencheru, 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
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 adaptable 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, Patencheru, 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 inter 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 exploiting 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
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 productive tillers per hill was observed 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 Y1 DT1, |
| II      | 38                  | IR 10C108, IR 10C 143, IR 10C161, IR 10C 167, NERICA 18, IR 10C 112, 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 68144-28-4-2-3-2, 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 10C 126, IR 71895-3R-26-2-1-2B-2, CPAU -26, DOMSIAH, FROIROZ, IR1552, HUANG ANZHAH, IR 70865-B-P-6-2, |
| III     | 17                  | WAB56-125, GANJIA RANGWALA, HHZ5 Y3 Y1 DT1, 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, JUAI, 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 7323-6-2-3, 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 10C 157, HHZ12 Y4 DT1 Y2, CR 547-1-2-3, TUTOROKIWASE, SADRI, ZAKHA, TEQING, TAREME, IR 11C170, LEMONT, IR 10C172, HHZ 5 SAL8 DT7 SAL1, GANJAY, IR 11C130, RJT 74, HHZ 8 SAL14 SAL1 SUB1, PEH-KUH-TSAO-TU, IR 11C173, GHRAB, HHZ8 SAL12 Y2 DT1, NERICA 17, IR 10C 113, HHZ 5 SAL 1O DT3 Y2, IR 10C139, HHZ 7 DT6 Y1 DT1, HHZ 12 SAL2 Y3 Y2, LAROME, HHZ5 SAL14 SALZ Y2, DARIAL, IR 11C119, HHZ 5 DT20 DT2 DT1, 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, |
| 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 72583-B-3-2-3-2B-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, 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 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 |
|-----------|------------|-------------|------------|-----------|------------|-------------|--------------|------------|-----------|------------|------------|-------------|-------------|-------------|
| 377.09 (19.42) | 1979.16 (44.49) | 6651.81 (81.56) | 3250.54 (57.01) | 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) |
| 3011.81 (70.79) | 1879.92 (43.36) | 2103.54 (45.86) | 3805.99 (31.13) | 1322.30 (55.88) | 9156.79 (95.69) | 3313.43 (57.56) | 2783.57 (63.93) | 4086.80 (49.20) | 11076.83 (105.25) | 18118.28 (63.15) | 2588.38 (50.88) | 3532.82 (59.44) | 9686.27 (99.34) |
| 5011.81 (70.79) | 3250.54 (57.01) | 2103.54 (45.86) | 3805.99 (31.13) | 1322.30 (55.88) | 9156.79 (95.69) | 3313.43 (57.56) | 2783.57 (63.93) | 4086.80 (49.20) | 11076.83 (105.25) | 18118.28 (63.15) | 2588.38 (50.88) | 3532.82 (59.44) | 9686.27 (99.34) |
| 1979.16 (44.49) | 6651.81 (81.56) | 3250.54 (57.01) | 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) |

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.)

| S. no. | Characters | 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) |
|--------|------------|------------------------|------------------|-------------------|---------------------|-----------------|-----------------------------|------------------|------------------------|----------------------|----------------------|-----------------------|
| 1      | Days to 50% flowering | 110.222                | 140.089          | 87.743            | 23.920              | 17.112          | 12.028                      | 142.786          | 83.826                | 20.354                | 71.111                | 29.154                |
| 2      | Days to maturity      | 102.461                | 132.904          | 84.458            | 22.219              | 15.815          | 12.478                      | 107.959          | 84.672                | 21.146                | 82.421                | 24.683                |
| 3      | Plant height (cm)     | 105.294                | 136.229          | 91.329            | 21.000              | 17.979          | 13.015                      | 70.615           | 62.818                | 19.976                | 62.000                | 13.106                |
| 4      | Panicle length (cm)   | 102.147                | 132.171          | 99.765            | 22.020              | 17.295          | 12.560                      | 81.997           | 80.808                | 20.395                | 83.985                | 19.218                |
| 5      | Number of tillers per hill | 101.722               | 130.839          | 105.895           | 22.325              | 16.151          | 12.017                      | 59.333           | 42.364                | 19.200                | 65.889                | 7.719                 |
| 6      | Number of productive tillers per hill | 103.500               | 135.700          | 88.790            | 21.951              | 17.140          | 14.895                      | 129.288          | 88.161                | 14.063                | 84.250                | 26.458                |
| 7      | Number of grains per panicle | 99.000                | 126.450          | 84.625            | 24.808              | 16.590          | 16.245                      | 129.154          | 87.401                | 14.036                | 84.250                | 30.853                |
| 8      | Spikelet fertility (%) | 110.500                | 143.200          | 88.995            | 20.961              | 14.090          | 4.720                       | 123.686          | 85.061                | 20.915                | 89.250                | 18.673                |
| 9      | 1000-grain weight (g) | 105.239                | 134.825          | 93.680            | 23.503              | 16.579          | 12.175                      | 129.588          | 79.727                | 19.927                | 76.212                | 24.126                |
| 10     | Pollen viability (%)  | 100.500                | 130.200          | 77.695            | 24.160              | 12.690          | 10.720                      | 90.986           | 79.151                | 23.395                | 49.250                | 19.472                |
| 11     | Single plant yield (g) | 99.500                 | 129.700          | 109.350           | 25.150              | 10.340          | 8.895                       | 135.635          | 42.016                | 17.994                | 29.250                | 21.253                |

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 eigenvalues, 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.)

| Traits                          | 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 CHOTA  | 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.   | TODOROKIWAISE | 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 71866-3R-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.  | JUAI            | 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.  | GHARIB          | 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                 | 182.225  | 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   | -17.352  | 85.165   |
| 129  | HHZ12 Y4 DT1 Y2     | 209.139  | 81.080   | -6.655   | -28.771  | 60.303   |
| 130  | HHZ 5 SAL 14 SAL2 Y1| 187.988  | 77.868   | 6.656    | -20.592  | 49.992   |
| 131  | HHZ 8 SAL14 SAL1 SUB1 | 205.095 | 77.778   | -0.318   | -13.057  | 81.368   |
| 132  | IR IOC 157           | 201.038  | 89.457   | -2.693   | -15.603  | 81.638   |
| 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 SALI| 212.248  | 86.037   | -3.888   | -26.716  | 73.210   |
| 136  | HHZ 5 DT20 DT2 DTI  | 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 10C 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 Y1 DTI     | 156.578    | 109.737    | 18.698     | -34.744    | 72.268     |
| 155  | HHZ 12 Y4 Y1 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 11C126          | 209.448    | 96.891     | 1.400      | -27.197    | 29.000     |
| 161  | IR 11C120          | 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 72593-3-3-2-3-2B-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    | 165.045   | 69.567    | 62.26     | 6.695    | 96.442    |
| 187  | CPAU -17    | 150.690   | 73.271    | 13.001    | -6.078   | 93.554    |
| 188  | CPAU -18    | 165.525   | 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, CPAU -29. |
| VII        | 4                | NERICA-L-45, NERICA-L-44, HHZ5 Y3 Y1 DT1, 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              | TODOROKIWARSE, 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 - 3R -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 IOC 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, JJAI, 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)

| Cluster | 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 PC1 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 PC1, and days to 50% flowering and maturity were loaded in PC2, and number of tillers per hill and number of productive tillers per hill in PC3, spikelet fertility, days to maturity and days to 50% flowering in PC4 and pollen viability
and plant height in PC2 towards variability. In the present study, D^2 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 D^2 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, D^2 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 D^2 cluster analysis and principal components analysis corroborated with each other.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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