# Genetic diversity analysis for yield and quality traits in rice cultivars of Manipur and Assam.

## ABSTRACT

The North–Eastern region of India is blessed with wide variability in rice. The present investigation was carried out with 41 diverse cultivars of rice collected from the farmers' fields of Manipur and Assam to estimate the nature and magnitude of genetic divergence among the genotypes using Mahalanobis $D^2$ statistics. The germplasm consisted of the popular black rice and some glutinous and non-glutinous rice which are commonly grown in both regions. The experimental materials were evaluated during the Kharif season of 2020-2021, following a randomized block design with three replications at the experimental field of BN College of Agriculture, Biswanath Chariali, Assam. The genotypes exhibited significant differences for all 24 characters under study. The cluster analysis indicated that 41 genotypes were grouped under 12 different clusters and cluster IV was the largest comprising the maximum number of genotypes with 12 genotypes, followed by cluster V with eight genotypes, cluster X with five genotypes, clusters II and XII with four genotypes each, cluster I with two genotypes and clusters III, VI, VII, VIII, IX & XI with one genotype each. Among all the characters studied, grain length exhibited maximum contribution towards divergence followed by kernel length after cooking, grain breadth, 100-grain weight and kernel breadth after cooking. Clusters X and XII showed the maximum inter-cluster distance and the maximum intra-cluster distance was exhibited by cluster XII, indicating the existence of a significant amount of variability within the cluster. The intra-cluster distance ranged from zero (clusters III, VI, VII, VIII, IX, XI) as they consist of a single genotype each to 1146.89 (cluster XII). Hybridization among the genotypes of ~~these two~~ clusters X and XII is expected to produce better heterotic combinations.

**Keywords:** Rice, diversity, $D^2$ statistics, hybridization.

## INTRODUCTION

Rice (*Oryza sativa* L. 2n=24) is the most important staple food crop in the world particularly the South East Asia including India. About 90% of all rice in the world is grown and consumed in the Asian region which is also known as the 'Rice Bowl of the World'(Khush and Virk [1]. Globally, India stands first in the area and second in production after China and contributing 25.1% of global rice production. Among the states, the North-

Eastern region of India is endowed with rich biodiversity. It is considered to be one of the hot pockets of rice genetic resources in the world with extremely diverse rice-growing conditions as compared to other parts of the country. Particularly in this region, rice has played an important role in ensuring food security and it has been known for its contribution to various cultural aspects since time immemorial. Currently, the production in the region has been facing many constraints including the decreasing cultivation of paddy, rapid population growth, and the increasing shortage of labor. Hence, it is necessary to perform the study on-field performances in grain yield and quality aspects. In the past few years, rice grain quality breeding has become a major attraction ~~in the past few years~~ and very limited studies have been done to evaluate the extent of genetic diversity for the grain quality attributes of rice in the region. With the increase in population, it is very important to analyze whether the production of rice can keep pace with population growth. Hence, to support the demand of the increasing population, emphasis should be given to the development of high-yielding rice with outstanding quality traits. This can be achieved by breaking the existing yield plateau and by utilizing more diversified parents in breeding programs as emphasized by Swamy *et al.*[2].

For a successful breeding program, the most essential prerequisite is the availability of genetic variability, and the development of superior hybrids with good qualities mainly depends on the existence of diversity among the genotypes. The study of genetic diversity allows us to know about the magnitude of genetic variability that is available in the population and also gives information about the genetic distance among the group of genotypes. The knowledge of genetic diversity in terms of nature and degree of divergence for grain yield, yield components, and quality characters help the breeders in the selection of parents for hybridization for developing potential high-yielding rice varieties with good grain qualities as reported by Ogunbayo *et al.* [3]. The more diverse the parents, the greater the chances of obtaining a higher amount of heterotic expression in $F_1$ s and a broad spectrum of variability in segregating generations as suggested by Singh *et al.* [4]. The use of Mahalanobis $D^2$ statistics for estimating genetic divergence has been emphasized by Shukla *et al.* [5] and Garh *et al.* [6]. Therefore, the present investigation was carried out to estimate the nature and magnitude of genetic divergence present in the 41 rice genotypes and to identify the diverse genotypes for a future breeding program.

## MATERIALS AND METHODS

41 rice genotypes (Table 1) collected from the farmers' fields of Manipur and Assam were transplanted in a randomized block design with three replications during the *Kharif*

season, (June to November) 2020. In each replication, the plants were grown with a spacing of 20 cm between the plants and 25 cm between the rows. Five plants from each plot in each replication were randomly sampled for observation for days to 50 percent flowering, days to maturity, plant height (cm), panicle length (cm), panicle number per plant, the total number of grains per panicle, number of filled grains per panicle, 100-grain weight (g), spikelet fertility, grain yield (g), biological yield (g), harvest index, panicle harvest index, grain length (mm), grain breadth (mm), grain length: breadth ratio, kernel length (mm), kernel breadth (mm), kernel length: breadth ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, kernel widening ratio and volume expansion ratio. The analysis of variance (ANOVA) was done using the RCBD design as suggested by Panse and Sukhatme [7]. Mahalanobis' $D^2$ statistic [8] was used for assessing the genetic divergence between the rice cultivars under study for 24 characters and the percent contribution of each character was estimated following Tocher's method as suggested by Rao [9] and described by Singh and Choudhury [10]. The data analysis was carried out using INDOSTAT software.

## RESULTS AND DISCUSSION

Analysis of variance for 24 characters revealed significant differences among the genotypes for all the characters under study at a 1% level of significance indicating the presence of greater variability among the genotypes studied suggesting that there is ample scope for selection from these diverse sources for yield and its components and quality traits. The details pertaining to ANOVA are presented in **Table 2**. These results were in accordance with Ketan *et al.* [11] and Devi *et al.* [12].

The distribution of 41 genotypes in different clusters is presented in **Table 3**. The genotypes could be clustered into 12 clusters based on Mahalanobis $D^2$ values. Sabesan *et al.* [13] calculated a similar clustering pattern for 26 rice genotypes into 13 different clusters based on 12 morphological and quality characters. The maximum number of genotypes were grouped in cluster IV with 12 genotypes, followed by cluster V with eight genotypes, cluster X with five genotypes, clusters II and XII with four genotypes each, cluster I with two genotypes and clusters III, VI, VII, VIII, IX & XI maintained their separate identities by forming monogenetic groups with one genotype each. The distribution of the germplasm into many clusters showed the presence of genetic diversity among the germplasm taken in the experiment which further indicated that the materials considered may serve as a good source for selecting the diverse parents for hybridization programs for isolating desirable segregants for grain yield and quality traits. These results concur with the results shown by Chandramohan *et al*. [14] and Devi *et al.* [15].

The grouping of the clusters revealed that the genotypes did not follow their geographical distribution as the varieties from diverse sources can be seen to be grouped into the same cluster. For example, in clusters IV and XII, the genotypes originating from both Manipur and Assam were included. The possible reason for clustering of genotypes of different states in a single cluster could be due to the free exchange of germplasm among the breeders of different regions, or unidirectional selection practiced by the breeder in tailoring the promising cultivars for different regions. Similar results were seen by Chaturvedi and Maurya [16] and Sabesan [17]. Whereas, clusters II and VI were observed to have only the Manipuri varieties, and clusters I, III, V, VII, VIII, IX, X, and XI consisted only of the genotypes from Assam. On the contrary, the genotypes originating from a common geographical location were also grouped into different clusters, which may be a result of differential adaptation to varied agroecosystems [18, 19]. This revealed that geographic diversity is not the sole factor in contribution to genetic diversity and that it may be due to different genetic backgrounds involved in the clustered genotypes.

The intra-cluster distance was minimum (68.59) for cluster I, and zero for clusters III, VI, VII, VIII, IX, and XI as they consist of a single genotype each. It was maximum (1146.89) for cluster XII. The inter-cluster distance was also recorded minimum of 104.43 (between clusters I and III) which indicated a close relationship and presence of similarity for most of the characters and was maximum (2678.57) between clusters X and XII, which indicates the presence of high diversity among the genotypes. Clusters X with five genotypes and cluster XII with four genotypes were the most divergent groups with a maximum inter-cluster distance of 2678.57 (**Table 3**). Therefore, it is expected that intercrossing between two genotypes of these clusters having high inter-cluster distance can exhibit a high heterotic effect and would yield better recombinants. These findings corroborate well with Chandra *et al.* [20], Anjali *et al.* [21] and Shivani *et al.* [22] regarding the use of parents with wide inter-cluster distances in hybridization programs since intercrossing between divergent parents is likely to produce wide variation and transgressive segregations. Rahaman *et al.* [23] and Souroush *et al.*, [24] also suggested the same**.**

Cluster means analysis with respect to 24 characters revealed a wide range of variation for all the traits under study and is presented in Table 5. Cluster II exhibited the maximum cluster means for grain length: breadth ratio, kernel length: breadth ratio and kernel widening ratio. Cluster III showed the maximum cluster means for kernel elongation ratio and volume expansion ratio and the highest cluster means for kernel length, grain yield per plant, biological yield and grain length were exhibited by cluster VI. Cluster VII showed maximum values for panicle length, the total number of grains per panicle, number of filled grains per panicle, 100-grain weight, spikelet fertility and panicle harvest index. The maximum cluster means for days to maturity, kernel breadth and kernel breadth after cooking were exhibited by cluster VIII. For panicle number per plant and harvest index, the maximum cluster mean values were shown by cluster IX; cluster XI genotypes exhibited the maximum cluster means for days to 50 percent flowering, days to maturity, plant height and grain breadth. Cluster XII exhibited the maximum cluster mean value for kernel length after cooking. It was observed that all the clusters did not contain genotypes with all the desirable traits which could be directly selected. The minimum and maximum cluster means were found to be distributed in relatively distant clusters. However, it can be estimated that the genotypes belonging to cluster V are endowed with many important traits.

The percent contribution of 24 characters to the total genetic divergence is presented in **Table 6**. Among all the characters studied, the maximum contribution towards divergence was found to be provided by grain length followed by kernel length after cooking, grain breadth, 100-grain weight, kernel breadth after cooking, days to 50 percent flowering, volume expansion ratio, panicle harvest index, biological yield, days to maturity, plant height, panicle length, kernel elongation ratio, panicle number per plant, grain yield per plant and kernel length. While characters *viz.* total number of grains per panicle, number of filled grains per panicle, spikelet fertility, harvest index, grain length: breadth ratio, kernel breadth, kernel length: breadth ratio and kernel widening ratio showed no contribution towards divergence and hence, they were of less importance. Therefore, those characters having maximum contribution towards divergence should be given importance during hybridization programs as selection and choice for potential parents mainly depend on their contribution and selection for these characters may be rewarding. The results corroborate well with the findings of Chandramohan *et al.* [14]; Bharathi *et al.* [25]and Saraswathi *et al.* [26].

Based on the mean performance of the genotypes for different traits, their genetic distance and their contribution to total divergence, genotypes with desirable characteristics can be selected for hybridization programs to produce a greater heterotic effect. Hence, it can be suggested that the earliness of Maizubiron from cluster XII concerning days to 50 percent flowering and maturity can be utilized in crossing with diverse genotypes from different clusters to develop early maturing plant varieties and for enhancing the performance of the genotypes with respect to different desirable traits.

**Table 1. List of 41 rice cultivars taken for the experiment**

| Sl. No. | Genotypes | Sl. No. | Genotypes |
|---|---|---|---|
| 1. | Bhogali | 22. | Kunkuni Joha |
| 2. | Biriabhonga Bao | 23. | Machuri |
| 3. | Biyoi Sali | 24. | Maguri Dhan |
| 4. | Black Rice | 25. | Maizubiron |
| 5. | Boga Joha | 26. | Maizubiron 1 |
| 6. | Bokul | 27. | Manipur Joha |
| 7. | Bonni | 28. | Manohar Sali |
| 8. | Bor Jahinga | 29. | Navin Dhan |
| 9. | Buthao Sticky Rice | 30. | Nepali Sokowa |
| 10. | Chaoren Phou | 31. | Noinoi Phou |
| 11. | Hacky Nagaland | 32. | Nolbora |
| 12. | Hemo Phou | 33. | Rangali Sali |
| 13. | Hindubor | 34. | Ranjit |
| 14. | Kaleja Phou | 35. | Sekmai Phou |
| 15. | Karbi Dhan | 36. | Solpuna |
| 16. | Kokua Bao | 37. | Sulsuli Bao |
| 17. | Kola Joha | 38. | Swarna Joha |
| 18. | Kola Manipuri | 39. | Thoibi Phou |
| 19. | Kolakon Joha | 40. | Til Bora 1 |
| 20. | Konguti | 41. | Xaru Jahinga |
| 21. | Kumol Dhan 1 | | |

**Table 2: Analysis of variance for yield, yield components and quality traits in rice cultivars.**

| Sl no. | Character | Mean Sum of Squares | | | CV (%) | CD (5 %) |
|---|---|---|---|---|---|---|
| | | Replication (d.f= 2) | Treatment (d.f= 40) | Error (d.f= 80) | | |
| 1. | Days to 50 percent flowering | 8.422 | 445.781** | 2.872 | 1.41 | 2.75 |
| 2. | Days to maturity | 2.203 | 487.536** | 5.311 | 1.52 | 3.74 |
| 3. | Plant height (cm) | 388.108 | 2818.96** | 89.081 | 5.99 | 15.33 |
| 4. | Panicle length (cm) | 10.847 | 27.021** | 3.309 | 6.74 | 2.95 |
| 5. | Panicle number per plant | 6.508 | 12.889** | 0.761 | 8.32 | 1.41 |
| 6. | Total number of grains per panicle | 222.038 | 5901.24** | 194.070 | 10.29 | 22.63 |
| 7. | Number of filled grains per panicle | 232.292 | 4979.98** | 123.042 | 10.66 | 18.02 |
| 8. | 100-grain weight (g) | 0.0007 | 0.566** | 0.002 | 2.13 | 0.07 |
| 9. | Spikelet fertility | 29.934 | 206.215** | 26.522 | 6.81 | 8.36 |
| 10. | Grain yield per plant (g) | 52.416 | 183.088** | 7.210 | 13.20 | 4.36 |
| 11. | Biological yield (g) | 166.696 | 716.824** | 19.546 | 8.62 | 7.18 |
| 12. | Harvest index | 20.969 | 507.929** | 9.972 | 7.73 | 5.13 |
| 13. | Panicle harvest index | 4.019 | 57.445** | 2.710 | 1.98 | 2.67 |
| 14. | Grain length (mm) | 0.010 | 2.861** | 0.003 | 0.71 | 0.09 |
| 15. | Grain breadth (mm) | 0.014 | 0.412** | 0.001 | 1.56 | 0.07 |
| 16. | Grain length: breadth ratio | 0.022 | 0.517** | 0.002 | 1.72 | 0.08 |
| 17. | Kernel length (mm) | 0.037 | 1.934** | 0.008 | 1.62 | 0.15 |
| 18. | Kernel breadth (mm) | 0.024 | 0.284** | 0.006 | 3.62 | 0.13 |
| 19. | Kernel length:breadth ratio | 0.048 | 0.482** | 0.006 | 3.06 | 0.13 |
| 20. | Kernel length after cooking (mm) | 0.012 | 3.687** | 0.006 | 0.95 | 0.12 |
| 21. | Kernel breadth after cooking (mm) | 0.008 | 0.627** | 0.001 | 1.15 | 0.07 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 22. | Kernel elongation ratio | 0.0004 | 0.017** | 0.0005 | 1.64 | 0.03 |
| 23. | Kernel widening ratio | 0.004 | 0.070** | 0.003 | 3.34 | 0.09 |
| 24. | Volume expansion ratio | 0.009 | 1.269** | 0.010 | 3.50 | 0.16 |

** Significant at 1 % level

**Table 3: Clustering pattern of 41 rice genotypes.**

| Clusters | No. of Entries | Name of genotypes |
|---|---|---|
| **I** | 2 | Navin Dhan, Swarna Joha |
| **II** | 4 | Buthao Sticky Rice, Sekmai Phou, Thoibi Phou, Hemo Phou |
| **III** | 1 | Karbi Dhan |
| **IV** | 12 | Kokua Bao, Til Bora 1, Manohar Sali, Ranga Sali, Black Rice, Xoru Jahinga, Manipuri Joha, Maguri Dhan, Hacky Nagaland, Bokul, Bonni, Kaleja Phou |
| **V** | 8 | Solpuna,Sulsuli Bao, Machuri, Kumol Dhan 1, Ranjit, Nolbora, Nepali Sokowa, Bor Jahinga |
| **VI** | 1 | Chaoren Phou |
| **VII** | 1 | Biria Bhonga Bao |
| **VIII** | 1 | Biyoi Sali |
| **IX** | 1 | Maizubiron 1 |
| **X** | 5 | Kola Joha, Kunkuni Joha, Boga Joha, Konguti, Kolakon Joha |
| **XI** | 1 | Hindubor |
| **XII** | 4 | Bhogali, Kola Manipuri, Noinoi Phou, Maizubiron. |

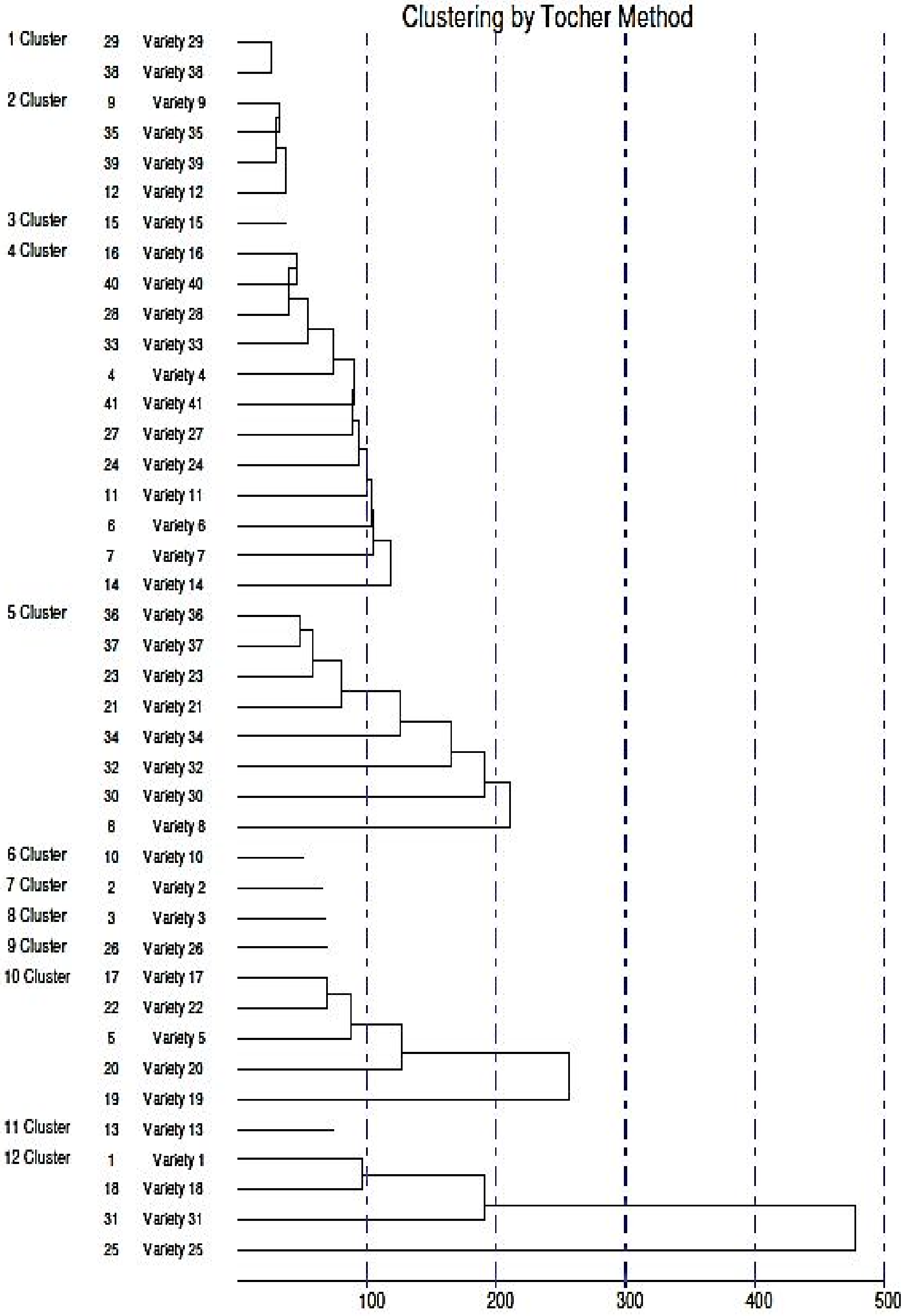

**Fig. 1: Dendrogram based on Cluster analysis by Tocher's method**

**Table 4: Average inter and intra cluster distances for yield, yield components and quality traits in rice genotypes**

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | **68.59** | | | | | | | | | | | |
| **II** | 221.38 | **120.39** | | | ` | | | | | | | |
| **III** | 104.43 | 427.62 | **0.00** | | | | | | | | | |
| **IV** | 365.78 | 340.45 | 607.25 | **289.77** | | | | | | | | |
| **V** | 454.73 | 583.02 | 626.10 | 425.82 | **495.24** | | | | | | | |
| **VI** | 418.41 | 192.33 | 661.17 | 375.63 | 728.20 | **0.00** | | | | | | |
| **VII** | 702.99 | 532.05 | 998.52 | 465.54 | 734.54 | 510.24 | **0.00** | | | | | |
| **VIII** | 691.86 | 623.38 | 933.23 | 572.23 | 723.92 | 824.91 | 181.64 | **0.00** | | | | |
| **IX** | 764.75 | 755.94 | 979.03 | 754.67 | 909.72 | 995.67 | 356.92 | 183.11 | **0.00** | | | |
| **X** | 1746.67 | 2050.57 | 1733.51 | 1836.43 | 1789.90 | 2374.78 | 1627.95 | 1378.13 | 915.10 | **565.72** | | |
| **XI** | 777.31 | 706.64 | 946.57 | 581.34 | 692.75 | 792.25 | 350.13 | 196.34 | 435.94 | 1460.08 | **0.00** | |
| **XII** | 656.91 | 690.18 | 822.44 | 696.87 | 872.67 | 683.98 | 1113.77 | 1200.91 | 1459.37 | 2678.57 | 1136.15 | **1146.89** |

* Diagonal values indicate intra cluster distances * Above and below diagonal values indicate inter cluster distances

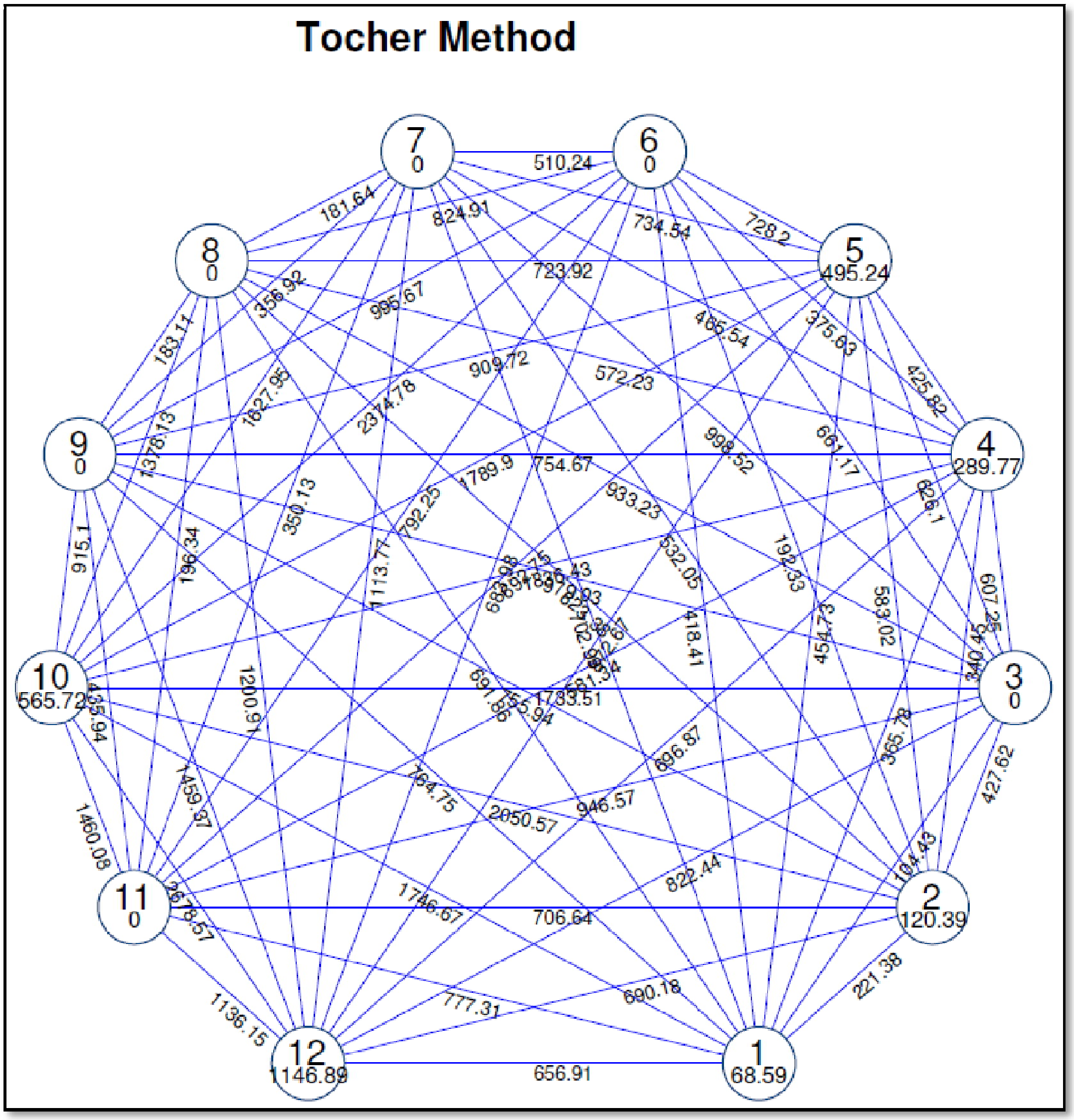

**Fig 2: Mahalonobis' Euclidean distance**

**Table 5: Cluster means for yield, yield components and quality traits in rice genotypes**

| Clusters | DF | DM | PH | PL | PN | TG | FG | 100 gw | SF | GYP | BY | HI |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 99.83 | 131.50 | 124.99 | 25.41 | 11.11 | 85.61 | 61.84 | 2.09 | 72.21 | 15.01 | 37.74 | 40.28 |
| II | 107.67 | 139.42 | 99.96 | 23.47 | 9.03 | 105.94 | 76 | 2.26 | 72.36 | 14.54 | 42.11 | 39.08 |
| III | 89.33 | 118.67 | 132.53 | 26.26 | 8.22 | 93.02 | 74.89 | 1.82 | 80.51 | 11.48 | 42.12 | 27.25 |
| IV | 123.17 | 155.03 | 171.06 | 27.44 | 11.13 | 149.32 | 116.02 | 2.32 | 77.18 | 22.66 | 52.59 | 44.34 |
| V | 127.42 | 159.17 | 167.44 | 26.65 | 10.90 | 145.48 | 113.23 | 1.96 | 75.28 | 23.23 | 49.77 | 44.84 |
| VI | 109.33 | 139.33 | 115.55 | 25.68 | 11.45 | 130.67 | 99.45 | 2.71 | 76.12 | 32.65 | 92.94 | 34.65 |
| VII | 126.33 | 155.33 | 190.29 | 33.28 | 7.67 | 201.45 | 174.44 | 2.92 | 86.62 | 28.23 | 73.76 | 38.28 |
| VIII | 129 | 166.33 | 162.64 | 29.22 | 9.44 | 107.89 | 84.22 | 2.29 | 78.07 | 19.77 | 45.33 | 43.63 |
| IX | 127.33 | 157.33 | 173.90 | 29.74 | 13.22 | 107.56 | 81.44 | 2.14 | 75.54 | 22.96 | 49.08 | 46.97 |
| X | 127.13 | 156.87 | 157.38 | 27.90 | 10.71 | 149.81 | 120.48 | 1.44 | 78.49 | 17.14 | 55.52 | 31.41 |
| XI | 133.33 | 166.33 | 193.45 | 28.51 | 9.33 | 82.89 | 52.78 | 1.88 | 63.98 | 9.35 | 68.50 | 13.52 |
| XII | 108.42 | 141.08 | 163.45 | 26.64 | 9.11 | 131.28 | 92.31 | 2.28 | 70.80 | 19.33 | 44.48 | 46.43 |

**Table 5 Contd…**

| Clusters | PHI | GL | GB | GL: B | KL | KB | KL: B | KLC | KLB | KER | KWR | VER |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 81.95 | 8.31 | 2.54 | 3.28 | 5.83 | 2.13 | 2.74 | 8.46 | 3.87 | 1.45 | 1.82 | 3.37 |
| II | 79.40 | 8.91 | 2.71 | 3.29 | 6.24 | 2.22 | 2.82 | 8.16 | 4.10 | 1.31 | 1.85 | 3.04 |
| III | 82.91 | 8.14 | 2.51 | 3.25 | 5.60 | 2.21 | 2.53 | 8.47 | 3.72 | 1.51 | 1.69 | 3.79 |
| IV | 83.98 | 8.55 | 2.87 | 3.01 | 6.14 | 2.31 | 2.69 | 8.65 | 3.85 | 1.41 | 1.68 | 2.90 |
| V | 84.11 | 8.38 | 2.69 | 3.17 | 6.08 | 2.18 | 2.81 | 8.83 | 3.72 | 1.46 | 1.72 | 3.31 |
| VI | 82.51 | 8.99 | 3.05 | 2.95 | 6.36 | 2.46 | 2.59 | 8.81 | 4.10 | 1.38 | 1.67 | 2.59 |
| VII | 91.71 | 8.04 | 3.00 | 2.69 | 5.36 | 2.42 | 2.22 | 7.55 | 4.24 | 1.41 | 1.76 | 3.16 |
| VIII | 86.49 | 7.88 | 3.11 | 2.54 | 5.13 | 2.74 | 1.87 | 7.29 | 4.30 | 1.42 | 1.57 | 3.28 |
| IX | 85.23 | 7.29 | 2.89 | 2.52 | 4.87 | 2.32 | 2.10 | 6.54 | 4.14 | 1.34 | 1.78 | 1.97 |
| X | 78.73 | 6.09 | 2.39 | 2.57 | 4.23 | 1.81 | 2.37 | 6.13 | 2.91 | 1.44 | 1.62 | 1.77 |
| XI | 75.63 | 8.09 | 3.37 | 2.40 | 5.44 | 2.63 | 2.07 | 7.88 | 4.15 | 1.45 | 1.58 | 3.74 |
| XII | 83.88 | 8.90 | 3.16 | 2.88 | 6.33 | 2.46 | 2.68 | 9.28 | 3.85 | 1.47 | 1.59 | 2.94 |

**Table 6. Percent distribution of each character towards divergence in rice genotypes ~~evaluated in field condition~~.**

| Sl no. | Character | Contribution (%) |
|---|---|---|
| **1** | Days to 50 percent flowering | 6.46 |
| **2** | Days to maturity | 0.37 |
| **3** | Plant height | 0.24 |
| **4** | Panicle length | 0.24 |
| **5** | Panicle number per plant | 0.12 |
| **6** | Total number of grains per panicle | 0.00 |
| **7** | Number of filled grains per panicle | 0.00 |
| **8** | 100- grain weight | 9.51 |
| **9** | Spikelet fertility | 0.00 |
| **10** | Grain yield per plant | 0.12 |
| **11** | Biological yield | 2.44 |
| **12** | Harvest index | 0.00 |
| **13** | Panicle harvest index | 2.68 |
| **14** | Grain length | 40.73 |
| **15** | Grain breadth | 9.88 |
| **16** | Grain length: breadth ratio | 0.00 |
| **17** | Kernel length | 0.12 |
| **18** | Kernel breadth | 0.00 |
| **19** | Kernel length: breadth ratio | 0.00 |
| **20** | Kernel length after cooking | 17.44 |
| **21** | Kernel breadth after cooking | 6.59 |
| **22** | Kernel elongation ratio | 0.24 |
| **23** | Kernel widening ratio | 0.00 |
| **24** | Volume expansion ratio | 2.8 |

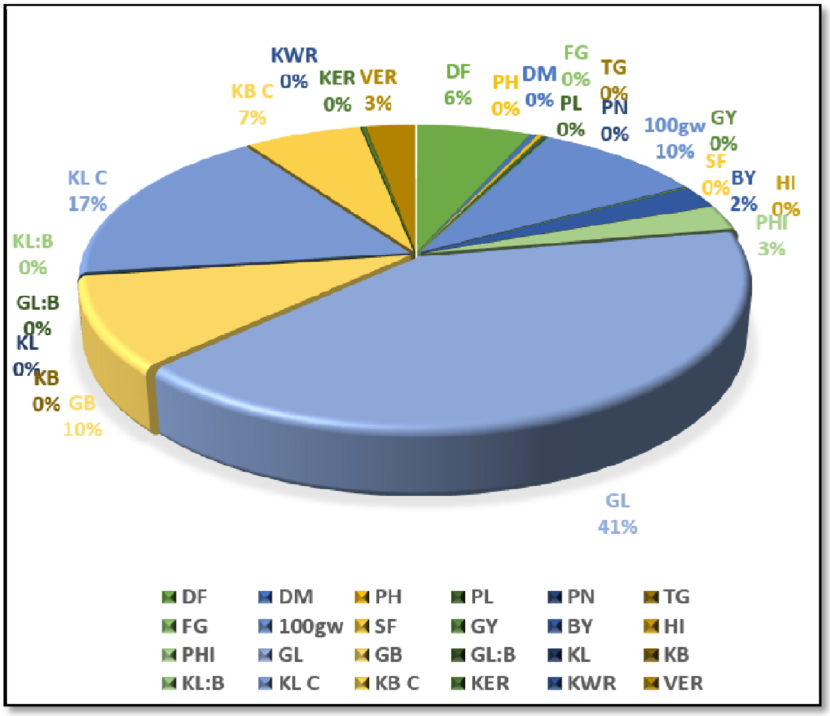

**Fig 3: Percent contribution of different characters towards genetic divergence in genotypes**

## CONCLUSION

From the above findings, it can be concluded that substantial genetic diversity was observed in the materials studied for all the traits. It can be estimated that these germplasm lines can be taken as breeding material in future regional breeding programs, mainly focusing on the rice grain quality. Recombination breeding can be suggested among the genotypes of cluster XII having a maximum intra-cluster distance to improve the yield potential. As the maximum inter-cluster distance was observed between clusters X and XII, crosses involving the genotypes from these two clusters would give wider and desirable recombinations. Hence, an efficient hybridization program can be formulated for breeding better quality grains with higher yields by crossing two distantly related superior rice genotypes.

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## AUTHORS' CONTRIBUTIONS

This work was carried out in collaboration among all authors. Author NSD designed the study, conducted the experiment, wrote the protocol, and wrote the first draft of the manuscript. Author SZ, MKS and JB supervised and made the final presentation of the manuscript. Author DDS, MPN, JCT and ASNA helped in performing the laboratory analysis, collection and tabulation of the data.

## ETHICAL APPROVAL

There is no involvement of ethical issues regarding the report on the manuscript.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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