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# Genetic diversity analysis of aromatic rice germplasm

**G Parimala[1]*, Ch Damodhar Raju[2], LV Subba Rao[3], K Uma Maheswari[4]**
[1] Department of Genetics and Plant Breeding, College of Agriculture, PJTSAU, Rajendra Nagar, Hyderabad, Telangana, India
[2] Department of Genetics and Plant Breeding, Rice Research Centre, Agricultural Research Institute, Rajendra Nagar, Hyderabad, Telangana, India
[3] Department of Genetics and Plant Breeding, Indian Institute of Rice Research (IIRR), Rajendra Nagar, Hyderabad, Telangana, India
[4] Department of Food and Nutrition, Post Graduate & Research centre, PJTSAU, Rajendra Nagar, Hyderabad, Telangana, India

**Abstract**
The present study was conducted at the agricultural Research Institute (ARI), Hyderabad, during 2018-19 to identify potential genotypes and suitable traits of aromatic rice (Oryza sativa L.) germplasm for breeding programs. Fifty genotypes were evaluated in a randomized block design with three replications. All genotypes exhibited a wide and significant variation for 18 traits. According to $D^2$ cluster analysis, 50 test genotypes were grouped into 8 clusters. Cluster IV was the largest consisting of 8 genotypes. Out of eight clusters, cluster I was the largest comprising of twenty genotypes followed by clusters II with sixteen genotypes. The clusters IV, V, VII and VIII were solitary clusters represented by single genotype exhibiting high degree of heterogeneity among the genotypes. Maximum inter cluster distance was exhibited between clusters VI and VIII (26082.43) and lowest inter cluster distance was observed between clusters IV and V (508.53). Intra cluster $D^2$ values were minimum (0.00) in cluster IV, V, VII and VIII as these were monogenotypic clusters. The diversity profiles and Shannon diversity index ensures the existence of high genetic divergence among the studied genotypes and can be used by breeders to develop high yielding rice varieties and have immense applications in rice improvement.

**Keywords:** diversity, $d^2$ analysis, aromatic rice, shannon-diversity index

## Introduction

Aromatic rice have a great demand both in the national and international market (Mannan *et al*., 2012) [3]. Traditional basmati rice varieties are very low yielding due to their poor harvest index and tendency to lodging. Despite inferior performance, the aromatic rice is highly regarded for their excellent aroma and superior grain quality (Wakte *et al*., 2017) [8]. Hence there is a need to develop new varieties combining the grain quality attributes of basmati with high yield potential (Amarawathi *et al*., 2008) [2]. The variability of key agronomic traits in available germplasm is indeed crucial for their fruitful utilisation via recombination, breeding and selection. Efficient use of germplasm collections in plant breeding relies on the understanding of the existing genetic diversity, including its characterisation, evaluation, and classifcation. The available cultivars, genotypes, breeding lines, mutants and land races in India impart a greater genetic diversity in the cultivated rice germplasm. Rice genetic resources are the common heritage of mankind and essential for genetic improvement of rice and developing desired rice varieties. However, the genetic diversity in rice has been drastically reduced due to aggressive introduction of modern varieties and disappearance of indigenous landraces. Due to the narrow genetic base, modern rice varieties are less adaptable to varying agro-climatic conditions. Their yield performance, biotic and abiotic stress tolerance ability and other agronomic traits can be genetically broken down due to narrow genetic base. Therefore these cultivars used to disappear after few years of cultivation.

Thus, exploration of genetic resources like landraces and indigenous rice varieties is an important and urgent issue in crop breeding for developing durable, climate resilient and high yielding rice varieties with desired quality attributes. Towards these understanding of genetic relationship among rice landraces will help their proper utilization in rice breeding program. This study presents a phenotypic characterisation of the aromatic rice germplasm, focusing on yield and quality characters.

## Materials and Methods

The germplasm used in this study consisted of 50 aromatic rice accessions and were sown during kharif 2018-19 at Rice Research Centre, Agricultural Research Institute, Professor Jayashankar Telangana State Agricultural University, Rajendranagar. Healthy nursery was raised and thirty one days old seedlings were transplanted in well prepared main field. Two rows for each entry with spacing of 20 x 15 cm in randomized block design with 3 replications and each row consists of 25 plants per entry. First weeding was carried out 20 days after transplanting and second weeding 30 days after first weeding. Fertilizer application was carried at recommended dosage. Necessary crop protection measures were taken up based on need of crop. Mean data were collected for seven quantitative and eleven qualitative characters before and after harvest respectively. The mean data after computing for each character was subjected to standard methods of analysis. $D^2$ analysis was performed using INDOSTAT software.

**Results and Discussion**

Fig. 1 displays the resultant diversity profile. Generally, the Shannon–Weaver diversity index value represents the degree of diversity prevailing among the tested samples. Higher value indicates higher diversity and vice versa. In this study, the Shannon–Weaver index values ranged from 3.75 for kernel L/B ratio to 3.911 for both days to 50% flowering and head rice recovery the latter showing considerable variation. Increase in the H-based evenness value across the traits indicates the efective representativeness of the diversity available in the germplasm. Evenness varies from 0 to 1. Table 1 presents the Shannon–Weaver diversity index and evenness for the 18 traits.

All genotypes under the study were grouped into eight clusters based on $D^2$ values using Tocher's method (Rao, 1952) [1]. Genotypes with an average smaller $D^2$ values were grouped into same cluster and genotypes with an average of larger $D^2$ values were grouped into different clusters. The distribution of genotypes into various clusters in (Table 2). Out of eight clusters, cluster I was the largest comprising of twenty genotypes followed by clusters II with sixteen genotypes, cluster III with eight genotypes and cluster VI with 2 genotypes. The clusters IV, V, VII and VIII were solitary clusters represented by single genotype exhibiting high degree of heterogeneity among the genotypes, when grouping of genotypes were done by considering both quantitative and qualitative traits. The genotypes were grouped to eight clusters which were similar to the findings of Mir *et al*. (2019) [4]. The number of genotypes were highest in cluster I followed by cluster II in accordance with the findings of Pragnya *et al*. (2018) [5].$D^2$ statistic measures forces of differentiation at two levels *i.e.*, intra cluster and inter cluster levels. The average intra and inter cluster $D^2$ values are presented in (Table 3).

Intra cluster $D^2$ values were minimum (0.00) in cluster IV, V, VII and VIII as these were monogenotypic clusters and genotypes in these clusters were more divergent and they could be utilized as parents for hybridization. These results are in accordance with Supriya *et al* (2017) [6].

Maximum intra cluster distance was observed in cluster I (473.99), followed by cluster III (414.65), cluster VI (406.46) and cluster II (403.53) similar to findings of Mohan *et al* (2016) [7], revealing that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean value for the desirable characters. The intra cluster distance was lower than inter cluster distance (Table 3), indicating the existence of genetic diversity among the genotypes under study. Maximum inter cluster distance was exhibited between clusters VI and VIII (26082.43) followed by clusters III and VI (19547.19), clusters IV and VIII (1792.34), clusters V and VIII (16529.24) clusters VI and VII (16307.62) and clusters I and VIII (13780.68). Greater the distance, wider the genetic diversity among the genotypes of those clusters. For high heterotic recombinants, highly divergent and high performing genotypes would be used as parents in recombination breeding programme. The lowest inter cluster divergence was observed between clusters IV and V (508.53) followed by clusters I and V (708.05), clusters I and IV (868.09) describing that the genotypes included in these clusters were closely related. These studies were simiar to the findings of Mir *et al* (2019) [4].

The cluster means for each of 18 characters are presented in (Table 4).

From the results of cluster means generated by Tocher method, it can be concluded that considerable differences existed for all the traits studied among the clusters. Cluster means data indicates days to 50% flowering was highest in cluster VIII (114.00) and lowest in cluster IV (101.00), plant height recorded highest in cluster VII (181.30) and lowest in cluster IV(98.00), no. of effective tillers per plant was observed highest in cluster VII (21.30) and lowest in cluster IV (10.00), panicle length was highest in cluster VIII (27.30) and lowest in cluster V (22.10), 1000 grain weight recorded highest in cluster V (21.51) and lowest in cluster III (8.32), no. of grains per panicle was found to be highest in cluster VII (217.60) and lowest in cluster VI (139.61), seed yield per plant was recorded was highest in cluster VI (27.46) and lowest in cluster VII (18.22).

Hulling% was highest in cluster VII (85.65) and lowest in cluster IV (51.67), milling% recorded highest in cluster VII (72.85) and lowest in cluster I (66.01), head rice recovery found to be highest in cluster VII (60.71) and lowest in cluster VI (41.99), kernel length was highest in cluster VI (7.02) and lowest in cluster III (3.36), kernel breadth was highest in cluster VIII (2.51) and lowest in cluster I (1.58), kernel L/B ratio was observed to be highest in cluster VI (4.35) and lowest in cluster VII (1.50), kernel length after cooking was highest in cluster VI (14.82) and lowest in cluster VIII (5.20), kernel elongation ratio was observed to be highest in cluster V (2.22) and lowest in cluster VII (1.37), amylose content was highest in cluster VIII (26.21) and lowest in cluster I (21.29), alkali spread value was found to be highest in cluster IV, V (6.83) and lowest in cluster VII, VIII (4.33) and gel consistency was observed to be highest in cluster VII (53.67) and lowest in cluster VIII (22.20).

It was observed that none of clusters contain all desirable traits. Therefore, it is required to carry out hybridization programme among selected genotypes to get desirable and heterotic hybrids.

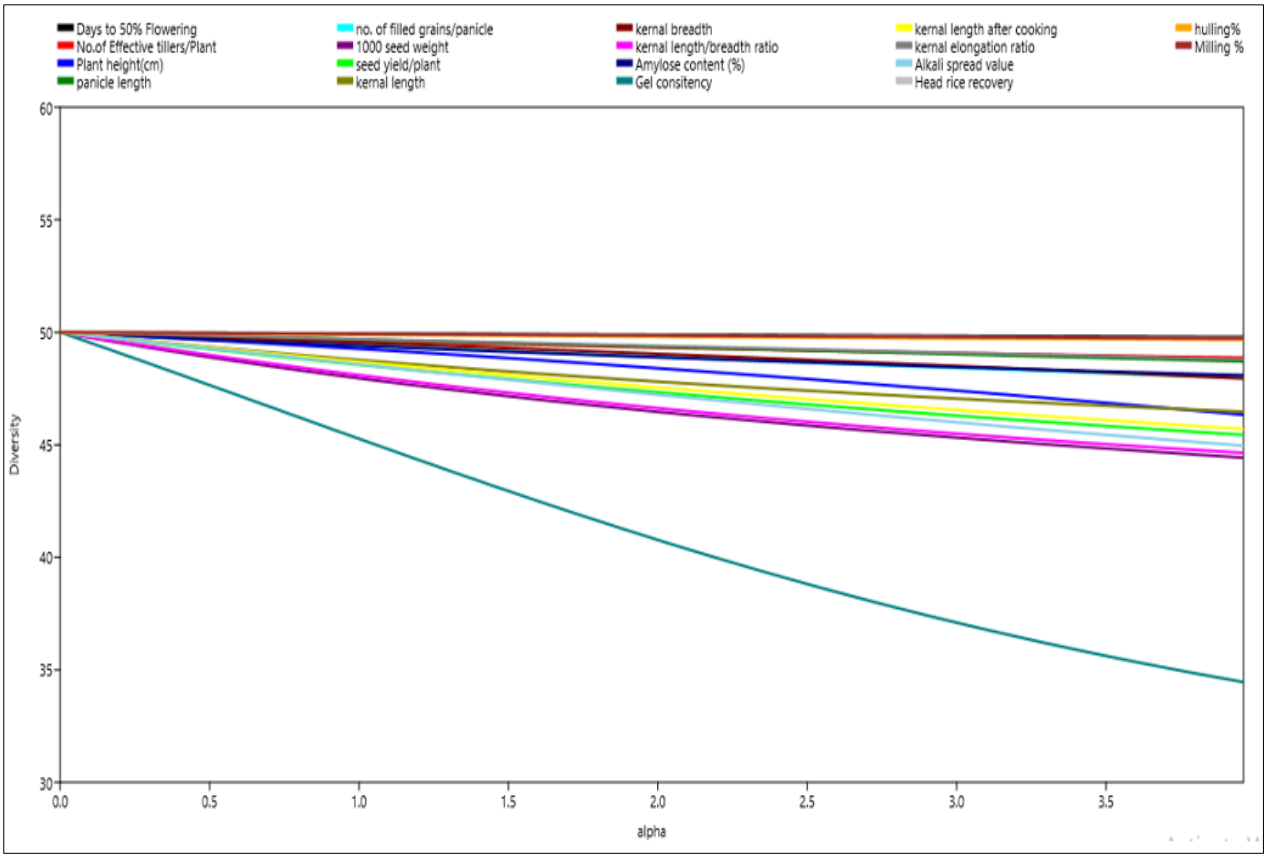


**Fig 1:** Diversity profile of eighteen characters.

**Table 1:** Phenotypic variation of 50 aromatic rice germplasm based on 18 traits.

| Sl.no | character | Shannon diversity index (H′) | Evenness |
|---|---|---|---|
| 1 | Days to 50% flowering | 3.911 | 0.998 |
| 2 | No. of effective tillers | 3.904 | 0.992 |
| 3 | Plant height | 3.897 | 0.985 |
| 4 | Panicle length | 3.906 | 0.993 |
| 5 | No. of filled grains per panicle | 3.9 | 0.988 |
| 6 | 1000-seed weight | 3.87 | 0.959 |
| 7 | Seed yield/ plant | 3.88 | 0.971 |
| 8 | Kernel length | 3.887 | 0.975 |
| 9 | Kernel breadth | 3.90 | 0.990 |
| 10 | Kernel L/B ratio | 3.75 | 0.962 |
| 11 | Amylose content | 3.9 | 0.988 |
| 12 | Gel consistency | 3.813 | 0.905 |
| 13 | Kernel length after cooking | 3.885 | 0.937 |
| 14 | Kernel elongation ratio | 3.906 | 0.993 |
| 15 | Alkali spread value | 3.883 | 0.971 |
| 16 | Head rice recovery | 3.911 | 0.998 |
| 17 | Hulling | 3.91 | 0.997 |
| 18 | Milling | 3.8 | 0.959 |

**Table 2:** Clustering pattern among 50 rice genotypes under study by Tocher method

| S. No | Cluster number | No. of Genotypes | Genotypes |
|---|---|---|---|
| 1 | I | 20 | RNR-28403, RNR-26058, RNR-17500, RNR-26010, RNR-28404, RNR17501, RNR-29301, RNR-29305, RNR-29420, RNR-29422, Sumathi, RNR-15488-2, PUSA-1121, RNR-15541, RNR-2600, RNR-26009, RNR-28408, RNR-28402, RNR 15541, RNR 28405. |
| 2 | II | 16 | RNR 28410, CR 2982-14-6-3, NVSR 406, CR 2981-16-2-6, NVSR 407, CR 3715-119-18-9-2, CR 3663-261-8-4, Ketekijoha, Shobini, R 1624-61-1-59-1, Dubraj, JDP-K-37, RNR-29423, OR (CZ)-70, NWGR 9081, RNR-29306. |
| 3 | III | 8 | RNR 15462-2, RNR 15459-1, RNR 15460-1, RNR-15459-6, RNR-15462-4, RNR-15453-2, Chittimutyalu, Sugandh Samba. |

| | | | |
|---|---|---|---|
| 4 | IV | 1 | Pusa Basmathi. |
| 5 | V | 1 | RNR-29296. |
| 6 | VI | 2 | RNR-26020, Vasumathi. |
| 7 | VII | 1 | BM 4. |
| 8 | VIII | 1 | R 1656-2151-1-412-1. |

**Table 3:** Intra (diagonal) and inter cluster distances of $D^2$ values of 50 genotypes under study

| Clusters | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 | Cluster 7 | Cluster 8 |
|---|---|---|---|---|---|---|---|---|
| Cluster 1 | 473.99 | 1785.21 | 9034.56 | 868.09 | 708.05 | 2672.58 | 7252.05 | 13780.68 |
| Cluster 2 | | 403.53 | 3822.97 | 2975.37 | 2709.99 | 7066.60 | 3090.99 | 7096.28 |
| Cluster 3 | | | 414.65 | 12449.96 | 11147.78 | 19547.19 | 1383.69 | 1476.16 |
| Cluster 4 | | | | 0.00 | 508.53 | 1325.79 | 10319.16 | 17972.34 |
| Cluster 5 | | | | | 0.00 | 1406.93 | 8876.38 | 16529.24 |
| Cluster 6 | | | | | | 406.46 | 16307.62 | 26082.13 |
| Cluster 7 | | | | | | | 0.00 | 5084.16 |
| Cluster 8 | | | | | | | | 0.00 |

**Table 4:** Cluster means of 50 rice genotypes under study by Tocher method.

| Characters | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 107.32 | 113.08 | 107.54 | 101.00 | 103.00 | 105.50 | 102.33 | 114.00 |
| Plant height | 107.75 | 117.36 | 105.53 | 98.0 | 98.20 | 112.38 | 181.30 | 130.53 |
| Effective tillers per plant | 17.81 | 18.11 | 18.77 | 10.00 | 16.33 | 17.42 | 21.30 | 17.47 |
| Panicle length | 25.21 | 24.21 | 22.41 | 25.46 | 22.10 | 26.65 | 25.90 | 27.30 |
| Panicle weight | 7.25 | 5.68 | 3.28 | 7.85 | 4.42 | 3.18 | 5.12 | 3.52 |
| 1000 grain weight | 17.84 | 17.17 | 8.32 | 20.71 | 21.51 | 20.15 | 14.83 | 16.72 |
| Grains per panicle | 147.87 | 175.38 | 155.18 | 205.33 | 143.67 | 139.61 | 217.67 | 183.00 |
| Seed yield per plant | 27.04 | 19.03 | 24.40 | 19.19 | 24.80 | 27.46 | 18.22 | 22.54 |
| Hulling | 77.40 | 81.45 | 80.80 | 51.67 | 80.78 | 78.46 | 85.65 | 82.92 |
| Milling | 66.01 | 67.93 | 66.58 | 66.73 | 68.13 | 67.28 | 72.85 | 71.68 |
| Head rice recovery | 55.01 | 56.61 | 55.49 | 55.61 | 56.78 | 41.99 | 60.71 | 59.73 |
| Kernel length | 6.34 | 5.51 | 3.36 | 6.98 | 5.84 | 7.02 | 3.68 | 3.80 |
| Kernel breadth | 1.58 | 1.84 | 1.73 | 1.85 | 1.71 | 1.61 | 2.45 | 2.51 |
| Kernel L/B ratio | 4.02 | 3.02 | 1.94 | 3.77 | 3.41 | 4.35 | 1.50 | 1.52 |
| Kernel length after cooking | 11.16 | 9.22 | 6.33 | 12.16 | 12.99 | 14.82 | 7.50 | 5.20 |
| Kernel elongation ratio | 1.77 | 1.68 | 1.89 | 1.74 | 2.22 | 2.13 | 2.04 | 1.37 |
| Amylose content | 21.29 | 25.54 | 23.24 | 23.67 | 21.31 | 23.84 | 24.62 | 26.21 |
| Alkali spread value | 5.83 | 4.88 | 4.88 | 6.83 | 6.83 | 5.17 | 4.33 | 4.33 |
| Gel consistency | 41.48 | 29.36 | 35.42 | 22.33 | 48.33 | 32.50 | 53.67 | 22.00 |

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