## Research Article

# GENETIC DIVERGENCE STUDIES ON YIELD AND YIELD ATTRIBUTING TRAITS IN RICE (*Oryza sativa* L.)

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**Abstract:** Fifty-eight genotypes of rice were studied for genetic diversity on the basis of yield and its attributing traits. Based on $D^2$ analysis, 58 rice genotypes were grouped into eight clusters. Cluster II consisted maximum of 16 genotypes followed by cluster III with 11 genotypes. Among different traits, test weight followed by days to 50% flowering, filled grains per panicle and plant height had maximum contribution towards the total divergence. PCA identified four components with eigen value more than one which contributed 85.028 percent of cumulative variance. Divergence studies indicated that selection for hybridization should be more based on genetic diversity rather than the geographical diversity.

**Keywords:** Rice, $D^2$analysis, Principal component analysis

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## Introduction

Rice (*Oryza sativa* L.) is the most important food crop in south and South East Asian countries particularly in developing countries like India and it is the third important staple food crop after maize and wheat of the world in particular. Most of the people in Asia, particularly in developing countries meet their calorific requirement through rice. Rice offers a great wealth of material for genetic studies because of its wide ecological distribution and enormous variation for various morphological and physiological characters. In the hybridization programme, diversity of parents was very much important, because the cross between the genotypes with maximum genetic divergence would be responsible for obtaining desirable improvement as they are likely to yield desirable recombinants in the progenies. Therefore, the present investigation was carried out with $D^2$ analysis, principal component analysis to study genetic divergence in 58 genotypes of rice by employing multivariate analysis.

## Material and Methods

The present experiment was carried out with 58 rice genotypes in randomized block design with two replications at Agricultural Research Station, Nellore, Andhra Pradesh during kharif 2015-16. The inter and intra row spacing adapted was 20cm x 15cm. Each plot consisted of three rows of 5m length and observations were recorded on five randomly selected plants from each plot per replication for characters viz., plant height, productive tillers per plant, panicle length, filled grains per panicle, total grains per panicle, spikelet fertility, test weight and grain yield per plant. However, days to 50% flowering and days to maturity were recorded on plot basis. The data were statistically analyzed to study genetic diversity using Mahalanobis, (1936) [1] $D^2$ statistic as per Rao, (1952) [2], principal component analysis as described by Jackson, (1991) [3].

## Result and Discussion

The analysis of variance showed significant differences among the genotypes for all the characters under study in rice indicating substantial genetic variability. Based on $D^2$ values 58 genotypes were grouped into eight clusters [Table-1]. Cluster II comprised of maximum 16 genotypes followed by cluster III with 11 genotypes, cluster V and VIII with eight genotypes, cluster I with seven genotypes and cluster VII with six genotypes while remaining clusters i.e. cluster IV and VI consisted of single genotypes indicating high degree of heterogeneity. The formation of distinct solitary clusters may be due to the fact that geographical barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. The distribution of genotypes indicated that the genetic diversity and geographical diversity were not related. This suggests that there are forces other than geographical separation such as natural or artificial selection, exchange of breeding material, genetic drift and environmental variation.

The intra cluster distance ranged from 44.32(cluster I) to 360.67 (cluster VIII). The maximum was observed between cluster VII and VIII (736.14) followed by cluster III and VII (733.51) suggesting that the genotypes from these clusters could be used as donors in hybridization programme to obtain good recombinants. These results were in accordance with the earlier findings of Ref no 3 [Table-2]. Test weight (62.86%) showed maximum contribution towards genetic divergence followed days to 50% flowering (16.45%), filled grains per panicle (9.8%) and panicle length (3.02%) [Table-3]. The relative importance of contribution of yield components towards divergence can be judged by comparing the group means of 10 characters. The highest mean values for days to 50% flowering (104.81), days to maturity (135.813), plant height (95.762), total grains per panicle (251.313) and grain yield per plant (38.80) were depicted by cluster VIII which consisted of eight genotypes viz., JGL17004, NLR33636, NLR40021, HMT Sona, NLR33641, NLR33892, NLR20084, BPT1768) [Table-4].

The principal component analysis identified five principle components in rice genotypes. The contribution by the first principal component was maximum in the groups.

Table-1 *Clustering pattern of 58 genotypes of rice by Tocher's method*

| Cluster No | No. of Genotypes | Genotypes |
|---|---|---|
| I | 7 | NLR 34449, ADT43, JGL11118, WGL 23985, Sumati, NLR3303, NDLR7 |
| II | 16 | NLR33359, NLR40058, NLR3042, NLR40065, NLR34242, NLR33671, NLR3010, ADT37, Pusa Basmati 1, Vasumati, Geetanjali, Kasturi, Suhasini, MTU 1001, NLR33654, Srikakulam sannalu |
| III | 11 | RNR2465, RNR2458, JGL11727, BPT5204, NDLR8, RNR2354, NLR3041, WGL14, WGL44, NLR20104, WGL32100 |
| IV | 1 | NLR33358 |
| V | 8 | NLR40024, NLR30491, ADT45, NLR40007, White Ponni, NLR145, NLR3083, CR1009 |
| VI | 1 | IR 64 |
| VII | 6 | ASD16, PS4, PS5, NLR33057, MTU1010, NLR34417 |
| VIII | 8 | JGL17004, NLR33636, NLR40021, HMT Sona, NLR33641, NLR33892, NLR20084, BPT1768 |

Table-2 *Average intra (bold, diagonal) and inter cluster $D^2$ values among eight clusters in 58 rice genotypes*

|  | 1 Cluster | 2 Cluster | 3 Cluster | 4 Cluster | 5 Cluster | 6 Cluster | 7 Cluster | 8 Cluster |
|---|---|---|---|---|---|---|---|---|
| Cluster I | 44.325 | 174.864 | 128.535 | 233.159 | 154.189 | 367.167 | 488.443 | 279.976 |
| Cluster II |  | 70.198 | 340.631 | 100.433 | 135.634 | 97.329 | 176.214 | 419.516 |
| Cluster III |  |  | 76.548 | 505.498 | 252.458 | 612.352 | 733.516 | 233.292 |
| Cluster IV |  |  |  | 0 | 170.639 | 83.902 | 163.282 | 581.689 |
| Cluster V |  |  |  |  | 122.144 | 218.533 | 317.592 | 356.259 |
| Cluster VI |  |  |  |  |  | 0 | 75.975 | 670.917 |
| Cluster VII |  |  |  |  |  |  | 72.654 | 736.141 |
| Cluster VIII |  |  |  |  |  |  |  | 360.671 |

Table-3 *Contribution of different characters towards genetic divergence among 58 genotypes of rice*

| Source | Times Ranked 1st | Contribution % |
|---|---|---|
| 1. Days to 50% Flowering | 272 | 16.45 |
| 2. Days to Maturity | 0 | 0.00 |
| 3. Plant Height cm | 88 | 5.32 |
| 4. Productive Tillers/ Plant | 5 | 0.30 |
| 5. Panicle Length | 50 | 3.02 |
| 6. Filled Grains/ Panicle | 162 | 9.80 |
| 7. Total Grains/ Panicle | 18 | 1.09 |
| 8. Spikelet Fertility | 18 | 1.09 |
| 9. Test Weight | 1039 | 62.86 |
| 10. Grain Yield/ Plant | 1 | 0.06 |

Table-4 *Mean values of eight clusters for 58 rice genotypes*

|  | Days to 50% Flowering | Days to Maturity | Plant Height cm | Productive Tillers/ Plant | Panicle Length(cm) | Filled Grains/ Panicle | Total Grains/ Panicle | Spikelet Fertility (%) | Test Weight(g) | Grain Yield/ Plant(g) |
|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 86.071 | 117.071 | 79.729 | 10.993 | 22.471 | 173.50 | 196.286 | 88.487 | 18.011 | 31.921 |
| Cluster II | 92.031 | 123.031 | 85.203 | 11.222 | 23.434 | 153.781 | 173.281 | 89.063 | 22.484 | 37.194 |
| Cluster III | 102.318 | 133.273 | 79.982 | 11.473 | 21.888 | 203.909 | 242.955 | 84.132 | 15.757 | 37.000 |
| Cluster IV | 78.000 | 109.000 | 76.300 | 10.800 | 18.700 | 115.000 | 129.500 | 88.640 | 24.005 | 18.200 |
| Cluster V | 94.625 | 125.625 | 81.887 | 12.531 | 20.794 | 135.125 | 171.313 | 79.938 | 20.609 | 32.575 |
| Cluster VI | 91.500 | 122.500 | 82.500 | 12.50 | 23.850 | 123.500 | 140.000 | 88.010 | 25.705 | 37.600 |
| Cluster VII | 92.917 | 123.917 | 90.583 | 10.452 | 22.892 | 139.667 | 160.750 | 86.121 | 26.577 | 37.525 |
| Cluster VIII | 104.81 | 135.813 | 95.762 | 10.962 | 22.275 | 202.625 | 251.313 | 81.436 | 16.917 | 38.800 |

Table-5 *Eigen values, proportion of the total variance represented by first five principal components, cumulative percent variance and component loading of different characters in rice*

|  | PC$_1$ | PC$_2$ | PC$_3$ | PC$_4$ | PC$_5$ |
|---|---|---|---|---|---|
| Eigene Value (Root) | 4.070 | 1.819 | 1.563 | 1.051 | 0.544 |
| % Var. Exp. | 40.704 | 18.186 | 15.629 | 10.509 | 5.441 |
| Cum. Var. Exp. | 40.704 | 58.890 | 74.519 | 85.028 | 90.469 |
| Days to 50% Flowering | 0.453 | 0.163 | 0.116 | 0.031 | 0.165 |
| Days to Maturity | -0.453 | -0.162 | -0.114 | -0.027 | -0.166 |
| Plant Height cm | 0.234 | -0.415 | 0.469 | 0.025 | -0.088 |
| Productive Tillers/ Plant | -0.326 | 0.011 | -0.146 | 0.555 | -0.280 |
| Panicle Length | -0.050 | 0.466 | -0.126 | -0.630 | -0.439 |
| Filled Grains/ Panicle | 0.330 | -0.341 | -0.324 | -0.294 | 0.180 |
| Total Grains/ Panicle | 0.371 | 0.167 | -0.188 | 0.368 | -0.217 |
| Spikelet Fertility | -0.215 | -0.557 | -0.275 | -0.222 | 0.055 |
| Test Weight | -0.154 | -0.079 | 0.695 | -0.145 | -0.224 |
| Grain Yield/ Plant | -0.333 | 0.312 | 0.130 | -0.023 | 0.731 |

The distribution of genotypes based on PCA values were shown in 3D plot where the genotypes NLR40021, NLR33641, BPT1768, NLR 33892, NLR20084 and NLR20104 were away from other genotypes on the basis of PCA I and PCA II scores [Fig-1]. The first four principle components showed eigen values more than one and they altogether accounted 85.028% of the variability. Principal components showing less than one were considered non-significant [Table-5].

The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated from the study that hybridization between the genotypes of cluster VII and VIII will be beneficial. The genotypes of these clusters may be used as parents selected for future breeding programme.
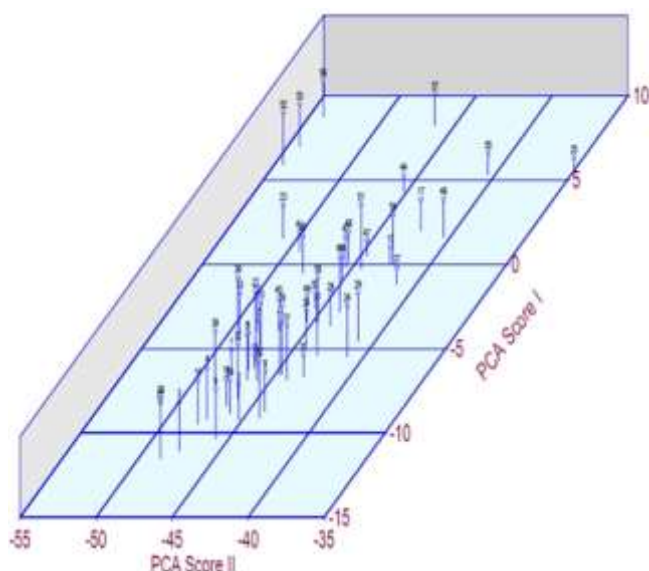
Fig-1 Three-dimensional graph showing relative position of 58 genotypes of rice based PCA scores

**Application of research:** Divergent genotypes can be selected and used as parents in plant hybridization programmes to develop superior rice varieties ultimately improvement of rice crop.

**Research Category:** Genetic divergence, Clustering of genotypes

**Abbreviations:** BPT-Bapatla, NLR- Nellore, JGL-Jagitial, HMT, PCA-Principle Component Analysis

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**Study area / Sample Collection:** Agricultural Research Station, Nellore, 532185

**Cultivar / Variety / Breed name:** Rice (*Oryza sativa* L.) genotypes and cultivars

**Conflict of Interest:** None declared

**Ethical approval:** This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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