# Genetic Diversity Analysis for Yield Traits in Upland Rice (*Oryza sativa* L.)

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## Abstract

The present experiment comprised with thirty seven advanced rice cultures and conducted during *Rabi* 2016-17 under upland rice ecosystem. They were evaluated for nine yield and yield related traits *viz.,* days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield, straw yield and harvest index using $D^2$ analysis. Based on the analysis, the genotypes were grouped into eight clusters. Maximum number of genotypes (21 genotypes) was grouped in cluster I. Cluster II consists of ten genotypes and others were represented by a single genotype each. Maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by between cluster III and VI (7.11) indicating wider genetic diversity between genotypes. Hence the genotype PM 16003 had wider diversity with IET 25134 and PM 14041 and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster I (4.07) followed by cluster II (3.88) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the nine traits studied, number of panicles per square metre area contributed maximum divergence (22.22%) followed by panicle length (17.12%), plant height (14.41), filled grains per panicle (11.26) and days to fifty per cent flowering (10.96%). Hence these altogether contribute more than seventy five per cent towards total divergence. Therefore these characters may be given importance during hybridization programme in upland rice ecosystem.

**Keywords:** Genetic diversity, yield traits, upland rice.

## Introduction

Rice is one of the principle food crops and one third of the world population and two thirds of the Indian population is utilizing rice as staple food. It contributes 43 per cent of caloric requirement and 20-25% of agricultural income. In India, rice is grown in an area of 43.5 million ha (23% of gross cropped area) with an annual production of 90 million tons. Most of the Asian countries have been able to keep pace between rice production growth rate and that of population during the last four decades. This has been mainly possible due to the contributions made by the green revolution technologies. However, it is of great concern to note that the rate of growth in rice production has started declining during 90's and there has been a plateauing effect. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth. With the current green revolution technologies it is estimated that by 2020 at least 115-120 million tons of milled rice is to be produced in India to maintain the present level of self-sufficiency. In order to meet the food requirement of growing population, development of high yielding varieties is essential.

The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekanandan and Subramanian, 1993). An attempt was made in the present investigation to assess the genetic diversity of thirty seven advanced rice cultures for yield traits in upland rice ecosystem.

## Materials and methods

The experimental material comprised with thirty seven advanced rice cultures collected from various research institutes which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during *Rabi* 2016-17. The experimental site is located at 9" 21' N latitude, 78" 22' E longitudes and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5x2 m plot keeping

15 x 10 cm spacing. The recommended agronomic practices followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz,* days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle and grain yield (kg), straw yield (kg) and harvest index. The genetic distance between the genotypes was worked out using Mahalanobis $D^2$ analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

## Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating existence of variability among the genotypes. Based on the relative magnitude of $D^2$ values, thirty seven genotypes were grouped into eight clusters (Table 1). Maximum number of genotypes (21 genotypes) was grouped in cluster I. Cluster II consists of ten genotypes and others were represented by a single genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non- correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al.,* (2000) and Nayak *et al.,* (2004). The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by

between cluster III and VI (7.11) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. Surprisingly the clusters identified with maximum inter cluster distance were possessed a single genotype in each cluster. Hence selection of parents for hybridization is already over. The minimum inter cluster distance was found between cluster III and V (3.44) followed by between cluster II and VI (4.55). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

**Table 2. Intra (diagonal) and inter cluster average distance of yield traits in 37 genotypes**

|  | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| **I** | 4.07 | 5.85 | 6.31 | 5.05 | 5.81 | 5.78 | 6.61 | 6.65 |
| **II** |  | 3.88 | 5.75 | 5.75 | 6.05 | 6.65 | 5.80 | 6.54 |
| **III** |  |  | 0.00 | 6.83 | 3.44 | 7.11 | 4.55 | 7.75 |
| **IV** |  |  |  | 0.00 | 6.64 | 4.65 | 6.42 | 6.46 |
| **V** |  |  |  |  | 0.00 | 6.96 | 5.97 | 6.55 |
| **VI** |  |  |  |  |  | 0.00 | 5.17 | 6.28 |
| **VII** |  |  |  |  |  |  | 0.00 | 6.09 |
| **VIII** |  |  |  |  |  |  |  | 0.00 |

The maximum intra cluster distance was observed in cluster I (4.07) followed by cluster II (3.88). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would

**Table 1. Clustering pattern of 37 genotypes**

| Cluster | No. of genotypes | Name of genotypes |
|---|---|---|
| I | 21 | IR12-L369 (G3), IR13-L382 (G6), IR13-L391 (G7), IR12-L356 (G2), IR13-L114 (G4), IR13-L137 (G5), IR12-L353 (G1), IR14-L235 (G12), IR13-L406 (G9), IR13-L400 (G8), IR13-L413 (G10), IET 25106 (G18), PM 14048 (G34), IET 25114 (G21), IET 24690 (G16), PM 14032 (G27), PM 14046 (G33), IR14-L177 (G11), PM 14049 (G35), PM 16002 (G14) and PM 16001 (G13). |
| II | 10 | PM 14030 (G26), PM 14044 (G32), PM 14018 (G25), PM 14038 (G28), Anna(R)4 (G37), PM 14050 (G36), IET 25107 (G19), PM 13017 (G24), PM 14042 (G30) and PM 14043 (G31). |
| III | 1 | PM 16003 (G15) |
| IV | 1 | IET 25118 (G22) |
| V | 1 | IET 25105 (G17) |
| VI | 1 | PM 14041 (G29) |
| VII | 1 | IET 25111 (G20) |
| VIII | 1 | IET 25134 (G23) |

**Table 3. Cluster mean of different yield characters in 37 rice genotypes**

| Cluster | Days to 50% flowering | Plant Height (cm) | Productive tillers per plant | No. of panicles per sq. metre | Panicle length (cm) | Filled grains / panicle | Grain yield (kg/ha) | Straw yield (kg/ha) | Harvest Index |
|---|---|---|---|---|---|---|---|---|---|
| I | 53.92 | 78.32 | 6.84 | 121.71 | 21.41 | 84.49 | 1420.32 | 4247.62 | 0.27 |
| II | 58.20 | 67.80 | 6.27 | 185.87 | 19.58 | 77.53 | 1931.33 | 4966.67 | 0.28 |
| III | 63.67 | 71.73 | 7.00 | 137.33 | 20.63 | 130.33 | 1533.33 | 3933.33 | 0.30 |
| IV | 52.00 | 77.27 | 7.67 | 104.33 | 17.17 | 57.67 | 666.67 | 2333.33 | 0.22 |
| V | 58.00 | 72.47 | 6.67 | 102.33 | 21.27 | 142.33 | 1943.33 | 3600.00 | 0.41 |
| VI | 46.67 | 73.87 | 8.33 | 118.67 | 16.83 | 64.00 | 1233.33 | 6800.00 | 0.15 |
| VII | 59.67 | 59.60 | 8.00 | 125.33 | 18.33 | 71.00 | 983.33 | 4733.33 | 0.24 |
| VIII | 57.00 | 60.47 | 4.33 | 77.33 | 18.90 | 57.67 | 733.33 | 700.00 | 0.54 |

be made use of in improvement through inter-varietal hybridization (Joshi *et al.,* 2008). A perusal of results of cluster means (Table 3) revealed that cluster I with twenty one genotypes exhibited highest mean value for panicle length (21.41) and plant height (78.32). Cluster II had genotypes with maximum number of panicles per square metre area (185.87) and the genotype in Cluster III (PM 16003) had taken more days for fifty per cent flowering (63.67). Cluster IV was characterized by lowest grain yield (666.67), while the cluster V had maximum number of filled grains per panicle (142.33) and grain yield (1943.33). The genotype PM 14041 with more straw yield (6800.00) and highest productive tillers per plant (8.33) was grouped in cluster VI. The Genotype IET 25111 (Cluster VII) had shown short stature (59.60). The genotype IET 25134 possessing lowest mean values for productive tillers per plant (4.33), number of panicles per square metre area (77.33), filled grains per panicle (57.67) and straw yield (700.00) but highest harvest index (0.54) was grouped in cluster VIII. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster II recorded desirable mean value for maximum number of productive traits *viz.*, productive tillers per plant, number of panicles per square metre area, panicle length, filled grains per panicle and grain yield. Similar results were also reported by Banumathy *et al.,* (2010) and *Rai et al.,* (2014), thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the *per se* performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in table 4. Among the traits studied, number of panicles per square metre area contributed maximum divergence (22.22%) followed by panicle length (17.12%), plant height (14.41), filled grains per panicle (11.26) and days to fifty per cent flowering (10.96%). The minimum percentage of contribution was observed in harvest index (3.75%) followed by productive tillers (5.41%), grain yield (6.76%) and straw yield (8.11%). The traits *viz.,* number of panicles per square metre area, panicle length, plant height, filled grains per panicle and days to fifty per cent flowering contributed more than seventy five per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

**Table 4. Percentage of contribution of each character towards total divergence**

| Character | No. of Times Ranked First | Contribution (%) |
|---|---|---|
| Plant Height (cm) | 73 | 10.96 |
| Days to 50% flowering | 96 | 14.41 |
| Productive tillers per plant | 36 | 5.41 |
| No. of panicles per sq. metre | 148 | 22.22 |
| Panicle length (cm) | 114 | 17.12 |
| Filled grains / panicle | 75 | 11.26 |
| Grain yield (kg/ha) | 45 | 6.76 |
| Straw yield (kg/ha) | 54 | 8.11 |
| Harvest Index | 25 | 3.75 |
| **Total** | **666** | **100** |

## References

Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D and Ramasubramanian GV. 2010. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic J Plant Breeding.* 1(4):500-504.

Joshi MA, Singh P, Sarao NK, Sharma RC and Bharaj TS. 2008. Genetic diversity among the rice varieties cultivated in Punjab. *Oryza*, 45(4):277-279.

Mahalanobis PC. 1936. On the generalized distance in statistics. *Proceeding Naturnal Institute Science India.* (2):49-55.

Nayak AR, Chaudhery D and Reddy JN. 2004, Genetic divergence in scented rice. *Oryza*, 41(3&4):79-82.

Rai SK, Ramesh C, Suresh BG, Rai PK, Kumar R and Sandhya. 2014. Int. J Life Sci. Res., 2(4):225-228.

Rao CR. 1952. Advanced statistical methods in biometrics research, New York:John Wiley & Sons.

Shanmugasundaram P, Souframanien J and Sadasivam S. 2000. Genetic divergence among rice varieties released from paddy breeding station, Coimbatore, India. *Oryza*, 37(3):225-228.

Vivekanandan P and Subramanian S. 1993. Genetic divergence in rainfed rice. *Oryza*. 30:60-62.