

**RESEARCH ARTICLE :**

Genetic diversity for yield, its contributing characters in rice (*Oryza sativa* L.)

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SUMMARY : A set of 48 rice genotypes were subjected to Mahalanobis D^2 analysis to assess the genetic diversity. All these genotypes were grouped into seven clusters with maximum inter cluster distance between cluster IV and cluster VII (55.28) and minimum inter cluster distance between cluster II and cluster IV (16.14). Among the eleven characters studied 1000 grain weight contributed maximum towards genetic divergence (51.77%) followed by days to 50 per cent flowering (35.55%) and days to maturity (7.89%).

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KEY WORDS :

Cluster analysis,
Genetic diversity,
Alpha lattice design

BACKGROUND AND OBJECTIVES

Rice is a main staple food for most people in the world and it is a crop with the longest history of cultivation. More than 90% of the world's rice is produced in Asia and for more than three billion people it is the staple food that accounts for 35–75% of the calorie intake (Khush, 2005). Rice occupies an important position in the agricultural development, history and civilization of Asian nations.

To fulfill the growing demand for rice, it becomes necessary to design new rice varieties with higher yield potential to enhance average farm yields that relies heavily on the availability and utilization of genetic diversity. Genetic diversity of crops plays an important role in sustainable development and food

security (Esquinas-Alcazar, 2005), as it allows the cultivation of crops in the presence of various biotic and abiotic stresses. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology which involves the intelligent use of available genetic variability. D^2 analysis is a powerful technique for measuring genetic divergence, which enables to discriminate between different cultivars according to the diversity present in the genotypes (Mahalanobis, 1936).

RESOURCES AND METHODS

The experimental material for the study comprised of 48 genotypes laid in alpha lattice design (ALD) with two replications at the Rice Research Center, Agricultural Research

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Institute (ARI), Rajendranagar, Hyderabad, Telangana during *Kharif*, 2015. The seedlings were transplanted to main field 15cm apart between rows and 10cm within the row. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per plant, panicle length (cm), number of filled grains per panicle, 1000 grain weight (g), grain yield per plant (g), grain length (mm), grain breadth (mm), L/B ratio and days to 50 per cent flowering, days to maturity were recorded plot basis. The analysis of variance was carried out for all the characters and then data was analyzed following multivariate analysis of Mahalanobis (1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

OBSERVATIONS AND ANALYSIS

The analysis of variance revealed significant differences among the genotypes for all the characters indicating existence of variability among the genotypes

for the characters studied. Based on the relative magnitude of D^2 values, 26 genotypes were grouped into nine clusters (Table 1). The cluster I was the biggest consisting of 26 genotypes followed by 11 in cluster III, 7 in cluster IV, cluster II, V, VI, VII with one germplasm line each.

The Maximum intra cluster distance was observed in cluster IV (22.27), followed by cluster III (16.82), cluster I (16.52) indicating the existing divergence among the germplasm lines within these clusters. This could be made use of in the yield improvement through recombination breeding. The relative divergence of each cluster from other cluster (inter-cluster) indicated greater divergence between cluster IV and VII (55.28) followed by cluster III and VI (52.64). The minimum inter-cluster distance was recorded between cluster II and IV (16.14) (Table 2). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield, which may enable further selection and genetic improvement.

The average cluster wise mean values for different characters are presented in (Table 3) which can be used

Table 1: Clustering pattern among 48 rice genotypes (in Mahalanobis D^2 analysis)

| Cluster No. | No. of germplasm lines | Names of the germplasm lines |
|-------------|------------------------|---|
| I | 26 | Bali, Shamphai, Daramphou, Kene, Khemaru, Wazhuhophek, Mancho Tsok, Rosolia, Phougak, Hasosil Mah, Runya, Nagaphou, Machang Kaoyeng, Nongrangphou, Chakhao, Thangmoi, Ngonolasha, Chingtui Mah, Phorel Utlou, Meghalaya Lefara, Gumdhan, Kushal, Ratkhara, Nerika-L-54, CO-39, Kahangam |
| II | 1 | Taichang Native1(TN ₁) |
| III | 11 | Chingtui, Kunta Mah, Moirangphou Angouba, Angatra, Sapet Maso, Ching Phourel Amubi, Tetep, Japanphou, Sanayanbi, Nerika-L-49, Pumpha Mah, |
| IV | 7 | Samba mahsuri (BPT-5204), Weshelora, Kemp Yaisha, Senebumap, Younyo Kangru, ARC-10531, Kapangra |
| V | 1 | Chingphou |
| VI | 1 | Desek Youso |
| VII | 1 | Bhobu Kangbu |

Table 2 : Intra (diagonal) and inter-cluster average of D^2 values of 48 rice genotypes

| Clusters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|-------------|-----------|------------|-------------|------------|-----------|------------|-------------|
| Cluster I | 16.52 | 24.61 | 23.38 | 30.74 | 24.79 | 34.70 | 38.39 |
| Cluster II | | 0.00 | 45.87 | 16.14 | 19.59 | 18.65 | 49.67 |
| Cluster III | | | 16.82 | 50.63 | 39.88 | 52.64 | 29.48 |
| Cluster IV | | | | 22.27 | 29.62 | 26.56 | 55.28 |
| Cluster V | | | | | 0.00 | 19.60 | 38.21 |
| Cluster VI | | | | | | 0.00 | 47.22 |
| Cluster VII | | | | | | | 0.00 |

Table 3 : Relative contribution of different characters to genetic diversity in rice germplasm lines

| Sr. No. | Characters | Times ranked first | Contribution (%) |
|---------|-------------------------------------|--------------------|------------------|
| 1. | Days to 50 % flowering | 401 | 35.55 |
| 2. | Plant height (cm) | 5 | 0.44 |
| 3. | Number of productive tillers/ plant | 0 | 0.00 |
| 4. | Panicle length (cm) | 0 | 0.00 |
| 5. | Number of filled grains/ panicle | 19 | 1.68 |
| 6. | Days to maturity | 89 | 7.89 |
| 7. | 1000 Grain weight (g) | 584 | 51.77 |
| 8. | Grain yield/ plant (g) | 4 | 0.35 |
| 9. | Kernel length (mm) | 1 | 0.09 |
| 10. | Kernel breadth (mm) | 5 | 0.44 |
| 11. | L/B ratio | 20 | 1.77 |

to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster IV recorded highest days to 50 per cent flowering and grain breadth. Cluster VII exhibited superior mean performance for plant height, number of filled grains per panicle, 1000 grain weight, grain yield per plant and L/B ratio. Cluster V recorded highest value for panicle length and days to maturity. Cluster II had highest mean value for number of productive tillers per plant while cluster VI recorded highest mean values for grain length.

The characters contributing maximum to the divergence need greater emphasis for deciding on the clusters for purpose of further selection and choice of parents for hybridization. Among the eleven characters studied, 1000 grain weight contributed maximum of 51.77 per cent, followed by days to 50% flowering (35.55 %), days to maturity (7.89%), L/B ratio (1.77%), Number of filled grains per panicle (1.68%), grain breadth (0.44 %), plant height (0.44%), grain yield per plant (0.35%) and grain length (0.09). The results were in conformity with Ramanjaneyulu *et al.* (2014) and Devi *et al.* (2015) for 1000 grain weight, Srinivas *et al.* (2015) for days to fifty per cent flowering and number of filled grains per panicle Padmaja *et al.* (2011) for plant height, Ramya and Kumar (2008) for number of productive tillers per plant and grain yield per plant, Vennila *et al.* (2011) number of filled grains per panicle, plant height, and grain breadth. Hence, these characters could be given due importance for selection of genotypes for further improvement. There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity.

The contribution mainly depends upon the genotypes included in the study and the environment influences over the character. Regarding the least contribution, number of productive tillers per plant and plant height contributed the least. The minimum contribution by these traits reveal that these traits were least affected in course of evolution.

The number of times that each of the eleven characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 3. The results showed that the contribution of 1000 grain weight was highest towards genetic divergence (51.77%) by taking 584 times ranking first, followed by days to 50% flowering (35.55%) by 401 times, days to maturity (7.89%) by 89 times, L/B ratio (1.77%) by 20 times, No. of filled grains per panicle (1.68%) by 19 times, kernel breadth (0.44 %) by 5 times, plant height (0.44%) by 5 times, grain yield per plant (0.35%) by 4 times, kernel length(0.09) by 1 time.

Conclusion :

The conclusion drawn by the cluster analysis is that in the studied population, high variability was observed between the germplasm lines in different clusters for different traits. Recombination breeding among germplasm lines belonging to cluster IV having maximum intra-cluster distance can improve the yield potential. As maximum inter-cluster distance was noticed between cluster IV and VII, cluster III and IV, cluster III and IV, cluster II and VII and cluster VI and VII crosses involving genotypes from these clusters would give wider and desirable recombination.

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