Assessment of genetic diversity of rice (*Oryza sativa* (L.) genotypes under aerobic condition

Abstract

The present study was carried out at Anbil Dharmalingam Agricultural College and Research Institute, Trichy under aerobic conditions. The experimental material comprised forty-nine rice genotypes, which were laid out in randomized complete block design with two replications. The data on ten quantitative characters were recorded to assess the magnitude of genetic diversity through D^2 analysis. Based on genetic distance, rice genotypes were grouped into five clusters. Among the five clusters, cluster I had the highest number of genotypes (42) and cluster V had the lowest number of one genotype. The range of inter-cluster distance was 65.33 (between clusters IV and V) to 7.91 (between clusters II and III). The genotypes in cluster IV and cluster V exhibited a high degree of genetic diversity due to the maximum inter-cluster distance between them, and these genotypes may be utilized under a hybridization program for getting high-yielding and desirable recombinants.

Keywords: rice genotype, Genetic diversity, Cluster, D^2 analysis

Introduction

Rice (*Oryza sativa* L.) is an important cereal crop that provides food for more than fifty percent of the world's population. Due to changes in climatic patterns, rice cultivation faces serious threats such as drought and flooding. To mitigate these situations and to reduce the cost of cultivation, farmers go for direct seeding and aerobic rice cultivation in marginal land areas. Currently, available rice varieties are more adapted to transplanted rice environment conditions. Hence, there is a need to identify the rice genotypes that are more suitable for aerobic conditions.

Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different traits and ultimately for a rational use of germplasm collections (Hossain *et al.*, 2021 and Hossain *et al.*, 2023). Similarly, quantification of genetic diversity existing within and between groups of genotypes is important and the crosses between parents with high genetic divergence are generally the most responsive for genetic improvement for realizing higher heterosis and obtaining superior recombinants in the segregating generations. In view of the above background, the present investigation was carried out with forty-nine rice genotypes to study the genetic divergence of ten yield and yield-related traits.

Materials and methods

The experiment was conducted at Anbil Dharmalingam Agricultural College and Research Institute, Trichy under aerobic conditions. The experimental material consisted of 49 rice genotypes which were raised in randomized block design with two replications. The observations such as days to 50% flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, spikelet fertility, grain yield per plant, straw yield per plant and harvest index were recorded and analysed statistically. The genetic divergence was estimated by multivariate analysis using Mahalanobis (1936) D^2 statistics described by Rao (1952).

Result and discussion

The forty-nine rice genotypes, which were collected from different research stations, were grouped into 5 clusters by using D^2 analysis. The D^2 analysis for genetic divergence studies was done by Kandhola and Panwar (1999), Shivani *et al.* (2006), Singh *et al.* (2006), Kuchanur *et al.* (2009), Kumari *et al.* (2013), Bhati *et al.* (2015), Vennela *et al.* (2017), Behera *et al.* (2018) have reported for studying the genetic divergence of rice genotypes.

The clustering composition and the grouping of genotypes into different clusters are depicted in Table 1. Among the five clusters, cluster I had the highest number of genotypes (42) and cluster V had the lowest number of one genotype. The cluster means with respect to ten characters were displayed in Table 2. Among the clusters, cluster IV was suitable for early flowering, dwarf plant type, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, and harvest index. Hence, cluster IV may be selected for developing early maturity types and also as a donor for dwarf plant type (Gnaneswari *et al.*, 2023). Cluster III had the maximum mean value for two traits, *viz*., spikelet fertility and straw yield per plant. The cluster I and cluster V had the genotypes with the highest mean value for grain yield per plant and panicle length respectively. Hence, these clusters may be chosen for transferring the traits through hybridization programme. The selection of genotypes based on cluster mean for the better exploitation of genetic potential was also reported by Muthuramu and Sakthivel (2017), Sudeepthi et al. (2020), Sharma *et al.* (2021) and Shanmugam *et al.* (2023)

The average D^2 distances within and between clusters which were presented in Table 3 (Fig. 1). The intra cluster distance ranged from 14.70 (cluster I) to 0.00 (cluster V). The higher intra cluster distance was recorded by the cluster I (14.70) followed by cluster IV (13.36), cluster III (10.05), cluster II (3.95) and cluster V (0.00) indicating that the genotypes present within a cluster were more diverse than other clusters. The least intra-cluster distance was found in cluster V, and cluster II, revealing the presence of more similarity between the genotypes present in these clusters. Similar rice genotypes grouping was also reported by Vennela *et al.* (2017) and Dey *et al.,* (2020).

The range of inter cluster distance was 65.33 (between cluster IV and V) to 7.91 (between cluster II and III). The genotypes in cluster IV and cluster V exhibited a high degree of genetic diversity due to the maximum inter-cluster distance between them, and these genotypes may be utilized under a hybridization programme for getting high-yielding and desirable recombinants. Likely, the crosses may be attempted between genotypes in clusters I and V, clusters II and V, and clusters I and II. The lowest inter-cluster distance was observed between clusters II and III, followed by clusters I and II and clusters I and IV, showing that these clusters were comparatively less divergent and that crosses between them cannot produce better recombinants. These results were in accordance with Mishra *et al.* (2003), Chaturvedi and Maurya (2005), , Ranjith *et al.* (2018), Amegan *et al.* (2020), Sudeepthi *et al.* (2020), Rathan *et al.* (2020), Chhodavadiya *et al.* (2023), Pathak *et al.* (2019) and Prakash *et al.* (2024)

Conclusion

From the D^2 analysis, it could be concluded that only five genotypes (TKM1, TKM 5, ASD 16, ADT 39, TKM 7) were more diverse and may be selected as parents for hybridization to throw desirable genes from both the parents.

Table 1. Cluster classification of rice genotypes

Cluster	Number of genotypes	Rice genotypes
I	42	ASD 17, ASD 19, TRY 2, ASD 20, ADT 41, ADT 36, TKM 11, ADT 45, ,ASD 10, Chandaikar, TRY 1, Maranellu, Vellaichithiraikar, ADT 44, ADT 50, CB-07-701-252Mattaikar, Norungan, TKM 9, TKM 12, Kuruvai kanangiyam, PMK 3, Kuliyadichan, GEB 24, ANNA 4, Sivappu Chithiraikar, IR 64, CB-08-701, CB-07-701-274, CO 51, CO 47, CB-07-701-279,

		ADT 37, CO 43, TKM 10, TKM 2, TRY 3, CO 29, TKM 8, TKM 3, CO 50, CB-08-702
II	2	Kattanur, Kalurundaikar
III	2	TKM1, TKM 5
IV	2	ASD 16, ADT 39
V	1	TKM 7

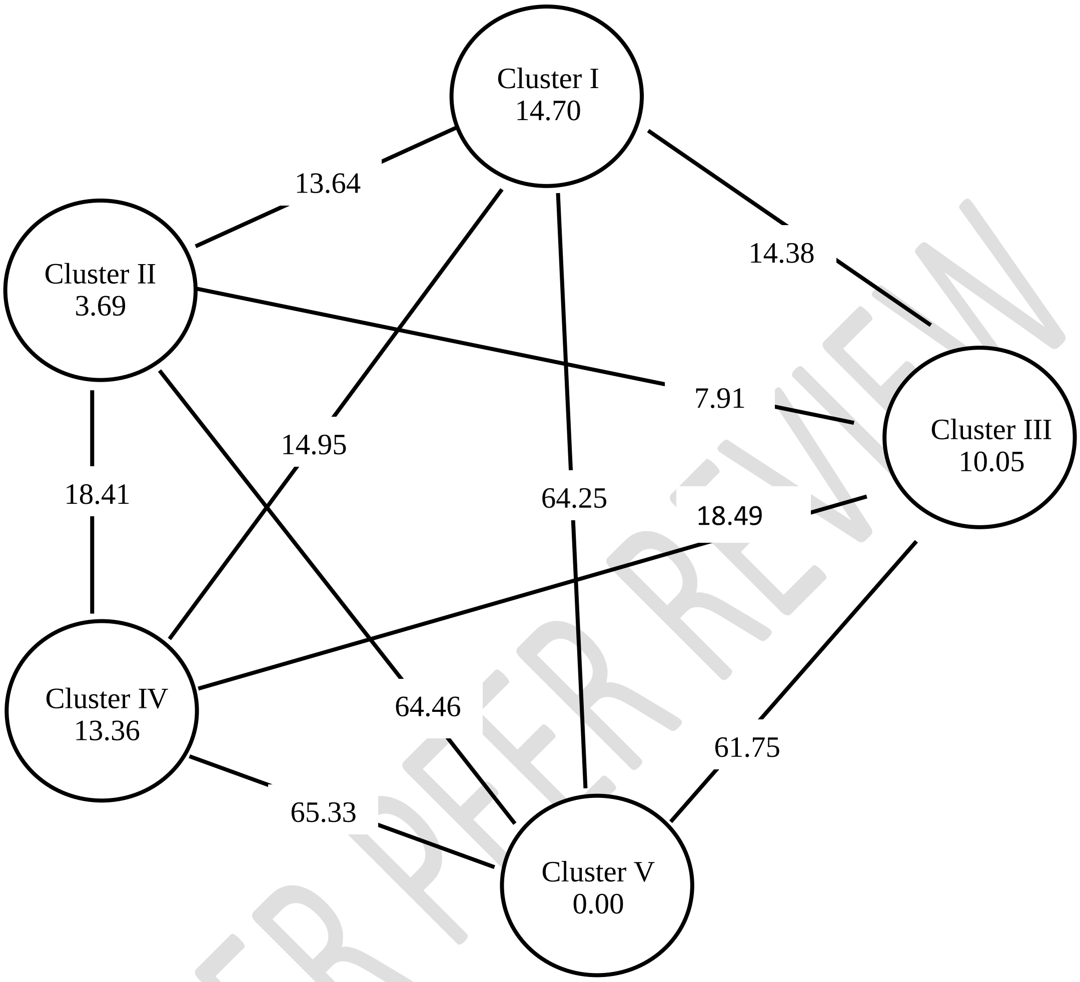
Table 2. Cluster mean values of ten quantitative characters

Character	Cluster				
	I	II	III	IV	V
Days to 50% flowering	72.10	64.50	70.75	77.0	70.50
Plant height	111.51	139.30	111.80	99.70	137.20
Number of tillers per plant	17.71	17.70	18.75	19.55	17.00
Number of productive tillers per plant	15.74	14.50	13.50	17.75	12.00
Panicle length	23.32	23.45	26.90	21.65	104.30
Number of grains per panicle	115.42	84.35	124.80	147.0	73.60
Spikelet fertility	77.22	74.00	89.00	83.50	69.00
Straw yield per plant	43.76	47.50	49.80	33.20	40.80
Grain yield per plant	28.54	19.60	20.60	34.20	28.00
Harvest index	0.39	0.29	0.28	0.49	0.40

Table 3. Intra (bold) and inter-cluster distances of various clusters

Cluster	I	II	III	IV	V
I	**14.70**	13.64	14.38	14.95	64.25
II		**3.95**	7.91	18.41	64.46
III			**10.05**	18.49	61.75
VI				**13.36**	65.33
V					**0.00**

Fig. 1 Intra and inter cluster distances of various clusters



Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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