Full Length Research Article

Analysis of Genetic Diversity Using Morphological Markers in 30 Landraces of Rice (*Oryza sativa* L.)

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Abstract

Rice (*Oryza sativa* L.) belongs to family Poaceae and chromosome number 2n = 2x = 24. Rice is a major staple food crop in the world. The 90% of the rice is grown and consumed in south and southeast Asia. Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study thirty landraces of rice were subjected to diversity analysis using morphological markers for the identification of diverse genotypes. This analysis was carried out during kharif season of 2021 at the Genetics and Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. Based on clustering pattern, 30 landraces of rice were grouped into 5 clusters. The intra cluster distance was maximum at cluster II and inter-cluster distance, indicated greater divergence between cluster IV and cluster V followed by cluster III and IV and cluster II and V indicating greater genetic divergence and these genotypes may be utilized in further breeding programme for the exploitation of hybrid vigour. Among the five clusters studied the cluster I, II and IV were recorded by high mean values for grain yield per plant than general mean. The relative contribution of individual characters towards the expression of genetic diversity estimated over character wise D^2 value revealed that with 58.40 per cent contribution for days to 50 per cent flowering, 12.91 per cent contribution of grains yield per plant, 8.50 per cent of number of grains per panicle and with 9.90 per cent from 1000 grain seed weight were the major traits contributing to the total divergence and may be utilized as parameters for selecting genetically diverse parents.

Key words: *Oryza sativa* L., Genetic diversity, Morphological markers, Landraces, Contributing traits

Rice (*Oryza sativa* L.) is a major staple food crop in the world belongs to family Poaceae and chromosome number 2n = 2x = 24. About one-third of the population gets more than 20% of their calories from the rice harvest [1]. For the majority of people in Asia, rice is a staple food, especially in south and south-east Asia, where more than 90% of the world's rice is produced and consumed. It contributes to the total agricultural income in Asian countries and is a significant source of calories [2]. Even though the green revolution technologies increased the production drastically in past decades, still there is a huge gap between production and the demand [3]. According to the estimates, there should be an increase in the production of rice by 4.90 per cent to feed the increasing Indian population by 2050 if the land resources remain constant. The current growth rate is only 2.42 per cent and unfortunately, the current cultivars have reached the yield plateau due to the reduced variability. Even though the technological advances including crop improvement are positively contributing to the yield, the growth is not satisfying the global demand especially for the food crops like rice [4]. Genetic diversity is a basic requirement for crop improvement programme because it facilitates the production of superior recombinants through the selection of parents with greater variability for various traits [5-6]. Many traditional varieties and improved cultivars have been released for cultivation in different regions of India. Despite abundant genetic resources, only a small proportion of the total rice germplasm collection has been used in breeding programs. Since the previous few centuries, rice has experienced a loss in diversity as native types have been replaced with high-yielding variants [7-8]. Genetic divergence analysis evaluates the genetic distance among the selected genotypes and shows the relative contribution of specific traits towards the total genetic divergence [9]. A higher heterosis could be achieved from crosses between genetically distant parents [10]. The current study thus sought to determine the type and extent of genetic divergence existing in the 30 rice landraces and to choose suitable diverse genotypes as parents for additional use in crop breeding projects.

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Table 1 List of land races of rice used for diversity analysis

Accession No.	Landraces
G1	Aathur Kitchali Samba
G2	Arupatham Kuruvai
G3	Garuda Samba
G4	Gomathi
G5	Sooran Kuruvai
G6	Kuzhali Adichan
G7	Salem Sannam
G8	Sivan Samba
G9	Illupam Poo Samba
G10	Mappilai Samba
G11	Ottu Kichali
G12	Chinnar
G13	Kothamalli Samba
G14	Rathasali
G15	Poongar
G16	Sigapu Kar
G17	Kulla Kar
G18	Kandha Sala
G19	Thooya Malli
G20	Kattuyanam
G21	Jeeraga Samba
G22	Sivapu Kavuni
G23	Madu Muzhangi
G24	Kuruvai Kar
G25	Karupu Kavuni
G26	Kallurndi
G27	Singini Kar
G28	Kalli Madiyan
G29	Molam Samba
G30	Manjal Ponni

MATERIALS AND METHODS

30 rice landraces are used as experimental material for genetic divergence analysis, which is shown in (Table 1). An experiment was carried out during kharif season of 2021 at the Genetics and Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. On end of May, the raised bed nursery is prepared and transplanted during June 25th using randomized block design with three replications was used to transplant 30-day-old seedlings onto the field. Standard agronomic procedures and planned plant protection measures were used. Each germplasm was raised with a 20X15 cm gap between rows and plants, respectively. Morphological marker observations were recorded for different quantitative traits such as Days to 50 per cent flowering, No. of tillers per plant, No. of productive tillers per plant, Plant height at maturity, Panicle length, Number of grains per panicle, Grain length, Grain breath, grain (L/B) ratio, Spikelet Fertility percentage, 1000 grain weight, and Grain yield per plant. Mahalanobis D^2 statistic was used for estimating the genotypic divergence among 30 landraces of rice. Analysis of variance was carried out using the method of Panse and Sukhatme [11] for each of the 30 landraces of rice. The germplasms were grouped into a number of clusters as described by Rao [12]. For the purpose of estimating the contribution of each character to divergence, each character was evaluated based on values in all landraces of rice.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) was based on the mean values of eleven quantitative traits observed for 30 rice landraces. The results of analysis of variance, presented in (Table 2), show significant differences for the characters such as Days to 50 per cent flowering, No. of tillers per plant, No. of productive tillers per plant, Plant height at maturity, Panicle length, Number of grains per panicle, Grain length, Grain breath, grain (L/B) ratio, Spikelet Fertility, 1000 grain weight, and Grain yield per plant. Employing Mahalanobis generalized distance, the divergence in 30 landraces of rice were assessed for yield and yield contributing characters. The results are presented in (Table 3-5). 30 landraces of rice were grouped into 5 clusters using clustering technique. The compositions of different clusters are presented in (Table 3). Cluster I, the largest cluster, comprised 17 genotypes, followed by cluster II with 10 genotypes. The cluster III, IV and V had 1 genotype respectively. Similar findings were also reported by [13-14]. The intra cluster distance was maximum at cluster II and the minimum intra-cluster value exhibited by cluster I indicated limited genetic divergence among the constituent genotypes. The cluster III, IV, V are monogenotypic clusters had zero intra cluster distance. The relative divergence of each from other cluster i.e., inter-cluster distance, indicated greater divergence between cluster IV and cluster V followed by cluster III and IV and cluster II and V indicating greater divergence of genotypes belonging to these clusters. Genotypes belonging to clusters separated by high genetic distance may be used hybridization programme to obtain a wide spectrum of variation among the segregants. Therefore, selection of divergent genotypes from the clusters would produce a broad spectrum of variability for different traits studied, which may enable further selection and improvement of grain yield. The hybrids developed from the selected genotypes with in the limit of the compatibility of these cluster may produce high magnitude of heterosis or desirable segregant which would be rewarding in a rice breeding programme.

Table 2 ANOVA for grain yield and yield contributing traits of 30 rice landraces

Source	df	Mean sum of square											
		DF	PH	NTPP	NPTPP	PL	SF	NGPP	GL	GB	L/B R	GW	GYPP
Replication	2	0.13	22.98	1.56	0.60	2.03	6.11	12.94	0.007	0.001	0.28	0.70	0.64
Genotype	29	660.45**	1003.56**	20.40**	28.35**	41.87**	139.98**	1703.01**	0.03**	0.006**	0.61**	32.77**	21.03**
Error	58	0.25	10.11	0.50	0.46	0.39	3.45	8.68	0.001	0.0006	0.13	0.28	0.81

**Significant at 1 per cent level, Days to 50 per cent flowering (DF), No. of tillers per plant (NTPP), No. of productive tillers per plant (NPTPP), Plant height at maturity (PH), Panicle length (PL), Number of grains per panicle (NGPP), Grain length (GL), Grain breath (GB), grain L/B ratio (L/B R), Spikelet Fertility (SF), 1000 grain weight (GW), and Grain yield per plant (GYPP)

The cluster mean values showed a wide range of variation for all the traits under study. Cluster IV had high mean earliness for flowering, maximum number of productive tillers per plant, highest 1000 grain weight, recorded maximum spikelet fertility and also characterized for higher value for grain yield per plant. The cluster V is registered for maximum

number of tillers per plant but late flowering and least grain L/B ratio. The cluster III is characterized by maximum grain L/B ratio, maximum grain length but low grain yield per plant, least number of productive tillers and lowest 1000 grain weight. The highest panicle length was observed in cluster II. Among the five clusters studied the cluster I, II and IV were recorded by high mean values for grain yield per plant than general mean.

Among these high yielding clusters, cluster IV shows a high mean than general mean for all 10 characters and cluster II for nine traits and cluster I for five characters. This indicates that none of the cluster has genotypes with all desirable traits which could be directly selected and utilized. Almost the minimum and maximum clusters mean values were distributed in relatively distance clusters.

Table 3 Composition of D² Clusters for 30 landraces of rice

S. No.	List of landraces of rice in each cluster	Total number of landraces
1	Kuzhali adichan, Manjal ponni, Kandha sala, Sigapu kar, Thooya malli, Sooran kuruvai, Kalli madiyan, Singini kar, Kallurndi, Karupu kavuni, Kuruvai kar, Kulla kar, Poongar, Illupam poo samba, Ottu kichali, Kothamalli samba, Rathasali.	17
2	Attur kitchaki samba, Molam samba, Gomathi, Jeeraga samba, Mappilai Samba, Garudan Samba, Madu muzhangi, Sigapu kavuni, Salem sannam, Sivan samba.	10
3	Chinnar	1
4	Kattuyanam	1
5	Arupatham kuruvai	1

Table 4 Average inter and intra cluster D values for 30 landraces of rice

Cluster number	I	II	III	IV	V
I	29.95	52.87	53.66	102.05	84.82
II		34.90	89.88	63.12	124.99
III			0.00	144.07	52.09
IV				0.00	180.13
V					0.00

Table 5 cluster mean of 30 landraces of rice for observed traits

Traits / Cluster	DF	pH	NTPP	NPTPP	PL	SF	NGPP	GL	GB	L/B R	GW	GYPP
I	86.32	122.70	17.19	13.74	24.08	84.50	118.54	0.71	0.29	2.55	20.01	25.00
II	104.00	123.02	19.00	13.93	26.93	83..93	124.96	0.73	0.31	2.60	19.90	29.96
III	76.00	74.81	13.05	9.66	17.05	76.54	79.63	0.91	0.26	3.51	15.12	20.85
IV	126.00	136.14	19.85	15.78	27.16	93.79	144.01	0.86	0.30	2.90	23.67	28.30
V	51.44	85.51	20.10	16.00	20.57	80.12	70.66	0.75	0.34	2.00	19.96	22.28
General mean	89.73	109.02	18.37	14.19	23.46	84.43	107.42	0.79	0.30	2.71	19.79	24.74

Days to 50 per cent flowering (DF), No. of tillers per plant (NTPP), No. of productive tillers per plant (NPTPP), Plant height at maturity (PH), Panicle length (PL), Number of grains per panicle (NGPP), Grain length (GL), Grain breath (GB), grain L/B ratio (L/B R), Spikelet Fertility (SF), 1000 grain weight (GW), and Grain yield per plant (GYPP)

Table 6 contribution of different characters for genetic diversity of landraces of rice

S. No.	Observed characters	Percentage of contribution
1	Days to 50% flowering	58.40
2	Plant height at maturity	3.13
3	No of tillers per plant	0.12
4	No of productive tillers per plant	2.66
5	Panicle length	3.38
6	Spikelet fertility	0.68
7	Number of grains per panicle	8.50
8	Grain length	0.30
9	Grain breath	0.00
10	Grain L/B ratio	0.00
11	1000 grain weight	9.90
12	Grain yield per plant	12.91

The relative contribution of individual characters towards the expression of genetic diversity estimated over character wise D² value revealed that with 58.40 per cent contribution for days to 50 per cent flowering, 12.91 per cent contribution of grains yield per plant, 8.50 per cent of number of grains per panicle and with 9.90 per cent from 1000 grain seed weight were the major traits contributing to the total divergence and may be utilized as parameters for selecting genetically diverse parents. Similar findings were made by [15] for grain yield per plant and number of grains per panicle.

CONCLUSION

The 30 rice landraces used for the genetic diversity assessment demonstrated a significant range of variance. The 30 rice landraces were divided into 5 clusters, which was consistent with the Mahalanobis D² clustering pattern. The parents for the hybridization programme should be chosen based on the genetic distance, the contribution of various characters to the total divergence, and the magnitude of the cluster means for various characters performing with the greatest heterosis. It is anticipated that crosses between the germplasms of clusters II and V, IV and V, and III and IV will exhibit substantial heterosis as well as an accumulation of advantageous genes in ensuing segregating generations.

LITERATURE CITED

1. GriSp. 2013. Rice almanac. International Rice Research Institute Los Banos, Philippines.

2. Saxena RC, Singh RK. 2004. Rice research in India and the Asian perspective. *Journal Asian Biotechnology and Development* 7(1): 81-96.

3. Fahad S, Adnan M, Noor M, Arif M, Alam M, Khan IA, Ullah H, Wahid F, Najafi E, Devineni N, Khanbilvardi R, Kogan F. 2018. Understanding the changes in global crop yields through changes in climate and technology. *Earth's Future* 6(3): 410-427.

4. Manonmani S, Khan F. 2003. Analysis of genetic diversity for selection of parents in rice. *Oryza* 40: 54-56.

5. Nayak AR, Chaudhury D, Reddy JN. 2004. Genetic divergence in scented rice. *Oryza* 41: 79-82.

6. Ovung CY, Lal GM, Rai PK. 2012. Studies on genetic diversity in rice (*Oryza sativa* L.). *Journal of Agriculture and Technology* 8(3): 1059-1065.

7. Olaniran A, Briggs J, Pradhan A. 2022. Stock-outs of essential medicines among community health workers (CHWs) in low- and middle-income countries (LMICs): A systematic literature review of the extent, reasons, and consequences. *Human Resource Health* 20: 58. https://doi.org/10.1186/s12960-022-00755-8

8. Iftekharuddaula KM, Khaleda A, Hassan MS, Fatema K, Badshah A. 2002. Genetic divergence, character association and selection criteria in irrigated rice. *Pakistan Journal of Biological Sciences* 2: 243-246.

9. Falconer DS. 1960. *Introduction to Quantitative Genetics*. The Ronald Press, New York.

10. Panse VG, Sukhatme PV. 1967. *Statistical Methods for Agricultural Workers*. 2nd Edition, Indian Council of Agricultural Research, New Delhi.

11. Rao CR. 1952. *Advanced Statistical Methods in Biometrics Research*. John Willey and Sons, New York.

12. Chandani Y, Noel M, Pomeroy A, Andersson S, Pahl MK, Williams T. 2012. Factors affecting availability of essential medicines among community health workers in Ethiopia, Malawi, and Rwanda: solving the last mile puzzle. *American Journal of Tropical Med. Hyg*. 87(5 Suppl): 120-126.

13. Mishra AK, Singh PK, Kumar R, Kumar P, Singh R, Kumar A, Kumar A. 2018. Genetic divergence study in advance Indica rice (*Oryza sativa* L.) lines for yield and quality attributes. *Int. Jr. Curr. Microbiol. App. Sci*. SI-7: 2924-2933.

14. Babu J. 2012. Genetic diversity, variability and character association in rice under saline condition. *M. Sc. (Agriculture) Thesis*, Annamalai University, Annamalainagar, Tamil Nadu, India.

15. Zhou Y, Tao Y, Yuan Y, Zhang Y, Miao J, Zhang R, Yi C, Gong Z, Yang Z, Liang G. 2018. Characterization of a novel quantitative trait locus, GN4-1, for grain number and yield in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics* 131: 637-648.