



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.1.223>

DIVERSITY ANALYSIS IN IMPROVED AND TRADITIONAL GENOTYPES OF RICE (*ORYZA SATIVA* L.)

S. Keerthana¹, P. Senthil Kumar², Gangadhara Doggalli¹, Vinutha S. Patil³, Santhoshini Elango⁴, C.A. Deepak⁵, Ashwini Lamani⁶ and D. Gireesha⁴

¹Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad - 580 005, Karnataka, India

²Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram-608 002, Tamilnadu, India

³Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur, Karnataka, India.

⁴Department of Plant Pathology, University of Agricultural Sciences, Dharwad - 580 005, Karnataka, India.

⁵Zonal Agricultural Research Station, V.C. Farm, Mandya, Karnataka, India.

⁶CSIR-CIMAP Research Centre, Bangalore - 560 065, Karnataka, India.

(Date of Receiving-13-12-2023; Date of Acceptance-25-03-2024)

ABSTRACT

The present study was carried out to study the diversity among the 35 different rice genotypes. The study was carried out in two seasons in randomized block design and evaluated for twelve yield and yield attributing characters. From this pooled diversity analysis was carried out, in that 35 rice genotypes were grouped into seven clusters. Maximum numbers of genotypes were grouped in the cluster II hence it was observed with high intra cluster distance and the cluster VI and VII had single genotype and thus observed with low intra cluster distance. The maximum inter cluster distance, which is a measure of greater genetic diversity had been observed between the cluster I and cluster V. Hence, hybridization between these clusters can be expected to produce transgressive segregants which can be utilized as effective parents. The character that contributed more for the divergence was found to be single plant yield among the twelve characters studied.

Key words : D², Genetic divergence, Rice, Yield.

Introduction

Rice is one of the crop that is fetching the place in the list of staple food crop after wheat and maize which is cultivated in almost all the continents of the world except Antarctica (Harihar Ram, 2019). Rice is the crop which is having the highest area, production and it is the most important cereal among the all in the Indian scenario. Rice fields cover about 9% of earth's arable land (Maclean *et al.*, 2002). As this much importance is found to Rice it is prerequisite to improve the rice varieties both in economical and nutritional aspects to build a better healthy society.

Hence, by utilizing the traditional cultivars in hybridization programmes we could incorporate various health benefits in improved varieties. Heterosis is the basic aim of hybridization programmes. Quantitative genetics

theory predicts that the mid parent heterosis is a function of genetic divergence between the parents of hybrid; Thus ultimately suggesting the heterotic cross combination (Singh and Singh, 2019). The present study is aimed to find out the genetic divergence among 35 traditional and improved cultivars of rice by using Mahalanobis D² statistics.

Materials and Methods

35 different genotypes were included in this study which comprising both traditional and improved cultivars of rice belonging to different regions including IRRI varieties, TNAU released varieties and traditional landraces of Tamilnadu (Table 1). The experiment was carried out in randomized block design with suitable agronomic practices over two seasons at Andipantal village, Thiruvarur, Tamilnadu (longitude 10°52' 11.666"N

Table 1 : Cluster formation in the Pooled analysis.

Cluster	No. of genotypes	Code of genotypes													
		G28	G29												
I	2	G28	G29												
II	14	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G25
III	7	G14	G15	G16	G17	G18	G19	G27							
IV	8	G20	G21	G22	G23	G24	G26	G30	G31						
V	2	G33	G35												
VI	1	G32													
VII	1	G34													

and latitude 79°38'36.563"E) during February to July and at Kekarai village, Thiruvarur, Tamilnadu (longitude 10°47'38.108"N and latitude 79°39'29.426"E) during September to February and pooled analysis of them was made. They were evaluated for twelve yield and yield attributing characters viz., plant height, number of tillers, number of productive tillers, days to 50% flowering, panicle length, panicle weight, number of grains per panicle, 1000 grain weight, grain length, grain breadth, length breadth ratio and single plant yield. From this information diversity among the genotypes was estimated by employing Mahalanobis D² analysis.

Results and Discussion

Evaluation of improved and traditional genotypes of rice for the genetic diversity study

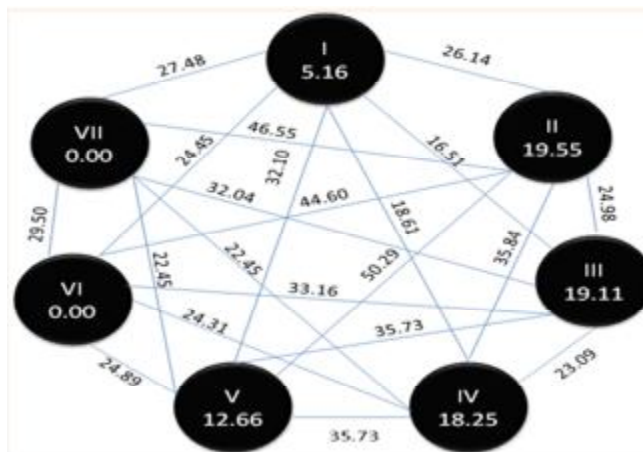
The analysis of variance showed significance difference among the genotypes for almost all the characters indicating the presence of variation among the genotypes and it is further directed to D² analysis. In the pooled analysis, the 35 genotypes were grouped into seven clusters and the cluster I had two genotypes, cluster II had fourteen genotypes, Cluster III had seven genotypes whereas cluster IV had eight genotypes. Cluster V had two genotypes and finally single genotype was included in the cluster VI and cluster VII. Genetic diversity was by the effect caused by either by geographical barrier or by genetic barrier in crossability (Singh and Singh, 2019). But, here it was found that genotypes belonging to the same geographical origin were grouped in different cluster but the genotypes belonging to the different geographical origin were grouped into same cluster. Similar findings was noted by Nayak *et al.* (2004) and Banumathy *et al.* (2010) (Table 1).

Intra and inter cluster distances

In simple terms genetic distance is the quantitative measure of genetic difference between two individuals in sense of difference in their nucleotide level and/or gene



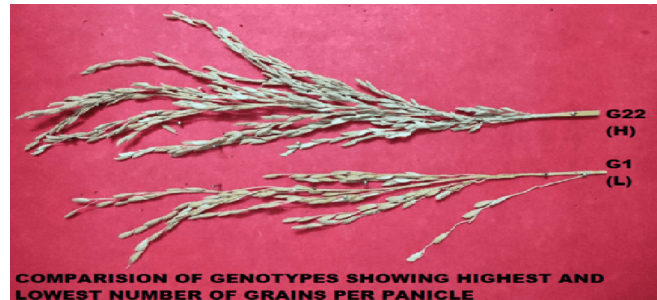
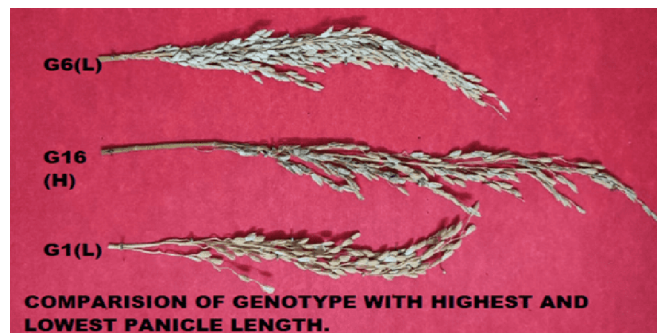
Field view of improved and traditional genotypes of rice plot

**Fig. 1 :** Cluster diagram for pooled analysis.

frequencies (Singh and Singh, 2019). So by evaluating the D² distance which is a measure of genetic distance or in terms genetic diversity, among the seven clusters maximum intra cluster is found in the cluster II (19.55) and the minimum intra cluster distance was observed in cluster I (5.16), while it was zero value for the cluster VI and VII as they had only single genotype in each. With this we may remark that the selection within the cluster II will be rewarding and with the cluster mean it is showed that the genotypes of this cluster have so many positive yield attributes such as reduced plant height thus producing dwarf plants, early flowering thus reducing the crop duration with maximum singleplant yield. Inter cluster distance is the important criteria for selection of genotype as a parent in hybridization programme (Singh and Narayanan, 2017). The inter cluster distance were found

Table 2 : List of genotype used in the experiment.

Code	Name of the genotype	Parentage	Release
G1	ADT 36	Tirriveni × IR 20	1981
G2	ADT 37	BG 280-12/PTB 33	1987
G3	ADT 42	AD9246/ADT 29	1997
G4	ADT 43	IR 50 × White ponni	1998
G5	ADT(R)45	IR 50 × ADT 37	2001
G6	ADT 48	IET 11412/IR 64	2005
G7	ADT 53	ADT 43/JGL 384	2019
G8	CO 51	ADT 43/RR 272-1745	2013
G9	ASD 16	ADT 31 × CO 39	1986
G10	ADT 38	IR 1529-680-3-2/IR 4432-52-6-4/IR 7963-30-2	1987
G11	ADT 39	IR 8/IR 20	1988
G12	ADT 46	ADT 38/CO 45	2002
G13	ADT 52	CR1008/ADT 49	2018
G14	TKM 13	WGL 32100/Swarna	2015
G15	CO(R)50	CO43 /ADT 38	2010
G16	IR 20	IR 262 × TKM 6	1969
G17	Bhavani	PETA × BPI 76	1973
G18	Kichili samba	Spontaneous Mutant	1921
G19	Zeeraga samba	Traditional variety of TN	-
G20	Thuyamalli	Traditional variety of TN	-
G21	Vellakar	Traditional variety of TN	-
G22	Vasundhara	Phalguna × IET-6858	2000
G23	Thanuska	Untraceable	-
G24	Arcot kichidi samba	Arcot region of TN	-
G25	Navara	Palaghat, Kerela	-
G26	BPT	GEB 24×T(N)1×Mashuri	2018
G27	ADT 40	RPW 6.13 × Sona	1994
G28	ADT 44	IR56/or142-99	2000
G29	ADT 50	BPT 5204/CR 1009	2012
G30	CR 1009	GEB-24 × Y(N) × Mashuri	1982
G31	ADT 51	BPT 5204 × I.W. Ponni	2018
G32	Kalanamak	Terrai belt of U. P.	-
G33	Karupukavuni	Chettinadu belt of TN	-
G34	Sivapukavuni	Sivagangai district of TN	-
G35	Mappillai samba	Villages (Kalapaganur) of Salem district	-

**Fig. 2 :** Panicles of genotypes showing higher number of grains per panicle.**Fig. 3 :** Comparison of panicles for number of grains per panicle (H- highest, L-lowest).**Fig. 4 :** Panicles of Genotypes showing higher panicle length.**Fig. 5 :** Comparison of panicle length (H- highest, L-lowest).

to be maximum than the intra cluster distance which indicate the existence of substantial diversity among the parents. Similar results of inter and intra cluster distances in rice were reported by Senapati and Sarkar (2005), Shahidullah *et al.* (2009) (Tables 3 and 4).

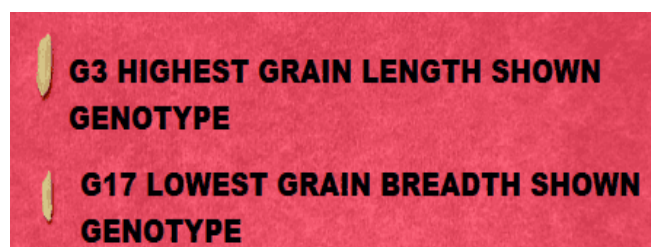


Fig. 6 : Grains of genotypes showing improved quality traits.

Table 3 : Intra and Inter Cluster D^2 values for pooled study.

	I	II	III	IV	V	VI	VII
I	26.16	26.14	16.51	18.61	32.40	24.45	27.48
II		19.55	24.98	35.84	50.29	44.61	46.55
III			19.11	23.09	35.73	33.16	32.04
IV				18.25	24.33	24.31	22.45
V					12.66	24.89	18.66
VI						0.00	29.50
VII							0.00



Fig. 7 : Panicles of genotypes showing good single plant yield.

cluster I and cluster VII (46.557) and the minimum inter cluster distance was found between cluster I and cluster III (16.511). The cluster I has some improved varieties

Table 4 : Cluster mean of various character studied in Pooled analysis.

PH	T	PT	DFP	PL	PW	NGPP	1000 GW	GL	GB	LB Ratio	SPY
107.78	21.07	18.04	121.56	26.87	3.28	183.48	21.93	0.63	0.23	2.70	23.28
84.99	17.65	15.05	88.76	22.11	2.41	159.16	19.38	0.74	0.32	2.43	24.04
101.83	18.98	17.14	106.85	25.55	3.05	203.97	21.15	0.78	0.28	2.84	20.52
120.99	19.40	17.10	113.06	27.64	3.10	227.01	21.70	0.74	0.29	2.61	23.11
137.23	20.61	18.27	135.02	23.80	2.98	135.91	23.21	0.85	0.32	2.62	19.51
134.01	23.41	20.86	129.45	24.93	2.73	122.50	18.57	0.48	0.24	1.99	20.75
131.42	17.25	14.75	132.34	29.32	3.22	183.66	29.16	0.80	0.33	2.39	18.20

Character abbreviation : PH-Plant height, T-Number of tillers, PT-Productive tillers, DFP-Days to 50% flowering, PL-panicle length, PW-Panicle weight, NGPP-Number of grains per panicle, 1000 GW-1000 grain weight, GL-grain length, GB-Grain breadth, LB Ratio-Length breadth ratio, SPY-Single plant yield.

Table 5 : Contribution of character towards divergence in the pooled analysis.

S. no.	Characters studied	Contribution (%)
1	Plant height	2.85
2	No. of Tillers	0.25
3	No. of Productive tillers	2.50
4	Days to fifty percent flowering	4.11
5	Panicle Length	9.43
6	Panicle weight	0.25
7	No. of Grains per Panicle	6.04
8	1000 Grain weight	4.62
9	Grain length	16.05
10	Grain Breadth	16.38
11	LB Ratio	6.47
12	Yield per Plant	31.07

The maximum inter cluster distance was found between cluster I and cluster V (50.29) followed by

and shows high mean for increased panicle length and length breadth ratio, thus it may contribute to both quality and in yield aspects. Similarly the genotype in the cluster VII shows increased panicle length, 1000 grain weight and grain length. Thus hybridization between the genotypes of these clusters will be rewarding for yield attributes and nutritional aspects too since the cluster VII was singly occupied by the traditional variety Sivapukavuni which is known to have anthocyanin with enormous anti oxidant property (Kalaivani *et al.*, 2020) (Fig. 1).

Contribution of characters towards total diversity

In the pooled analysis, among all the character the maximum contribution to the diversity was made by Single plant yield (35.54%), followed by grain breadth, grain length and panicle weight. The lowest contribution to genetic divergence was provided by Number of Tillers. Thus in the hybridization programme the maximum

importance could be given to those character that contributing maximum to the divergence (Table 5 and Fig. 7).

References

- Banumathy, M., Manimaran B., Sheeba A., Manivanan N., Ramya B., Kumar D. and Ramasubramanian G.V. (2010). Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Elect. J. Plant Breed.*, **1(14)**, 500-504.
- Hari, Har Ram (2019). *Crop breeding and biotechnology* (2nd ed.). Ludhiana: Kalyani Publishers.
- Kalaivani, R., Bakiyalakshmi S.V. and Nandhini R. (2020). An integrated approach on study of nutritional and *in vitro* anti cancerous properties of traditional pigmented rices against MC7 cell line. *J. Nat. Remed.* **21(8)**, 1.
- Maclean, J.L., Dawe D.C. and Hettel G.P. (2002). *Rice almanac: Source book for the most important economic activity on earth*. International Rice Research Institute, Manila, Philippines.
- Nayak, A.R., Chaudhery D. and Reddy J.N. (2004). Genetic divergence in scented rice. *Oryza*, **41(3 and 4)**, 79-82.
- Senapati, B.K. and Sarkar G. (2005). Genetic divergence in Indica rice (*Oryza sativa* L.) under rainfed saline soil of Sundaban. *Oryza*, **42(1)**, 70-72.
- Shahidullah, S.M., Hanafi M.M., Ashrafuzzaman M., Ismail M.R. and Khair A. (2009). Genetic diversity in grain quality and nutrition of aromatic rices. *Afr. J. Biotechnol.*, **8(7)**, 1238-1246.
- Singh, P. and Narayanan S.S. (2017). *Biometrical techniques in plant breeding* (6th ed.). Ludhiana: Kalyani Publishers.
- Singh, B.D. and Singh A.K. (Eds) (2019). *Marker assisted plant breeding: Principles and practices*. New Delhi: Springer.