Received: 13 Oct 2022 | Revised: 08 Nov 2022 | Accepted: 14 Nov 2022

Electronic Journal of Plant Breeding

Research Article

Genetic diversity analysis for yield and yield attributing characters in rice (*Oryza sativa* L.)

B. Hema Sai[1]*, B. Rupesh Kumar Reddy[1], M. Shanthi Priya[2] and Lakshminarayana R. Vemireddy[3]

[1]Department of Genetics and Plant Breeding, S. V. Agricultural College, Tirupati-517 502, Andhra Pradesh, India
[2]Department of Genetics and Plant Breeding, Agricultural Research Station, Perumallapalle, Tirupati -517 505, Andhra Pradesh, India
[3]Department of Molecular Biology and Biotechnology, S. V. Agricultural College, Tirupati-517 502,Andhra Pradesh, India
***E-Mail**: hemasaibavisetti1998@gmail.com

Abstract
In the present study, 60 rice genotypes were selected to evaluate the genetic divergence for 15 yield and yield attributing characters. Based on Mahalanobis D^2 statistic, the 60 genotypes were grouped into nine clusters. On the basis of genetic distance and cluster means, clusters IV and IX, VI and IX, I and IX, were identified as clusters with high inter-cluster distance. Genotypes of these clusters could be used as parents in crop improvement programmes for generation of promising segregants. Days to maturity and thousand grain weight were observed to contribute highly towards divergence. Hybridisation between the genotypes SMB3 (cluster VIII) and Juma (cluster IV) could be recommended for recombination breeding to get superior transgressive segregants for earliness and desirable yield attributing characters.

Keywords: D^2 Mahalanobis, Diversity Analysis, yield and yield attributing characters.

INTRODUCTION

Rice (*Oryza sativa* L.) is a staple food and a major source of food for about three million people globally. It is the second most consumed food in the world. In order to meet the growing demands of increasing global population, the development of high yielding rice varieties is essential. Crop improvement programmes are dependent on the nature and magnitude of genetic diversity that exists among the genotypes and the prerequisite for success of any breeding program is to select divergent parents for hybridisation. Multivariate analysis like Mahalanobis D^2 statistic is a useful tool for measuring genetic diversity by considering different characters in a given population and also identify the characters which significantly contribute to divergence among the genotypes. Numerous researchers have underlined the significance of genetic diversity for the selection of desirable parents (Lakshmi *et al*., 2022; Rathan *et al*., 2020 and Palaniyappan *et al*., 2020).The present experiment was carried out to estimate the genetic diversity of rice genotypes for yield and yield attributing characters for their utilization in the development of high yielding rice varieties.

MATERIALS AND METHODS

The current investigation consisted of 60 diverse rice genotypes (**Table 1**) and the experiment was carried out during *kharif,* 2021 at Wetland Farm, S.V. Agricultural College, Tirupati. All 60 genotypes were sown and raised in separate lines on a nursery bed and 21 days old seedlings were transplanted in the main field in a randomized block design (RBD) with two replications. In each replication, each genotype was transplanted in two rows of two meters length with a spacing of 20 cm × 15 cm. All the recommended packages of practices were followed to raise a healthy crop.

Observations were recorded for 15 yield and yield attributing characters *viz.,* days to 50% flowering, days to maturity, plant height, panicle length, the total number of effective tillers plant^{-1}, number of chaffy grains panicle^{-1}, the number of filled grains panicle^{-1}, the number of spikelets panicle^{-1}, spikelet fertility, grain yield plant^{-1}, thousand grain weight, grain length, grain width, grain thickness and grain L/B ratio. The observations were recorded on five randomly selected plants from each genotype in each replication except for days to 50% flowering and days to maturity. Observations for thousand grain weight were obtained from random grain sample drawn from each genotype in individual replications using standard procedures.The collected data were subjected to Analysis of Variance (ANOVA), as per the method proposed by Panse and Sukhatme (1961), Genetic divergence analysis was carried out following the D^2 statistics proposed by Mahalanobis (1928) and described by Rao (1952).

RESULTS AND DISCUSSION

The 60 genotypes were grouped into nine distinct clusters using Tocher's method (Rao, 1952) and the cluster composition is furnished in **Table 2**. Out of nine clusters, clusters I and III were the largest ones comprising of 12 genotypes each followed by cluster IV with 11 genotypes and cluster II with 10 genotypes. Clusters VI had seven genotypes while clusters V and VII had three genotypes each. Clusters VIII and IX had only one genotype each. The genotypes present in the solitory clusters are unique and could be very useful for breeding purposes.

The results of intra and inter-cluster distances are presented in **Table 3**. The D^2 values of intra clusters are lesser than that of inter clusters, indicating lesser divergence within the cluster than among the clusters. The average intra-cluster distance ranged from 0.00 to 1257.64. The maximum intra-cluster distance was observed in cluster VI (1257.64) followed by cluster IV (982.15), cluster II (741.04), cluster VII (578.36), cluster III (572.44), cluster I (469.88) and cluster V (414.78). Genotypes from these highly divergent clusters could be considered for selection of parents for hybridization programs, which could result in better segregants. Clusters VIII and IX were solitory clusters.

The cluster VIII was constituted by the genotype SMB3. This genotype was observed to record good perse performance for most of the important characters like panicle length, spikelet fertility, grain yield plant^{-1}, thousand grain weight, grain width and grain thickness. Similarly, cluster IX comprised of NLR33892, which exhibited late flowering and maturity nature. The genotypes of cluster V recorded maximum values for the number of filled grains panicle^{-1}, the number of spikelets panicle^{-1} and grain L/B ratio and recorded minimum values for plant height which is desirable. Cluster IV registered minimum values for days to 50% flowering, days to maturity which are

Table 1. List of genotypes included under the study and their pedigree

S. No.	Genotypes	Parentage	Group
1	MTU 1153 (Chandra)	MTU1010 x MTU1081	Indica
2	Vasundhara	Phalguna x IET-6858	Indica
3	BPT 1235 (DhanyaLakshmi)	Sabarmathi x W12708	Indica
4	KalamKheti	Landrace	Landrace
5	IC 454277	Indigenous collection	Indica
6	Mandhyavijaya	Sona x Mahsuri	Indica
7	DRR dhan 38	BPT5204/KMR-3	Indica
8	Heera	CR-404-48 x Cr-289-1208	Indica
9	RP bio226	Samba mahsuri (BPT5204)*4/SS 1113	Indica
10	Kesari	Kumar x Jagannath	Indica
11	NLR 4002	Selection from ARS, Nellore	Indica
12	Kolong	Chilarai/Kalinga III	Landrace
13	IR 1552	Selection from IRRI	Indica
14	Gulmurali	Local Selection	Indica
15	BPT 5204 (SambaMahsuri)	GEB24 x TN1 x Mahsuri	Indica
16	Ranbir Basmati	Pureline selection from basmati 370-90-95	Aromatic

https://doi.org/10.37992/2022.1304.161

Table 1. Continued..

S. No.	Genotypes	Parentage	Group
17	SMB3	Swarna Mutant	indica
18	N22	selection from landrace Rajbhog (Nepal)	Landrace
19	Dhariabolia	Land race	Landrace
20	MTU 1121 (Sridhuti)	BPT5204 x MTU BB 8-24-1	Indica
21	MTU 7029 (Swarna)	Vasista x Mahsuri	Indica
22	Haryana Basmati	Sona x Basmati-370	Aromatic
23	Sharbati	Local selection from uttarpradesh	Aromatic
24	AC 38460	Germplasm collection	Japonica
25	IR 8	Dee-gee-woo-gen x Peta	Indica
26	PR 118	/ PR 11 //	Indica
27	BPT 2295 (BapatlaMahsuri)	BPT1768 x NLR33641	Indica
28	NLR 34242	Selection from NLR30491	Indica
29	Badshabhog	Local Selection	Aromatic
30	HIM 299	IR28/Shensi var./IR28	Indica
31	Pantdhan12	Govind/UPR 201	Indica
32	NLR 2422	Selection from ARS, Nellore	Indica
33	Aditya	M-63-83/Cauvery	Indica
34	Vikramarya	RPW 6-13/PTB 2	Indica
35	WGL 32100	Divya/BPT 5204	Indica
36	Anjali	Sneha x RR149-1129	Indica
37	Mahi Sugandh	BK79/Basmati370,	Aromatic
38	Ranjith	Pankaj x Mahsuri	Indica
39	Varalu	Erramallelu/CR 544-1-2	Indica
40	Pusa Sugandh15	Basmati370/sadari/buharul/muskan41	Aromatic
41	Warangal Sambha	BPT 5204/ARC5566/BPT3291	Indica
42	Juma	Local selection	Indica
43	T309	Local selection	Landrace
44	Siddhi	BPT5204/ARC5984/45Kavya/Kavya/BPT5204	Indica
45	Luit	Heera x Annada	Indica
46	Sonasali	RP-1015-348-84-1/SONA/Manoharsali	Indica
47	Tetep	Local selection	Landrace
48	MGD 101	Teqing/Binam// Teqing///Teqing	Indica
49	IC 455374	Indigenous collection	Japonica
50	Azucena	Traditional landrace	Landrace
51	NLR 33671	Selection from ARS, Nellore	Indica
52	Krishna Hamsa	Rasi x Fine Gora	Indica
53	Gandhi Birion	Local selection	Landrace
54	Ravi 003	-	Indica
55	RNR 19186	BPT 5204 / Tellahamsa	Indica
56	MTU 1061 (Indra)	PLA 1100 x MTU 1010	Indica
57	MTU 1190 (Varam)	MTU1081 x Swarna Sub1	Indica
58	MTU 3626 (Prabhat)	IR8 x MTU3	Indica
59	Pusa Basmati	Pusa-167/Karnal Local	Aromatic
60	NLR 33892 (Parthiva)	NLR27999 x MTU 4870	Indica

Table 2. Distribution of 60 rice genotypes into nine clusters based on Tocher's method

Cluster	Number of Genotypes	Rice genotypes
I	12	Dhariabolia, IC 455374, Pusa Basmati, Vikramarya, Mahi Sugandh, Badshabhog, NLR 33671, Kesari, WGL 32100, IR 1552, PusaSugandh 15, AC 38460
II	10	IC 454277, Azucena, PR 118, Haryana Basmati, Gandhi Birion, MTU 3626(Prabhat), Vasundhara, Sonasali, Tetep, T 309
III	12	RP bio 226, Ranjith, Warangal Sambha, MTU 1190(Varam), Mandhyavijaya, MTU 1121(Sridhuti), BPT 2295(BapatlaMahsuri) BPT 5204(Samba Mahsuri), Ranbir Basmati, MTU7029(Swarna), Siddhi, BPT 1235(Dhanya Lakshmi)
IV	11	KalamKheti, NLR 2422, Aditya, Heera, Kolong, Anjali, Varalu, Juma, N22, HIM 299, Luit
V	3	Ravi 003, RNR 19186, IR 8
VI	7	MTU 1153(Chandra), NLR 34242, Gulmurali, MGD 101, Pant dhan 12, NLR 4002, DRR dhan 38
VII	3	Krishna Hamsa, MTU 1061(Indra), Sharbati
VIII	1	SMB 3
IX	1	NLR 33892 (Parthiva)

Table 3. Average Inter (above diagonal) and Intra cluster (diagonal) D^2 and D values (in parenthesis) for 15 characters in 60 rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	469.88 (21.68)	1529.47 (39.11)	4211.21 (64.89)	10057.54 (100.29)	1233.72 (35.12)	2955.16 (54.36)	18243.47 (135.07)	6235.04 (78.96)	80088.68 (283.00)
II		741.04 (27.22)	2950.97 (54.32)	15722.90 (125.39)	2815.01 (53.06)	6243.55 (79.02)	12551.28 (112.03)	2632.98 (51.31)	67452.27 (259.72)
III			572.44 (23.93)	25438.96 (159.50)	2868.56 (53.56)	12350.67 (111.13)	6392.27 (79.95)	2960.87 (54.41)	50244.86 (224.15)
IV				982.15 (31.34)	13314.45 (115.39)	3499.07 (59.15)	53620.52 (231.56)	28661.67 (169.30)	144411.40 (380.01)
V					414.78 (20.37)	4956.73 (70.40)	16357.06 (127.89)	7370.14 (85.85)	74239.60 (272.47)
VI						1257.64 (35.46)	33206.64 (182.23)	14903.04 (122.08)	109031.80 (330.20)
VII							578.36 (24.05)	5475.41 (74.00)	22591.07 (150.30)
VIII								0.00 (0.00)	47586.11 218.14)
IX									0.00 (0.00)

desirable for development of short duration genotypes. The cluster I and cluster II exhibited high cluster mean value for the number of effective tillers panicle^{-1} and grain length respectively.

The inter-cluster D^2 values ranged from 1233.72 to 144411.40. The maximum inter-cluster distance (144411.40) was observed between clusters IV and IX followed by clusters VI and IX (109031.80), clusters I and IX (80088.68), clusters V and IX (74239.60) and clusters II and IX (67452.27). Minimum inter-cluster distance of 1233.72 was recorded between clusters I and V, followed by clusters I and II (1529.47), clusters II and VIII (2632.98), clusters II and V (2815.01) and clusters III and V (2868.56) indicating that genotypes of these clusters were genetically close. To realize much variability and high heterotic effect, the parents should be selected from highly divergent clusters which could lead to the generation of a wide range of desirable recombinants in the F_2 and subsequent generations (Mishra *et al*., 2020).

The cluster means for yield attributing characters are presented in **Table 4**. It indicated that early and late flowering genotypes were grouped in cluster IV and cluster IX respectively. The cluster V was observed to record the least mean plant height whereas cluster VIII registered the maximum plant height. The panicle length was observed to be maximum in cluster VIII . The number of effective tillers plant^{-1} was more in cluster I whereas it was least in clusters V and IX. The number of chaffy

Table 4. Cluster means for yield and yield attributing characters among 60 rice genotypes

Cluster	DFF	DAM	PH	PL	ET	CG	FG	TS
I	98.04 (3)	125.88 (3)	116.35 (4)	25.87 (4)	9.71 (1)	39.08 (5)	185.60 (5)	224.68 (4)
II	103.35 (5)	131.75 (5)	124.73 (7)	26.46 (2)	8.02 (7)	31.93 (4)	159.52 (8)	191.45 (8)
III	109.13 (6)	139.04 (6)	117.02 (5)	25.00 (8)	8.45 (6)	49.88 (8)	218.12 (2)	268.00 (2)
IV	78.41 (1)	105.41 (1)	119.06 (6)	25.39 (7)	9.15(3)	31.27 (3)	157.84 (9)	189.11 (9)
V	100.00 (4)	127.33 (4)	111.10 (1)	25.90 (3)	7.00 (8)	63.87 (9)	259.00 (1)	322.87 (1)
VI	88.71 (2)	115.71 (2)	115.53 (3)	25.84 (5)	8.77 (4)	43.40 (6)	169.06 (7)	212.46 (5)
VII	125.67 (8)	154.33 (8)	113.20 (2)	24.47 (9)	9.33 (2)	27.93 (2)	174.73 (6)	202.67 (7)
VIII	113.50 (7)	139.50 (7)	182.50 (9)	32.50 (1)	8.70 (5)	16.00 (1)	190.40 (4)	206.40 (6)
IX	155.00 (9)	186.50 (9)	142.30 (8)	25.70 (6)	7.00 (8)	45.80 (7)	199.70 (3)	245.50 (3)
MEAN	107.98	136.16	126.87	26.35	8.46	38.80	190.44	229.24

Cluster	SF	GY	TGW	GL	GW	GT	L/B	Productivity Traits	
								Total score	Final Rank
I	82.00 (5)	22.62 (2)	20.68 (5)	9.15 (2)	2.71 (6)	1.67 (5)	3.42 (2)	56	1
II	82.32 (4)	18.16 (6)	25.56 (2)	9.42 (1)	2.91 (2)	1.73 (3)	3.27 (5)	69	4
III	80.73 (7)	17.46 (8)	16.78 (7)	8.21 (7)	2.50 (8)	1.56 (9)	3.31 (4)	93	8
IV	83.86 (3)	19.44 (5)	22.56 (4)	8.99 (5)	2.88 (4)	1.75 (2)	3.19 (7)	69	4
V	79.54 (9)	16.09 (9)	15.20 (9)	8.38 (6)	2.45 (9)	1.58 (8)	3.45 (1)	82	7
VI	80.34 (8)	20.53 (3)	22.64 (3)	9.15 (2)	2.89 (3)	1.73 (3)	3.23 (6)	62	2
VII	85.83 (2)	17.68 (7)	19.53 (6)	9.12 (4)	2.71 (6)	1.63 (6)	3.39 (3)	78	6
VIII	92.08 (1)	32.38 (1)	27.60 (1)	8.14 (8)	3.36 (1)	1.96 (1)	2.43 (9)	62	2
IX	81.22 (6)	19.72 (4)	16.50 (8)	7.47 (9)	2.76 (5)	1.62 (7)	2.71 (8)	100	9
MEAN	83.10	20.45	20.78	8.67	2.80	1.69	3.16		

DFF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
PL : Panicle length (cm)
ET : Total number of effective tillers plant^{-1}
CG : Number of chaffy grains panicle^{-1}
FG : Number of filled grains panicle^{-1}
TS : Number of spikelets panicle^{-1}
SF : Spikelet fertility (%)
GY : Grain yield plant^{-1}(g)
TGW : 1000 grain weight (g)
GL : Grain length (mm)
GW : Grain width (mm)
GT : Grain thickness (mm)
L/B : Grain L/B ratio

grains panicle^{-1} was observed to be less in cluster V whereas the number of filled grains panicle^{-1} and number of spikelets panicle^{-1} were high in cluster IV. Low and high spikelet fertility %, grain yield plant^{-1} and thousand grain weight were observed for Cluster V and Cluster VIII respectively. Longer grain length was observed in cluster II whereas shorter in cluster IX. Wider grain width and L/B ratio were observed in cluster VIII and narrow grain width and L/B ratio in cluster V. High and low grain thickness was recorded for cluster VIII and cluster III respectively.

Since no cluster was observed to record all the desirable characters, the possibility of direct selection for immediate use was ruled out. In order to improve a character in a hybridization programme, genotypes from clusters with high cluster means for a particular character are recommended for selection. Further, hybridization between the genotypes from divergent clusters is suggested for a desirable combination of all the characters. Hence, the selection of genotypes from clusters VIII and IV could be recommended for recombination breeding to get superior transgressive segregants for earliness and desirable yield attributing characters.

The results on per cent contribution of various traits towards diversity are presented in **Table 5**. The maximum contribution towards genetic divergence is recorded by days to maturity (78.81 %) followed by thousand grain weight (19.49 %). The characters grain L/B ratio (0.68 %), grain length (0.62 %), days to 50% flowering (0.11%), plant height (0.11%), the number of chaffy grains panicle-1 (0.11%) and grain width (0.06%) contributed least towards genetic divergence. Hence, days to maturity and thousand grain weight were found to be the best discriminatory characters for the selection of divergent parents which would be useful for developing desirable recombinants for high yielding rice genotypes in breeding programme. The results were supported by earlier findings of Kumar *et al*. (2015) for days to maturity and Saraswathi *et al*. (2012) for thousand grain weight.

Table 5. Per cent contribution of various characters towards genetic divergence in 60 rice genotypes

S.No.	Characters	Number of times	% contribution
1	Days to 50% flowering	2	0.11
2	Days to maturity	1395	78.81
3	Plant height (cm)	2	0.11
4	Panicle length (cm)	0	0.00
5	Total number of effective tillers plant^{-1}	0	0.00
6	Number of chaffy grains panicle^{-1}	2	0.11
7	Number of filled grains panicle^{-1}	0	0.00
8	Number of spikelets panicle^{-1}	0	0.00
9	Spikelet fertility (%)	0	0.00
10	Grain yield plant^{-1}(g)	0	0.00
11	Thousand grain weight (g)	345	19.49
12	Grain length (mm)	11	0.62
13	Grain width (mm)	1	0.06
14	Grain thickness (mm)	0	0.00
15	Grain L/B ratio	12	0.68

From the study, it could be concluded that the cross between SMB3 (cluster VIII) and Juma (cluster IV) would be better for recombination breeding to get superior transgressive segregants for earliness and desirable yield attributing characters. Similarly, the crosses *viz.,* IC455374 (cluster I) x Juma (cluster IV), SMB3 (cluster VIII) x MTU1153 (cluster VI) and Ranjith (cluster III) x Juma (cluster IV) could be exploited for hybridization for the development of high yielding rice genotypes.

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