Int.J.Curr.Microbiol.App.Sci (2020) *9*(9): 3369-3376

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 9 (2020)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2020.909.419

Genetic Divergence for Important Economic and Quality Traits in Improved Lines of Rice (*Oryza sativa* L.)

Aditya Bora, Dhanraj Meena*, Mukesh Kumar Karnwal and Himanshu Chaudhary

Department of Genetics and Plant Breeding, College of Agriculture G.B. Pant University of Agriculture and Technology, Pantnagar-263145(U.S.Nagar, Uttarakhand), India

**Corresponding author*

ABSTRACT

Keywords

Rice (*Oryza sativa* L.), Mahalanobis D^2 analysis, Genetic divergence and Cluster

Article Info

Accepted:
24 August 2020
Available Online:
10 September 2020

The present investigation was carried out for two years during *kharif* season (2012 and 2013) of 28 rice genotypes including 2 local checks and layout in Randomized Complete Block Design (RBD) with 3 replications under irrigated condition. Nature and magnitude of genetic divergence was assessed using Mahalanobis D^2 statistics through which the genotypes were grouped inti 6 clusters. In the first year cluster III having 13 genotypes whereas, in next season cluster I containing of 12 genotypes was largest. While cluster V, VI during 2013 were found monogenotypic clusters. The highest inter-cluster divergence (74.537) was found between cluster I and IV in the year 2012 and cluster II and III (79.081) in 2013. Thus, the genotypes selected from cluster I (C-1446-5-18-17-1-MLD-2, JGL-1718, WGL-365, UPR-3411-1-1-1, UPR-3305-6-1-2, CR-77-3-1-1, NP-14-3-1, GontraBidhan-3, UPR-3027-10-1-1) for number of productive tillers, cluster IV (UPRI-3425-14-3-1, UPR-3443-7-2-1, NP-218, KAGR-559-1) for number of grains per panicle and cluster VI (Pant Dhan 4) for panicle length and grain yield per plant could be used in crossing programmes to achieve desired segregants.

Introduction

Rice is the seed of the grass species *Oryza sativa* (Asian rice) or *Oryza glaberrima* (African rice). As a cereal grain, it is the most widely consumed staple food for a large part of the world's human population, especially in Asia. It is the agricultural commodity with the third-highest worldwide production (rice, 741.5 million tons in 2014), after sugarcane (1.9 billion tons) and maize (1.0 billion tons).Major rice producing countries India, China, Indonesia, Thailand and Bangladesh make up a little over two-thirds of total area under rice. The World Rice Production in 2017/18 will be 481.04 million metric tons, which is 2.06 million tons less than the last year production i.e. 483.1 million tons (USDA). In India, estimated rice production in 2016/17 is 105 million tons from 44 million hectares as compared to 103.5 million tons harvested from 43.46 million hectares in 2015-16. India is 2nd largest rice producing country in the world after China (145MT). Rice cultivation is well-suited to countries and regions with low labor costs and high rainfall, as it is labor-intensive to cultivate and requires ample water. However, rice can be grown practically anywhere, even on a steep hill or mountain area with the use of water-controlling terrace systems. The varieties of rice are typically classified as long, medium, and short-grained. The grains of long-grain rice (high in amylose) tend to remain intact after cooking, medium-grain rice (high in amylopectin) becomes stickier and short grain rice contents low amylose.

Genetic diversity and the diverse gene pools are the basis of plant breeding. In addition to new gene pool providing building blocks for further improvement, genetic diversity is essential if higher level of productivity is to be achieved and sustained during the process of varietal development. The more diverse the parents, within overall limits of fitness, greater are the chances of obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in segregating generations(Singh and Bains 1968).Thus genetic divergence among parents is of paramount importance in selecting parental genotype for crossing programmes. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Shukla *et al.,* (2006), Sarawgi and Binse, 2007 and (Ramya and Senthilkumar, 2008). Hence the present investigation was carried out to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programmes.

Materials and Methods

The experimental material for the present study comprised of 28 genotypes of rice laid in randomized complete block design (RCBD) with 3 replications at the Norman E. Borlaug Crop Research Centre, GovindBallabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, during two seasons *kharif* 2012 and *kharif* 2013. Observations were recorded on randomly selected plants per replication for days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of panicle per plant, number of tillers, number of grains per panicle, flag leaf length (cm), flag leaf breadth (cm), flag leaf area (sq. cm), 1000 grain weight (g), grain yield per plant (g), dry weight of plant (g), harvest index. (%), decorticated grain length (mm), decorticated grain breadth (mm), decorticated L/B ratio, gelatinization temperature through alkali spreading value and Endosperm: amylosecontent. The data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

Results and Discussion

By using Tocher's methods the twenty eight genotypes were grouped into six clusters in both the seasons (*kharif* 2012 and 2013) and over the seasons. Cluster I during 2013 and in pooled estimates was the largest cluster having 12 and 9 genotypes; whereas cluster III during 2012 (13 genotypes) was largest. Cluster III in 2013, Cluster V in both the seasons (2012, 2013) and over the seasons were monogenotypic cluster. Cluster IV in both the seasons and cluster V in 2013 had five genotypes each. Cluster II in 2012 and cluster V in over the seasons had 6 genotypes each. Cluster II, III, and IV in pooled estimates had 4 genotypes each. Cluster I in 2012 had two genotypes and cluster II in 2013 had 3 genotypes (Table 1). In 2012 the maximum inter-cluster D^2 values were obtained between clusters I and IV (74.537), followed by cluster I and VI (74.289). During 2013, cluster II and III (79.081) followed by cluster III and V (76.819); whereas in pooled estimates cluster IV and V (50.044) followed by cluster I and V (46.633) had maximum inter-cluster D^2 values. Parental lines selected from these three clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects. Such recommendations were also made by Murty and Arunachalam (1966), Rao and Gomanthinayagam (1997) Mishra *et al.*, (2003), Chaturvedi and Maurya (2005) and Sandhya Kishore *et al.*, (2007).

Table.1 Cluster Pattern of 28 Genotypes of Rice (On The Basis Of D^2 Values)

Cluster number	**Year**	**Genotypes included**	**Number of genotypes**
I	2012	C 1446-5-18-17-1-MLD 2, CR-2995-1-2-3-1-1	2
	2013	C 1446-5-18-17-1-MLD 2, NLR- 40024, JGL-17183, UPRI-2009-9, NP-6226, R-1570-2644-2-1547, CR-2995-1-2-3-1-1, PR-113, CR-77-3-1-1, NP-218, KAGR-559-1, Pant Dhan-12	12
	Pooled	C 1446-5-18-17-1-MLD 2, JGL-17183, WGL- 365, UPR-3411-1-1-1, UPR-3305-6-1-2, CR-77-3-1-1, NP-107-5, GontraBidhan -3, UPR-3027-10-1-1	9
II	2012	NLR- 40024, UPRI- 3425-14-3-1, UPR-3411-1-1-1, Pant Dhan-12, UPR-3027-10-1-1, Pant Dhan-4	6
	2013	OR 2324-25-1, UPRI- 3425-14-3-1, UPR-3305-6-1-2	3
	Pooled	NLR- 40024, UPRI-2009-9, UPR-2805-14-1-2, NP-6226	4
III	2012	JGL-17183, OR 2324-25-1, UPR-3443-7-2-1, WGL-365, PAU-3832-79-4-3-1, UPR-3305-6-1-2, R 1576-1700-1-560-1, CR-77-3-1-1, KJT-1-11-15-23-26-22, NP-218, KAGR-559-1, NP-107-5, GontraBidhan -3	13
	2013	UPR-2805-14-1-2	1
	Pooled	OR 2324-25-1, R-1570-2644-2-1547, Pant Dhan-12, Pant Dhan-18	4
IV	2012	UPRI-2009-9, NP-6226, JGL- 17196, R-1570-2644-2-1547, PR-113	5
	2013	UPR-3443-7-2-1, WGL- 365, JGL- 17196, PAU-3832-79-4-3-1, UPR-3027-10-1-1, Pant Dhan-18	5
	Pooled	UPRI- 3425-14-3-1, UPR-3443-7-2-1, NP-218, KAGR-559-1	4
V	2012	UPR-2805-14-1-2	1
	2013	UPR-3411-1-1-1, R 1576-1700-1-560-1, KJT-1-11-15-23-26-22, NP-107-5, GontraBidhan -3	5
	Pooled	JGL- 17196, PAU-3832-79-4-3-1, R 1576-1700-1-560-1, CR-2995-1-2-3-1-1, PR-113, KJT-1-11-15-23-26-22	6
VI	2012	Pant Dhan-18	1
	2013	Pant Dhan-4	1
	Pooled	Pant Dhan-4	1

Table.2 Averages Inter and Intra-Cluster (Diagonal) D^2values in rice genotypes

Cluster	**Year**	**I**	**II**	**III**	**IV**	**V**	**VI**
I	2012	10.692	64.250	57.761	74.537	26.868	80.288
	2013	45.769	42.463	43.882	14.937	39.024	18.733
	pooled	28.702	21.231	26.357	7.984	46.633	29.671
II	2012		32.440	11.411	15.297	58.117	19.583
	2013		17.549	79.081	28.896	11.391	35.120
	pooled		50.256	13.348	23.597	29.259	20.415
III	2012			39.238	17.909	52.859	26.082
	2013			0	54.148	76.819	57.983
	pooled			36.562	28.595	26.015	8.445
IV	2012				28.069	66.439	19.695
	2013				40.112	25.182	14.182
	pooled				35.995	50.044	32.087
V	2012					0	74.289
	2013					25.669	31.552
	pooled					32.178	28.405
VI	2012						0
	2013						0
	pooled						0

Table.3 Cluster mean values for different characters in rice

Clusters	Season	Days To 50 % Flowering	Days To Maturity	Plant Height (cm)	Panicle Length (cm)	No of tillers	No of productive tillers	No of Grain/ Panicle	Leaf Length (cm)	Leaf Breadth (cm)	Flag Leaf Area (sq.m)	1000 Grain Weight (g)	Grain Yield/ Plant (g)	Dry Weight (g)	Harvest Index (%)	Grain length (mm)	Grain breadth (mm)	L/b Ratio	Alkali Digestion	Amylose Content (%)
I	**2012**	97.670	127.670	94.300	25.630	8.870	9.000	258.630	33.730	1.600	40.650	19.870	11.930	50.730	23.530	6.000	1.800	3.340	3.760	20.250
	2013	109.000	140.000	93.733	27.633	9.000	9.067	187.667	33.867	1.433	36.467	21.521	13.690	56.833	24.435	5.067	1.867	2.722	6.192	20.670
	pooled	101.667	131.889	99.889	24.418	9.433	9.520	210.806	33.427	1.597	41.780	20.687	12.419	47.686	30.052	5.580	1.894	2.955	5.322	20.546
II	**2012**	101.000	131.000	101.340	24.560	8.930	9.000	194.700	34.200	1.670	42.810	20.280	12.960	50.670	25.590	5.500	1.870	2.940	5.640	20.100
	2013	107.667	137.667	98.900	25.000	9.267	9.267	176.967	39.867	1.660	49.614	20.407	10.830	54.500	19.925	5.600	1.900	2.952	5.524	20.523
	pooled	106.500	136.875	99.881	25.571	10.446	10.575	192.067	37.455	1.591	46.418	23.003	12.425	45.865	29.145	5.671	1.921	2.956	5.046	21.321
III	**2012**	110.000	141.000	95.930	26.810	9.330	9.400	195.330	35.600	1.610	43.090	19.670	13.190	57.800	23.240	5.030	1.930	2.600	6.130	20.020
	2013	98.333	129.333	104.433	25.133	10.467	10.533	240.733	43.800	1.813	59.591	25.987	12.690	41.800	30.502	6.133	1.933	3.178	4.592	21.997
	pooled	107.542	137.917	101.486	25.690	9.463	9.625	187.025	32.775	1.549	37.551	24.299	14.091	51.419	32.309	5.700	2.050	2.782	4.602	21.152
IV	**2012**	111.330	141.330	102.340	25.690	8.530	8.600	169.770	32.670	1.470	35.820	20.620	11.560	45.390	26.000	5.200	2.070	2.490	3.710	20.890
	2013	104.000	134.000	105.833	27.733	8.067	8.133	175.900	28.300	1.663	35.092	25.947	17.520	50.833	34.524	6.200	2.067	3.006	5.885	22.200
	pooled	102.792	133.667	99.898	26.665	9.083	9.183	213.633	37.800	1.486	43.030	21.461	12.995	51.958	32.476	5.517	1.892	2.918	5.156	21.032
V	**2012**	96.000	126.000	103.160	26.980	10.330	10.330	239.530	44.330	1.840	61.560	26.400	15.070	43.680	33.430	6.000	2.070	2.940	4.110	21.710
	2013	101.000	131.000	97.733	27.167	9.733	9.867	180.533	36.233	1.693	45.932	20.385	12.970	46.400	28.116	5.567	1.767	3.153	5.779	20.287
	pooled	102.222	132.639	96.596	24.481	8.872	8.972	164.464	35.601	1.474	40.811	21.407	11.161	45.689	28.425	5.556	2.033	2.766	5.852	20.537
VI	**2012**	105.670	135.670	104.470	26.320	9.300	9.800	175.530	26.500	1.670	33.190	25.550	16.800	53.670	31.400	6.570	2.200	2.990	5.280	21.990
	2013	106.000	136.000	104.700	27.167	9.133	9.400	193.800	29.700	1.467	33.514	24.273	17.167	53.833	31.871	6.100	2.133	2.871	4.944	21.931
	pooled	106.833	136.833	104.867	27.973	9.350	9.533	185.967	29.167	1.467	32.631	24.328	16.647	53.817	31.148	6.150	2.100	2.934	4.639	22.027

Table.4 Contribution of different characters towards genetic divergence in rice

S. No.	Character	Contribution (per cent)		
		2012	**2013**	**Pooled**
1	Days to 50% Flowering	3.36	3.42	3.57
2	Days to Maturity	2.64	2.66	2.79
3	Plant Height	1.98	2.04	2.00
4	Panicle Length	4.11	3.52	3.77
5	No. of Productive Tillers	3.84	4.16	3.96
6	No. of Tiller	3.79	4.16	3.89
7	No. of Grain Per Panicle	10.01	11.35	11.20
8	Leaf Length	6.90	5.86	7.05
9	Leaf Breadth	4.78	4.53	4.44
10	Flag Leaf Area	9.51	8.27	8.99
11	1000 Grain Weight	6.87	6.36	6.93
12	Grain Yield Per Plant	6.36	7.37	7.08
13	Dry Weight	6.59	5.66	5.28
14	Harvest Index	5.72	7.45	4.71
15	Grain Length	3.99	3.88	4.08
16	Grain Breadth	3.86	3.27	3.59
17	L/B Ratio	4.73	4.82	4.82
18	Alkali Digestion	9.77	9.86	10.32
19	Amylose Content	1.53	1.80	1.71

The minimum inter-cluster distance was found between clusters II and III (11.411) during 2012, between clusters II and V (11.391) during 2013 and between clusters I and IV (7.984) in pooled estimates. This suggested that the lines belonging to these clusters were relatively closer to each other hence to maintain broad genetic base hybridization between lines of these clusters should be avoided.

The largest intra-cluster D^2 values were recorded in cluster III (39.238), cluster I (45.769), cluster II (50.256) during 2012, 2013 and over the season respectively. The lines included in clusters III, I and II were relatively more diverse than those in the other clusters (Table 2). The diversity was also supported by the appreciable amount of variation among the cluster means for different characters.

During 2012 cluster I showed the maximum cluster means for number of grains per panicle and L/B ratio, the lines from Cluster III had maximum means for dry weight and alkali digestion value. Cluster IV showed maximum means for 50% flowering and days to maturity. Cluster V showed the maximum cluster means for panicle length, number of productive tillers, flag leaf length, flag leaf breadth, flag leaf area, 1000 grain weight and harvest index. Cluster VI had maximum cluster means for plant height, grain yield per plant, grain length, grain breadth and amylose content. During 2013 cluster I had maximum means for 50% flowering, days to maturity, panicle length, dry weight per plant and alkali digestion value. Cluster III had maximum means for number of productive tillers per plant, number of tillers, number of grain per panicle, flag leaf length, flag leaf breadth, flag leaf area, 1000 grain weight and L/B ratio.

Cluster IV had maximum means for plant height, grain yield per panicle, harvest index, grain length and amylose content. Cluster VI showed maximum means for grain breadth.

However, when data from both the seasons were pooled cluster I had maximum cluster mean value for flag leaf breadth. Cluster II had maximum mean values for number of productive tillers per plant, number of tillers per plant, flag leaf length, flag leaf area and L/B ratio. Cluster III showed maximum means for days to 50% flowering, days to maturity and harvest index. In cluster IV exhibited highest cluster mean values for number of grains per panicle. Cluster V had highest cluster mean value for alkali digestion value. In Cluster VI highest cluster mean values were observed for plant height, panicle length, 1000 grain weight, grain yield per plant, dry weight per plant, grain length, grain breadth and amylose content (Table 3).

The number of grains per panicle (10.01, 11.35, and 11.20) had maximum contribution and amylose content (1.53, 1.80, and 1.71) had minimum contribution towards diversity in both the season as well as over the seasons. 1000 grain weight, dry weight per plant, flag leaf area, flag leaf length and grain yield per plant showed moderate contribution towards diversity in both the seasons as well as over the seasons (Table 4).

In conclusion the considering the importance of genetic distance, relative contributions of characters towards total divergence and yield potential of genotypes, the present investigation suggests that, parental lines elected from cluster I (C-1446-5-18-17-1-MLD 2, JGL-17183, WGL- 365, UPR-3411-1-1-1, UPR-3305-6-1-2, CR-77-3-1-1, NP-107-5, GontraBidhan-3, UPR-3027-10-1-1) for number of productive tillers, cluster IV (UPRI- 3425-14-3-1, UPR-3443-7-2-1, NP-218, KAR-559-1) number of grains per panicle and cluster VI (Pant Dhan-4) for panicle length and grain yield per plant could be used in crossing programmes to achieve desired segreants. Since No. of grains per panicle contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

On the basis of above observations, it is quite obvious that material have sufficient amount of diversity for desired traits. The diversity between clusters can be utilized for restoration of hybridization and trait selection related to divergence. Thus, it would be beneficial for selection of superior lines which could be used in hybridization programme.

References

Chaturvedi, H.P. and Maurya, D.M. (2005). Genetics divergence analysis in rice (*Oryza sativa* L.), *Adv. Pl. Sci.*, 18(1): 349-353. Mahalanobis, P.C. (1936). On generalized distance in statistics. *Proceedings of National Institute of Science*, India, 2: 49-55.

Mishra, L.K., Sarawgi, A.K. and Mishra, R.K. (2003). Genetic diversity for morphological and quality traits in rice (*Oryza sativa* L.), *Adv. in Pl. Sci.*, 16(1): 287-293.

Murty, B.R. and Arunachalam, V. (1967). Computer programmes for some problems in biometrical genetics-I. Use of Mahalanobis D^2 in classification problem. *Ind. J. Genet. Pl. Breed.*, 27:60-69.

Ramya, K. and Senthilkumar, K. (2008). Genetic divergence in rice. Crop Improv.35(2): 119-21.

Rao, C.R. (1952). The concept of distance and the problem of group constellation. In Advance Statistical Methods in Biometric Research. *John Willey and Sons. Inc.*, *New York*, USA, pp. 351-

378.

Rao, T.P., Gomathinayagam, P. (1997). Genetic diversity in semi dry rice under different environments. Madras Agr. J. 84, 314–317.

Sandhyakishore, N., Babu, V.R., Ansari, N.A. and Chandran, R. (2007). Genetics divergence analysis using yield and quality traits in rice (*Oryza sativa* L.), *Crop Improv.*,34:12-13.

Sarawgi, A.K. and Rita Binse. (2007). Studies on genetic divergence of aromatic rice germplasm for agro-morphological and quality characters. *Oryza*, 44(1): 74-76.

Singh, R. B., and Bains, S. S. (1968). Genetic divergence for ginning outturn and its components in upland cotton. *Indian Journal of Genetics and Plant Breeding (The)*, 28(3), 262-268.

How to cite this article:

Aditya Bora, Dhanraj Meena, Mukesh Kumar Karnwal and Himanshu Chaudhary. 2020. Genetic Divergence for Important Economic and Quality Traits in Improved Lines of Rice (*Oryza sativa* L.). *Int.J.Curr.Microbiol.App.Sci.* 9(09): 3369-3376.
doi: https://doi.org/10.20546/ijcmas.2020.909.419