Assessment of Genetic Diversity in RiceGenotypes (*Oryzasativa* L.)

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(Received : November, 2016 : Revised : January, 2017; Accepted : January, 2017)

Abstract

Present investigation was carried out among the thirty seven genotypes of rice to study the nature and magnitude of genetic divergence usingMahalanobis D^2 statistic revealed considerable amount of genetic diversity was found among all the genotypes based on twelve important quantitative characters. All the genotypes were grouped into seven clusters with cluster VI containing the maximum of 9 genotypes followed by cluster III and IVeach containing 7 genotypes. This suggested that the genotypes grouped within a particular cluster are high or less genetically similar to each other.The maximum intra cluster distance exhibited for cluster V (96.944) while lowest intra cluster distance was recorded for cluster III (43.122). The maximum intra cluster distance was revealed between clusters V and V (277.703); whereas, minimum inter cluster distance was between clusters III and IV (94.944).Cluster VII showed the highest mean values for number of productive tillers per plant, panicle length, biological yield per plant and grain yield per plant. Hence on the basis of higher cluster mean for almost all important component characters, cluster VII has been isolated as most divergent cluster containing genotypes like NLR 40058, PAU 3832-79-4-3-1 and cluster V containing CRR 644-B-12-B, CR 2929-57-4-2-3 and CR 2995-1-2-3-1-1. Thus, crosses involving the parents from these clusters may exhibit high heterosis as well as grain yield. The characters like number of grains per panicle (37.99), grain yield per plant (g) (12.31) and 1000-grain weight with husk (12.31) wererecorded as high percentage to the genetic divergence could be play major role to select the elite genotypes among them and the selecting genotypes may be used in further breeding programme to develop new high yielding rice varieties to the farmers for commercial cultivation.

Key words: Genetic diversity,intra-clusters distance, rice, grain yield.

Introduction

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Published by Indian Society of Genetics, Biotechnology Research and Development,
5, E Biotech Bhawan, Nikhil Estate, Mugalia Road, Shastripuram, Sikandra, Agra 282007 Online management by www.isgbrd.co.in , www.irjgbt.org

Rice (*Oryzasativa*L.) is the most important cereal food crop for the developing world and it is one of the agronomically and nutritionallyeconomic crop of India. More than 70 percent of the Indian population with more than 4,000 varieties and hybrids of rice grown throughout the country.It is the most important source of dietary energy in India.Rice is also used for processed products like snaks (puffed rice), savories and bakery items.Rice has become a highly strategic and priority commodity for food security in our country as well as other emerging countries. Consumption is growing faster than that of any other major staple on the continent because of high nutritive value, population growth, rapid urbanization and changes in eating habits of the humans (Seck*et al*., 2013).In the year 2015-16 rice production of the India was at 103.5 million tonnes from 43.46 million hectares, however it is expected increase and reaches 105 million tonnes from 44 million hectares in 2016-17 (Anonymous, 2015-16).Genetic diversity is pre-requisite for any crop improvement programme as it helps in the development of superior recombinants. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). A quantitative estimation of genetic diversity guides the breeder for rapid progress of the breeding programme. Inthe hybridization programmes, diversity of the parental material is being very much emphasized, because crosses between genetically divergent parents would be more suitable for obtaining appreciable improvement, as they are likely to yield desirable recombination in segregating generations. Generally phenotypic or geographic diversity is considered as a measure of genetic diversity. However, this being an inferential criterion may not be so effective in quantifying or differentiating between populations occupying ecologically marginal habitats. The D^2 technique is based on multivariate analysis developed by (Mahalanobis, 1936) had been found to be a potent tool in quantifying the degree of divergence in germplasm.

Genetic diversity analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely divergent clusters are likely to produce hecterotic combinations and wide variability in segregating generation. The knowledge of the extent and pattern of genetic diversity in the crop species is a pre-breeding approach for any crop improvement because it helps breeders in deciding suitable breeding strategies for their furthergenetic improvement in the rice genotypes to get the desired results.

Material and Methods

Thirty seven diverse genotypes of rice were grown in randomized block design (RBD) with three replications during kharif 2011 at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each genotype was transplanted in three rows of 7.5 m. length spaced 20 cm. apart with plant to plant distance of 15 cm.The observations

were recorded on five randomly selected plants per replication forplant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, biological yield per plant (g), grain yield per plant (g), harvest index (%), 1000-grain weight with husk and 1000-grain weight without husk were evaluated on individual plant basis five randomly selected plants on each genotype. The analysis of genetic divergence was carried out while observations on days to panicle emergence, days to 50 % flowering and days to maturity were recorded on plot basis. The data was calculated by method of Mahalanobis'D^2' statistic as described by (Rao, 1952).The clustering was done following Wardmethod as suggested by (Rao, 1952). The intra and inter-cluster distances (D^2 value) and mean performance of the cluster for quantitative characters were also computed. The objective of the present study is to investigate the genetic diversity among thirty seven rice genotypes differing in their genetic value and to identify the best genotype to be used in breeding programme in the future for the genetic enhancement and development of new high yielding and disease resistance rice varieties that are equally beneficial for farmers and the breeder community.

Results and Discussion

Actual assessment of the level and clustering pattern of genetic diversity is of great value for crop breeding in any crop. To initiate any crop breeding programme, breeder should know the genetic architecture of the genotypes to be used in the crop improvement programme. After that he could be in a position to select the elite genotypes for further breeding programme. That point of view, genetic diversity analysis is used for estimating and establishing of genetic relationship in germplasm collection, identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection and introgression of desirable genes from diverse germplasm into the available genetic stock (Islam *et al.* 2012). Genetic diversity analysis guides breeders for rapid progress of breeding programme.

The results of D^2 analysis indicated the presence of high amount of genetic diversity among the genotypes studied. Based on relative magnitude of D^2 values, thirty-seven genotypes of the present study were grouped into seven clusters. The clustering pattern of the genotypes is presented in Table 1. Cluster VI was the largest, comprising of 9 genotypes followed by cluster IV & cluster III with 7 genotypes in each, cluster II with 6, and cluster I & V with 3 genotypes in each and cluster VII with 2 genotypes. All the clusters observed to be heterogeneous which included genotypes from different geographical regions. The clustering pattern obtained in the present study confirmed that genetic diversity is not necessarily parallel to the geographical diversity. These results are similar to those reported earlier by several workers in rice regarding the geographical diversity (Doddabhimappa*et al.* 2014);(Parimalan, 2008); Babu*et al.* 2003); (Ubarhande*et al.* 2009); (Ramya and Senthilkumar, 2008).The average intra and inter cluster

distances have been given in Table 2.The maximum intra cluster distance (96.944) was observed for cluster V, whereas the minimum intra cluster distance (43.122) was recorded in case of cluster III.The maximum intra cluster distance was due to wide genetic diversity among the genotypes. On the basis of inter cluster distance hybridization programme may be taken up between the genotypes of cluster V and II. In earlier studies, several workers on the basis of higher inter cluster distance suggested hybridization programme involving more divergent genotypes for yield improvement in rice. For an efficient breeding programme, selection of genetically divergent and superior genotypes is important before making crosses between genotypes, which would ensure the exploitation of heterosis and development of transgressivesegregants.

In any crop improvement programme, germplasmmaterial serves as a valuablesource of base population and providing scope forwide genetic variability. The more genetically diverse parents, thegreater are the chances of obtaining higher amount of heterotic value in F_1's and broad spectrum ofvariability in further segregating generations. Information onnature and degree of genetic divergence would helpthe plant breeder in choosing the desirable parents forthe crop breeding programme.In the present research, the maximum inter-cluster distance was found between cluster V and II, (277.703) followed by clusters VII and I (269.371), VI and V (267.404), VII and V (251.529), VI and II (236.970), VII and IV (227.910), VII and II (218.173), V and I (217.477), IV and II (203.593), VII and VI (200.259), V and III (183.023), V and I (164.255), VII and III (135.808), VI and III (129.889), VI and IV (128.844), IV and I(122.384), II and I (121.656), III and I (119.169), V and IV (116.919), IV and III (94.942),III and II (90.273). Maximum inter cluster distance indicated that genotypes of cluster V and II are not so closely related suggesting wide diversity between these clusters. Thus, crosses involving the parents from these clusters may exhibit high heterotic combinations and thus produce large variability and better recombinants in the segregating generations for high yield. The minimum inter cluster distance was recorded between cluster II and III (90.273) followed by cluster III and IV (94.944). The minimum inter cluster suggested that thegenotypes of these clusters had close genetic relationship and so, may not be utilized in the future breeding programme. The cluster mean computed for twelve quantitative characters under study are presented in Table 3. Days to panicle emergence showed highest mean in cluster number V (88.33) and lowest mean for this character was observed in cluster number VI (69.66).Cluster VII indicated the highest mean values for number of productive tillers per plant, panicle length, biological yield per plant and grain yield per plant. Hence on the basis of higher cluster mean for almost all important component characters, cluster VII has been isolated as most divergent cluster containing genotypes like NLR 40058, PAU 3832-79-4-3-1 and cluster V containing CRR 644-B-12-B, CR 2929-57-4-2-3 and CR 2995-1-2-3-1-1. Thus, crosses involving the parents from these clusters may exhibit high heterosis as well as grain yield. Therefore, hybridization involving above mentioned genotypes is

suggested in further breeding programme, in order to achieve high heterotic combinations and thus produce large variability and better recombinants in the segregating generations for high yield.

The percent contribution of twelve quantitative characterstowards total genetic divergence was computed in Table 4. Numbers of grains per panicle recorded highest percent contribution followed by grain yield per plant, 1000-grain weight with husk, harvest index and panicle length have contributed more for the divergence. Remaining characters played very little role towards genetic divergence. Similar results were reported byearlier researchers (Nayak,*et al.*2004); (Sharma *et al.*2008): (Bardhan and Thangavel, 2011) and (Ramanjaneyulu,*et al.* 2014) intheir findingsthat the selection of parents mainly depends on the contribution of traits toward genetic divergence.Thus, the above 5 characters were useful as they have contributed 76.13% towards genetic divergence.Consequently, these characters could be given due importance for effective selection of desirable genotypes for further genetic improvement in rice.The promising genotypesselected from diverse clusters for desirable characters with mean value were mentioned in Table 5. The cluster IV had maximum three genotypes namely, REWA 862-1, CR 2926-15-3-4-2 and GOVIND for days to panicle emergence (81.15), 1000-grain weight with husk (18.54 g), days to 50% flowering (89.48), plant height (107.55 cm), and days to maturity (125.10). Therefore, based on these traits genotypes of cluster IV can be used as parents in hybridization programme to get desirable segregentsts.

Conclusion

Our results demonstrated that the rice genotypes were having huge amount of genetic diversity. ClusterV and II will result in maximum hybrid vigorwhich may be usedin hybridization programme tocreate genetic variability and to obtained superior and high heterotic recombinantsso that breeders can develop high yielding varieties of rice for commercial cultivation.

Acknowledgement

The authors are highly thankful to Directorate of Rice Research Rajendranagar, Hyderabad (A.P.) to provide the genotypes of rice for completion of this experiment.

Table 1: Grouping of 37 rice genotypes in seven clusters

Clusters No.	No. of genotypes	Name of genotypes
I	3	HKR06-47, NDR6206, CR273-11
II	6	PUSA1121, NDR 6263, VDN-94-10, AD06084, RP5210-BIO-FBR 1-12-4-18, CR2903-7-5
III	7	TM07575, GONTRA BIDHAN3, RP5210-BIO-FBR1-15-3-22, CR2928-21-5-3-1, RP5219-9-6-7-3-2-1-1, NLR400024, CR2995-2-6-1-1-1
IV	7	2K3-430-144-8-56-5-1-15-5-6, 2K3-430-144-8-56-5-1-15-5-1, REWA862-1, CR2926-15-3-4-2, GOVIND, CR2994-5-3-2-1-1, CR2881-19-1(A)
V	3	CRR646-B-12-B , CR2929-57-4-2-3, CR2995-1-2-3-1-1
VI	9	CN1794-2-1, SAHBHAGI DHAN, CHR10, NP107-5, CR2927-42-2-3-2, CR2930-26-2-2-1, RP5128-110-6-3-8-2-5-B , PAU3832-196-4-1-2, CR2881-19-1
VII	2	NLR40058, PAU3832-79-4-3-1

Table 2: Average intra and inter cluster distance (D^2)values in rice

Clusters	I	II	III	IV	V	VI	VII
I	**82.660**	121.656	119.169	122.384	164.255	217.477	269.371
II		**49.873**	90.273	203.593	277.703	236.970	218.173
III			**43.122**	94.942	183.023	129.889	135.808
IV				**50.898**	116.919	128.844	227.910
V					**96.944**	267.404	251.529
VI						**73.487**	200.259
VII							**46.053**

Diagonal and bold values are intra cluster distance

Table 3:Clusters mean values for twelve quantitative characters in rice genotypes

Sl.No.	Characters	Clusters						
		I	II	III	IV	V	VI	VII
1.	Days to panicle emergence	78.43	83.15	81.33	83.25	**88.33**	69.66	80.66
2.	Days to 50% flowering	86.53	91.03	90.37	91.00	**101.00**	77.00	89.00

3.	Plant height (cm)	105.66	109.03	102.18	107.00	108.33	**138.66**	129.00
4.	No. of productive tillers/ plant	11.52	14.06	13.17	12.60	10.46	15.76	**16.60**
5.	Panicle length (cm)	22.31	21.13	21.57	20.96	23.26	19.90	**25.63**
6.	No. of grains/ panicle	118.26	137.09	85.40	77.50	**157.33**	136.33	156.00
7.	Days to maturity	124.90	127.54	123.59	126.00	**129.66**	114.00	117.00
8.	Biological yield/plant (g)	66.59	62.26	66.87	78.45	60.50	78.48	**95.55**
9.	Grain yield/plant (g)	19.93	17.35	16.22	26.07	14.28	15.87	**30.31**
10.	Harvest index (%)	30.01	30.04	24.88	**36.76**	28.65	20.21	35.78
11.	1000-grain weight with husk (g)	19.28	18.42	17.21	19.61	**22.22**	15.60	19.44
12.	1000-grain weight without husk (g)	14.46	13.81	12.9	14.71	**16.67**	11.70	14.57

Bold values are highest for that character

Table 4: Characters contribution percentage to the divergence in rice based on Mahalanobis D^2 analysis

Sl. No.	Characters	Percentage of contribution to divergence
1.	Days to panicle emergence	0.00
2.	Days to 50% flowering	1.20
3.	Plant height (cm)	0.30
4.	Number of productive tillers per plant	2.57
5.	Panicle length (cm)	6.61

6.	Number of grains per panicle	37.99
7.	Days to maturity	0.75
8.	Biological yield per plant (g)	0.60
9.	Grain yield per plant (g)	12.31
10.	Harvest index (%)	6.91
11.	1000- grain weight with husk (g)	12.31
12.	1000-grain weight without husk (g)	0.45

Table 5: Promising genotypes selected from diverse clusters

Clusters number	**Genotypes**	**Desirable character (s) with mean value**
I	NDR 6206, CR 273-11	1000-grain weight with husk (g) (18.54 g),Days to panicle emergence (81.15), Days to 50 percent flowering (89.48),Panicle length (cm)(21.68)
II	PUSA1121, RP5210-BIO-FBR 1-12-4-18	Harvest index (%) (29.35 %), Number of productive tillers per plant (13.02)
III	CR 2928-21-5-3-1, RP5219-9-6-7-3-2-1-1	Number of productive tillers per plant(13.02),Biological yield per plant (g)(67.59 g)

IV	REWA 862-1, CR 2926-15-3-4-2, GOVIND	Days to panicle emergence (81.15), 1000-grain weight with husk (g)(18.54 g),Days to 50 percent flowering (89.48),Plant height (cm) (107.55),Days to maturity (125.10)
V	CRR 646-B-12-B , CR 2995-1-2-3-1-1	Biological yield per plant (g)(67.59 g), Panicle length (cm) (21.68), Number of grains per panicle (114.02)
VI	CN 1794-2-1	Number of grains per panicle (171.00)
VII	NLR 40058	Harvest index (%) 29.35 %

References

1. **Anonymous**.(2015-16) Governments rice procurement and PDS operation. Food Corporation of India, and GOI Budget.

2. **Arunachalam V**. (1981) Genetic divergence in plant breeding. *Indian J. Genet*. (14): 226-236.

3. **Babu S., Anbumalarmathi J., Yogameenakshi P., Sheeba A. and Rangasamy P**. (2003) Genetic divergence studies in rice.*Crop Res*.**25**: 280-286.

4. Bardhan G., Thangavel P. (2011)D^2 analysis in rice (*Oryzasativa*L.). *Plant Archives,* **11**(1): 373-375.

5. **Doddabhimappa R., Gangapur K. Thiyagarajan S.M.,Malarvizhi D.**(2014) Genetic Diversity Analysis of Rice Genotypes for Yield and Yield Attributing Traits, *Environment & Ecology,***32**(3): 803-807.

6. **Islam A.S.F., Ali M.R., Gregorio G.B., Islam M.R**. (2012) Genetic diversity analysis of stress tolerant rice (*Oryzasativa* L.). *African J. Biotech*.**11**(85): 15123-15129.

7. **Mahalanobis P.C**. (1936) On the generalized distance in statistics. *Proc. Natl. Inst. Sci. Indi.* (2): 49-55.

8. **Nayak A.R., Chaudhury D. and Reddy J.N**. (2004) Genetic divergence in scented rice. *Oryza*.**41**(384): 79-82.

9. **Parimalan R., John Joel A. and Vanniarajan C**. (2008) Genotypes clustering in rice (*Oryzasativa*L.). Centre for Plant Breeding and Genetics, TNAU, Coimbatore.*Crop Improvement*.**35**(2): 115-118.

10. **Ramanjaneyulu A.V., Gouri Shankar V., Neelima, T.L. and Shashibhusahn D**. (2014) Genetic Analysis of Rice (*Oryzasativa*L.) Genotypes Under Aerobic Conditions on Alfisols. *SABRAO Journal of Breeding and Genetics.***46** (1) 99-111.

11. **Ramya K. and Senthilkumar N**. (2008) Genetic divergence in rice (*Oryzasativa*L.). Genetics and Plant Breeding, Department of Agriculture Botany, Faculty of Agriculture, Aannamalai University, Annamalaiinagar. *Crop Improvement,***35**(2): 119-121**.**

12. **Rao C.R**. (1952) Advance statistical methods in biometrical research. John Wiley and Sons, Increased. New York.

13. **Seck P.A., Toure A. A., Coulibaly J. Y., Diagne A. and Wopereis M. C. S**. (2013) Impact of rice research on income, poverty and food security in Africa: an ex-ante analysis. In: Wopereis, M. C. S., Johnson, D. E., Ahmadi, N., Tollens, E., and Jalloh, A. (Eds.), Realizing Africa's Rice Promise. CAB International, Wallingford, UK. pp. 24-33.

14. **Sharma, Arun. Gupta, K.R. and Kumar, Rakesh**. (2008) Genetic divergence in basmati rice (*Oryzasativa*L.) under irrigated ecosystem. Rice Research Station, Kaul (Kaithal).*Crop Improvement*,**35**(1): 8-10.

15. **Ubarhande V.A., Prasad R., Sing R.P., Singh S.P. and Agrawal R.K**. (2009) Variability and diversity studies in rainfed rice (*Oryzasativa*L.). *Indian J. Plant Genet. Resour*: **22**(2): 134-137.