Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.4073

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (4):** 54-58 (2017)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

D^2 Statistics for Grain Yield and Quality Traits in Rice (*Oryza sativa* L.)

A. J. Rathod[1], P. M. Mistry[2], A. G. Pampaniya[1], H. R. Patel[1] and C. P. Chetariya[3*]
PG Scholar[1], Assistant Professor[2], Ph. D. Scholar[3]
Department of Genetics and Plant Breeding, Main Rice Research Centre, Navsari Agricultural University, Navsari-396 450. (Gujarat) India
[3]Junagadh Agricultural University, J.A.U., Junagadh-362001
*Corresponding Author E-mail: chetariyachana89@gmail.com

Received: 16.06.2017 | Revised: 27.06.2017 | Accepted: 29.06.2017

ABSTRACT

Genetic divergence was studied for different yield and quality component traits for 54 rice genotypes. The analysis of variance revealed presence significant differences among the genotypes for all the characters studied. Based on genetic distance all the 54 genotypes were grouped under nine different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like zinc content, iron content, amylose content and grains per panicle contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster III and V. Selection of genotypes in these clusters which may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with different quality traits.

Key words: *Rice, Genetic divergence, D^2 analysis, Quality traits*

INTRODUCTION

Rice is a staple food for millions of people and having great importance in food and nutritional security. Rice is the second most widely consumed in the world next to wheat. From poorest to richest person in this world consume rice in one or other form. In the last two decades, new research findings generated by the nutritionists have brought to light the importance of micronutrients, vitamins and proteins in maintaining good health, adequate growth and even acceptable levels of cognitive ability apart from the problem of protein energy malnutrition. Development of varieties containing higher amounts of Fe and Zn would improve nutrition in regions where population depend on rice as a staple food. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes[1]. This helps in the choice of parents for hybridization in yield and quality improvement programmes.

Cite this article: Rathod, A.J., Mistry, P.M., Pampaniya, A.G., Patel, H.R. and Chetariya, C.P., D^2 Statistics for Grain Yield and Quality Traits in Rice (*Oryza sativa* L.), *Int. J. Pure App. Biosci.* **5(4):** 54-58 (2017). doi: http://dx.doi.org/10.18782/2320-7051.4073

Hence, estimation of genetic diversity for yields and quality components among genotypes is important for planning the future crossing programme. In the present study an attempt was made to assess the genetic divergence using Mahalanobis D^2 statistics and different clustering procedures, based on yield and its component characters and assessing the relative contribution of different components to total divergence[6].

MATERIAL AND METHODS

The experimental material consisted of 54 rice genotypes from different geographical regions. All the genotypes were evaluated in replicated thrice adopting statistical design RBD during *Kharif* 2016 at Main Rice Research Centre, Navsari agricultural university, Navsari. The seedlings were transplanted to main field at the rate of one seedling per hill with a spacing of 20 cm between rows and 15 cm within plants. Recommended agronomic practices and need based plant protection measures were taken up. Observations were recorded on fourteen agronomical and quality characters, *viz.,* days to 50% flowering, plant height, Productive tillers per plant, panicle length, grains per panicle, grain yield per plant, L/B ratio, hulling per cent, milling per cent, head rice recovery, amylose content, protein content, zinc content and iron content. Genetic diversity analysis was carried out following D^2 statistics proposed by Mahalanobis[5].

RESULTS AND DISCUSSION

Based on the relative magnitude values, 54 genotypes studied were grouped into nine clusters (Table 1). The cluster I bearing maximum number of 22 genotypes, while clusters V, III and II had 16, 8 and 3 genotypes respectively. Whereas, clusters IV, VI, VII, VIII and IX were mono genotypic. The genotypes obtained from different eco-geographical regions were distributed into different clusters was at random, which indicates that geographical distribution and genetic diversity are not related. This suggests that forces other than geographical separation such as exchange of breeding material, genetic drift, natural and artificial selection, environmental variation were also responsible for the genetic diversity. Similar results have been obtained by Chakma *et al*[2]., and Chanbeni *et al*[3]. Lack of correlation between genetic and geographic diversity was also reported by Kandamoorthy and Govindarasu[4]. The intra cluster distance ranged from 0.00 to 11.21. The cluster V exhibited maximums intra cluster distance (11.21) followed by the cluster III (8.94), cluster II (8.77) and cluster I (7.52). The intra cluster distance was zero for clusters IV, VI, VII, VIII and IX indicating limited genetic diversity among genotypes representing this cluster (Table 2). The relative divergence of each cluster from other inters-cluster indicated greater divergence between cluster III and V (19.89) followed by cluster II and V (18.02). The minimum cluster distance was observed between cluster VI and VIII (8.82) followed by that of clusters I and VII (9.38), I and IV (9.56), I and VI (9.71), I and II (10.04) and IV and V (10.52). The inter cluster distance is the criterion used for selection of genotypes as parents in hybridization programme[7]. The hybrids developed from the selected genotypes within the limits of compatibility of these clusters may produce high magnitude of heterosis or desirable segregants. The average cluster wise mean values for different characters are presented in (Table 3). The cluster mean is another criterion to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster I exhibited moderate mean value for almost all the characters except hulling percent (67.41%), which had the highest and the second highest mean value for milling percent (68.21%). Cluster II showed the moderate mean value for all the character, which had second highest mean value for zinc content (27.25 ppm), while minimum mean value for head rice recovery (58.98 %). Cluster III exhibited the highest mean value for plant height (146.25 cm), grains per panicle (257), L/B ratio (3.73) and zinc content (27.76 ppm), whereas, second highest value for panicle length (28.55 cm).

Cluster IV revealed second lowest value for days to 50 % flowering (81.00), highest for panicle length (29.15 cm), grain yield per plant (49.52 g), milling percent (69.33 %) and protein content (8.12 %), whereas, second highest for head rice recovery (73.01 %). Cluster V depicted moderate mean value for most of the traits. Whereas, second highest mean value for productive tillers per plant (8.31), L/B ratio (3.54) and protein content (7.66 %). Cluster VI showed high to moderate mean values for all traits. Lowest mean value was expressed by days to 50 % flowering (78.00 days), plant height (101.47 cm), panicle length (24.85 cm), grains per panicle (101.97). Whereas, highest mean value manifested by number of productive tillers per plant (9.87). Cluster VII exhibited moderate mean values for most of traits. Where, the highest mean value was expressed by grains per panicle (271.47) and Fe content (29.35 ppm) and lower mean value expressed by amylose content (17.60 %). Cluster VII depicted highest mean value for days to 50 % flowering (103.00 days) and iron content (29.35 ppm), whereas lowest mean value for amylose content (17.60 %). Cluster VIII revealed maximum number of traits with lowest mean values *viz.*, productive tillers per plant (4.93), L/B ratio (2.69), hulling percent (49.92 %) and milling percent (55.70 %). whereas only one trait head rice recovery (75.88 %) had showed highest mean value. Cluster IX exhibited lowest mean value for protein content (6.36 %) and iron content (12.09 ppm) and highest mean value for amylose content (29.00 %). Selection of promising genotypes from each of these clusters based on per se of yield and its component characters.

Table 1: Composition of cluster based on D^2 values

Cluster	No. of genotypes	Genotypes			
I	22	NVSR-312	NVSR-365	NVSR-320	NVSR-324
		NVSR-357	NVSR-371	NVSR-373	NVSR-331
		NVSR-389	NVSR-378	NVSR-383	NVSR-326
		NVSR-330	NVSR-356	NVSR-360	NVSR-374
		NVSR-367	NVSR-368	NVSR-376	NVSR-381
		NVSR-318	NVSR-366		
II	8	NVSR-334	NVSR-386	NVSR-384	NVSR-364
		NVSR-382	NVSR-335	NVSR-388	NVSR-363
III	3	NVSR-351	NVSR-370	NVSR-369	
IV	1	NVSR-348			
V	16	NVSR-310	NVSR-390	NVSR-319	NVSR-328
		NVSR-317	NVSR-355	NVSR-372	NVSR-338
		NVSR-313	NVSR-323	NVSR-375	NVSR-339
		NVSR-322	NVSR-329	NVSR-352	NVSR-350
VI	1	NVSR-387			
VII	1	NVSR-362			
VIII	1	NVSR-359			
IX	1	NVSR-343			

Table 2: Intra and inter-cluster distances (D) between 54 genotypes of rice (D = $\sqrt{D^2}$)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**7.52**	10.04	12.24	9.56	13.50	9.71	9.38	10.455	11.77
II		**8.77**	11.41	14.69	18.02	12.73	10.84	10.32	13.33
III			**8.94**	14.57	19.89	17.44	15.06	16.24	11.52
IV				**0.00**	10.52	12.18	11.75	15.24	12.54
V					**11.21**	13.30	14.66	17.00	15.75
VI						**0.00**	11.30	8.82	14.50
VII							**0.00**	10.81	17.14
VIII								**0.00**	15.99
IX									**0.00**

Table 3: Cluster mean for fourteen characters in rice

Clusters	**Days to 50% flowering**	**Plant height (cm)**	**Number of productive tillers per plant**	**Panicle length (cm)**	**Grain per panicle**	**L/B Ratio (Kernel)**	**Hulling percent (%)**	**Milling percent (%)**	**Head rice recovery (%)**	**Amylose content (%)**	**Protein content percent (%)**	**Zn content (ppm)**	**Fe content (ppm)**	**Grain yield per plant**
I	93.82	117.39	6.99	26.11	191.82	3.43	67.41	68.21	68.17	22.98	7.28	22.50	22.29	38.34
II	98.50	133.16	6.57	27.64	224.88	3.14	62.32	64.88	58.98	23.86	6.90	27.25	23.51	41.33
III	99.89	146.25	7.27	28.55	257.00	3.73	65.32	65.35	70.87	21.75	7.00	27.76	16.23	42.84
IV	81.00	134.07	7.00	29.15	161.80	3.53	65.52	69.33	73.01	18.85	8.12	16.29	19.62	49.52
V	92.15	126.60	8.31	26.95	188.44	3.54	60.68	62.84	63.97	24.05	7.66	12.91	22.67	36.86
VI	78.00	101.47	9.87	24.85	101.90	3.47	63.77	65.31	61.34	25.00	6.39	21.11	25.22	27.31
VII	103.00	124.03	8.07	28.32	271.47	3.35	64.04	66.67	62.02	17.60	6.87	21.78	29.35	38.06
VIII	93.00	107.80	4.93	27.11	115.63	2.69	49.92	55.70	75.88	26.55	7.31	26.71	28.87	32.70
IX	96.00	124.40	7.40	27.69	187.67	3.46	49.97	56.09	60.40	29.00	6.36	21.93	12.09	43.63

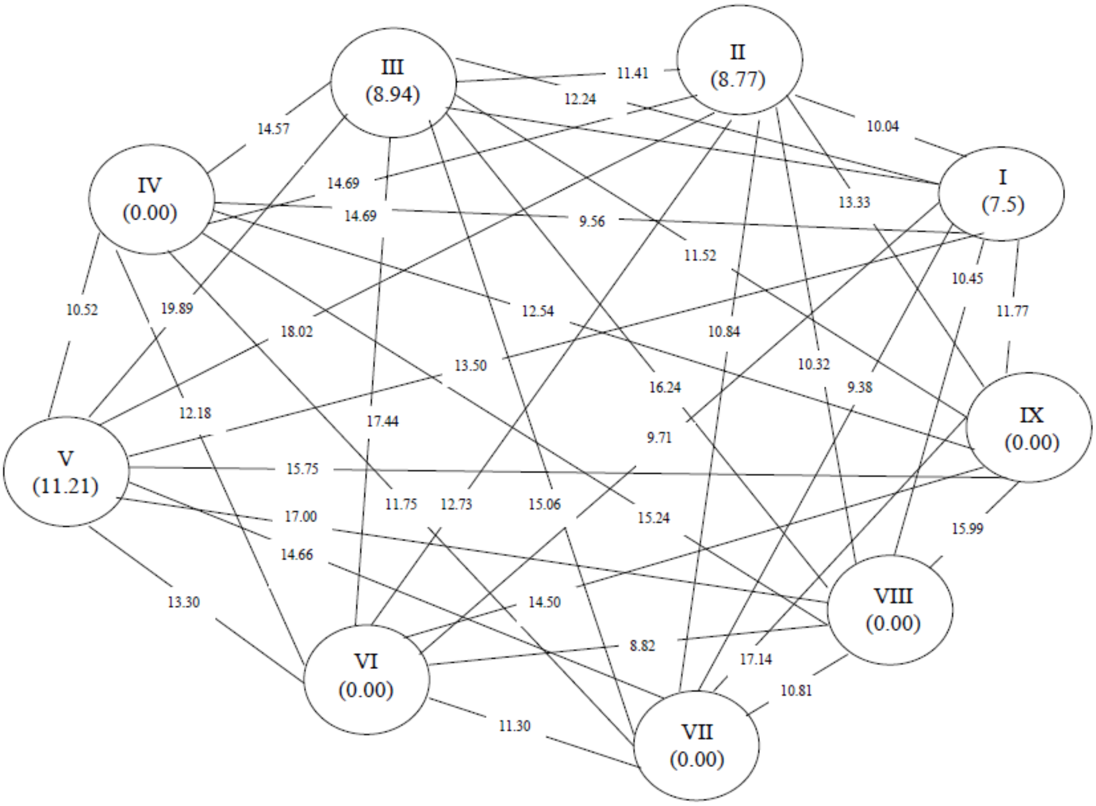

Fig. 1: Intra and Inter- cluster distances (D) between 54 genotypes of rice $D = \sqrt{D}$

CONCLUSION

Thus from the present study, it is inferred that the genetic divergence studies of different genotypes of cluster IV and cluster VI may be used for intercrossing to produce higher grain yielding plant with better quality characters. Intercrossing between the genotypes of clusters (cluster VII and IX) and (cluster III and V) may produce transgressive segregants for zinc and iron content respectively.

REFERENCES

1. Allard, R.W., Principles of plant breeding. Wiley and Sons Inc., New York (1960).
2. Chakma, S.P., Haq, H., Mahmud, F. and Husna, A., Genetic diversity analysis in rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet,* **25(1):** 31-39 (2012).
3. Chanbeni, Y.O., Lal, G.M. and Rai, P.K., Studies on genetic diversity in rice (*Oryza sativa* L.). *Journal of Agricultural Technology*, **8(3):** 1059-1065 (2012).
4. Kandamoorthy, S. and Govindarasu R., *Indian J. Genet.*, **65:** 43 – 44 (2005).
5. Mahalanobis, P.C., *Proc. Nat. Inst. Sci*., India. **2:** 49 – 55 (1936).
6. Rao, C.R., Advanced statistical methods in biometrical research. Edn. I. John Wiley & Sons, New York. pp. 390 (1952).
7. Singh and Narayanan, Biometrical Techniques in Plant Breeding. Kalyani Publishers. Chennai (2000).