

Genetic Divergence Studies for Yield and Quality Traits in Rice (*Oryza sativa* L.)**Ramesh Babu P and Sreelakshmi Ch**

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Received: 16th June, 2017 Accepted: 23rd April, 2017**Abstract**

Genetic divergence was assessed among fifty genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Based on the genetic distance the fifty genotypes were grouped into six clusters. Of the six clusters formed, cluster I having maximum number of genotypes (12) followed by cluster II with nine entries. Maximum intra cluster distance (746.9) was observed in cluster VI and minimum in Cluster III (327.8). Days to 50% flowering, gelatinization temperature score and water uptake together contributes around 72% to total divergence. Maximum inter cluster distance was recorded between clusters III and VI (827.45) followed by cluster III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Keywords: Divergence, Rice genotypes, Mahalanobis D^2 **Introduction**

Rice is the most important food crop of the world, providing over 21% of the calorific intake of the population of South East Asia. Genetic improvement of any crop mainly depends upon the genetic variability present in the population. The nature and magnitude of genetic divergence would help the plant breeder in choosing right choice of the parents in order to obtain high amount of heterotic expression in F_1 s and broad spectrum variability in subsequent generations. Besides yield, improvement of physical, milling and cooking quality characters in rice is important factor to be considered in breeding. Hence, there is an imperative need for a shift in emphasis towards development of high quality rice. This is achieved by evaluating the available germplasm lines for quality traits, and by generation of knowledge regarding their inheritance pattern to use in further breeding programmes. Keeping this in view, the present investigation was undertaken to study the nature and degree of genetic divergence among fifty rice genotypes. A meaningful classification of experimental material depending upon different characters helps to distinguish genetically close and diverse genotypes which were a pre-requisite for any genetic study.

Several workers *viz.*, Ravindra Babu *et al* (2006), Subudhi *et al* (2009), Garg *et al* (2011) proposed to choose diverse parents for quality traits such as head rice recovery, kernel length after cooking, gel consistency, kernel elongation ratio and amylose content from the most divergent clusters so that they produce larger variability and desirable segregants. Similarly, Kumar *et al* (2015) for days to maturity, Senapathi and Sarkar (2005) for ear bearing tillers per plant, panicle length, Ramesh Chandra *et al* (2007) and Iftekharuddaula *et al* (2010) for test weight, Bose and Pradhan (2005) for grain yield, Suman *et al* (2005) for

harvest index, Ramya and Kumar (2008) for number of filled grains per panicle, Raut *et al* (2009) for Kernal L/B ratio and Ubarhande *et al* (2009) for chlorophyll content contributes maximum towards total divergence.

Material and Methods

Fifty diverse genotypes from different geographic origin were transplanted in randomized block design with three replications during *rabi* season at Agricultural Research Station, Nellore, Andhra Pradesh. In each replication single seedling was transplanted per hill in 5 rows of 3 meters length with 15 x 15 cm spacing. Recommended package of practices were followed to obtain a normal crop. The observations were recorded on five randomly taken plants from each plot for days to 50% flowering, Plant height (cm), Number of ear bearing tillers, Panicle length (cm), Primary branches per panicle, secondary branches per panicle, filled grains per panicle, unfilled grains per panicle, test weight (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio, hulling percentage, milling percentage, gelatinization temperature score, water uptake, volume expansion, and kernel elongation ratio. The analysis of genetic divergence was done using Mahalanobis D^2 (1936) statistics. The genotypes were grouped into different clusters by Tocher's method described by Rao (1952).

Results and Discussion

The analysis of variance revealed that significant differences among the genotypes for all the characters studied (Table 1). Based on D^2 analysis all the 50 genotypes could be grouped in to six clusters using Tocher's method (Singh and Chaudhary., 1977). However, with variable number of entries in each cluster revealing considerable amount of



Table 1. Distribution of 50 genotypes of rice in different clusters

Cluster	Number of genotypes	Identity of genotypes
I	12	NLR 33657, NLR 33656, NLR 33359, NLR 33637, NLR 33655, IR 50-15, IET 9994, IET 7563, W 1263, SUREKHA, ADT 39, CO 43
II	9	NLR 13969, NLR 33658, MTU 1005, MTU 1004, NLR 6802-1, WGL 20471, IET 10158, IET 10746, IR 60
III	5	BPT 5204, IET 10021, PANKAJ, IR 20, DV 85
IV	9	NLR 5050-13-1-1, NLR 5144-1-2-6, NLR 5110-16-2-1, NLR 5144-7-5-3, NLR 5144-5-3-1, NLR 30491, PR 164, MTU 1003, MTU 1002
V	5	NLR 145, NLR 5144-1-7, MTU 9992, KARJAT 1, WHITE PONNI
VI	10	NLR 33636, WGL 44645, RASI, POTTINALLAVARI, IET 4141, IET 7302, KHAO-DAWK-MALI, IR 72, IR 62, IR 64

genetic diversity in the material studied (Table1). It was observed that the cluster I had maximum number of 12 genotypes followed by cluster II with 10 genotypes and cluster II and IV with 9 genotypes each. Whereas, Cluster III and V had 5 genotypes in each cluster. The clustering pattern indicated that there was some degree of similarity of genotypes clubbed together in a cluster on the basis of their origin. The genotypes from Nellore, Warangal, Hyderabad, IRRI and Thailand were included in the same cluster (cluster X). Similar findings were reported by Singh *et al* (2008) and Allam *et al* (2014). Grouping of materials of similar origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin. So, genotypes originating from same place may have different genetic architecture or vice – versa as the genotypes developed at Agricultural Research Station, Nellore had fallen in clusters I, II, IV, V and VI Similar

kind of results were also reported by Pradhan and Mani (2005), Sharma *et al* (2011) and Nirmaladevi *et al* (2015).

Average intra and inter cluster distance values among six clusters were presented in Table 2 and it revealed that the intra cluster average D^2 values ranged from 327.8 (cluster III) to 746.87 (Cluster VI). The maximum intra cluster distance was observed in cluster III revealed that existence of diverse genotypes that fell in these clusters. While the minimum distance was observed in the cluster VI indicating that the genotypes fell in this cluster was found similar. The average inter cluster D^2 value between clusters III and VI was maximum (827.45) followed by cluster III and cluster IV (760.71) which indicates that genotypes include in these clusters are genetically diverse and may give rise to high heterotic response. Minimum inter cluster D^2 values were observed between cluster I and II (223.86)

Table 2. Intra and inter cluster average distances (D^2) values of six clusters from 50 genotypes

Cluster	I	II	III	IV	V	VI
I	700.87	223.86	506.62	324.39	267.85	593.09
II		681.69	720.88	238.26	390.96	590.40
III			327.80	760.71	292.04	827.45
IV				536.20	504.02	690.91
V					582.80	645.08
VI						746.90

indicating the close relationship among the genotypes included in these clusters.

Considerable differences were found among the clusters for most of the characters studied (Table 3). The cluster I had the highest mean value for milling percentage (70.59), elongation ratio (1.64) and GT score (6.10). Clusters III, IV and VI had highest mean value for only one character each *viz.*, Days to 50% flowering (127.30), water uptake (264.40) and L/B ration of the kernel (3.18) respectively. On the other hand, cluster V had highest mean values for more number of characters *viz.*, primaries per panicle, secondary branches per panicle, grain yield per plant, hulling

percentage and volume expansion. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters (Mishra and Parvin 2004).

Percentage contribution of the each character towards total divergence is presented in table 4. The data revealed that maximum percentage of contribution came from the trait days to 50% flowering (41.5%) followed by G.T score (20.33), water uptake (9.84%), hulling percentage (7.76), elongation ratio (4.08%), L/B ratio of the kernel (3.18%), and number of primary branches per panicle (2.20%). The other traits had very low contribution to total

Table 3. Mean values of clusters from 50 genotypes of rice for different characters

Sl. No.	Character	I	II	III	IV	V	VI
1	Days to 50% flowering	102.92	91.11	127.30	105.58	113.20	89.0
2	Primaries per panicle	9.87	9.11	10.85	9.26	11.21	9.35
3	Secondaries per panicle	28.58	26.04	30.98	22.70	37.70	30.39
4	Grain yield per plant	13.97	17.93	18.33	16.45	21.50	19.43
5	L/B ration of the kernel	2.76	3.01	2.71	3.01	2.97	3.18
6	Hulling percentage	78.85	74.76	70.92	75.29	78.86	74.80
7	Milling percentage	70.59	66.69	64.33	69.71	68.83	69.76
8	G T score	6.10	5.64	4.10	5.55	4.60	2.22
9	Water uptake	233.29	29.17	230.5	264.40	240.45	245.64
10	Volume expansion	4.22	4.26	4.45	4.29	4.54	4.45
11	Kernal elongation ratio	1.64	1.50	1.53	1.49	1.50	1.54

Table 4. Relative contributing on (%) of individual trait to the divergence among genotypes

S. No	No. of times Ranked first	Contribution (%)
Days to 50% flowering	1	41.55
Primaries per panicle	7	2.20
Secondaries per panicle	8	0.73
Grain yield per plant	11	0.00
L/B ration of the kernel	6	3.18
Hulling percentage	4	7.76
Milling percentage	0	0.08
G T score	2	20.33
Water uptake	3	9.84
Volume expansion	9	0.24
Kernal elongation ratio	5	4.08

divergence. Relative importance of these parameters on these characters in inter varietal divergence on rice were reported by Patil *et al* (2005), Sandhya kishore *et al* (2007) and Garg *et al* (2011).

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the rank first. Hence, days to 50% flowering, GT score, water uptake, hulling percentage, elongation ratio, L/B ratio of the kernel may be used as selection parameters in the segregating generations from the present material studied. The traits which had low or zero contribution towards divergence were of less importance as per the material studied in the experiment. Since genotypes with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes. Availability of genetically more divergent genotypes were important for hybridization programme. Since, days to flowering contributed maximum towards the genetic divergence, we may go for direct selection for this trait for diversity purpose.

References

- Allam CR, Jaiswal HK and Qamar A. 2014. Divergence analysis for yield and quality traits in some indigenous basmati rice genotypes (*Oryza sativa* L.) *International Journal of Applied Biology and Pharmaceutical Technology*. 5(4):257-263.
- Bose LK and Pradhan SK. 2005. Genetic divergence in deep water rice genotypes. *Journal of Control European Agriculture*. 6 (4):635-640.
- Garg P, Pandey DP and Kaushik RP. 2011. Genetic divergence for yield and quality traits in rice (*Oryza sativa* L.). *Journal of Rice Research* 4(1&2):1-5.
- Iftekharuddaula KM, Khaleda Akter Hassan MS, Kaniz Fatema and Adil Badshah. 2010. Genetic divergence, character association and selection criteria in irrigated rice. *Online Journal of Biological Sciences*. 2 (4):243-246.



- Kumar N, Tiwari B, Lal GM, Mishra SP, Katiyar A and Khunthey Y. 2015. Evaluation of rice hybrids (*Oryza sativa* L.) for yield and its component characters. *Indian Research Journal of Genetics and Biotechnology*. 7 (1):41-43.
- Mahalanobis PC.1936. On the generalized distance in statistics.Proc.Nat.Inst.Sci.of India 2:49-55.
- Mishra LJ and Parvin 2004. Variability and genetic diversity in rice (*Oryza sativa* L.) *Mysore Journal of Agricultural Sciences* 38:367-375.
- Nirmaladevi G, Padmavathi G, Suneetha Kota and Babu VR. 2015. Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.) *SABRAO Journal of Breeding and Genetics* 47 (4) 424-433.
- Patil SG, Mairan NR and SahuVN. 2005. Genetic divergence of traditional rice germplasm accessions. *Journal of Soils and Crops*. 15:308-314.
- Pradhan S K and Mani SC. 2005. Genetic diversity in Basmati Rice. *Oryza* 42 (2):150-152.
- Ramesh Chandra, Pradhan SK, Sanjay Singh Bose LK and Singh ON. 2007. Multivariate Analysis in Upland Rice Genotypes. *World Journal of Agricultural Sciences*. 3 (3):295-300.
- Ramya K and Senthilkumar N. 2008. Genetic divergence in rice. *Crop Improvement*. 35 (2):119-121.
- Rao CR. 1952. Advanced Staistical Methods in Biometrical research. John Wiley and Sons.Inc.New York.
- Raut KR, Harer PN and Yadav PS. 2009. Genetic divergence in rice. *Journal of Maharashtra Agricultural Universities*. 34 (2):172-174.
- Ravindrababu V, SandhyaKishore ShobhaRani N and Ravichandran. 2006. Genetic divergence analysis using quality traits in rice (*Oryza sativa* L.). *Oryza*. 43 (4):260-263
- Sandhya Kishore N, Babu VR, Ansari NA and Chandra R 2007. Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.) *Crop improvement*. 34:12-15.
- Senapati BK and Sarkar G. 2005. Genetic divergence in tall indica rice under rainfed saline soil of Sundarban. *Oryza*. 42 (1):70-72.
- Sharma SK, Nandan R, Singh SK, Sharma AK, Kumar S, Sharma P K, Singh M K, Kumar V. 2011. Genetic divergence in rice (*Oryza sativa* L.) genotypes under irrigated condition, *Progressive Agriculture* 11(2):321-325.
- Singh RK and Chaudhary BD. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India.Pp:229-252.
- Singh YR, Pradhan SK, Anita Bajpai and Singh U S 2008. Divergence analysis for quality traits in some indigenous basmati rice genotypes. *Crop Improvement* 45(4):263-267.
- Subudhi, H.N., Meher, J., Bose, L.K. and Sanjukta Das. 2009. Genetic diversity studies of promising rice varieties of eastern India based on quality characters. *Oryza* 46(3):224-227.
- Suman A, Shankar VG, Rao LVS and Sreedhar N. 2005. Analysis of genetic divergence in rice (*Oryza sativa* L.) germplasm. *Research on Crops* 6 (3):487-491.
- Ubarhande VA, Prasad R, Singh RP, Singh SP and Agrawal RK. 2009. Variability and diversity studies in rainfed rice (*Oryza sativa* L.). *Indian Journal of Plant Genetic Resources*. 22 (2):134-137.