

Studies on Nature of Genetic Diversity in Slender Grain Rice Genotypes

Biswaranjan Behera, Simanchal Sahu, Rajesh Kumar Kar,
 Ritu Kumari Pandey

Received 13 July 2017 ; Accepted 16 August 2017 ; Published online 2 September 2017

Abstract Forty-nine elite slender grain rice genotypes collected from different parts of the country were evaluated to elicit the information on nature and magnitude of genetic divergence. Based on the relative magnitude of D^2 values, following Tocher's method, all the test entries were grouped into eight clusters. The clustering pattern showed no relationship between geographic distribution and genotypic diversity. The cluster I was the biggest cluster consisting of 23 genotypes followed by cluster III, IV (7 genotypes each), cluster II (5 genotypes), cluster V, VI, VII (2 genotypes each). The cluster VIII was monogenic. Average inter-cluster distance ranged from 2468.28 (clusters VI and V) to 248.12 (clusters IV and VIII) and the intra cluster distances ranged from 346.64 (cluster VII) to 0.00 (VIII). The cluster means indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Hence recombination breeding between genotypes of different clusters may be followed. The selection of most divergent clusters would produce broad spectrum of variability for

yield and other attributing traits, which may enable further selection and genetic improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants that would be useful in rice breeding program. Therefore, it is suggested that in the present investigation parents should be chosen from the most divergent groups i.e., between cluster V and cluster VI for hybridization.

Keywords Slender grain rice, Genetic diversity, Mahalanobis D^2 , Clustering.

Introduction

Rice is staple food for more than 70% of people and a source of livelihood for 120—150 millions rural households of the country. It contributes to 43% of total food grain production and 53% of cereal production. It provides more than 50% of daily calorie intake and considered as the cheapest source of food, energy and protein in the developing countries. It contributes to 43% of total food grain production and 53% of cereal production, thus, continues to hold the key to sustain food sufficiency in the country. Understanding the importance, it is important to know the amount of diversity present in the rice genotypes so that they can be further improved. Genetic diversity is one of the key factors in adapting a effective breeding program in any crop. Success of hybridization followed by selection depends largely on the

B. Behera, S. Sahu, R. K. Kar*
 Department of Plant Breeding and Genetics, College of
 Agriculture Bhubaneswar, OUAT, India

R. K. Pandey
 Department of Nematology, College of Agriculture
 Bhubaneswar, OUAT, India
 e-mail: rajeshkar023@gmail.com

*Correspondence

Table 1. Clustering of forty-nine medium slender rice genotypes.

Cluster	No. of genotypes	Name of genotype
I	23	CB09123, CR3511-3-2-2-5-1-1, NP-3003, RTN28-1-5-3-2, RP 5947-123-6-2-1-1-B, WGL-14 (NC-1), NP-9917-54, NVSR 6127, RP 4926-352-99-76-23-18-1, Improved samba mahsuri (RC), NP-9359-9, R 1130-80-1-52-1-R-1, PUSA 1850-20-11-22, NLR 3350, NP 5682-2, WGL-810, BPT 5204 (NC 2), CR 3505-7-1-1-1-2-1, RTN 14-1-1-1-1, R 1502-HR-Heera sel.1, WGL-401, RP 5951-121-51-6-1-1-B, RTN 65-1-2-2-2
II	5	PUSA 1701-10-5-8, PUSA 1850-16, UBKVR-59, CR 3861-37-6-3, Manaswini (LC)
III	7	GNV-14-25, GNV-14-96-1, WGL-821, MTU 110 (MTU 2142-9-2-1), CBMAS 14065, CB 12186, RP 5950-24-6-2-1-1-B
IV	7	BPT 2595, RGL 7012, BPT 2673, AD 12079, AD 12074, BPT 2644, AD 13121
V	2	RP 5949-122-2-5-1-1, AD 12182
VI	2	NLR 3337, BPT 2743
VII	2	NLR 3313, BPT 2675
VIII	1	RGL 7011

selection of parent with high genetic variability for different characters. The genetically diverse parents are likely to produce heterotic effects and desirable segregants. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents. Slender grain rice varieties collected from different parts of the country will help to identify varieties suitable for cultivation in this region as well as select promising varieties for use as parent material in future breeding program. Therefore, the magnitude of genetic divergence and characters contributing to the genetic divergence were studied among forty-nine elite slender grain rice genotypes.

Materials and Methods

The experimental material used in the present investigation consisted of forty-nine elite slender grain rice genotypes. The test genotypes were evaluated under normal situations at Rice Research Station, Orissa University of Agriculture and Technology, Bhubaneswar during *kharif*, 2015. Trials were laid out in a randomized block design with two replications with the spacing of 15 × 20 cm and the recommended cultural practices were followed. Observations were recorded on the following thirteen characters Days to 50% flowering, Plant height, Panicle length, Number of effective tillers per plant, Flag leaf area, Fertile grain number, Fertility percentage, Kernel length, Kernel breadth, L/B ratio, 100-seed weight, Harvest index, Grain yield per plant were recorded. The data gener-

ated was utilized to estimate the genetic divergence by using Mahalanobis D^2 analysis.

Results and Discussion

The analysis of variance revealed the existence of significant differences among the genotypes for all the traits, indicating the existence of sufficient variation in the material studied. Based on D^2 values the forty-nine genotypes were grouped into eight clusters (Table 1). The clustering pattern showed no relationship between geographic distribution and genotypic diversity as the genotypes from different geographic origins were grouped in the same cluster. This may be due to free exchange of breeding material from one place to another besides unidirectional selection for a particular trait under the respective domestication. Earlier reports also indicated that geographic diversity can not always be used as an index of diversity [1].

Cluster I was the largest accommodating twenty-three varieties, followed by cluster III and cluster IV seven varieties each, cluster II includes five varieties. Cluster V, cluster VI and cluster VII includes two varieties each, where as the cluster VIII consisted of one variety. Grouping of large number of varieties in cluster-I might have resulted due to similar selection pressure favoring identical expression of characters influencing grain yield during course of selection. The inter cluster and intra cluster D^2 values are presented

Table 2. Average inter-cluster distances (D^2) in forty-nine medium slender rice genotypes. * Diagonal values are intra cluster distances.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	236.04							
II	658.02	165.45						
III	462.76	1551.48	224.67					
IV	870.84	1199.58	1228.44	246.96				
V	921.55	2457.20	421.50	1367.21	182.56			
VI	1354.29	1270.73	1972.36	454.90	2468.28	345.24		
VII	963.98	1967.04	758.76	624.81	874.82	963.12	346.64	
VIII	1057.40	1314.86	1463.39	248.12	1546.03	568.89	916.96	0.00

in Table 2. The divergence within the cluster indicates the divergence among the genotypes falling in the same cluster. On the other hand inter cluster distance suggest the divergence between genotypes of different clusters. The data suggested maximum distance between the genotypes falling under cluster VII (346.64) followed by cluster VI (345.24), cluster IV (246.96), cluster I (236.04) and cluster III (224.67). Average inter-cluster distance revealed that most divergent clusters were VI and V (2468.28), followed by II and V (2457.20), II and VII (1967.04) and III and VI (1972.36). On the other hand, the minimum inter-cluster divergence was found between IV and VIII (248.12), followed by III and V (421.50), thus indicating closeness between themselves. Thus from the foregoing observations it is observed that genotypes included in divergent clusters had large differences among themselves for more number of characters where as clusters having closeness among them-

selves contained genotypes with more or less similar for majority of traits.

A glance of cluster means for different characters (Table 3) indicated genotypes in cluster I were characterized by intermediate for all the characters. Genotypes in cluster II were characterized by early maturity, small plant height, medium panicle length, small leaf area, low number of fertile grains per panicle, high kernel length, high L/B ratio, medium harvest index and low grain yield. Cluster III is characterized by high harvest index and high grain yield. Cluster V having high flag leaf area and lower number of effective tiller per plant, lower kernel length and lower 100-seed weight. Cluster VI characterized by late maturity, higher plant height, lower L/B ratio, medium panicle length, low number of effective tillers, low fertility percentage and low harvest index. Cluster VII having higher fertile grains per panicle and me-

Table 3. Cluster means of 49 medium slender rice genotypes of 13 characters.

Clusters/characters	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	99.48	97.10	102.00	122.00	104.25	129.25	127.25	120.50
Plant height (cm)	102.56	90.52	103.64	102.67	110.23	106.50	96.45	115.00
Panicle length (cm)	24.80	23.05	25.69	25.48	25.80	24.25	22.98	29.30
No. of effective tillers/plant	12.02	12.34	11.40	12.24	10.80	9.15	11.65	13.30
Flag leaf area (cm ²)	41.17	31.34	47.32	46.24	60.88	35.21	45.71	51.82
Fertile grains/panicle	145.51	94.98	181.66	126.93	178.65	134.15	187.85	105.40
Fertility percentage	78.56	71.07	77.85	62.76	70.26	50.92	62.17	63.68
Kernel length (mm)	5.57	6.04	5.74	5.42	5.25	5.44	5.58	5.93
Kernel breadth (mm)	1.83	1.81	1.91	1.86	1.66	2.03	1.88	2.06
L/B ratio	3.09	3.37	3.00	2.94	2.99	2.72	2.99	2.88
100 seed wt (gm)	1.58	1.75	1.66	1.50	1.40	1.51	1.56	2.00
Harvest index	0.40	0.39	0.44	0.31	0.39	0.25	0.33	0.33
Grain yield/plant (g)	12.83	10.12	17.12	12.57	14.65	13.24	15.19	17.37

dium fertility percentage. Cluster VIII are having higher panicle length, number of effective tiller per plant, kernel breadth, 100-seed weight and grain yield per plant. The cluster means indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Hence recombination breeding between genotypes of different clusters may be followed.

The present study revealed that considerable diversity existed both within and between the clusters. To realize much variability and high heterotic effect earlier [2—4] recommended that parents should be selected from two clusters having wider inter cluster distance. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants that would be useful in rice breeding program. Therefore, it is suggested that in the present investigation parents should be chosen from the most divergent groups i.e., between cluster V and cluster VI for hybridization.

Conclusion

The clustering pattern showed no relationship between geographic distribution and genotypic diversity as the genotypes from different geographic origins were grouped in the same cluster. Cluster I was the largest accommodating twenty-three varieties, followed by cluster III and cluster IV seven varieties each, cluster II includes five varieties. Cluster V, cluster VI and cluster VII includes two varieties each, where as the clusters VIII consisted of one variety. Grouping of large number of varieties in cluster I might have resulted due to similar selection pressure favoring identical expression of characters influencing grain yield during course of selection. The data suggested maximum distance between the genotypes

falling under cluster VII (346.64) followed by cluster VI (345.24), cluster IV (246.96), cluster I (236.04) and cluster III (224.67). Average inter-cluster distance revealed that most divergent clusters were VI and V (2468.28), followed by II and V (2457.20), II and VII (1967.04) and III and VI (1972.36). Thus from the foregoing observations it is observed that genotypes included in divergent clusters had large differences among themselves for more number of characters where as clusters having closeness among themselves contained genotypes with more or less similar for majority of traits. The cluster means indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Hence recombination breeding between genotypes of different clusters may be followed. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants that would be useful in rice breeding program. Therefore, it is suggested that in the present investigation parents should be chosen from the most divergent groups i.e., between cluster V and cluster VI for hybridization.

References

1. Chandra Ramesh, Pradhan SK, Singh S, Bose LK, Singh ON (2007) Multivariate analysis in upland rice genotypes. *World J Agric Sci* 3 : 295—300.
2. Yadav VK, Singh Y, Soni SK, Yadav AK (2011) Genetic divergence analysis in salt tolerance rice (*Oryza sativa* L.) genotypes. *Pl Arch* 11 : 593—595.
3. Vennila S, Anbuselvam Y, Palaniraja K (2011) Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.). *Int J Recent Scient Res* 2 : 237—239.
4. Latif MA, Rahman MM, Kabir MS, Ali MA, Islam MT, Rafii MY (2011) Genetic diversity analyzed by quantitative traits among rice (*Oryza sativa* L.) genotypes resistant to blast disease. *Afr J Micro Res* 5 : 4483—4491.