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Genetic Divergance Analysis of some Genotypes of Aerobic Rice

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Abstract The experiment was conducted during 2015-16 on 26 genotypes of aerobic rice. The 26 rice genotypes were classified into 5 clusters, using mahalanobis D^2 statistic. Based on 10 morphological characters namely, days to 50% flowering, plant height, effective tillers/m^2, flag leaf area, panicle length, fertile grains/panicle, fertility percentage, 1000 grain weight, L/B ratio and plot yield, these genotypes were grouped into 5 clusters. Cluster I contains 16 genotypes , cluster II contains 4 genotypes. Cluster III contained 4 genotypes and cluster IV and V contained one genotype each and the intra-cluster distance is more in cluster III (146.15) and less in cluster I (81.36). Cluster I and V are more divergent from each other with an inter-cluster distance 716.72 and cluster III and IV were less divergent from each other with intercluster distance 192.39. So selecting parents from more divergent clusters are important in hybridization program to get better segregant.

Keywords Aerobic rice, Genetic divergence, Genotype.

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Introduction

Rice is the life and the prince among cereals as this unique grain helps to sustain two thirds of the worlds population. Asia is the biggest rice producer and consumer, accounting for 90% of the worlds production and consumption of rice. Rice is the major consumer of irrigated water, particularly in the dry season. Lack of rainfall makes cropping impossible without irrigation. Farming commeunities just have to cope with this water scarcity scenario, by reducing irrigation water to their fields. To safeguard the food industry and conserve water, aerobic rice was introduced . It is fundamentally a different approach of rice cultivation where a high yielding rice is grown in non-puddled and non-saturated fields with supplementary irrigation and high external inputs [1]. As, aerobic system of rice cultivation can save wa-

ter up to 50%. Aerobic rice is a new way of cultivating rice that requires less water than lowland rice. Success of hybridization and subsequent selection between aerobic genotype of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The more diverse the parents, greater are the chances of obtaining higher amount of heterotic expression in F_1 and broad spectrum of variability in segregating generations. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Shukla et al. [2] and Sarawgi and Bins Rita [3]. The present experiment was conducted to find out the magnitude of genetic diversity of 26 aerobic rice genotypes and to select suitable genotypes for further utilization in breeding program.

Materials and Methods

The experiment was conducted at Rice Research Station, O.U.A.T., Bhubaneswar during 2015 *kharif* season. 22 aerobic rice genotypes and 4 check varieties were collected from AICRP trails on aerobic rice, conducted in a randomized block design with three replications. The plot size was 5.28 meter square with spacing 20 × 15 cm. Observations were recorded for ten metric traits taking five competitive plants selected randomly from middle rows of each plot; where as, characters like plot yield and days to 50% flowering were recorded on plot basis and number of effective tillers was observed on square meter basis. The characters studied were days to 50% flowering, plant height, effective tillers/m^2, flag leaf area, panicle length, fertile grains/panicle, fertility percentage, 1000 grain weight, L/B ratio and plot yield. The replicated data were subjected to Mahalanobis D^2 analysis which was used to estimate genetic divergence among the 26 genotypes. Grouping of genotypes into clusters was carried out by tocher's method. Mean values of the variables, calculated based on measurements on plants from blocks for each genotype, were used in the cluster analysis.

Results and Discussion

The analysis of variance of randomized complete block design revealed the existence of highly significant genetic variance for all the eighteen characters studied. Based on D^2 analysis, all the 26 rice genotypes were classified into 5 clusters (Table 1). Cluster I contains 16 genotypes, cluster II contains 4 genotypes. Cluster III contained 4 genotypes, cluster IV and V contained one genotype each. From the obervations of Table 2 indicated cluster I and V are more divergent from each other with an inter cluster distance 716.72. Cluster III and IV were less divergent from each other with inter-cluster distance 192.39 and the intra-cluster distance in more in cluster III (146.15) and less in cluster I (81.36).

Table 3 indicated genotypes in cluster I were characterized by shorter duration with medium plant

Table 1. Clustering of 26 aerobic rice genotypes.

Cluster	No. of Genotypes	Name of genotypes
	16	TRC 2014-14/IR 82589-B-B-2-2,CR DHAN202, RCPR-19-IR-84899-B-179-13-1-1-1, RAU1484-Aer-04,PA 6129, MANDAKINI, CR DHAN201,TRC2014-11/IR83377-B-B-123-2,RCPR8 (IR84899-B-179-16-1-1-1), KMP 128, KPH272 (HYBRID), RCPR-20-IR83929-B-B-291-2-1-1-2, BRR0006(IR87759-2-2-1-1), R1986-296-2-86-1, NPH912(HYBRID), BRR0007 (IR87638-10-1-13)
	4	NPH8899 (HYBRID), RP5587-B-B-B-305-13,CR3947-1-3-1-1-1, TRC-2015-14
	4	MC13,R1973-206-2-86-1,TRC-2015-12,CR3856-44-22-2-1-10-3-1
	1	CR 3948-2-1-2-2-1
	1	CR3580-3-1-1-1-1-1

Table 2. Inter and intra-cluster distance of 26 aerobic rice genotype.

Cluster	1	2	3	4	5
1	81.36	215.60	311.33	575.26	716.72
2		120.40	503.82	682.15	501.39
3			146.15	192.39	581.46
4				0.000	419.29
5					0.000

Table 3. Cluster means of 26 aerobic rice genotypes.

Sl. No.	Clusters/Characters	I	II	III	IV	V
1.	Days to 50% flowering	81.13	87.42	82.25	82.00	103.00
2.	Plant height (cm)	108.29	94.22	101.95	100.60	103.00
3.	Panicle length (cm)	244.35	204.50	188.75	119.67	197.00
4.	No. of tiller/m^2	24.35	21.84	22.47	23.40	21.42
5.	Flag leaf area (cm^2)	26.50	32.03	24.47	42.00	62.40
6.	No. of fertile grain/panicle	71.81	32.67	109.75	108.00	84.33
7.	Fertility %	71.40	41.38	72.66	55.84	62.96
8.	L-B Ratio	3.48	4.22	3.42	3.19	2.72
9.	100 grain weight (g)	2.29	1.96	2.11	2.19	1.47
10.	Plot yield (kg/ha)	1540.35	464.17	1609.75	1136.33	455.00

having longer panicle length and more no. of tiller per m^2 with higher grain weight than other. Genotypes in cluster II were characterized by smallest plant height than other with lowest fertile grains per panicle with lower fertility percentage and having more slender grains. Cluster III is characterized by medium duration, medium plants with lower flag leaf area and more no. of fertile grains per panicle with higher fertility percentage. Cluster IV is characterized by medium height plants with smaller panicle than other. Cluster V is characterized by medium height plants with lower grain weight, bold grains, highest flag leaf area than other and low grain yield.

A number of techniques involving multivariate analysis are currently used to quantify diversity among the individuals in the population. In the recent part researchers have extensively used Mahalanobis D^2 statistics to assess genetic diversity among the genotypes in a number of crops [4—6]. Generally geographical diversity has been considered as an index of genetic diversity. Published reports are highly conflicting with regard to relation between geographical origin and genetic diversity. A number of workers in rice found no parallelism between genetic diversity and ecogeographic distribution [6,7]. The results obtained in the present study did not show relationship between the two.

Cluster I contained 16 genotypes from different sources (Table 3). Similarly cluster II contained 4 genotypes cluster III contained 4 genotypes. Cluster VI and VII contained one genotype each. Thus it indicated that geographical distance *per se* is not that important in varietal diversity. It may be visualized that the genotypes developed at one location are showing similarity with those developed else where.

Conclusion

The 26 genotypes were grouped into 5 clusters on the basis of Mahalonobis's D^2 analysis.Cluster I contained 16 genotypes from different sources (Table 1). Similarly cluster II contained 4 genotypes. Cluster III contained 4 genotypes. Cluster VI and VII contained one genotype each. Thus it indicated that geographical distance *per se* is not that important in varietal diversity.

Table 3 indicated genotypes in cluster I were characterized by shorter duration with medium plant having longer panicle length and more no. of tiller per m^2 with higher grain weight than other. Genotypes in cluster II were characterized by smallest plant height than other with lowest fertile grains per panicle with lower number of fertile grains /panicle and fertility percentage and having more slender grains. Cluster III is characterized by lower flag leaf area and more no. of fertile grains per panicle with higher fertility percentage and higher yield. Cluster IV is characterized by medium height plants with smaller panicle than other. Cluster IV is characterized by medium duration and medium height plats with lower grains weight, bold grain weight, bold grains and lower number of tiller/m^2 highest flag leaf area than other and low grain yield.

This result reveals that more divergent clusters are cluster I and V followed by cluster II and IV (Table 2) . So selecting parents from more divergent cluster are important in hybridization program to get better segregant.

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