Research Article

GENETIC DIVERSITY ANALYSIS IN FEW GENOTYPES OF RICE FOR YIELD AND ITS COMPONENT TRAITS

VANGARU SATHISH[1]*, BHATTACHARYYA SOMNATH[1], MUKHERJEE SUBHRA[1] AND MONDAL SUBHASIS[2]

[1]Department of Genetics and Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Nadia, Mohanpur, 741252, West Bengal, India
[2]Department of Plant Physiology, Bidhan Chandra Krishi Viswavidyalaya, Nadia, Mohanpur, 741252, West Bengal, India
*Corresponding Author: Email- sathish.agrico@gmail.com

Abstract- Twenty-one genotypes of rice were evaluated in Randomised block design with three replications during Kharif season of 2015. Observations recorded for characters like days to 50% flowering, Chl-a (mg/kg), Chl-b (mg/kg), Chl a/b, Plant Height (cm), No of tillers, No of effective tillers, 1000 seed weight, number of filled grains, floret Sterility (%), Dry weight (g) and Seed yield (g).Twenty-one genotypes were grouped into seven clusters, according to depicted distances among the genotypes based on D^2 values. Among the all seven clusters, maximum genotypes present in Cluster-IV, possessing six genotypes followed by cluster-I, which had five genotypes and the remaining clusters had two genotypes each. According to D^2 values, highest inter cluster distances were witnessed between cluster-III and cluster-V (18248.23), followed by cluster III and VII (11764.44), cluster V and VI (104.22.98). Lowest inter cluster distances were observed between cluster-II and cluster-VI (856.26), signifying close relationship among the genotypes of this group. During hybridization programmes, parents from distant clusters should be selected and maximum emphasis should be given to characters like number of grains per panicle, seed yield, 1000 grain weight, floret fertility and number of tillers per plant which together contributed more than 89% towards divergence.

Key words- Rice, Genetic diversity, D^2 statistic and cluster.

Introduction

Rice (*Oryza sativa* L.) has been cultivated as a crop for at least 8000 years. Rice is the world's second most important cereal crop and staple food for more than 60% of the global population [1]. According to a survey conducted in 18th century, population was increasing faster than food production, and people frightened eventual global starvation. However, modern technology expanded food production, but observations about how populations increase were important. The food grains increase in arithmetical progressions while the population increases in geometrical progression[2], which is why the numbers can increase so quickly. In 1950, the world had 2.5 billion people; and in 2017, the world had 7.5 billion people. By 2050, this number could rise to more than 9 billion. Maintaining stable rice production is extremely important to feed the constantly growing population. In the present scenario, the rice productivity has reached a plateau [3]. For breaking the yield barrier level and make rice cultivation more attractive, it is now necessary to explore alternative approaches. Among the all-possible alternatives, heterosis is an important approach for increasing rice production [4] Knowledge about germplasm diversity and genetic relationships among breeding materials could be an invaluable aid in crop improvement strategies [5]. Genetic diversity is the main source of variability in any crop improvement program. An assessment and classification of this diversity is important for effective utilization of the germplasm [6]. It serves as a reservoir for identifying superior alleles controlling key agronomic and quality traits through allele mining/ association mapping [7]. The success of any crop improvement programme largely depends on the existence of diversity among the genotypes [8]. This helps in the choice of parents for hybridization in yield improvement programmes. Selection of diverse parents could yield highly desirable combinations not only in segregating generations.

With this background information, genetic diversity was assessed in 21 rice genotypes of Rice.

Materials and Methods

Twenty-one genotypes of Rice were collected from West Bengal and Odisha, evaluated in Randomised block design with three replications. Experiment conducted during Kharif season of 2015, at Instructional farm, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal. In order to raise good crop, recommended cultural and management practices were followed during entire crop growing period. Five randomly selected plants were utilised for taking various observations in each replication. Observations recorded for characters like Plant height, days to 50% flowering, Chlorophyll a (mg/kg), Chlorophyll-b (mg/kg), Chlorophyll a/b ratio, Plant Height(cm), number of tillers, number of effective tillers, 100 seed weight, number of filled grains, floret sterility (%), Dry weight(g) and Seed yield(g). Biochemical characters like chlorophyll-a, b and a/b ratios were estimated according to methods suggested by Krishnan, *et al.* [9]. Mahalanobis's D^2 statistic was used to estimate genetic diversities among the germplasm chosen under the study, which is suggested by C. R. Rao [10] for selection of parents in plant hybridization. Clustering of genotypes was done by adopting Tocher's method. All statistical calculations were done utilizing GENRES software.

Results and Discussion

Analysis of variance revealed that significant differences were observed for all characters chosen for study and presented in [Table-1]. Twenty-one genotypes were grouped into seven clusters, according to depicted distances among the genotypes based on D^2 values [Table-2]. Among the all seven clusters, maximum

genotypes present in Cluster-IV, possessing six genotypes followed by cluster-I, which had five genotypes. Rest of the clusters had two genotypes in each. Remarkably, land races which were collected from West Bengal present were grouped in cluster-I. Most of the Landraces of collected from Odisha were shared cluster-IV. The all other genotypes observed to present in remaining clusters. This finding suggesting that there was an association between clustering pattern and eco-geographical distribution of genotypes, which is corroborated with earlier findings of Yahiaoui, *et al.*[11].

Table-1 *Analysis of variance for various characters in 21 genotypes of rice*

Character Name	Source of Variation with Df		
	Replication (2)	Treatment (20)	Error (40)
Days to 50% flowering	21.81	9810.857**	448.19
Chla (mg/kg)	0.03	24.387**	0.15
Chlb (mg/kg)	0.00	6.132**	0.02
Chl a/b	0.01	21.348**	0.00
Plant Height	57.33	39967.971**	326.61
No of tillers	0.21	497.536**	5.36
No of effective tillers	1.33	504.149**	11.98
1000 seed weight	1.15	1039.09**	37.48
No of filled grains	12.97	28269.814**	1023.66
floret Steriity %	1.98	23782.318**	29.42
Dry weight(g)	0.93	3554.289**	22.31
Seed yield(g)	0.15	884.055**	30.68

Table-2 *Clustering pattern of 21 genotypes of rice (Oryza sativa L.) by Tocher's method.*

Cluster No	No of genotypes	Name of Genotype
Cluster-I	5	Bhudeb, Tulaipanji, Sathidhan, Sadanunia and GopalBhog
Cluster-II	2	Bardhan and Bhoi
Cluster-III	6	Srabani, Golaka, Udaygiri, Luna Sankhi, Khandagiri andMandakini
Cluster-IV	2	Daya and Sarasa
Cluster-V	2	Pyari and PS-4
Cluster-VI	2	CN-365 and WR-4-3
Cluster-VII	2	NC-678 and NC-1281

Cluster means of characters

Cluster means of twelve characters revealed that significant variability present among the genotypes chosen for study. Cluster means of each cluster is depiction of mean value of particular characters for genotypes present in that cluster. Character wise cluster mean values were presented in [Table-3]. Maximum plant heights were recorded by genotypes present in cluster-II, whereas shortest statured plants among the all genotypes in this study were observed in cluster-VI. Genotypes present in cluster-VII were noticed as earliest to flower. Cluster-V recorded for maximum 50% flowering values.

Table-3 *Mean values of seven clusters for 21 genotypes of rice (Oryza sativa L.).*

	Days to 50% flowering	Chla (mg/kg)	Chlb (mg/kg)	Chl a/b	Plant Height	No of tillers	No of effective tillers	1000 seed weight	No of filled grains	floret Steriity %	Dry weight(g)	Seed yield(g)
Cluster-I	96.133	1.946	0.675	2.860	108.980	10.800	10.663	25.411	93.273	27.013	22.389	17.982
Cluster-II	106.167	2.618	0.935	2.800	141.252	8.502	8.405	28.418	103.567	8.652	21.130	19.013
Cluster-III	101.333	1.890	0.61	3.188	108.918	7.417	6.208	23.962	87.146	32.908	29.766	15.824
Cluster-IV	104.167	2.032	0.697	2.908	102.085	8.874	8.874	21.398	73.585	28.127	22.865	18.232
Cluster-V	108.333	2.322	1.508	1.507	116.465	11.335	10.807	21.990	82.897	29.112	32.025	18.897
Cluster-VI	100.000	3.233	1.23	2.560	126.300	8.848	8.493	21.990	82.897	29.112	32.025	18.897
Cluster-VII	89.167	2.910	0.792	3.785	98.533	9.788	8.775	22.180	91.905	81.848	19.573	14.418
Overall mean	**100.757**	**2.421**	**0.921**	**2.801**	**114.647**	**9.366**	**8.889**	**23.621**	**87.895**	**33.824**	**25.681**	**17.609**

Maximum values for chlorophyll-a were observed in cluster-VI and lowest chlorophyll-a values recorded in genotypes present in cluster-III. Higher chlorophyll-b values were perceived in genotypes of cluster-V, whereas cluster-III has shown lowest phenotypic values for this character. Maximum and minimum Chlorophyll a/b ratios were recorded in cluster-III and cluster-V respectively. Number of tillers and effective tillers per plant observations recorded in cluster-V and Cluster-III as highest and lowest respectively. Genotypes present in cluster-II were recorded highest 1000 grain weights and genotypes of cluster VIII were lowest in this regard. Highest phenotypic values for No. of grains per panicle were observed in cluster-II. Interestingly, a member of same cluster genotypes has shown less floret sterility among all the genotypes in this cluster. Cluster -II also had highest seed yield per plant. Lowest values for No. of grains per panicle, floret sterility and seed yield were observed in cluster-IV, cluster VII and cluster-VII respectively. Maximum dry weights were shown in genotypes of cluster-V and cluster VI, whereas lowest was recorded against cluster VI.

Inter and intra cluster distances

According to d2 values, highest inter cluster distances were witnessed between cluster-III and cluster-V (18248.23), followed by cluster III and VII (11764.44), cluster V and VI (104.22.98). Lowest inter cluster distances were observed between cluster-II and cluster-VI (856.26), signifying close relationship among the genotypes of this group. Selection of parents from distant clusters would help in achieving highly heterotic hybrids or novel recombinants in segregating generations, suggested in rice by Ashok, *et al.* [3] and Sathish V. and Senapati B.K. [12]. Hence, genotypes present in Cluster-III *viz.,* Srabani, Golaka, Udaygiri, Luna Sankhi, Khandagiri, Mandakini were distantly related to the members of cluster-V(CN-365 and WR-4-3), choosing of parents from the members of these clusters could be recommended.

Highest intra cluster distance observed in cluster-VII, whereas cluster-II exhibited very less intra cluster distances. Therefore, it was evident that the genotypes in this cluster are less variable. Intra and inter cluster distance of 64 rice genotypes are showed in [Table-4].

Table-4 *Average intra (bold) and inter cluster D2 values among seven clusters in 21 rice genotypes*

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII
Cluster-I	**1320.15**	1420.46	8064.58	1404.15	6472.20	2048.65	2344.11
Cluster-II		**335.04**	10140.09	1977.05	4556.52	856.26	2528.78
Cluster-III			**589.37**	6240.84	18248.23	9674.69	11764.44
Cluster-IV				**1580.14**	7391.36	2337.14	3018.95
Cluster-V					**935.14**	3573.65	10422.98
Cluster-VI						**1386.07**	3915.13
Cluster-VII							**1820.13**

Character contribution towards divergence

Relative contributions of various characters under the study were presented in [Table-5]. Highest contribution towards divergence were recorded by number of filled grains per panicle(30%), followed by seed yield per plant(28.09), 1000 seed weight(19.04), floret sterility(7.14) and number of tillers per plant (4.76). All these characters together contributed more than 89% towards divergence. The remaining characters were observed as low contributors towards divergence. Therefore, during hybridization programmes maximum emphasis should be given to characters like number of grains per panicle, seed yield, 1000 grain weight.

Conclusion: It was concluded that emphasis should be given for characters like number of filled grains per panicle, 1000 seed weight, and for improvement of the rice yields by selecting the parents from cluster-III and Cluster-V might generate superior combinations in segregating generations.

Table-5 *Percent contribution of important characters towards diversity in rice genotypes*

CHARACTER	NO. OF FIRST RANK	% CONTRIBUTION
Days to 50% flowering	0	0.00
Chla (mg/kg)	4	1.90
Chlb (mg/kg)	4	1.90
Chl a/b	0	0.00
Plant Height(cm)	5	2.38
No of tillers	10	4.76
No of effective tillers	4	1.90
1000 seed weight(g)	40	19.05
No of filled grains	63	30.00
floret Steriity %	15	7.14
Dry weight(g)	6	2.86
Seed yield(g)	59	28.10
Total	210	100.00

Application of research: This article helps to identify genetically distant parents for hybridization programmes for crop improvement in rice.

Research Category: Genetic diversity in Crop improvement

Abbreviations: cm: centimetre, Df: degreed of freedom, mg:milli gram, kg:kilo gram, g:gram, *et al.*: et elia, *viz.*, videlicet.

*Research Guide: Dr Subhra Mukherjee
University: Bidhan Chandra Krishi Viswavidyalaya, Nadia, Mohanpur, 741252, West Bengal, India
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