RESEARCH ARTICLE

STUDIES ON GENETIC DIVERGENCE ANALYSIS FOR QUALITY TRAITS IN RICE (*ORYZA SATIVA* L.) GERMPLASM

Madhuri Singh, Prabharani Chaudhari*, Sandeep Bhandarkar and Ishu Kumar Khute

Department of Genetics and Plant Breeding, College of Agriculture,
Indira Gandhi Krishi Vishwavidyalaya, Raipur, 492012
Email: chau.prabha@gmail.com

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Abstract: Genetic diversity among fifty rice germplasm was evaluated analysis of variance revealed the presence of considerable amount of variability among the germplasm. Based on cluster analysis, the germplasm were grouped into five clusters. For quality characters, the cluster III constituted of 18 accessions, forming the largest cluster followed by cluster IV constituted of 14 accessions, Cluster V constituted of 8 accessions, Cluster I constituted of 6 accessions and Cluster II constituted of 4 accessions. This type of pattern of cluster group confirms the continuation of significant number of variability. The inter cluster distance was maximum between cluster II and V and minimum inter cluster distance was observed between cluster III and IV. Cluster II exhibited highest mean value for head rice recovery %, Cluster III exhibited highest mean value for endosperm content of amylose, Cluster IV exhibited highest mean value for hulling %, milling %, grain width, decorticated grain width, kernel width, alkali spreading value, Cluster V exhibited highest mean value for grain length, decorticated grain length, decorticated grain length width ratio, kernel length, kernel length width ratio. The germplasm falling in different clusters with high mean for hulling % and other component characters can be utilized for hybridization programme to obtain elite segregants. These traits hence could be focused for selection while improving grain yield.

Keywords: Genetic divergence, Cluster analysis, Yield attributes, Rice

INTRODUCTION

Rice is prime food crop of India, producing 43% of caloric requirement for more than 70% Indian population. Rice gives a great wealth of material for genetically studies because of its wide ecological distribution and enormous discrepancies encountered for multitudinous morphological and physiological characteristic. The Rice germplasm provide with ample of genetic diversity and a treasury of valuable genes. It is a rich pool of important genes that plant breeders can exploit for crop improvement (Yadav *et al*., 2013). It is the unique grain that is nearly entirely used as human food, unlike other cereals, which are also used extensively as feed (Swaminathan, 1999). Therefore, evaluation of rice germplasm is an important step for the fulfilment of human demand and options. Quality of rice may be considered from the view point of size, shape and appearance of grain, milling quality and cooking properties (Dela Cruz and Khush, 2000). The breeders and nutritionists seek rice grain with higher content of protein, vitamins and minerals.

In crop improvement program, genetic variability for agronomic traits as well as quality traits in almost all the crops is important, since this component is transmitted to the next generation (Singh, 1996). Study of genetic divergence among the plant materials is a vital tool to the plant breeders for an efficient choice of parents for plant improvement. Genetically diverse parents are likely to contribute desirable segregants and/or to produce high heterotic crosses. Parents identified on the basis of divergence for any breeding program would be more promising (Arunachalam, 1981). Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis' D 2 -statistic has proved to be a powerful technique (Murty and Arunachalam, 1966).

Genetic diversity is the pre-requisite for any crop improvement programme because it helps in the development of superior recombinants (Manonmani and Fazlullah Khan 2003), through selection of parents having wider variability for different characters (Nayak *et al.* 2004). Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence. A higher heterosis could be achieved from crosses between genetically distant parents (Falconer 1964). Therefore, the present investigation aimed to assess the nature and magnitude of genetic divergence present in the fifty-rice germplasm and to select suitable diverse genotypes as parents for further utilization in crop improvement program.

MATERIALS AND METHODS

Fifty indigenous rice germplasm were grown in randomized complete block design with two replications at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during

*Corresponding Author

Kharif 2018. Each entry was sown where row to row spacing was 20 cm and plant to plant spacing was 15 cm. Crop was raised following recommended package of practices. Observations were recorded on five randomly tagged plants of each genotype per replication. Data were recorded on 14 quality characters which includes Hulling (%), Milling (%), Grain length (mm), Grain width (mm), Grain length/width ratio, Decorticated grain length (mm), Decorticated grain width (mm), Decorticated grain L/W ratio, Kernal length (mm), Kernal width (mm), Kernal L/W ratio, Alkali spreading value, Endosperm content of amylase, Head rice recovery (%). In the current study, Euclidian distance between genotypes was estimated from the standardized data matrix by Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method and clustering was done by Agglomerative Hierarchical method using XLSTAT 2014 software.

RESULTS AND DISCUSSION

Analysis of variance was based on the mean values of quality traits observed for fifty rice germplasm (Table 1). The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied. This indicated presence of high variability among the genotypes, which provides ample scope for selection for different quality characters. The 50 germplasm accessions are distributed into 5 clusters. Between the clusters the accessions were not evenly distributed. The cluster II comprised of 17 accessions, followed by cluster IV constituted of 13 accessions, cluster I constituted by 9 accessions, cluster III cluster constituted of 6 and V cluster constituted 5 accessions. The pattern of collection proved the survival of remarkable amount of variability.

Inter and intra cluster distances among five clusters were computed and have been given in Table 3. The intra cluster distance ranged from 2.104 (cluster II) to 2.878 (cluster I). The inter cluster distance was maximum between cluster II and V (7.471) and minimum inter cluster distance was observed between cluster III and IV (2.404). To realize much variability and high heterotic effect, parents should be selected from two clusters having wider inter-cluster distance.

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4). Cluster II exhibited highest mean value for head rice recovery %, Cluster III for Endosperm content of amylase, Cluster IV for hulling %, milling %, grain width, decorticated grain width, kernel width, alkali spreading value and Cluster V exhibited highest mean value for grain length, decorticated grain length, decorticated grain length width ratio, kernel length, kernel length width ratio. These traits hence could be focused for selection while improving grain yield.

Table 1. Analysis of variance for different Quality characters

S. No.	Sources of variation	Mean sum of square		
		Replication	Treatment	Error
	Degree of freedom	(1)	(49)	(49)
1	Hulling (%)	0.43	213.52**	0.37
2	Milling (%)	0.031	222.35**	0.11
3	Grain length (mm)	0.21	1.38**	0.13
4	Grain width (mm)	0.17	0.18**	0.04
5	Grain lenth/width ratio	0.027	0.32**	0.012
6	Decorticated grain length(mm)	0.0029	1.23**	0.12
7	Decorticated grain width(mm)	0.22	0.204**	0.098
8	Decorticated grain L/W ratio	0.088	0.32**	0.033
9	Kernal length(mm)	0.608	0.84**	0.14
10	Kernal width(mm)	0.15	0.12**	0.047
11	Kernal L/W ratio	0.072	0.14**	0.022
12	Alkali spreading value	0	1.39**	0.46
13	Endosperm content of amylase	0.031	48.56**	10.55
14	Head rice recovery (%)	7.44	311.39**	4.2

(Note- ** Significant at 1% level of probability, * Significant at 5% level of probability)

Table 2. Distribution of 50 germplasm accessions among five clusters for quality characters

Cluster no.	No. of genotypes in each cluster	Name of genotypes
I	6	Hundar, R-RKM-1, Laycha, IR-64, MTU-1010, Zinc rice-2
II	4	Kalajeera, Jauphool, Tilkasturi, Chaptimathyala,
III	18	Karanga, Lal banko, Raj banko, Karela, Lal dhan, Parra, Davar, Barhasal, Kujjii, Karangi, Sendursingha, Bhejari, Baisoor, Resari, Soth, Karhani, Swarna, Madhuraj dhan-55
IV	14	Nagpurigurmatiya, Khutbuti, Sathaka, Nagkeshar, Sathaka, Korma, Parwatkala, Paveetra, Krishnanjan, Gathuwan, Danwar, Suldhan, Mehardhan, Cheptigurmatiya
V	8	Ramshri, Kali much, Sathi, Aalcha, Bora, Maharaji, Saraiphool, Zinc rice-1

Table 3. Distance between cluster centroids (intra and inter cluster D^2 values)

Cluster	I	II	III	IV	V
I	**2.878**	7.271	3.72	5.577	3.866
II		2.104	5.681	5.298	7.471
III			**2.524**	2.404	3.993
IV				**2.204**	4.561
V					**2.485**

Table 4. Cluster mean values of five clusters for different quality characters

Class	H(%)	M(%)	GL(mm)	GW(mm)	GLWR	DGL(mm)	DGW(mm)	DGLWR	KL(mm)	KW(mm)	KLWR	ASV	ECA	HRR(%)
I	49.61	40.99	8.65	2.76	3.13	6.95	2.44	2.82	5.85	2.56	2.32	3.17	20.08	14.73
II	69.99	64.4	5.98	2.78	2.18	4.62	2.4	1.98	4.34	2.25	1.83	2.62	15.97	**38.51**
III	67.62	55.35	8.39	3.11	2.71	6.52	2.89	2.25	5.53	2.7	2.04	3.06	**23.07**	20.01
IV	**76.87**	**68.63**	8.06	**3.24**	2.49	6.27	**2.9**	2.14	5.6	**2.73**	2	**3.64**	22.75	37.9
V	74.26	66.1	**8.84**	2.81	**3.18**	**7.24**	2.56	**2.93**	**6.52**	2.51	**2.53**	2.81	20.29	28.91

Note – H(%) =Hulling percentage, M(%)= Milling percentage, GL= Grain length, GW= Grain width, GLWR= Grain length width ratio, DGL= Decorticated grain length, DGW= Decorticated grain width, DGLWR = Decorticated grain length width ratio, KL= Kernel length, KW = Kernel width, KLWR= Kernel length width ratio, ASV= Alkali spreading value, ECA = Endosperm content of amylase, HRR%= Head rice recovery percentage.

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