

Variability and Diversity Studies in Rain-fed Rice (*Oryza sativa* L.)

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Forty four indica rice cultivars were evaluated under rain-fed condition for sixteen quantitative traits to examine the nature and magnitude of variability and genetic divergence. Among all the traits grain yield per plant exhibited highest estimate of PCV (29.11) and GCV (28.48) followed by filled grains/panicle and effective tillers/plant. Broad sense heritability (98.90) was highest for chlorophyll content followed by grain length and grain breadth. On the basis of D^2 analysis 44 rice genotypes were grouped into nine clusters and three ungrouped clusters. Cluster I was the largest and contained 22 genotypes. Rest of the clusters contained 2-3 genotypes. The genotype belonging to ungrouped cluster X, namely, NDR 1130-1 showed promise for early maturity, long grain size and grain yield/plant. The highest intra-cluster distance was observed in cluster IX, containing two genotypes differing mainly for maturity and grain yield/plant. The most distant clusters were Cluster IV and ungrouped cluster XII. The genotypes of cluster IV showed promise for rain-fed condition with regard to days to maturity, effective tillers/plant, grain yield/plant and chlorophyll content. Contribution (%) towards the total divergence was maximum through grain breadth followed by chlorophyll content, grain length and total tillers/plant.

Key Words: D^2 analysis, Variability, Heritability, Rice, Clusters

Introduction

Rice (*Oryza sativa* L.) is the most important cereal food crop of the world and about 90 per cent of the people of South-East Asia consume rice as staple food. According to FAO, the productivity level of rice in India is very low (3.21 t/ha) as compared to the average productivity of the China (6.35 t/ha) and world (4.15 t/ha) (Anonymous, 2008). Further, a majority of area under rain-fed rice cultivation suffer from poor productivity due to lack of promising rice cultivars under such eco-climatic condition. Thus, in order to improve the productivity level, a breakthrough would be desirable by way of increasing biological efficiency through hybridization and the productivity of new varieties suited to rain-fed condition. Perhaps there is no other single crop possessing as enormous variation as in rice. However, due to the ever-increasing demand of food grains, there is still a great scope to develop rice varieties suited to rain-fed conditions for higher production. The success of this to a large extent would depend on the exploitation of existing variability and therefore it is desirable to collect, evaluate and utilize the available diversity to suit specific need with regards to specific ecosystem. Study of variability parameters and D^2 -statistics are expected to provide reliable basis for selecting out desirable elite and diverse parents for hybridization and exploitation of variability. Grouping of genotypes on the basis of D distance finally provides a

clear picture about the inter-relationship of the genotypes and helps to pick up appropriate genotype.

Materials and Methods

The experimental material comprised of 44 rain-fed rice genotypes obtained from Directorate of Rice Research Institute, Hyderabad. These genotypes were evaluated in Completely Randomized Block Design with three replications during Kharif 2008-2009 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The crop was directly seeded under the rain-fed condition on 16th June, 2008. Each plot consisted of three rows of 2.25 m length. Spacing was maintained at 15 × 10 cm excluding the artificial irrigation; the normal recommended agronomic practices were followed. Fertilizers were applied at the rate of 60 Kg N₂, 40 Kg P₂O₅ and 30 Kg K₂O per hectare. Ten plants from the middle row of each entry in each replication were randomly taken for recording observations on grain yield and 15 yield attributing traits namely, days to first panicle initiation (DI), days to 50% flowering (DF), Days to 75% maturity (DM), total tillers plant⁻¹ (TN), total effective tillers plant⁻¹ (TE), plant height (PH), length of flag leaf (LF), breadth of flag leaf (BF), panicle length (PL), filled grains panicle⁻¹ (FG), fertility per cent (F%), grain weight (GW), grain length (GL), grain breadth (GB), grain yield plant⁻¹ (GY) and chlorophyll content (CL). Plot means were used for statistical analyses. Analysis of variance and variability parameter were estimated following Panse and Sukhatme (1985).

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Mahalanobis (1936) D^2 -statistics was employed to measure the genetic distance between genotypes. The genotypes were grouped in to possible number of clusters by Tocher's method as described by Rao (1952).

Results and Discussion

(A) Analysis of Variance, Range, Mean, Variability, Heritability, Genetic Advance, Phenotypic and Genotypic Coefficient of Variation

The analysis of variance for 16 traits including grain yield and its related traits in the present set of rice genotypes revealed significant differences for most of the traits. This suggested that there is an inherent genetic difference among the genotypes. Similar finding for various traits in the rice genotypes were also reported by many rice workers (Akter *et al.*, 2004 and Singh *et al.*, 2007). The estimates of range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance are presented in Table 1. Considerable range of variation was observed for all the traits under study indicating enough scope for bringing about improvement in the desirable direction. Some genotypes showed promise for more than one character viz., RAU 3036 recorded it for fertility per cent, grain yield per plant, and chlorophyll content. Rewa 691 IR 78908-1015 had maximum mean grain yield per plant followed by Rewa 673-RR 418. Both PCV and GCV estimates were highest for grain yield per plant (29.11/28.48) followed by filled grain per panicle (25.87/24.71) and total number of effective tillers per plant (24.57/24.37). Lowest magnitude of PCV was recorded for grain length (8.03) followed by panicle length (8.31). The differences between PCV and GCV were very small for most the traits indicating lesser contribution of

environmental variation towards expression of these traits. Similar observations were also recorded by Karad and Pol (2008) in rice genotypes. The Broad sense heritability was highest for the chlorophyll content (98.9%) followed by both grain length and grain breadth (98.7%). Madhaviatha *et al.* (2005) studying with 54 rice genotypes reported high broad sense heritability for kernel L/B ratio. Genetic advance as percent of mean was, highest for grain yield per plant (57.40) followed by total number of effective tillers per plant (49.79), filled grain per panicle, effective tillers and grain weight. High heritability coupled with high genetic advance as percent of mean in the in the present set of rice genotypes was recorded for total number of tillers per plant, total number of effective tillers per plant, grain yield per plant and filled grain per panicle indicating predominance of additive gene effects and the possibilities of effective selection for the improvement of these traits. This is in consonance with the reports of Singh *et al.* (2007) in a variability study of 117 diverse rice lines. The characters like panicle length and grain length recorded high heritability but poor genetic advance which may be due to comparatively more non-additive gene effects. Hence selection would not be much effective for such characters. Similar report was also made by Satyanarayana *et al.* (2005).

(B) Genetic Divergence

χ^2 test applied to 'V' statistic was significant, indicating significant difference between the means in respect of pooled effect of 16 traits under study and between different populations. Forty four genotypes in the present study could be grouped into nine distinct clusters and three ungrouped clusters on the basis of Tocher's method of clustering utilizing D^2 values. Clustering pattern indicated that 22 out of 44 genotypes belonged to a single cluster

Table 1. Variability parameters for 16 traits in 44 genotypes of rice

Parameter		Traits															
		DI	DF	DM	TN	TE	PH	LF	BF	PL	FG	F%	GW	GL	GB	GY	CL
Range	Min.	63.00	66.33	88.67	7.00	6.10	75.13	23.61	0.96	20.59	64.33	50.16	9.93	5.83	1.50	6.60	23.03
	Max.	105.00	109.67	133.00	20.10	18.40	158.67	53.59	1.85	29.30	168.33	94.67	27.20	8.10	2.97	34.54	44.73
Mean		78.80	82.06	103.47	10.71	9.50	103.54	34.56	1.30	25.43	104.01	74.28	19.87	6.90	2.17	19.25	35.35
SEm (±)		1.317	1.395	1.197	0.244	0.238	2.254	1.468	0.039	0.653	6.491	4.019	0.953	0.051	0.025	0.950	0.359
PCV (%)		14.20	13.72	11.39	23.81	24.57	16.95	17.69	14.23	8.31	25.87	14.69	19.05	8.03	12.60	29.11	11.64
GCV (%)		14.06	13.57	11.30	23.65	24.37	16.74	16.90	13.74	7.69	24.71	13.12	18.13	7.98	12.52	28.48	11.57
Heritability (%)			97.9	97.7	98.5	98.6	98.4	97.5	91.4	93.3	85.7	91.3	79.7	90.5	98.7	98.7	95.7
98.9																	
Genetic advance (K= 2.06)		22.58	22.67	23.91	5.18	4.73	35.25	11.50	0.36	3.73	50.59	17.91	7.06	1.13	0.56	11.05	8.38
Genetic advance (% of mean)		28.65	27.63	23.11	48.37	49.79	34.04	33.28	27.69	14.67	48.64	24.11	35.53	16.38	25.80	57.40	23.71

i.e. cluster I. On the other hand, cluster II, III and IV comprised three genotypes each and cluster V, VI, VII, VIII and IX comprised two genotypes each. Three of the forty four genotypes namely NDR 1130-1, NDR 8588 (IR77770-115-MFT-B-47-6) and RAU 3036 were ungrouped and belonged to ungrouped clusters, X, XI and XII, respectively. Genotype NDR 1130-1 had highest 1000-grain weight and the longest grain length was observed for the genotype belonging to ungrouped cluster XI followed by the genotype of ungrouped cluster X (Table 3). Intra and inter-cluster distances ($\sqrt{D^2}$) among nine clusters and three ungrouped clusters have been presented in Table 2. Highest intra-cluster distance was observed for cluster IX (30.23) which comprised two genotypes differing mainly for plant height, flag leaf length, filled grains per panicle and grain yield per plant. The genotype Rewa 691 IR 78908-1015 belonging to this cluster on the basis of *per se* performance was recorded as highest yielder with early maturity and thus showed promise for rain-fed condition. The highest inter-cluster

distance (67.56) was found between cluster IV and ungrouped cluster XII followed by inter-cluster distance between cluster IV and cluster V (59.04) and between cluster V and VII (58.50). The genotypes of the most distant cluster and ungrouped cluster i.e. cluster IV and XII were quite contrasting in performance with respect to grain yield per plant and chlorophyll content. The genotypes of cluster IV showed promise with regard days to maturity, effective tillers number, grain yield per plant & chlorophyll content (Table 3). The contrasting genotypes of these two clusters are expected to yield desirable segregants on hybridization following single plant selection in later generations, suitable for rain-fed condition with early maturity and high yield potential. The smallest inter cluster distance (28.17) was observed between cluster III and ungrouped cluster X which differed mainly for the characters grain length and grain yield per plant. The small inter cluster distance indicates less diversity between the genotypes contained in these clusters. However, these genotypes can be undertaken for hybridization in order

Table 2. Average Intra and Inter-cluster " D^2 -values among twelve clusters of 44 rice genotypes

I. Clusters											
25.19	35.68	34.56	39.72	42.82	36.12	32.42	29.97	30.90	32.02	29.92	44.03
28.39	36.07	52.63	44.89	34.38	35.82	40.67	42.14	40.76	37.02	47.20	
26.39	47.47	41.42	44.49	43.92	37.02	34.90	28.17	39.56	57.33		
26.67	59.04	57.94	42.96	45.69	37.83	40.88	51.24	67.56			
28.31	46.32	58.50	53.97	47.15	35.91	45.60	43.38				
14.83	37.96	36.05	39.07	51.17	44.17	41.24					
25.70	30.52	39.81	47.35	37.45	55.05						
24.36	32.21	44.37	37.75	54.92							
30.23	36.12	45.10	54.53								
0.00	31.85	50.13									
0.00	36.85										
0.00											

Cluster numbers X to XII are assigned to ungrouped genotypes

Table 3. Cluster mean values for different traits

Clusters	DI	DF	DM	TN	TE	PH	LF	BF	PL	FG	F%	GW	GL	GB	GY	CL
	76.61	79.78	101.42	10.66	9.54	103.48	33.81	1.28	25.92	100.44	74.04	20.36	6.96	2.11	19.15	34.85
	99.67	103.89	125.89	9.48	8.26	89.47	35.47	1.36	23.73	105.73	69.44	19.27	7.04	2.27	16.73	37.46
	67.89	71.56	93.67	9.46	7.93	108.01	38.59	1.48	25.285	113.16	75.08	21.73	6.96	2.66	19.82	38.57
	70.00	73.44	93.22	17.83	16.00	96.00	30.54	1.17	23.22	76.18	78.54	21.27	6.81	2.17	25.91	39.19
	86.67	89.17	107.17	8.98	7.55	156.67	43.47	1.61	26.00	118.70	77.88	22.80	7.13	2.72	20.45	29.05
	94.50	97.83	119.67	8.00	7.70	98.27	41.50	1.58	24.83	161.20	64.46	12.80	5.92	2.00	16.28	31.95
	90.33	92.50	115.17	11.48	10.08	89.80	30.07	1.22	27.41	114.83	63.55	15.90	6.92	1.75	18.50	41.35
	68.33	70.50	90.33	9.30	7.90	97.42	34.07	1.16	22.39	85.27	92.07	19.30	6.35	2.00	13.79	39.15
	67.17	70.50	96.17	11.80	10.83	102.90	30.48	1.32	24.93	117.10	88.23	21.40	5.98	2.32	27.30	34.13
	67.67	74.00	93.33	11.30	9.40	112.57	35.01	1.41	26.58	118.53	77.14	23.40	7.77	2.50	26.25	33.60
	84.67	86.67	104.33	8.00	7.20	90.30	36.03	0.97	26.93	93.93	70.36	18.73	8.10	2.00	13.05	34.90
	102.67	107.33	128.33	7.900	6.90	105.87	32.57	1.05	27.43	74.93	50.16	12.93	7.43	2.00	6.60	23.03
% (**)	6.34	0.00	3.80	15.33	0.32	5.40	0.32	0.53	0.32	0.21	0.00	0.74	19.98	23.04	1.70	21.99

DI = Days to first panicle initiation, DF = Days to 50% flowering, DM = Days to 75% maturity, TN = Total tillers plant⁻¹, TE = Total effective tillers plant⁻¹, PH = Plant height (cm), LF = Length of flag leaf (cm), BF = Breadth of flag leaf (cm), PL = Panicle length (cm), FG = Filled grains panicle⁻¹, F% = Fertility %, GW = Grain weight (g), GL = Grain length (mm), GB = Grain breadth (mm), GY = Grain yield plant⁻¹ (g), and CL = Chlorophyll content. ** = Contribution of traits towards divergence.

to exploit variability for the specific characters for which the genotypes of the two clusters showed marked difference. The genotypes contained in cluster V, VIII and ungrouped cluster XII seem to be quite promising for many of the yield attributing traits under study such as, flag leaf length, flag leaf breadth, grain weight, chlorophyll content etc. Percentage contribution of the individual character towards divergence was maximum through grain breadth (23.04 %) followed by chlorophyll content (21.99%), grain length (19.98) and total number of tillers per plant (15.33%). More than 75 per cent contribution towards total divergence was mainly because of these four characters. Kole (2000) reported that the characters grain length, panicle number, grain weight and days to flowering were the major contributing traits to total diversity in a set of 20 Aromatic rice genotypes. It is observed that the genotypes desirable for different traits belonged to different clusters. The selection of diverse genotypes with desirable traits and intercrossing them for multiple crossing programme amongst themselves is expected to be effective in accumulation of favorable genes for bringing together different desirable traits in to the common genetic background. Thus, an improved genotype suitable for rain-fed ecosystem can be developed by utilizing such diverse genotypes in rice.

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