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# STUDY OF GENETIC VARIABILITY AND D<sup>2</sup> ANALYSIS IN ELITE RICE GENOTYPES

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## ABSTRACT

An investigation was carried out with 32 elite rice genotypes to identify diverse genotypes. They were evaluated for thirteen yield and yield attributing characters *viz.* days to 50 percent flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, flag leaf length, flag leaf width, number of spikelets per panicle, days to maturity, biological yield, test weight, harvest index and grain yield per plant using Mahalanobis  $D^2$  statistics. The analysis of variance revealed significant differences among the genotypes for all the characters studied. On the basis of  $D^2$  values the genotypes were grouped into six clusters. Cluster I and VI was the largest containing 8 genotypes followed by cluster IV with 6 genotypes. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The maximum intercluster distance was recorded between clusters V and VI and the maximum intra-cluster distance was found in cluster IV followed by I. The characters like number of number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 percent flowering contributed maximum towards genetic diversity. Hence these characters could be given due importance for selection of genotypes for further crop improvement programme.

Keywords: GCV, PCV, Genetic Variability, D<sup>2</sup> Analysis

# INTRODUCTION

Rice (Oryza sativa L.) is the prime food crop of the world for more than half of the global populations. India is the second largest producer and consumer of rice next to China. As the population is increasing alarmingly, it is projected that the demand of rice in 2025 A.D. would be 140mt as against the production of about 131.9 mt. Hence, in order to meet the indispensable demand, improvement through genetic manipulation is the only way. The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent (Daniel, 2000). Even though self pollinated crops are highly homozygous there is every possibility of genetic variation among the parents collected from different eco-geographical regions (Vennila et al., 2011). In the present study, an attempt was made to assess the genetic divergence using Mahalanobis  $D^2$  statistics and different clustering procedures, based on yield and quality characters and assessing the relative contribution of different components to total divergence. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different yield and quality characters (Sarawgi and Rita Binse, 2007). The available diversity in the germplasm also serves as an insurance against unknown future needs and conditions, thereby contributing to the stability of farming systems at local, national and global levels (Singh et al., 2000). Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population. The  $D^2$  statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, it helps to quantify the degree of divergence between populations and to choose genetically diverse parents for obtaining desirable recombination (Thomas and Lal, 2012).

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## MATERIALS AND METHOD

The experimental material for the study comprised of 32 genotypes laid in randomized block design (RBD) with three replications at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad (U.P.), during Kharif, 2013. The seedlings were transplanted to main field 20cm apart between rows and 15cm within the row. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per plant, number of panicles per plant, panicle length (cm), spikelets per panicle, flag leaf length (cm), flag leaf width (cm), biological yield (g), harvest index (%), test weight (g), grain yield per plant (g) and observations on days to 50% flowering and days to maturity were recorded on plot basis. The analysis of variance was carried out for all the characters and then data was analyzed following multivariate analysis of Mahalanobis (1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

## **RESULTS AND DISCUSSION**

A wide range of variation was observed among 32 elite rice (Oryza sativa L.) genotypes for thirteen quantitative characters. The perusal of data revealed that variance due to treatment was significant for all the characters exhibited by the genotypes. Significant genetic variation in various component characters might be effective. Phenotypic variance was higher than genotypic variance for all the characters thus indicated the influence of environment factor on these traits. Similar findings were earlier reported by Devi et al., (2006) and Prajapati et al., (2011). Among coefficient of variation, phenotypic coefficient of variation (PCV) estimates highest for grain yield (29.59) followed by number of spikelets per panicle (26.74) and biological yield per plant (25.40). Lowest estimation of phenotypic coefficient of variation was observed for days to maturity (4.92) and days to 50% flowering (6.35). And highest genotypic coefficient of variation (GCV) was estimated for grain yield (27.58) followed by number of spikelets per panicle (25.67) and biological yield per plant (23.80). Lowest estimates of genotypic coefficient of variation were observed for days to maturity (4.15) and days to 50% flowering (5.64). The coefficient of variation doesn't offer the full scope of heritable variation. It can be find out with greater degree of accuracy when heritability is conjunction with genetic advance study. Heritability and genetic advance were determined to study the scope of improvement in various characters through selection. Heritability and genetic advance are important selection parameters. High heritability estimates along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johanson et al., 1955). Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. High estimates of heritability in broad sense were recorded for all the thirteen characters under study, which ranges from 18.00% (flag leaf width) to 92.17% (number of spikelets per panicle). High heritability was observed for number of spikelets per panicle (92.17%), biological yield (87.79%), grain yield per plant (86.84%), days to 50% flowering (78.77%), test weight (77.34%), harvest index (72.38%), days to maturity (70.21%) number of panicles per plant (68.42%) and number of tillers per plant (64.60%), which suggested that these traits would respond to selection owing is their high genetic variability and transmissibility (Table 1). Similar inding was earlier reported by Anandrao et al., (2011). While moderate estimates were observed for plant height (47.81%) and lowest estimates of heritability was observed for flag leaf width (18.00%). A perusal of genetic advance for all the quantitative characters under study ranged from 0.07 (flag leaf width) to 99.83 (number of spikelets per panicle). High genetic advance was observed for number of spikelets per panicle (99.83) and biological yield (28.95). Grain yield per plant (12.85), plant height (12.67) harvest index (12.38) and days to 50% flowering (10.27) show moderate genetic advance. Lowest genetic advance was observed for flag leaf width (0.07) followed by panicle length (2.92), number of tillers per plant (3.51), number of panicle per plant (3.63), flag leaf length(5.39), test weight (7.04) and days to maturity (9.17). Vivek et al., (2005) also

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reported similar findings. High heritability coupled with high genetic advance was registered for number of spikelets per panicle, biological yield, grain yield per plant, test weight and harvest index suggesting predominance of additive gene action in the expression of these traits. The thirty two genotypes under study were grouped into six clusters using Mahalanobis  $D^2$  analysis (Table 2). Cluster I and VI consist of 8 genotypes forming the largest cluster followed by cluster IV (6 genotypes), clusters III (5 genotypes), Cluster II (3 genotypes) and cluster V (2 genotypes). The pattern of group constellation proved the existence of significant amount of variability.

Characters	$V_{g}$	Vp	Coefficient	of variation	h <sup>2</sup> (bs) (%)	GA	GA as (%)
	0	-	PCV (%)	GCV (%)			
Days to 50% flowering	31.58	40.09	6.35	5.64	78.77	10.27	10.31
Plant height	79.18	165.60	11.01	7.62	47.81	12.67	10.85
Flag leaf length	9.76	13.90	10.04	8.41	70.21	5.39	14.51
Flag leaf width	0.01	0.04	12.86	5.46	18.00	0.07	4.78
Number of tillers/ plant	4.49	6.95	19.66	15.80	64.60	3.51	26.17
Number of Panicles/ plant	4.53	6.62	20.57	17.01	68.42	3.63	28.99
Panicle length	2.84	4.03	7.58	6.37	70.47	2.92	11.02
Number of Spikelets/ panicle	2547.90	2764.13	26.74	25.67	92.17	99.83	50.78
Days to maturity	27.79	39.00	4.92	4.15	71.25	9.17	7.22
Biological yield/ plant	224.98	256.27	25.40	23.80	87.79	28.95	45.93
Harvest index	49.89	68.92	21.38	18.19	72.38	12.38	31.89
Test weight	15.09	19.51	19.73	17.35	77.34	7.04	31.44
Grain yield/ plant	44.83	51.62	29.59	27.58	86.84	12.85	52.94

Table 1: Estimation	of components	of varianc	e and geneti	c parameters	for 13	characters	in 1	rice
germplasm								

## Table 2: Distribution of 32 genotypes of rice into different clusters

Cluster	Cluster number	Cluster members
Ι	8	NWGR-6072,KMP-128,TRC 2008-6,LALAT,SKL-3-27-19-31-55-11,CR -2706,TRC 2008-
		5, PAU 3879-87-1-1
II	3	CB 08-534,CRK-27,NP-128
III	5	UPR 3528-12-1-12,RP 5212-56-12-9-3-2-1-1,RP 5213-69-3-3-4-1-2-B,OR 1946-2,IR-64
IV	6	JGL-18065,NP-6226, CR 2641-30,CN 1446-5-8-17-1 MLD4,NDR-359
V	2	CR 2644-2-6-4-3-2,R 1535-1382-1-1667-1
VI	8	ORJ-7,KJT 20-3-35-1-17,KJT 15-1-36-5-23-16,OR 2324-25-16,NDR 370133,UPR 3413-8-
		2-1,NVSR-178,CR 2701-1-47-IR 84882-B-120

The intra cluster distance ranged from 22.84 (cluster I) to 30.54 (cluster IV). The inter cluster distance was maximum between cluster V and VI (209.32) and minimum inter cluster distance was observed between cluster I and cluster II (33.53), Thomas and Lal (2012). To realize much variability and high heterotic effect, recommended that parents should be selected from two clusters having wider inter cluster distance (Table 3). The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4). Cluster IV exhibited highest mean value for grain yield per plant, biological yield and flag leaf width, while cluster VI contained genotypes with highest mean value for number of tillers per plant, number of panicles per plant, flag leaf length, panicle length and test weight. Cluster V recorded highest value for spikelets per panicle while highest mean value for grainty to 50% flowering and days to maturity was recorded by cluster II. Cluster I had highest value for plant height, while cluster III recorded highest mean values for harvest index. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004). The highest contribution in manifestation of genetic divergence was exhibited by number of spikelets per panicle (21.17%), biological yield per plant (20.77%), test weight (15.93%), harvest index (13.10%) and days to 50 percent flowering (10.08%), Ovung *et al.*, (2012). In other words, selection for these characters may be

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rewarding (Table 5). The results concluded that characters like number of spikelets per panicle, biological yield, grain yield per plant, test weight and harvest index show high heritability coupled with genetic advance as percent of mean therefore should be given top priority during selection. Further cluster V and cluster VI were most diverse to each other. These clusters are suggested to provide a broad spectrum of variability in segregating generations and the genotypes present in them may be used as parents for future hybridization programme to develop desirable types.

Tuble 5. Average mita (bold) and met cluster distance (b) values									
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI			
Cluster I	22.845	33.538	38.134	100.457	85.492	62.406			
Cluster II		0.000	46.940	116.972	111.575	79.531			
Cluster III			0.000	94.860	100.395	63.832			
Cluster IV				30.544	71.731	184.893			
Cluster V					0.000	209.329			
Cluster VI						0.000			
							_		

#### Table 3: Average intra (bold) and inter cluster distance (D) values

#### Table 4: Mean values of 6 clusters for 13 morphological characters in 32 rice genotypes

					1	0			0	11		
Days to	Plant	Flag Leaf	Flag	Tillers	Panicles/	Panicle	Spikelets/	Days to	Biological	Test	harvest	Grain
50%	Height	Length	Leaf	/Plant	Plant	Length	Panicle	Maturity	Yield/	Weight	Index	Yield
Flowering	(cm)	(cm)	Width			-		-	Plant	(g)		(g)
99.76	119.02	37.29	1.55	13.25	12.45	26.41	187.01	127.00	60.61	23.19	37.56	22.66
110.66	94.94	28.48	1.26	14.20	13.40	27.37	132.00	138.00	61.36	17.50	37.80	23.22
101.66	100.30	34.14	1.55	12.26	9.80	26.28	202.93	125.13	52.85	23.08	67.93	35.39
99.66	118.94	37.14	1.71	13.90	12.93	25.48	308.46	128.83	105.98	15.52	38.30	39.77
93.33	110.34	34.61	1.47	12.96	12.20	25.13	355.60	121.66	47.94	16.84	33.20	15.86
90.33	100.66	47.49	1.27	17.26	15.26	30.78	121.86	119.33	66.90	25.10	50.23	33.62
	Days to 50% Flowering 99.76 110.66 101.66 99.66 93.33 90.33	Days toPlant50%HeightFlowering(cm)99.76119.02110.6694.94101.66100.3099.66118.9493.33110.3490.33100.66	Days toPlantFlag Leaf50%HeightLengthFlowering(cm)(cm)99.76119.0237.29110.6694.9428.48101.66100.3034.1499.66118.9437.1493.33110.3434.6190.33100.6647.49	Days to 50%Plant HeightFlag Leaf LengthFlag LeafFlowering(cm)(cm)Width99.76119.0237.291.55110.6694.9428.481.26101.66100.3034.141.5599.66118.9437.141.7193.33110.3434.611.4790.33100.6647.491.27	Days to 50%Plant HeightFlag Leaf LengthFlag Leaf LeafTillers /PlantFlowering 99.76(cm)(cm)Width99.76119.0237.291.5513.25110.6694.9428.481.2614.20101.66100.3034.141.5512.2699.66118.9437.141.7113.9093.33110.3434.611.4712.9690.33100.6647.491.2717.26	Days to 50%Plant HeightFlag Leaf LengthFlag LeafTillers /PlantPanicles/ PlantFlowering 99.76(cm)(cm)Width99.76119.0237.291.5513.2512.45110.6694.9428.481.2614.2013.40101.66100.3034.141.5512.269.8099.66118.9437.141.7113.9012.9393.33110.3434.611.4712.9612.2090.33100.6647.491.2717.2615.26	Days to 50%Plant HeightFlag Leaf LengthFlag LeafTillers Panicles/Panicles/ Panicle50% HeightLength (cm)Leaf (PlantPlant PlantPlant Length99.76 119.02119.02 37.2937.29 1.5513.25 13.2512.45 13.4026.41 27.37 21.66101.66 99.66100.30 118.9434.14 37.141.55 1.71 13.9012.93 12.9325.48 25.48 25.13 90.3390.33100.66 47.4947.49 1.271.26 17.2615.26 15.2630.78 30.78	Days to 50%PlantFlag Leaf LengthFlag LengthTillers LeafPanicles/ PlantPanicleSpikelets/ PanicleFlowering 99.76(cm)(cm)WidthPlantPlantLengthPanicle99.76119.0237.291.5513.2512.4526.41187.01110.6694.9428.481.2614.2013.4027.37132.00101.66100.3034.141.5512.269.8026.28202.9399.66118.9437.141.7113.9012.9325.48308.4693.33110.3434.611.4712.9612.2025.13355.6090.33100.6647.491.2717.2615.2630.78121.86	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	$ \begin{array}{c c c c c c c c c c c c c c c c c c c $

#### Table 5: Relative contribution of different characters to genetic divergence

Source	Contribution %
1 Days to 50% Flowering	10.08
2 Plant Height(cm)	0.81
3 Flag Leaf Length (cm)	4.03
4 Flag Leaf Width	0.20
5 Tillers/ Plant	2.22
6 Panicles/ Plant	0.00
7 Panicle Length	8.87
8 Spikelets/ Panicle	21.17
9 Days to Maturity	2.42
10 Biological Yield/ Plant	20.77
11 Test Weight (g)	15.93
12 harvest Index	13.10
13 Grain Yield (g)	0.40

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