



# GENETIC DIVERGENCE STUDIES OF ELITE GERMPLASM ACCESSIONS OF RICE (*ORYZA SATIVAL.*)

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## Abstract

The present investigation was conducted to examine the genetic diversity existing among 100 genotypes of rice, during kharif 2014 under randomized block design with two replications. The data were recorded for fifteen quantitative characters to obtain estimates of variability, heritability, genetic advance and genetic divergence. Significant differences were observed among the genotypes for all the characters studied. High estimates of GCV and PCV were observed for grain yield per plant and biological yield. High heritability coupled with high genetic advance as per cent of mean was observed for ear bearing tillers, number of grains /panicle, biological yield, test weight and grain yield / plant. Hundred genotypes were grouped into eleven heterogeneous clusters. Among these clusters, Cluster I had maximum number of genotypes (66 genotypes) Cluster IV is the second largest with 16 genotypes followed by cluster II including 10 genotypes. test weight, Days to 50 % flowering, plant height, number of Grains per panicle, Grain yield/ plant, biological yield and earbearing tillers should be given top priority for effective selection. The present investigation revealed that Cluster I and IV are most diverse to each other and the genotypes constituted in these clusters may be used as parents for future hybridization.

**Key words:** Genetic advance, GCV, Heritability, PCV, Genetic diversity.

## Introduction

Rice is one of the most important food crop and a primary food source for more than one third of world's population. More than 90 per cent of the world's rice is grown and consumed in Asia, known as rice bowl of the world, where 60 percent of the earth's people and two thirds of world's poor live. Globally it is cultivated in an area of 161.8 m ha with an annual production of about 748.0 million tones and an average productivity of 4.6 t ha<sup>-1</sup> (FAO, 2016). India ranks first in the world in area of rice cultivation with 43.97 million ha and second in production with 104.32 million tons (Directorate of Economics & Statistics (D & ES 2016-17). The basic objective of this crop improvement programs is to realize a marked improvement in crop yield through various breeding methods. For planning and execution of a successful breeding program, the most essential prerequisite is the availability of substantial desirable genetic variability for *important* characters in the germplasm collections of the plant species. Information on the nature and degree of genetic divergence would help the plant

breeder in choosing the right parents for breeding programme. (Vivekananda and Subramanian, 1993). The D<sup>2</sup> technique is based on multivariate analysis developed by Mahalanobis (1936) had been found to be a potent tool in quantifying the degree of divergence in germplasm. It is therefore logical to assess the genetic divergence in the available germplasm, as the importance of genetic diversity for successful selection of parents to be used in hybridization has been emphasized earlier (Soni *et al.*, 1999; Bansal *et al.*, 1999). The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype.

## Materials and Methods

The material for the present study comprised 100 rice germplasm accessions evaluated in a randomized block design at Research Farm of Department of Genetics and Plant Breeding, SHUATS, Allahabad during

*khariif*, 2014. Twenty five days old seedlings were transplanted with 20 cm × 15 cm spacing. All the standard packages of practices were followed to raise a good and healthy crop. In each entry, five random plants were selected, data recorded on fourteen quantitative traits *viz.*, days to 50% flowering, plant height, flag leaf length, flag leaf width, number of tillers per plant, ear bearing tillers, panicle length, number of grains/ panicle, days to maturity, biological yield, spikelet fertility %, spikelet sterility %, harvest index, test weight and grain yield / plant. 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

### Genetic Parameters

A wide range of variation was observed among 100 rice (*Oryza sativa* L.) genotypes for fifteen quantitative characters. The perusal of data revealed that variance due to treatment was highly

**Table 1:** Analysis of variance for Fifteen quantitative characters in 100 rice Genotypes.

Degree of freedom		Replication	Treatment	Error
S. No.	Source	1	99	99
Mean squares				
1	Days to 50 % flowering	3.1250	171.4555**	2.1856
2	Plant Height (cm)	10.2152	183.8499**	5.4042
3	Number of tillers per plant	0.1741	6.8982**	1.6950
4	Ear bearing tillers	1.9110	7.5695**	0.6773
5	Panicle length (cm)	0.0772	13.5290**	2.1206
6	Flag leaf length (cm)	0.0136	19.4166**	1.3857
7	Flag leaf width (cm)	0.0005	0.0387**	0.0156
8	Number of grains /panicle	13.3335	1340.6851**	80.8774
9	Days to maturity	0.0315	175.9741**	2.2423
10	Spikelet Fertility %	0.0040	51.6491**	7.0258
11	Spikelet Sterility %	0.0040	51.6491**	7.0258
12	Biological yield	87.8077	362.1344**	42.5433
13	Harvest index	0.0123	7.1565**	1.1339
14	Test weight (g)	0.0150	24.1454**	0.4877
15	Grain yield /plant (g)	14.3434	74.6448**	7.2370

\*, \*\* significant at 5 and 1 percent level of probability respectively.

**Table 2 :** Clustering pattern of 100 genotypes of rice (*Oryza sativa* L.)

S. No	Cluster	Number of genotypes	Name of the Genotypes
1.	I	66	NLR-3350, NLR-3276, MTU-1075, KNM-118, BPT-2618, JGL-19621, MTU-1175, MTU-11365-62-1-1, RPHR-650-2-5, OR-2560-3, IRRI-105, IRRI-154, MTU-2051-3-2-3, NLR-3302, JGL-11727, BPT-3291, NLR-3213, OR-2542-12, NLR-3238, MTU-1161, MTU-1121, NLR-3349, JGL-18629, RGL-2538, MTU-1155, WGL-821, WGL-14, NLR-3350, WGL-810, NDR-2064, NDR-2065, NDR-3112-1, BPT-3252, NLR-33654, RNR-M7, JGL-11470, JGL-3844, JGL-1798, NDLR-8, RAMAPPA-WGL-23985, PANTDHAN-10, PANTDHAN-11, SUVARNA, PUSHYAMI, RGL-7004, RGL-7005, RGI7006ZHONGHAU-1, MTU-1156, MTU-1010, RNR-15048, MTU-126-1-6-1, MTU-1182, MOTIGOLD, SONAM, RGL-1880, BPT-2570, MTU-1155, MTU-1177, MTU-1181, BPT-2613, WGL-14, SWETHA, NLR-34449, NDR-7007, RP BIO-216.
2.	II	10	JGL-20171, NLR-3241, MTU-1190, BPT-2231, MTU-1064, INDRA 1061, AKSHAYA, LSD-1, ADO94933, RNR-2465
3.	III	1	MTU-2152-5-1-5
4.	IV	16	WGL-536, BPT-2676, RP-4978-60-3-2-2, IRRI-104, WGL-580, NLR-3353, OR-2573-4, ERRAMALLELU-WGL-20471, MTU-1001, BPT-2411, LAKSHMI, OR-2560-6, NDR-359, BM71, RGL-2624, SHAHABHAGIDHAN
5.	V	1	JGL17004
6	VI	1	BPT-1768
6.	VII	1	BPT-5204
8	VIII	1	PLA1100
9	IX	1	SHIATS DHAN-1
10	X	1	BPT-2615
11	XI	1	RGL-11226

**Table 3 :** Average intra-and inter –cluster D<sup>2</sup> values among eleven clusters in rice

	1	2	3	4	5	6	7	8	9	10	11
	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster
1 Cluster	86.332	192.286	121.565	179.147	361.65	641.948	220.075	681.237	252.175	286.054	1137.077
2 Cluster		139.922	240.939	354.983	684.658	317.857	203.063	336.209	275.579	460.881	691.959
3 Cluster			0	185.832	555.392	665.52	302.96	718.807	293.485	447.431	1106.446
4 Cluster				175.032	391.335	879.753	377.3	956.75	410.5	396.611	1438.135
5 Cluster					0	1511.607	500.858	1658.22	574.033	293.438	2339.132
6 Cluster						0	469.034	114.152	713.435	1147.108	269.99
7 Cluster							0	541.605	116.098	409.043	939.099
8 Cluster								0	607.954	1123.843	232.158
9 Cluster									0	410.195	1111.532
10 Cluster										0	1447.306
11 Cluster											0

**Table 4 :** Contribution of different characters to genetic divergence in rice (*Oryza sativa* L.)

Sl. No.	Character	% Contribution towards divergence
1	Test weight	26.44
2	Days to 50 % flowering	20.20
3	Plant height	14.89
4	Days to maturity	13.29
5	Number of Grains / panicle	6.73
6	Spikelet Fertility	4.95
7	Flag leaf length	4.34
8	Ear bearing tillers	2.89
9	Biological yield	1.72
10	Grain yield / plant	1.70
11	Harvest index	1.19
12	Panicle length	1.03
13	Flag leaf width	0.32
14	Spikelet Sterility	0.25
15	Number of tillers per plant	0.20

significant for all the characters exhibited by the genotypes. The analysis of variance revealed significant difference among the genotypes for all the characters studied. Hundred genotypes were grouped into 11 distinct clusters (table 2). Among these clusters, Cluster I had maximum number of genotypes (66 genotypes), Cluster IV is the second largest with 16 genotypes followed by cluster II with 10 genotypes. Clustering pattern of genotypes showed lack of any relationship between geographic origin and genetic diversity reported by (Vivekanandanand Subramanian, 1993, Nayak et al., 2004). The maximum intra cluster D<sup>2</sup> value was 175.03 for cluster IV followed by 139.92 for cluster II, 86.33 for cluster I, while it was zero for clusters III, V, VI, VII, VIII,

IX, X and XI (table 3). High intra cluster distance in cluster IV indicated the presence of wide genetic diversity among the genotypes. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied. Genotypes present in these clusters may be used as parents for hybridization programme to develop desirable types. To realize much variability and high heterotic effect, Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance. The crossing between superior genotypes of above diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties of rice. Intercrossing of divergent genotypes with desirable traits would lead to greater opportunity for maximum amount of heterosis and utilize them for multiple crossing programmes to accumulate favourable genes in single genotypes. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak et al., 2004). (table 4) The highest contribution in manifestation of genetic divergence was exhibited by test weight (26.44), Days to 50% flowering (20.20) plant height (14.89) number of grains per panicle (6.73) and Grain yield / plant (1.70g) showed maximum contribution towards total divergence, Usha Kumari and Rangasamy (1997) also reported that the characters, plant height and grain yield/plant have contributed maximum to divergence and should form the basis of selection for genotypes. Pandey and John (2010) also reported that the characters test weight and days to 50% flowering contributed maximum to divergence and should form the basis of selection for genotypes.

The present study concluded that high heritability coupled with high genetic advance as per cent of mean

was observed for ear bearing tillers, number of grains/panicle, biological yield, test weight and grain yield/ plant hence these parameters could be used for selection. The present investigation further revealed that cluster I and IV are most diverse to each other. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability in segregating generations and may be used for future parents in hybridization programme to develop desirable Rice varieties.

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