

## Study of genetic variability and diversity in germplasm lines of rice

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### ABSTRACT

*A set of 96 germplasm lines of rice belonging to IRRI, Philippines were studied to know the extent of genetic variability and diversity based on yield and yield contributing traits. The analysis of variance showed significant differences among the genotypes for all the traits studied, exhibited considerable range of variation among the genotypes indicating enough scope for breeding for crop improvement in desirable direction. The estimate of heritability (broad sense) for different traits under study ranged between 68.11 to 91.86 per cent. The high estimate of heritability revealed that selection for traits namely days to 50 per cent flowering, plant height, grain yield per plant, panicle length and grains per panicle could be effective for breeding program. Based on D<sup>2</sup> analysis 96 lines were grouped into nine clusters in which cluster first consisted of maximum numbers of genotypes (35) followed by cluster 3 (19), 2(17), and 4 (02) while cluster fifth, seventh and eighth were having only single genotype each. The highest intra cluster distance has been observed for cluster 6 (119.16) and highest inter cluster distance (75.53) between cluster 6 and 9. High inter cluster distance would mean high phenotypic diversity for genotypes contained in cluster which would be mainly because of magnitude of genetic diversity when environmental influence is small. Therefore, the genotypes selected from different distant cluster would be expected to yield wide spectrum of variability on hybridization in segregating generations. The mean values of cluster 5, 6 and 7 exhibited highest mean for most of the traits. The genotypes belonging to the clusters exhibiting high cluster mean for specific traits may be selected and utilized for breeding program.*

**Key words:** Rice, heritability, genetic advance, variability, diversity

Rice (*Oryza sativa* L.) is one of the most paramount food crops and a primary food source for more than one third of world's population (Singh and Singh, 2008). In India, rice is being cultivated in more than 42 m ha and is the major food crop for more than 70 per cent of the population. Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding (Manohara and Singh, 2013). Recently diversity in rice has been well utilized with respect producing high yielding genotypes along with another desirable back ground to solving the food problems. The narrow genetic base of rice genotypes is likely to make vulnerable to biotic and biotic factors. It is therefore, to meet the over increasing demand of food grain for high production, the emphasis should be given to genetic improvement of the existing rice genotypes for yield as well as another desirable

traits too. The success of breeding program regarding crop improvement for trait of interest is possible through collection of genetically diverse genotypes and their proper evaluation for development of superior genotypes. In light of above issues, the present effort has been made to collect and characterize the set of 96 established rice germplasm lines for various quantitative characters and to study the genetic diversity among them and then to utilize in the hybridization programme for development of new promising lines with improved grain yield along with other desirable traits as well.

### MATERIALS AND METHODS

The present investigation was carried out during wet season 2010-2011 at Agricultural Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The genotypes under investigation were a

set of ninety six well established diverse germplasm lines obtained from International Rice Research Institute (IRRI), Philippines (Table 1). All the genotypes were directly grown during wet season in Completely Randomized Block Design with two replications. Each plot consisted of two rows of 1.5 m length. Spacing was maintained at 0.15x0.10 m excluding the induced irrigation. Normal recommended fertilizer dose and agronomic practices were followed during crop seasons to raise healthy crops. The plant was tagged randomly from each genotype in each replication and their means were used to analyze the data. Observations were recorded on yield and yield contributing traits such as days to 50% flowering, plant height, tillers per plant, effective tillers per plant, chlorophyll content, panicle length, grain per panicle, grain length/bread ratio, test weight and grain yield per plant. Data of ten traits were subjected to analysis following the method of Panse and Sukhatme (1995). The genetic divergence amongst different genotypes was assessed inter se genetic distance using methodology of Mahalanobis (1928). After arranging the  $D^2$  values of all combinations of one genotype with the others in ascending order of magnitudes the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952).

## RESULTS AND DISCUSSION

The analysis of variance for ten quantitative traits including grain yield in the present set of 96 rice germplasm lines revealed that treatment (genotypes) differences were highly significant for all the traits under study (Table not shown). It shows that there are inherent genetic differences among the genotypes. Similar findings were also reported by Prasad *et al.* (2009) and Ali *et al.* (2000). The significant variability for various traits in rice genotypes were also reported by Mustafa *et al.* (2007) and Singh *et al.* (2007). The estimates of range, mean, phenotypic coefficient of variation (PCV) genetic coefficient of variation (GCV), heritability (broad sense), genetic advance are presented in Table 2. There was considerable range of variation observed for all the traits under investigation, indicating enough scope for breeding for improvement of desirable direction. The line number 2 showed lowest values for three characters namely plant height (72.8 cm), tillers per plant (3.4) and effective tillers per plant (3.1). The lowest values for days to 50% flowering (75.09) and panicle length (17.11) was recorded for

line number 1 while the poorest yielding ability was exhibited by the line number 63. Out of 96 genotypes no single genotype was found to exhibit highest mean values for two or more than two different characters. A maximum value for grain yield per plant (35.29) was recorded for line 30. Similarly, maximum values for plant height (135.55), effective tillers per plant (13.6), panicle length (32.97) and grains per panicle (197.10) were observed for line 31, line 97, line 92 and line 58 respectively. Considerably high range of variation observed for most of the traits in the present set of genotypes suggested a positive scope improvement through simple selection. Variability for grain yield per plant and yield related traits such as number of tillers per plant, effective tillers per plant and grain per plant were significantly higher than the other traits. Similar findings were also reported by Kuchanur *et al.* (2009). Genotypes which showed promise for yield and some of the yield components would be more suitable for direct selection for targeted trait or for hybridization in order to make desirable improvement in yield. In present investigation, the difference between PCV and GCV were found to be smaller for all the characters. Similar observations were also made by Karad and Pol (2008). Both PCV and GCV were higher for grain yield per plant followed by tillers per plant, effective tillers per plant and grain yield per plant; whereas Manna *et al.* (2006) reordered the highest GCV for flag leaf, grains per panicle and panicle weight in their study. This suggests that these characters are under the major influence of genetic control and less variable due to environmental factors. Hence, such characters could be relied upon and simple selection can be practiced for further improvement. This finding regarding variation was in agreement with the reports made by Shanthi and Singh (2001). The estimate of heritability (broad sense) for different traits under study ranged between 68.11 and 91.86 per cent. The highest heritability values were obtained for days to 50% flowering (91.86) followed by grain yield per plant (84.64) and panicle length (84.04). Lowest heritability value was recorded for test weight (68.11) per cent. In the present investigation, high estimate of heritability indicated that selection for traits such as days to 50% flowering, plant height, grain yield per plant, panicle length and grains per panicle could be effective for breeding programme. Ali *et al.* (2000) observed the maximum heritability for plant height followed by 100

**Table 1.** List of 96 established rice germplasm lines of IRRI used in the study

Sl.No.	Line No	Genotypes	Sl.No.	Line No	Genotypes
1	Line 1	Zhonghua 10	49	Line 51	IR 82590-B-B-32-2
2	Line 2	WAB880SG14	50	Line 52	IR 83750-B-B-30-3
3	Line 3	IR 83750-B-B-131-1	51	Line 53	IR 84984-27-1
4	Line 4	IR 826539-B-B-103-4	52	Line 54	IR 82589-B-B-7-2
5	Line 5	IR 83749-B-B-65-1	53	Line 55	IR 82590-B-B-87-4
6	Line 6	IR 83749-B-B-55-1	54	Line 56	IR 78914-B-22-B-B-B
7	Line 7	IR 82310-B-B-67-2	55	Line 57	IR 72860-107-3-1-2
8	Line 8	IR 825-B-B-117-2	56	Line 58	IR 82635-B-B-59-2
9	Line 9	IR 83754-B-B-40-2	57	Line 59	IR 83748-B-B-15-4
10	Line 10	IR 83754-B-B-46-4	58	Line 60	IR 81422-B-B-200-4
11	Line 12	IR 82589-B-B-138-2	59	Line 61	BP277D-MR-2-8
12	Line 13	IR 82635-B-B-32-4	60	Line 62	IR 55419-04
13	Line 14	IR 82635-B-B-82-2	61	Line 63	BIO530-A-5-10-1-2-8
14	Line 15	IR 82638-B-B-147-1	62	Line 64	IRAT 112
15	Line 16	IR 82639-B-B-118-3	63	Line 65	IR 77298-14-1-2-10
16	Line 17	IR 83384-B-B-102-3	64	Line 66	IR 83222-161-1-1-1-1-1
17	Line 18	IR 83749-B-B-46-1	65	Line 67	IR 70175-22-1-1-2-2
18	Line 19	IR 82589-B-B-51-4	66	Line 68	IR 71137-184-3-2-3-3
19	Line 20	IR-82589-B-B-114-3	67	Line 69	IR 78937-B-3-B-B-1
20	Line 21	IR 82589-B-B-114-4	68	Line 70	IR 78937-B-3-B-B-2
21	Line 22	IR 82589-B-B-124-2	69	Line 71	IR 78940-B-22-B-B-B-SB-1
22	Line 23	IR 82589-B-B-13-3	70	Line 72	KMP 34
23	Line 24	IR 82589-B-B-2-2	71	Line 73	CT 15673-8-4-7-1-4-M
24	Line 25	IR 82590-B-B-98-2	72	Line 74	CT 15672-2-2-4-1-1-M
25	Line 26	IR 82616-B-B-64-3	73	Line 75	IR 60080-46A
26	Line 27	IR 82635-B-B-143-1	74	Line 76	CT 15671-15-4-2-2-2-M
27	Line 28	IR 82635-B-B-47-2	75	Line 77	CT 15691-4-5-2-2-1-M
28	Line 29	IR 82635-B-B-58-1	76	Line 79	CT 15671-15-1-4-1-5-M
29	Line 30	IR 82635-B-B-88-2	77	Line 80	IR 78942-B-2-B-B-1
30	Line 31	IR 84135-11-6-B-B	78	Line 81	CT 15672-12-1-1-2-3-M
31	Line 32	IR 82635-B-B-25-4	79	Line 82	CT 15679-17-1-2-1-2-M
32	Line 33	IR 82635-B-B-145-1	80	Line 83	CT 15679-17-1-4-1-1-M
33	Line 34	IR 82639-B-B-140-1	81	Line 84	CT 15691-4-3-1-1-2-M
34	Line 36	IR 72876-62-2-2-2	82	Line 85	CT 15716-6-1-2-1-5-M
35	Line 37	IR 82589-B-B-2-3	83	Line 86	UPL-RI-5
36	Line 38	IR 82589-B-B-44-2	84	Line 87	CT 15679-17-1-1-1-4-M
37	Line 39	IR 82589-B-B-84-3	85	Line 88	CT 15679-17-2-3-1-4-M
38	Line 40	IR 82635-B-B-47-1	86	Line 89	CT 15691-4-3-4-1-3-M
39	Line 41	IR 82635-B-B-72-2	87	Line 90	CT 15691-4-3-4-5-1-M
40	Line 42	IR 82635-B-B-75-2	88	Line 91	CT 15699-1-5-3-1-3-M
41	Line 43	IR 83747-B-B-81-1	89	Line 92	IR 43
42	Line 44	IR 82639-B-B-3-3	90	Line 93	CT 15671-16-1-7-1-1-M
43	Line 45	IR 82635-B-B-93-2	91	Line 94	CT 15673-8-1-4-1-1-M
44	Line 46	IR 82589-B-B-121-3	92	Line 95	CT 15765-13-7-2-1-2-M
45	Line 47	IR 82589-B-B-149-4	93	Line 96	CT 15696-3-3-5-1-1-M
46	Line 48	IR 82589-B-B-36-2	94	Line 97	CT 15675-2-2-3-1-2-M
47	Line 49	IR 82589-B-B-95-2	95	Line 98	PR 26703-3B-PJ 7
48	Line 50	IR 82590-B-B-102-4	96	Line 99	WAB 881-10-37-18-9-P 1-HB

seed weight, number of tillers per plant, panicle length; whereas Akter *et al.* (2004) reported high heritability for all the tested characters except grains per panicles. Among the traits under investigation, grains per panicle (55.62) recorded highest genetic advance followed by

plant height (23.02). Lowest genetic advance was obtained for L/B ratio (0.72) followed by effective tillers per plant (3.50) and tillers per plant (3.88). Genetic advance as per cent of mean obtained for days to 50 per cent flowering (11.0). This suggests that there is

**Table 2.** Variability Parameter for 10 characters in 96 rice genotypes

	Characters	DF	PH (cm)	TN	ET	CL	PL	G/P	TW	L/B	GY/P (gm)
Range	Min.	75.09	72.8	3.40	3.10	19.20	17.11	42.10	10.13	2.23	3.90
	Max.	111.11	135.55	14.10	13.60	40.41	32.97	197.1	30.5	4.76	35.25
Mean		90.26	109.29	7.68	7.66	28.99	25.34	125.7	23.63	3.58	18.59
PCV (%)		5.81	12.18	30.55	29.07	16.96	11.86	26.08	13.72	12.33	37.09
GCV (%)		5.57	11.16	25.56	25.38	14.83	10.87	23.67	11.32	10.98	34.12
Heritability (%)		91.86	83.96	70.00	76.18	76.30	84.04	82.37	68.11	79.37	84.64
Genetic Advance (k=2.06)		9.93	23.03	3.38	3.50	7.74	5.20	55.62	4.55	0.72	12.07
Genetic Advance (% of mean)		11.00	21.07	44.05	45.63	26.69	20.53	44.25	19.25	20.16	64.92

## Abbreviations:

DF = Days to 50% flowering, PH = Plant height, TN = Tillers Numbers, ET = Effective tillers, CC=Chlorophyll Content, PL = Panicle length, G/P = Grains per panicle, TW = Test Weight, LB = Length breadth ratio of grain GY = Grain Yield per plant, GCV= Genotypic coefficient of variation, PCV= Phenotypic Coefficient of Variation.

greater scope for improvement of characters which exhibit high magnitude of expected genetic advance as per cent of mean compared to another trait. High genetic advance as per cent of mean indicated pre-dominance of additive effects. High heritability estimate accompanied by large genetic advance would be desirable for exploitation of variability in desirable direction. The researchers should be cautious in making selection based on heritability as it includes both additive and non additive gene action. Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure. In the present set of material, high heritability coupled with high genetic advance as per cent of mean was recorded for grains per panicle and grain yield per plant indicating effectiveness of selection for the improvement of these traits. High heritability coupled with high genetic advance for effective tillers per plant, grain yield per plant, and 1000 grain weight was also reported by Chaubey and Singh (1994). Akter *et al.* (2004) observed high heritability with high genetic advance as per centage of mean for panicles per square meter, 1000 grain weight and flag leaf area respectively. In order to study genetic divergence 96 rice germplasm lines were subjected to D<sup>2</sup> analysis. Analysis employed Tocher's method, through which 96 genotypes made 9 distinct clusters Table 3. Out of nine clusters, cluster first was consisted of 35 genotypes followed by cluster 3 (19 genotypes), cluster 2 (17 genotypes) and cluster 4 (10 genotypes). Cluster fifth, seventh and eighth were having only single genotype. The highest intra cluster distance (D values) observed for cluster 6 (119.16) which comprises of Lines (30, 37, 75, 91 and 97). Similarly, lowest intra cluster distance (0.00) was

noticed for cluster 5, 7 and 8 respectively which itself reveals that each of these clusters are formed of single genotype *viz.*, Line 93 (cluster 5), Line 92 (cluster 7) and Line 26 (Cluster 8). The highest inter cluster distance (75.53) has been found between cluster 6 (Line 30, 37, 75, 91 and 97) and cluster 9 (Line 1, 2, 10, 63, 65, 66 and 69) followed by inter cluster distances (61.00), (58.36) and (55.06) between cluster 4 and 6, 7 and 9 and 8, 9 respectively. Maximum intra cluster distance exhibits maximum diversity among the genotypes within the group but not to the extent so that they can form separate clusters as there existed genetic similarities among themselves on the basis of multiple characters causing them to belong into a single cluster. High inter cluster distance would mean high phenotypic diversity for genotypes contained in cluster which would be mainly because of genetic diversity when environmental influence is small. Thus, the genotypes selected from different distant cluster would be expected to yield wide spectrum of variability on hybridization in segregating generations (Prasad *et al.* 2009). The mean values of different traits for different clusters as per Tocher's method have been presented in Table 4. Cluster 5, 6 and 7 exhibited highest mean values for most of the traits. Cluster 5 exhibited highest values for total tillers per plant, test weight and grain L/B ratio. Cluster 6 recorded highest values for effective tillers per plant and grain yield and cluster 7 expressed highest mean values for chlorophyll content, panicle length and grains per panicle. Only maximum cluster mean values for plant height was exhibited by cluster 3. The genotypes contained in clusters exhibiting high cluster mean for specific traits may be selected from the above mentioned cluster for breeding programme. Based on

**Table 3.** Average Intra- and Inter-cluster D<sup>2</sup> values among nine clusters of 96 rice genotypes (dry season 2010)

Cluster	1	2	3	4	5	6	7	8	9
1	<b>30.28</b>	209.40	197.50	753.86	69.22	1196.01	375.32	265.03	1786.30
2		<b>33.21</b>	715.47	217.20	268.64	2272.39	952.22	796.83	870.24
3			<b>42.83</b>	1604.06	207.14	512.03	159.63	96.15	3000.12
4				<b>35.79</b>	856.34	3721.42	1911.03	1676.24	285.26
5					<b>0.00</b>	1192.67	251.78	377.60	1950.28
6						<b>119.16</b>	584.33	528.29	5704.46
7							<b>0.00</b>	329.10	3405.83
8								<b>0.00</b>	3032.11
9									<b>102.61</b>

**Table 4.** Cluster mean values for different quantitative traits (dry season 2010)

Cluster	DF	PH	TN	ET	CL	PL	GP	TW	L/B	GY/P
1	91.84	111.26	7.50	7.49	28.26	25.57	136.86	23.95	3.57	19.94
2	90.71	113.72	7.53	7.37	27.40	25.45	124.32	24.48	3.63	14.91
3	92.19	115.08	8.42	8.56	31.17	26.76	128.21	24.39	3.65	24.69
4	88.30	104.62	6.82	6.64	28.16	23.75	118.72	22.29	3.42	10.01
5	98.64	119.85	9.70	9.20	34.06	29.83	145.70	30.18	4.46	20.38
6	89.84	106.72	9.58	10.20	25.87	25.65	129.73	23.49	3.79	32.83
7	111.11	112.15	7.80	8.20	40.04	32.97	162.93	23.85	3.96	23.81
8	88.87	105.45	6.90	7.70	31.93	21.87	42.10	13.74	3.23	24.67
9	85.01	80.06	6.60	6.09	31.33	19.86	77.21	20.29	3.28	4.57

the information from cluster means contrasting genotypes for different traits may be utilised for making divergent crosses. The distribution of maximum and minimum mean values for different traits in distinct cluster indicated that the traits contributing to the total divergence. In this regards, grain yield per plant contributed maximum to total divergence followed by tillers per plant, effective tillers per plant and grains per panicle. Banumathy *et al.* (2010) reported maximum contribution was made by grain yield followed by days to 50 per cent flowering, total grains per panicle and plant height and Vennila *et al.* (2011) in their studies accounted maximum contribution to number of grains per panicle, plant height, grain length and breadth. The major contributing characters towards genetic divergence was found to be grain yield per plant (28.52) followed by effective tillers per plant (19.59), tillers per plant (18.24) and grains per panicle (17.20).

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