



# **Studies on Genetic Variability, Divergence and Characters Associated with Yield Components in Rice**

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## **Authors' contributions**

*This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.*

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## **ABSTRACT**

The current study was carried out to evaluate genetic factors such as Genotypic Coefficient of Variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) along with correlations, path coefficients and Genetic divergence from data collected on 22 rice genotypes. The results demonstrated significantly significant mean squares owing to genotypes for all variables investigated, demonstrating that there is adequate variation among genotypes and thus ample possibility for successful selection. Only seed yield per plant showed a high Phenotypic Coefficient of Variation (PCV). Moderate phenotypic coefficient of variation and Genotypic Coefficient of Variation (GCV) observed for number of tillers/plant, number of spikelets/panicle, flag leaf length, flag leaf width, number of filled grains/panicle, 1000-grain weight and biological yield. High heritability and genetic advance as per cent of mean was observed for number of tillers/plant, number of spikelets/panicle, flag leaf length, flag leaf width, number of filled grains/panicle, 1000-grain weight, biological yield and seed yield per plant, indicating the effectiveness of direct selection for improvement of these traits. Panicle length, 1000-grain weight and biological yield had recorded positive and significant association with seed yield per plant. The results on path analysis also revealed high and positive direct effect for biological yield followed by harvest index, days to 50% flowering, plant height, panicle length and number of spikelets/panicle and hence, these traits were identified as the most effective selection criteria for

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improvement of seed yield per plant in rice genotypes. The results on divergence analysis revealed that the genotypes were grouped into five clusters. Cluster I constituted maximum number of (10) genotypes. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster IV (18.33) followed by cluster I, II, III. Cluster V showed zero intra-cluster distance. The genotypes contained in Clusters IV and V (20.20) displayed the greatest intercluster distance, indicating that they might be employed as parents in a future hybridization experiment.

**Keywords:** Hybridization; *Oryza sativa*; rice cultivation; spikelets.

## 1. INTRODUCTION

Rice (*Oryza sativa* L.) is a plant belonging to the family of grasses (Gramineae) Poaceae. It is one of the world's most important cereal crops, forming the staple diet of almost half of the world's population. The Asia Pacific Region is the world leader in rice production, accounting for around 90% of global output. People in Asian countries eat more than 75% of the world supply, making rice critical to Asia's food security. The demand for rice is predicted to rise in tandem with the world's population growth.

Rice farming has a long and extensive history in India. India is the world's leader in terms of rice output and rice farming area, coming in second to China. 30% of the world's rice is produced there. In the nation, rice accounts for one-fourth of all cropped land, contributes 40–43% of all food grain output, and is nevertheless essential to the nation's system of food and livelihood security. In India, rice is cultivated over an area of about 45.0 million hectares. About 40% of the area in India is rainfed which 23% of the rainfed rice area is upland and 77% is lowland. The Rice is grown in a vast diverse geographical and climatic conditions ranging from below sea level areas like Kuttanad in Kerala to high altitude valley of Kashmir.

In India Rice is grown in 43.78 million ha, the production level is 118.43 million tonnes, and the productivity is about 20705 kg/ha during 2019-2020 (Agriculture statistics at a glance-2020). India occupies the first position in rice under the area of cultivation and second position in production which almost tripled its production during the second half of the last century. Global demand for rice is projected to grow at least equal to population growth, thus requiring a 70% (765 mt) increase in the supply of rice by the year 2025. To meet the demand for rice as the population increases the future demand for rice also increases, we have to work on the increasement of production to match the rate of increase in population growth. India is one of the

leading exporters of rice, particularly basmati rice. *Oryza sativa* has many ecotypes or cultivars adapted to various environmental conditions.

A critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adopting appropriate selection techniques. Correlation is the measure of the mutual relationship between two variables. Further studies on correlations help the plant breeder to know what exactly and how one character brings improvement in another character. Path coefficient analysis is a type of regression coefficient that assesses the direct influence of one variable on another. Since the environment has an impact on direct selection for yield, it is not a trustworthy method. Therefore, it is crucial to pinpoint the individual qualities that can boost yield. The correlation coefficient is used to quantify the degree of correlation between yield, yield components, and any other characteristic that significantly affects yield.

“Earlier workers considered distances in place of origin as an index of genetic diversity and used it for the selection of parents for hybridization programmes. However, the genetic diversity of the selected parents has not been found to be based on factors such as geographic diversity/place of release or ploidy level” [1].

The current study has the goals of estimating genetic variability, correlation, path analysis, and genetic divergence.

## 2. MATERIALS AND METHODS

The experimental material for the present study comprised of 22 genotypes of rice laid in Randomized Block Design (RBD) with three replications at Research farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab., during kharif season, 2021. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly

selected plants per replication for days to 50% flowering, plant height (cm), panicle length (cm), number of tillers per plant, number of spikelets/panicle, flag leaf length (cm), flag leaf width (cm), number of filled grains/panicle, days to maturity, 1000-grain weight (gm), biological yield (gm), seed yield per plant (gm), harvest index (%) on plot basis. The data was subjected to Analysis of variance Panse and Sukhatme [2], Heritability Hanson et al. [3], Genetic advance Johnson et al. [4], Correlation coefficient analysis Miller et al. 1958, Path coefficient analysis Dewey and Lu [5], Genetic diversity using D2 analysis Mahalanobis 1936.

### 3. RESULTS AND DISCUSSION

Analysis of variance (ANOVA) indicated that the mean sum of square (MSS) due to genotypes were highly significant for all the characters at 1% and 5% level of significance and it indicated the presence of consisted amount of genetic variability for all the traits (Table 1). As a result, there is a lot of scope for effective selection. Table 2 shows the results for yield and yield component characteristics in terms of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as a percentage of mean. A perusal of these results revealed maximum range of variability for the trait number of spikelets/panicle (112.53-242.03) while minimum range (0.9-1.56) was recorded for flag leaf width. In the present study, the phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits. It means the observed variation is not only due to the genotypes, but also due to suitable influence of environment. PCV and GCV were estimates classified into low (below 10%); medium (10-20%) and high (above 20%) in order to draw conclusions about these parameters. In the present study, there is only high PCV for and moderate GCV for seed yield per plant, indicating the existence of high amount of variability for effective selection towards improvement of these traits. However, the magnitude of PCV and GCV were moderate for the number of tillers per plant, number spikelets per panicle, 1000 grain weight, biological yield, flag leaf length, flag leaf width, plant height and harvest index. Similar kind of results were found by Sumanth et al. [6] for number of tillers/plant, number of spikelets/panicle and flag leaf length, Keerthiraj & Biju [7] flag leaf width and 1000-grain weight and Srujana et al. [8] for biological yield. Low PCV and low GCV were observed for traits viz., days

to 50% flowering, panicle length and days to maturity, however indicating little scope for improvement of these traits through selection. Similar kind of results found by Singh et al. [9] for days to 50% flowering and panicle length, Lipi et al. [10] for days to maturity. Heritability estimates for the various traits studied ranged from 60.25 (harvest index) to 98.09 (flag leaf length). High estimates of heritability (> 60%) were recorded for all the 13 traits studied. Similar kind of results found by Sumanth et al. [11], Srujana et al. [8]. A perusal of the results on genetic advance as percent of mean revealed high values (>20%) number of tillers/plant, number of spikelets/panicle, flag leaf length, flag leaf width, number of filled grains/panicle, 1000-grain weight, biological yield and seed yield per plant. It indicates that maximum genetic gain can be received by using these characters and these characters are transfer from parent to their offspring. Similar kind of results found by Sandeep et al. [12] for number of tillers/plant and 1000-grain weight, Singh & Verma [13] for number of spikelets/panicle, biological yield, Keerthiraj & Biju [7] for flag leaf length and flag leaf width. Moderate genetic advance as percentage of (10-20%) mean was recorded for days to 50% flowering, plant height and harvest index. It indicates partially genetic gain by selection. Similar kind of results were found by Sandeep et al. [12] for days to 50% flowering, Kishore et al. [14] for plant height.

High heritability coupled with high genetic advance as per cent of mean was recorded for number of tillers/plant, number of spikelets/panicle, flag leaf length, flag leaf width, number of filled grains/panicle, 1000-grain weight, biological yield and seed yield per plant. Indicating that heritability observed was due to additive gene effects and therefore selection would be effective in improvement of these traits. High heritability coupled with moderate genetic advance observed in traits viz., days to 50% flowering and plant height. While moderate heritability with moderate genetic advance was observed only for harvest index. Low heritability with low genetic advance was not observed in any character. In the present study traits like number of tillers/plant, number of spikelets/panicle, flag leaf length, flag leaf width, number of filled grains/panicle, 1000-grain weight, biological yield and seed yield per plant indicating the pre-ponderance of additive gene action and therefore, scope for effective improvement of these traits through selection.

**Table 1. Analysis of variance for seed yield and yield components in rice**

Sl. No.	Characters	Source of variation			CV
		Replications	Treatments	Error	
		Degree of freedom 2	20	40	
1	Days to 50% flowering	19.69	108.71	13.34	3.77
2	Plant height (cm)	485.54	511.49	107.40	8.71
3	Panicle length (cm)	2.58	6.20	1.32	6.79
4	Number of tillers/plant	0.31	16.70	0.72	4.91
5	Number of spikelets/panicle	114.56	3539.45	68.20	4.37
6	Flag leaf length (cm)	0.54	75.74	1.44	3.75
7	Flag leaf width (cm)	0.001	0.09	0.004	5.50
8	Number of filled grains/panicle	72.57	2254.78	155.64	6.89
9	Days to maturity	4.80	100.48	8.23	2.20
10	1000 Grain weight (gm)	1.06	28.53	1.18	8.81
11	Biological yield (gm)	33.98	236.13	21.23	6.17
12	Seed yield per plant	19.37	76.25	4.63	8.86
13	Harvest index	51.15	71.75	28.519	11.31

**Table 2. Genetic parameters of variability for yield and yield attributing characters in Rice**

Sl. No.	Characters	Range		Mean	Coefficient of variation		Heritability in broad sense (%)	Genetic advance in per cent of mean
		min	max		GCV	PCV		
1	Days to 50% flowering	87.33	106.33	96.87	5.81	6.21	87.72	11.22
2	Plant height (cm)	95.62	147.43	118.95	9.75	10.97	79.00	17.86
3	Panicle length (cm)	8.30	16.36	12.55	5.43	6.13	78.58	9.92
4	Number of tillers/plants	20.44	26.16	23.46	18.37	18.37	95.65	37.02
5	Number of spikelets / panicles	112.53	242.03	188.83	18.01	18.19	98.07	36.74
6	Flag leaf length (cm)	22.52	41.99	32.03	15.53	15.68	98.09	31.68
7	Flag leaf width (cm)	0.9	1.56	1.17	14.62	14.96	0.9549	29.44
8	Number of filled grains / panicle	131.95	233.50	180.83	14.62	15.16	93.10	29.07
9	Days to maturity	119.86	141.06	130.18	4.25	4.44	91.80	8.40
10	1000 Grain weight (gm)	16.47	34.45	24.43	17.13	17.50	95.86	34.56
11	Biological yield (gm)	12.62	24.69	17.61	16.27	17.06	91.01	31.99
12	Seed yield per plant	31.86	64.86	51.98	19.99	20.63	93.92	39.91
13	Harvest index	36.03	56.72	47.17	8.04	10.36	60.25	12.86

**Table 3. Genotypic and phenotypic correlation among 13 different characters in 21 rice genotypes**

Sl. No.	Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of tillers/plants	Number of spikelet /panicle	Flag leaf length (cm)	Flag leaf width (cm)	Number of filled grains/panicle	Days to maturity	1000 grain weight	Biological yield	Harvest index	Seed yield per plant
1	Days to 50% flowering	<b>1.0000</b>	-0.1809	-0.2387	-0.2976	-0.1058	-0.0973	0.1639	0.0084	0.6019**	-0.0148	-0.0668	-0.2460	-0.1788
		<b>1.0000</b>	-0.1972	-0.2748	-0.3633	-0.1197	-0.0929	0.1824	0.0172	0.6601**	-0.0328	-0.0875	-0.2864	-0.1782
2	Plant height (cm)		<b>1.0000</b>	-0.1481	0.4831*	0.2676	0.7574**	-0.1497	-0.2170	0.3499	-0.1380	-0.3290	0.1681	-0.2276
			<b>1.0000</b>	-0.1621	0.5362**	0.3172	0.8528**	-0.1863	-0.2312	0.3879	-0.1749	-0.3701	0.2879	-0.2464
3	Panicle length (cm)			<b>1.0000</b>	-0.5596**	-0.0321	-0.4409*	-0.3224	-0.4688*	-0.4540*	0.3297	0.5978**	0.1267	0.5785**
				<b>1.0000</b>	-0.6476**	-0.0343	-0.4551*	-0.3325	-0.4855*	-0.4834*	0.3446	0.6323**	0.2124	0.6223**
4	Number of tillers/plant				<b>1.0000</b>	0.0900	0.6335**	0.1672	0.1434	0.1229	0.1065	-0.4133	0.2367	-0.2479
					<b>1.0000</b>	0.1119	0.7253**	0.1719	0.1757	0.1474	0.1152	-0.4904*	0.2496	-0.3199
5	Number of spikelets/panicle					<b>1.0000</b>	0.2769	0.1652	0.2302	0.1341	-0.2926	-0.1153	0.0411	-0.0779
						<b>1.0000</b>	0.2835	0.1797	0.2475	0.1377	-0.3000	-0.1225	0.0692	-0.0755
6	Flag leaf length(cm)						<b>1.0000</b>	0.0634	-0.0174	0.4176	-0.1169	-0.6565**	0.1875	-0.5082*
							<b>1.0000</b>	0.0691	-0.0203	0.4345*	-0.1135	-0.6907**	0.2446	-0.5263**
7	Flag leaf width (cm)							<b>1.0000</b>	0.0588	0.1973	0.0405	-0.3359	0.2871	-0.1504
								<b>1.0000</b>	0.0671	0.1987	0.0407	-0.3470	0.3324	-0.1667
8	Number of filled grains/panicle								<b>1.0000</b>	0.0714	-0.1444	-0.1143	0.0534	-0.0423
									<b>1.0000</b>	0.0994	-0.1576	-0.1451	0.0702	-0.0618
9	Days to maturity									<b>1.0000</b>	0.0436	-0.2795	-0.2131	-0.3639
										<b>1.0000</b>	0.0313	-0.3170	-0.2494	-0.3887
10	1000 grain weight										<b>1.0000</b>	0.4457*	0.3810	0.5738**
											<b>1.0000</b>	0.4710*	0.5074*	0.6034**
11	Biological Yield											<b>1.0000</b>	-0.0215	0.8603**
												<b>1.0000</b>	0.1144	0.9135**
12	Harvesting index												<b>1.0000</b>	0.4853*
													<b>1.0000</b>	0.5089*

**Table 4. Genotypic direct and indirect effect of different characters on seed yield per plant in rice**

Sl. No	Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of tillers / plant	Number of spikelets / panicle	Flag leaf length (cm)	Flag leaf width (cm)	Number of filled grains / panicle	Days to maturity	1000 grain weight	Biological yield	Harvest index	Seed yield per plant
1	Days to 50% flowering	<b>0.0461</b>	-0.0091	-0.0127	-0.0167	-0.0055	-0.0043	0.0084	0.0008	0.0304	-0.0015	-0.0040	-0.0132	-0.1782
2	Plant height (cm)	-0.0290	<b>0.1472</b>	-0.0239	0.0790	0.0467	0.1256	-0.0274	-0.0340	0.0571	-0.0257	-0.0545	0.0424	-0.2464
3	Panicle length (cm)	0.0403	0.0238	<b>-0.1468</b>	0.0951	0.0050	0.0668	0.0488	0.0713	0.0710	-0.0506	-0.0928	-0.0312	0.6223
4	Number of tillers/plant	0.0221	-0.0327	0.0394	<b>-0.0609</b>	-0.0068	-0.0442	-0.0105	-0.0107	-0.0090	-0.0070	0.0299	-0.0152	-0.3199
5	Number of spikelets/ panicle	-0.0097	0.0256	-0.0028	0.0090	<b>0.0807</b>	0.0229	0.0145	0.0200	0.0111	-0.0242	-0.0099	0.0056	-0.0755
6	Flag leaf length(cm)	0.0219	-0.2012	0.1074	-0.1712	-0.0669	<b>-0.2360</b>	-0.0163	0.0048	-0.1025	0.0268	0.1630	-0.0577	-0.5263
7	Flag leaf width (cm)	-0.0109	0.0112	0.0199	-0.0103	-0.0108	-0.0041	<b>-0.0599</b>	-0.0040	-0.0119	-0.0024	0.0208	-0.0199	-0.1667
8	Number of filled grains/panicle	0.0000	0.0004	0.0009	-0.0003	-0.0005	0.0000	-0.0001	<b>-0.0019</b>	-0.0002	0.0003	0.0003	-0.0001	-0.0618
9	Days to maturity	-0.0733	-0.0431	0.0537	-0.0164	-0.0153	-0.0482	-0.0221	-0.0110	<b>-0.1110</b>	-0.0035	0.0352	0.0277	
10	1000 grain weight	-0.0048	-0.0257	0.0506	0.0169	-0.0440	-0.0167	0.0060	-0.0231	0.0046	<b>0.1467</b>	0.0691	0.0745	
11	Biological Yield	-0.0620	-0.2624	0.4483	-0.3477	-0.0868	-0.4897	-0.2460	-0.1029	-0.2248	0.3340	<b>0.7090</b>	0.0811	
12	Harvesting index	-0.1189	0.1195	0.0882	0.1036	0.0287	0.1015	0.1380	0.0291	-0.1035	0.2106	0.0475	<b>0.4150</b>	

**Table 5. Clustering pattern of 21 Rice genotypes & based on Mahalanobis's D2 Statistic**

Cluster No.	No. of Genotypes	Genotypes
Cluster 1	10	RNR2458, RNR15048, JYOTHI, JGL11727, EXP092, NLR34449, NLR3049, CHECK -PR126, WGL32100, BPT5204
Cluster 2	4	KPS2879, AMAN, MTU1010, MTU1153
Cluster 3	3	DAMINI, PLA1100, JAYSRI
Cluster 4	4	JGL24423, ADT39, PLA1100, ADT37
Cluster 5	1	RNR18833

**Table 6. Estimates of average intra and inter-cluster distances for the five clusters in rice**

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	10.10	14.48	13.32	14.58	15.88
Cluster 2		11.28	16.64	14.66	16.60
Cluster 3			7.91	18.29	20.20
Cluster 4				13.32	20.45
Cluster 5					0.00

**Table 7. Cluster means for different characters in rice**

Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of tillers/plant	Number of spikelet/panicle	Flag leaf length (cm)	Flag leaf width (cm)	Number of filled grains /panicle	Days to maturity	1000 Grain weight (gm)	Biological Yield (gm)	Seed yield per plant	Harvesting index
Cluster 1	98.27	118.83	11.92	23.20	201.41	31.66	1.13	191.55	130.78	22.09	15.60	50.50	43.89
Cluster 2	92.00	120.42	13.66	24.26	159.44	33.28	1.00	168.76	127.45	27.42	21.17	58.16	47.52
Cluster 3	93.22	134.26	11.24	24.96	209.60	40.10	1.40	177.67	132.40	20.06	16.98	38.17	52.61
Cluster 4	99.00	106.74	15.07	22.21	190.26	25.76	1.29	169.45	127.05	31.70	19.85	61.79	51.48
Cluster 5	105.00	117.33	8.33	23.50	112.57	31.80	1.23	177.10	141.07	20.03	16.53	44.50	45.23

**Table 8. Contribution of 13 traits of Rice towards divergence**

Sl. No.	Source	Times Ranked 1 <sup>st</sup>	Contribution %
1	Days to 50% Flowering	1	0.43 %
2	Plant height (cm)	0	0.00 %
3	Panicle length (cm)	13	5.63 %
4	Number of tillers/plants	0	0.00 %
5	Number of spikelets/panicles	60	25.97 %
6	Flag leaf length (cm)	67	29.00 %
7	Flag leaf width (cm)	26	11.26 %
8	Number of filled grains/panicle	14	6.06 %
9	Days to maturity	2	0.87 %
10	1000 Grain weight (gm)	17	7.36 %
11	Biological Yield (gm)	29	12.55 %
12	Seed yield per plant	2	0.87 %
13	Harvesting index	0	0.00 %

The correlation analysis among the thirteen characters studied is presented in Table 3. In the present findings, the magnitudes of genotypic correlation coefficient were greater than corresponding phenotypic correlation coefficient in general. In genotypic correlation coefficient Seed yield per plant exhibited positive and high significant correlation with the characters namely panicle length, flag leaf length, 1000-grain weight, and biological yield. While harvest index had showed positive and significance correlation for seed yield per plant. For days to 50% flowering, plant height, number of tillers/plant, number of spikelets/panicle, flag leaf width, number of filled grains/panicle and days to maturity where significance had not shown for the negative correlation with seed yield per plant. Similar findings were found with seed yield per plant exhibit for 1000-grain weight Shrestha et al. [15]; Rashid et al. [16], similar findings for panicle length by Rashid et al. [16] and for harvest index by Moosavi et al. [17]; Idris et al. [18]. In phenotypic correlation coefficient seed yield per plant exhibited positive and high significant correlation with the characters namely 1000-grain weight, panicle length and biological yield. while harvesting index are shown positive and significance only at 5 % level and Flag leaf length had shown negative and significant correlation with the seed yield. Days to 50% flowering, plant height, no of tillers per plant, no of spikelets per panicle, flag leaf width, number of grain per panicle, days to maturity. Similar findings were found by Idris et al. [18]. The results revealed that there is scope for simultaneous improvement of these traits through selection.

With the help of path coefficient analysis, the correlation coefficient is partitioned into direct and indirect effects (Table 4). The highest positive direct effect on seed yield per plant was exhibited by biological yield followed by harvest index, days to 50% flowering, plant height, panicle length and number of spikelets/panicle. Negative direct effect on seed yield per plant was exhibited by panicle length, flag leaf length followed by 1000-grain weight, number of filled grains per panicle, and days to maturity. The highest positive indirect effect on seed yield per plant was exhibited by biological yield, harvest index, 1000-grain weight, panicle length, followed by flag leaf width had shown indirect negative effect on seed yield, number of filled grains/panicle, days to 50% flowering, flag leaf length, number of spikelets/panicle, plant height, number of tillers per plant, days to maturity. Similar findings were found with Days to 50%

flowering Ekka et al. [19], Plant height Gour et al. [20], Panicle length and number of filled grains/panicle Moosavi et al. [17]; Idris et al. [18]; Ekka et al. [19] number of spikelets/panicle and flag leaf width Jeke et al. [21], days to maturity and harvest index Gour et al. [20]; Moosavi et al. [17], number of tillers/plant Shrestha et al. [15], Laxmi et al. [22], flag leaf length Reddy et al. [23], 1000- grain weight Nirmaladevi et al. [24]; Rashid et al. [16], biological yield Reddy et al. [23]. Therefore, harvest index, days to 50% flowering, plant height, panicle length and number of spikelets/panicle are the traits which can be directed in selection programmes to obtain higher grain yield.

The twenty-two genotypes under study were grouped into five clusters using Mahalanobis D2 analysis (Table 5). Among five clusters, cluster I was the biggest with 10 genotypes followed by cluster II (4 genotype), cluster III (3 genotype), IV (4 genotype) and V (1 genotype). The separation of genotypes into discrete clusters indicated the presence of a high level of genetic variety in the material tested. The presence of significant genetic variety among the parental material evaluated in this study suggested that this material could be a suitable source for selecting diverse parents for a hybridization programme. In conformity to the present investigation, similar findings were found by Koli et al. [25]; Ranjith et al. [26].

The inter and intra average distances among nine clusters were computed and have been given in Table 6. Divergence analysis exhibited were shown by cluster IV (12.68) followed by cluster II (11.28), followed by cluster I (10.10), followed by cluster III (7.91), followed by cluster V showed zero intracluster distance. Cluster IV and V (20.45) showed maximum inter cluster distance followed by that between cluster III and V (20.20), cluster III and IV (18.29), cluster III and II (16.64), cluster II and V (16.60), cluster I and V (15.88), cluster II and IV (14.66), cluster I and IV (14.58), cluster I and II (14.48) and cluster I and III (13.32), cluster I and III (13.32). To realize much variability and high heterotic effect, Mishra et al. (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance [27-29].

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 7). The maximum cluster mean for days to 50% flowering in cluster V, plant height in



cluster III, panicle length in cluster IV, number of tillers/plant in cluster III, number of spikelets/panicle in cluster III, flag leaf length in cluster III, flag leaf width in cluster III, number of filled grains/panicle in cluster I, days to maturity in cluster V, 1000-grain weight in cluster IV, biological yield in cluster II, seed yield per plant in cluster IV, harvest index in cluster III. The above observation confirms wide variation from one cluster to another in respect of cluster mean, which indicated that genotypes having distinct different mean performance for various characters were separated into different clusters. The genotypes of heterogeneous origin were frequently found in the five clusters in the aforementioned divergence analysis. Despite the fact that the genotype originated in the same location or geographic region, they were discovered to be clustered together in the same cluster. In all five clusters, there were examples of genotypes from different origins or geographical regions being grouped together in the same cluster. This shows that there is no parallelism between genetic and geographic diversity. As a result, just selecting parental material for a hybridization programme based on geographic variety may not be a successful exercise in selecting suitably divergent parents. Genetic divergence analysis-based selection would be more lucrative than geographic diversity-based selection.

The contribution of each trait to total divergence is presented in Table 8. Among the traits studied, flag leaf length contributed maximum divergence (29.00%) followed by number of spikelets/panicle (25.97%), flag leaf width (11.26%) and biological yield (12.55%). The minimum percentage of contribution was observed in 1000-grain weight (7.36%), number of filled grains/panicle (6.06%), panicle length (5.63%) followed by days to 50% flowering (0.43%), days to maturity (1.43%), days to maturity (0.87%), seed yield per plant (0.87%) and plant height, number of tillers/plant, harvest index contributed zero percent divergence. The traits viz flag leaf length contributed maximum divergence followed by number of spikelets/panicle, flag leaf width and biological yield contributed 78.78 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

#### 4. CONCLUSION

The findings indicate that the genotypes studied have adequate genetic variability. Characters

viz., panicle length, flag leaf length, 1000-grain weight, biological yield and harvest index. Path analysis revealed high and positive direct effect for biological yield followed by harvest index, days to 50% flowering, plant height, panicle length and number of spikelets/panicle and hence, these traits were identified as the most effective selection criteria for improvement of seed yield per plant in rice genotypes. Genetic diversity analysis was carried out through D2 analysis in order to assess the genetic divergence among genotypes under study. Based on D2 analysis twenty-two rice genotypes were grouped into five clusters. Cluster I constituted maximum number of genotypes. Further, the results on divergence analysis revealed that Cluster I constituted maximum number of genotypes. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster I followed by cluster II, III, IV. In contrast, cluster V displayed a zero intra-cluster distance. Clusters III and V had the greatest distances between them, indicating that the genotypes included in these clusters might be employed as parents in a future hybridization experiment.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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