

# Assessment of Genetic Diversity for yield and yield-related traits in Rice (*Oryza sativa* L.) using Mahalanobis' $D^2$

## ABSTRACT

Genetic improvement mainly depends on the amount of genetic variability present in the population. Hence an effort was made to classify and understand the nature and magnitude of genetic diversity by using Mahalanobis (1936)  $D^2$  statistics using 112 rice genotypes. All genotypes exhibited a wide and significant variation for sixteen traits. A slight difference between PCV and GCV was found, suggesting that genetic control of traits is higher than environmental influence. Characters such as harvest index (99.60 percent and 31.48 percent), days to first flowering (99.10 percent and 25.35 percent), days to 50 percent flowering (99.00 percent and 22.98 percent) and plant height (89.40 percent and 24.34 percent) showed high heritability coupled with high genetic advance as percent of mean respectively, suggesting that selection for the improvement of these traits may be rewarding. The cluster analysis indicated that 112 genotypes were grouped into seven clusters, where cluster I has highest number of genotypes followed by cluster III consisting of 73 and 22 genotypes respectively. The maximum inter cluster distance was recorded between clusters V and VII with an inter-cluster distance of 58981.07, followed by clusters II and V (51875.13). The number of spikelets per panicle (52.17%) and number of grains per panicle (27.26%) were found to be the most contributing traits towards genetic diversity. Hence information on the nature and degree of divergence would help the plant breeder in selection and hybridization procedure for choosing the right type of parent to improve the quality characters.

**Keywords:** Heritability, GAM, genetic advance, Mahalanobis  $D^2$ , Tocher's method, Rice.

## INTRODUCTION

Rice (*Oryza sativa* L.) being the staple food for more than 70% of our national population, is also the source of livelihood for 120-150 million rural households and the backbone of Indian agriculture. The ever-increasing population in the country is creating a dire need for national food security and thus there is a demand for improving rice varieties in terms of quality and quantity. Hence rice is of paramount importance for improving its production and productivity. Thereby, knowledge of the nature and magnitude of the genetic

variation governing the inheritance of quantitative characters in rice is essential for a plant breeder. In a crop improvement program, to increase productivity breeder needs to maintain a pool of diverse desirable donor parents (Joshi *et al.* 2013). An obvious knowledge of genetic diversity is critical for the productive management and use of genetic tools for rice breeding. The genetic assortment is a source of variation, the unrefined material for the effort to achieve crops, which is essential for reducing crop vulnerability to abiotic and biotic stresses, ensuring long-term selection through genetic enhancement and promoting rational use. Success in crop improvement generally depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. Genetic diversity in crop plants is essential to sustain the level of high productivity (Tripathi *et al.*, 2013). The characters with a high coefficient of variation and high heritability coupled with high genetic advance may be governed by additive genes and can be directly selected for improvement through simple plant selection. In contrast, the characters with low GCV, PCV, heritability and genetic advance may be used in heterosis breeding. Hence, an attempt has been made in this study to find out the genetic variability and diversity of 112 rice genotypes and their heritability, genetic advance as percent mean which would help in the selection and further improvement of rice genotypes.

## **MATERIAL AND METHODS**

The experimental material comprised 112 rice genotypes obtained from the IRRI AGGRi Alliance project and was conducted during *Kharif* 2019 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, U.P. India. Seeds of 112 rice genotypes were sown in a raised nursery bed and the seedlings were transplanted in the main field with a spacing of 20 cm between rows and 15 cm between plants in an alpha lattice design with three replications and four blocks. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded in five randomly selected plants for different traits *viz.*, Number of effective tillers per plant, Plant height(cm), Panicle length(cm), Number of spikelets per panicle, Number of grains per panicle, Spikelet fertility (%), Grain weight per panicle(g), Grain yield per plant (g), 1000-grain weight(g) and Kernel L/B ratio. Whereas for traits like Days to first flowering, Days to 50% flowering, Days to maturity, Grain yield per plot (kg), Biomass yield per plot (kg), and Harvest index (%) the data was collected on a plot basis. The data was recorded for all the characters whose mean values were subjected to analysis of variance to test the significance for each character as per methodology proposed by Patterson and

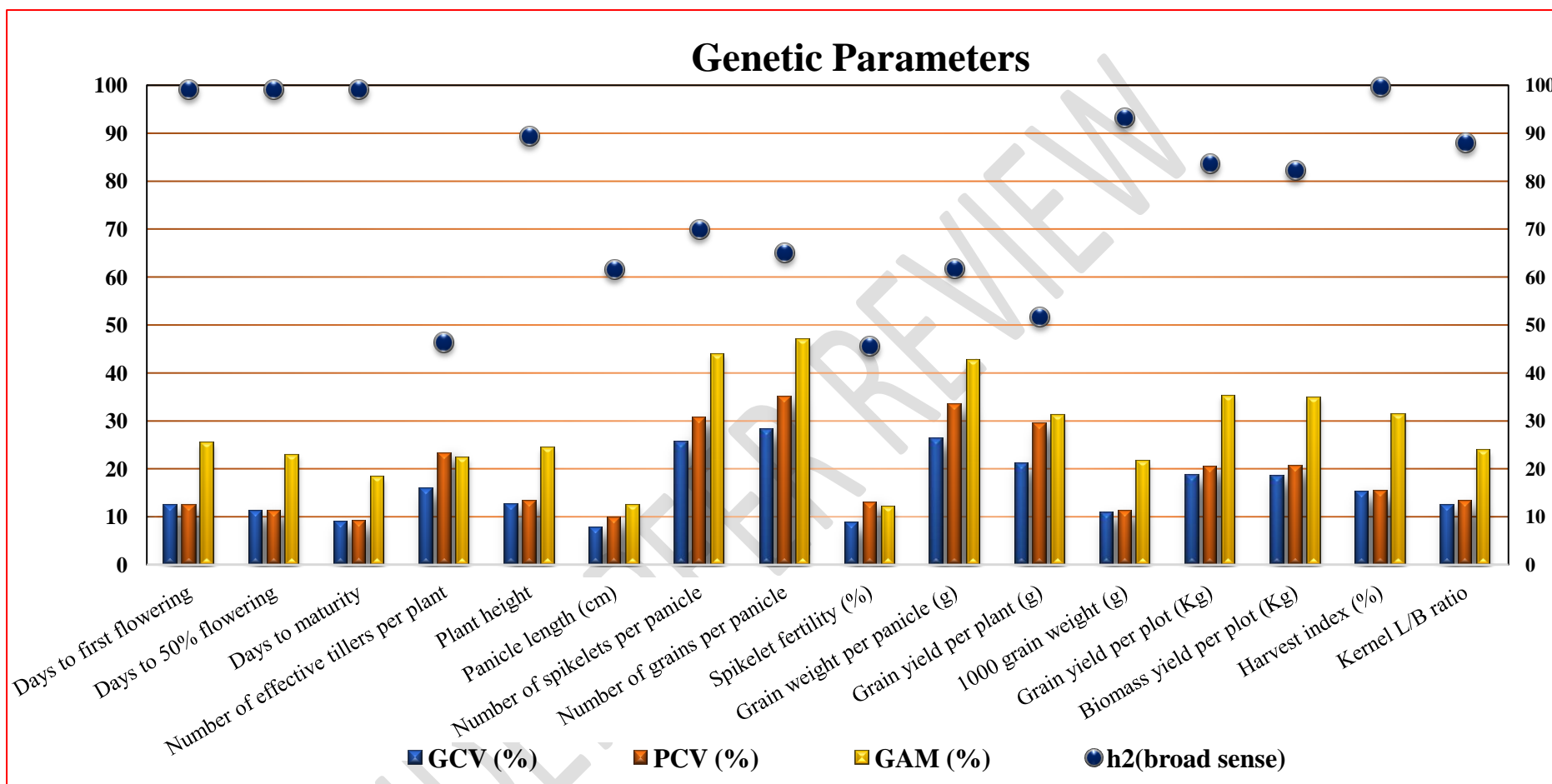
Williams (1976). The genotypic and phenotypic variances, as well as the genotypic (GCV) and phenotypic (PCV) coefficient of variation, were calculated by the formulae given by Burton (1952). Heritability in a broad sense was calculated using the formula given by Allard (1960) and genetic advance (GA) as per cent mean was estimated by the formula given by Johnson *et al.* (1955). Genetic divergence was estimated by Mahalanobis'  $D^2$  statistics (1936). The germplasms were grouped into several clusters by Tocher's method as described by Rao (1952).

## RESULTS AND DISCUSSION

The examination of variation for all the characters showed fair variations between the genotypes under study, suggesting the existence of appropriate heterogeneity. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense  $h^2$  (bs), genetic advance and genetic advance as percent of mean estimated for yield and quality traits are presented in Table 1 and Figure 1.

**Table 1: Estimates of variability, heritability and genetic advance as percent of mean for grain yield and yield components in Rice (*Oryza sativa* L.)**

Sl.No.	Genetic Parameters	GCV (%)	PCV (%)	$h^2$ (broad sense)	GAM (%)
1	Days to first flowering	12.36	12.42	99.10	25.35
2	Days to 50% flowering	11.21	11.27	99.00	22.98
3	Days to maturity	8.95	8.99	99.00	18.34
4	Number of effective tillers per plant	15.84	23.28	46.30	22.22
5	Plant height	12.50	13.22	89.40	24.34
6	Panicle length (cm)	7.70	9.82	61.50	12.44
7	Number of spikelets per panicle	25.55	30.56	69.90	44.00
8	Number of grains per panicle	28.22	34.99	65.00	46.88
9	Spikelet fertility (%)	8.66	12.83	45.50	12.03
10	Grain weight per panicle (g)	26.32	33.50	61.70	42.61
11	Grain yield per plant (g)	21.09	29.37	51.60	31.20
12	1000 grain weight (g)	10.88	11.27	93.10	21.63
13	Grain yield per plot (Kg)	18.72	20.47	83.60	35.25
14	Biomass yield per plot (Kg)	18.59	20.50	82.20	34.73
15	Harvest index (%)	15.31	15.35	99.60	31.48
16	Kernel L/B ratio	12.39	13.21	87.90	23.92



**Fig 1. Diagrammatic representation of variability, heritability and genetic advance as percent of mean for grain yield and yield components in rice (*Oryza sativa* L.)**

The magnitude of genetic variability in a population decides the effectiveness of selection. It is a fact that greater the variability among the genotypes better is the chance for further improvement in the crop. In this study, there is a presence of narrow difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicating less influence of environment on the manifestation of these characters. These findings were similar to the findings of Kurmanchaliet *al.* (2019), Singh *et al.* (2018), Bagudamet *al.* (2018), Mishuet *al.* (2016), Pal *et al.* (2016) and Dhurailiet *al.* (2014). A high estimate of phenotypic and genotypic coefficients of variation was recorded for number of grains per panicle (34.99% and 28.22% respectively) followed by grain weight per panicle (33.50% and 26.32% respectively) indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. Therefore, these traits can be used for further improvement in rice breeding. These findings are in close agreement with the results of Perween *et al.* (2020) and Singh *et al.* (2018).

Heritability describes the proportion of genetic diversity which is passed from parents to progeny. Burton (1952) proposed that genetic variation, along with heritability, would offer a clearer understanding of the selection efficiency predicted. Estimates of heritability along with genetic progress are more useful in forecasting the benefit under selection (Johnson *et al.*, 1955). In the present set of materials, high heritability coupled with high genetic advance as percent of mean was recorded for harvest index (99.60% and 31.48%), days to first flowering (99.10% and 25.35% respectively), days to 50% flowering (99.00% and 22.98% respectively) and plant height (89.40% and 24.34% respectively), indicating the effectiveness of selection for the improvement of these traits (**table 1**). These results are in line with the findings of Perween *et al.* (2020), Kurmanchaliet *al.* (2019), Tiwari *et al.* (2019), Bagudamet *al.* (2018), and Singh *et al.* (2018).

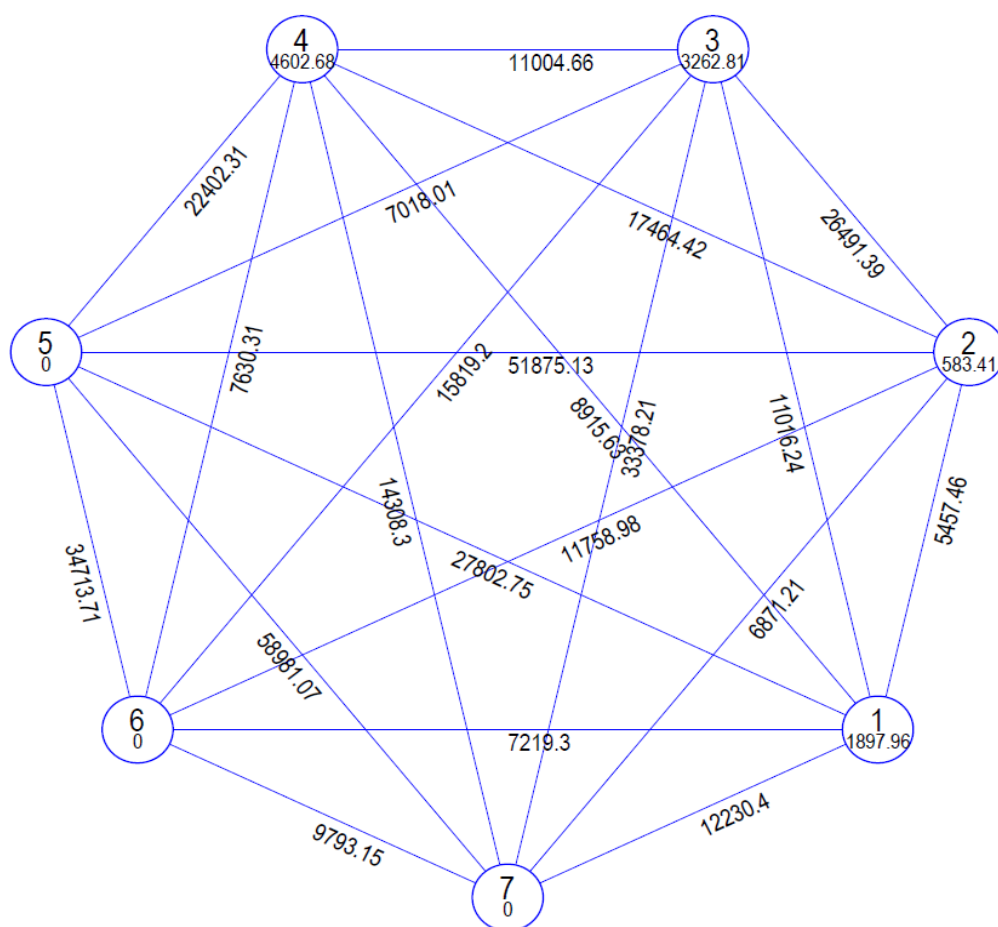
Genetic diversity is a prerequisite for any crop improvement program and it helps in the development of superior segregants. The importance of genetic diversity in selecting parents to recover transgressive segregants has been repeatedly emphasized by many workers (Devi *et al.*, 2017). The crosses between parents with maximum genetic divergence are responsive to genetic improvement. The multivariate analysis developed by Mahalanobis (1936) is most suitable in quantifying the degree of divergence in the available germplasm.  $D^2$  statistics is a numerical approach for measuring genetic diversity in a population. In the present study with 112 rice genotypes,  $D^2$  statistics grouped the whole set of genotypes into seven different clusters based on genetic distances (Fig. 3). The composition of the various clusters obtained from the  $D^2$  analysis is presented in Table 2, which indicates the presence of quite diverse material in the set of rice germplasm under study. Detailed insight into the diversity is therefore important to select desirable genotypes to be utilized in the breeding

programs. The clustering pattern indicated that 73 out of 112 germplasms belong to the same cluster, *i.e.* cluster I. On the other hand, 22 genotypes belong to cluster III, 10 belong to cluster II, 4 belong to cluster IV whereas clusters V, VI, and VII contain one genotype each. The highest intracluster distance was observed in cluster IV (4602.68) which comprised of 4 genotypes meaning these four genotypes are found to be more diverse in the same cluster. The highest inter-cluster distance (58981.07) was found between clusters V and VII indicating that hybridization between genotypes of these clusters would yield desirable segregants with the accumulation of favorable genes in segregating generations, followed by clusters II and V (51875.13) and clusters V and VI (34713.71). The smallest inter-cluster distance (5457.41) was observed between clusters I and II. The average intra and inter-cluster distances have been presented in Table 3 and diagrammatically represented in Figure 2.

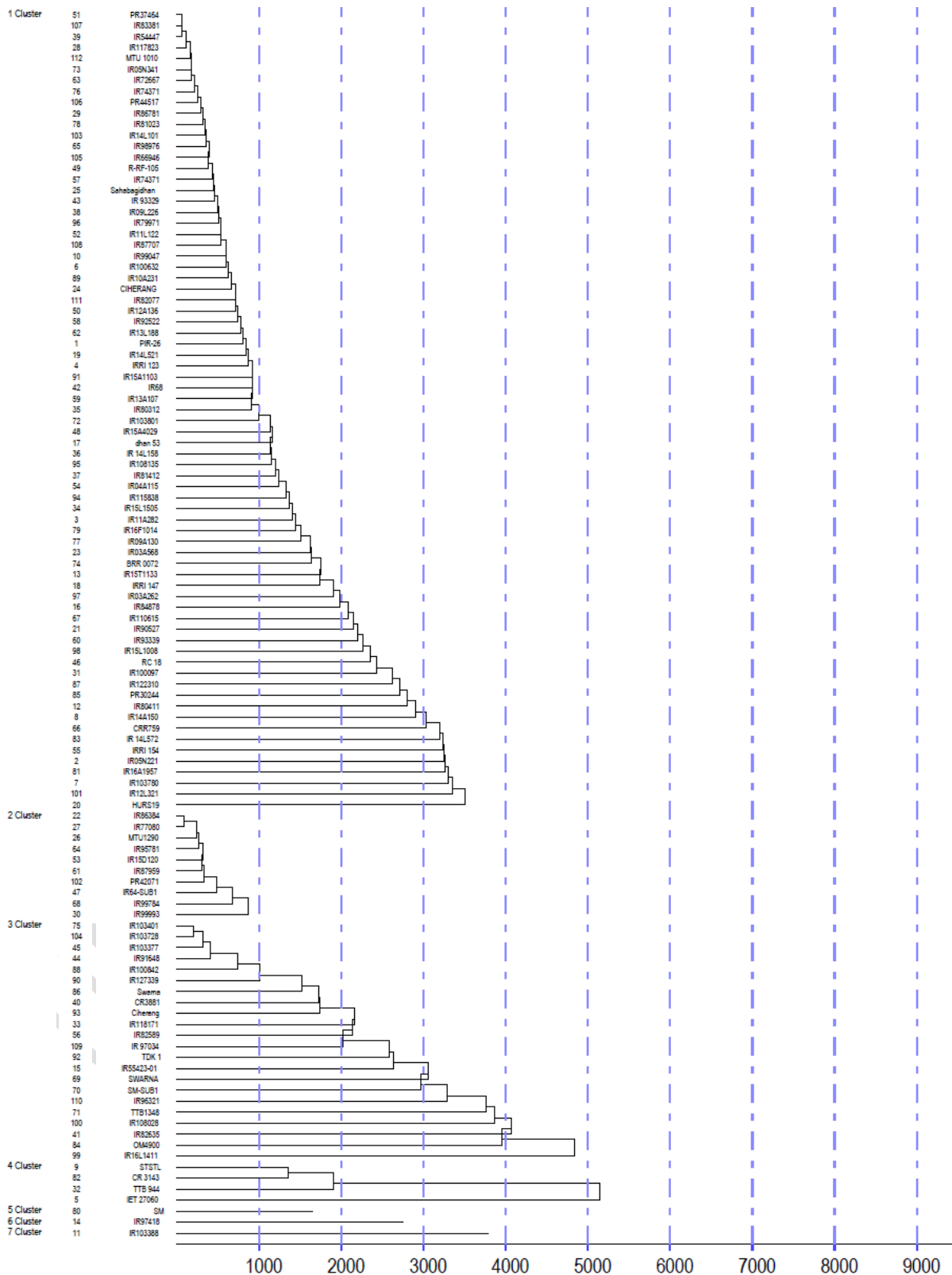
**Table 2: Grouping of 112 rice germplasm into seven clusters (by Tocher's method) using Mahalanobis'  $D^2$  method**

Clusters	Germplasm	Number
<b>I</b>	PR37464-31-3-2-2-2-3-1-B-5-1-1, IR83381-B-B-137-3, IR54447-3B-10-2, IR117823-B-43-1-1-1, MTU 1010, IR05N341, IR72667-16-1-B-B-3, IR74371-54-1-1, PR44517-10-2-1-B, IR86781-3-3-1-1, IR81023-B-116-1-2, IR14L101, IR98976-20-1-2-2, IR66946-3R-149-1-1 (BINA dhan 8), R-RF-105, IR74371-46-1-1, Sahabagidhan, IR 93329-61-B-21-12-21-IRGA-2RGA-, IR09L226, IR79971-B-191-B-B, IR11L122 (IR87761-39-2-3-2), IR87707-446-B-B-B, IR99047-B-B-B-B-47, IR100632-37-AJY 3-CMU 1, IR10A231, Ciherang, IR82077-B-B-71-1, IR12A136, IR92522-45-3-1-4, IR13L188, PIR-26>C0-2071-1-4-2-1, IR14L521, IRRI 123, IR15A1103, IR68, IR13A107, IR80312-6-B-3-2-B, IR103801-B-B-3-1, IR15A4029 (IR107051:15-1-1), BRRI dhan 53, IR 14L158, IR108135-B-1-AJY 1-B-1, IR81412-B-B-82-1, IR04A115, IR115838:5-5-5, IR15L1505, IR11A282, IR16F1014, IR09A130, IR03A568, BRR 0072, IR15T1133, IRRI 147 (BRRI dhan 47), IR03A262, IR84878-B-60-4-1, IR110615-C1-B-B-B-1-1, IR90527-B-577-2-B?B, IR93339:29-B-7-7-B-B-B-16, IR15L1008, RC 18, IR100097-B-B RGA-B RGA-8, IR122310:7-2-2, PR 30244-AC-V2 (NSICRC186), IR80411-B-49-1, IR14A150, CRR759-11-B-1, IR 14L572, IRRI 154, IR05N221 (KOMBOKA), IR16A1957, IR103780-B-B-6-2, IR12L321, HURS 19-4	73
<b>II</b>	IR86384-55-2-1-B, IR77080-B-34-3, MTU1290 (DST38-15-3-1), IR95781-15-1-1-4, IR15D120, IR87959-6-2-3-1-2-BAY B-CMU 1, PR42071-14-2-2-2, IR64-SUB1, IR 99784-255-29-1-1-1-2, IR99993-B-B RGA-B RGA-B RGA-1	10
<b>III</b>	IR103401-B-B-3-3, IR103728-B-B-B-B-1, IR103377-B-B-3-3, IR91648-B-20-B-3-1, IR100842-B-B RGA-B RGA-B RGA-9, IR 127339-10-1-1-1, Swarna, CR 3881-4-1-3-7-2-3(IET-26820), Ciherang-Sub1, IR118171-B-22-3-1-4, IR82589-B-B-84-3, IR	22

	97034-21-2-1-3, TDK 1, IR55423-01, Swarna-Sub1, Sambha mahsuri-Sub1, IR96321-1447-651-B-1-1-2, TTB 1348-1-1, IR108028-B-B-B-1-B-B, IR82635-B-B-75-2, OM4900, IR16L1411	
<b>IV</b>	SALT TOL SIN THWE LATT, CR 3143-1-1-1-2-1, TTB 944-31-10-1-2, CR 2860-S-B-189-1-1-1 (IET 27060)	4
<b>V</b>	Sambha mahsuri	1
<b>VI</b>	IR97418-32-3-1-AJY 1-1	1
<b>VII</b>	IR103388-B-B-2-3	1



**Figure 2.**Cluster diagram depicting Intra and inter-cluster distances



**Fig 3. Dendrogram representing the grouping of 112 rice genotypes by Tocher's Method**



**Table 3: Average Intra and inter Cluster Distances among 7 clusters (Tocher's method)**

	<b>Cluster I</b>	<b>Cluster II</b>	<b>Cluster III</b>	<b>Cluster IV</b>	<b>Cluster V</b>	<b>Cluster VI</b>	<b>Cluster VII</b>
<b>Cluster I</b>	1897.96	5457.46	11016.24	8915.63	27802.75	7219.30	12230.40
<b>Cluster II</b>	5457.46	583.41	26491.39	17464.42	51875.13	11758.98	6871.21
<b>Cluster III</b>	11016.24	26491.39	3262.81	11004.66	7018.01	15819.20	33378.21
<b>Cluster IV</b>	8915.63	17464.42	11004.66	4602.68	22402.31	7630.31	14308.30
<b>Cluster V</b>	27802.75	51875.13	7018.01	22402.31	0.00	34713.71	58981.07
<b>Cluster VI</b>	7219.30	11758.98	15819.20	7630.31	34713.71	0.00	9793.15
<b>Cluster VII</b>	12230.40	6871.21	33378.21	14308.30	58981.07	9793.15	0.00

Analysis of cluster means indicates the existence of considerable differences in the mean values of different traits (Table 4). The highest mean values for first flowering, 50% flowering, maturity, the weight of 1000 grains, grain yield per plot, and biomass yield per plot were seen in cluster VII. The highest mean values were seen in cluster V for number of spikelets in a panicle, number of grains in a panicle and spikelet fertility % with minimum values for plant height, weight of 1000 grains, and kernel L: B ratio. Cluster VI displayed the highest mean values for plant height and length of panicle whereas in the case of effective tillers per plant, the highest mean value was seen in cluster II and that for grain weight of a panicle in cluster III. Hence, germplasm included in clusters II, III, V, VI & VII seems to be promising, with various traits under study.

**Table 4: Mean values of different characters of 112 rice germplasms**

<b>Characters</b>	<b>Cluster I</b>	<b>Cluster II</b>	<b>Cluster III</b>	<b>Cluster IV</b>	<b>Cluster V</b>	<b>Cluster VI</b>	<b>Cluster VII</b>
<b>DF</b>	94.21	90.60	104.45	127.58	118.00	102.67	128.67
<b>D<sub>50</sub></b>	98.80	94.70	108.50	131.33	122.00	107.67	133.67
<b>DM</b>	127.13	123.60	138.00	160.58	152.00	136.67	162.67
<b>ET</b>	10.79	13.10	10.62	9.33	10.67	11.33	10.67
<b>PH</b>	105.35	98.02	108.78	134.39	91.97	181.67	140.03
<b>PL</b>	25.85	23.73	26.26	25.68	23.93	30.47	22.73
<b>SP</b>	132.29	82.73	196.76	172.67	243.67	131.67	74.67
<b>GP</b>	104.33	63.57	167.38	103.42	215.67	101.67	51.00
<b>SF%</b>	78.92	77.02	85.02	61.52	88.45	75.69	68.04
<b>GWP</b>	2.34	1.34	3.34	2.27	2.90	2.20	1.27
<b>GYP</b>	19.99	16.38	22.66	24.50	19.13	22.43	13.60
<b>GW</b>	23.54	23.81	21.84	22.80	15.33	22.80	24.53
<b>GY</b>	1.59	1.32	1.86	1.51	1.67	1.50	1.93

<b>BYP</b>	3.65	3.36	3.92	4.75	3.77	4.84	5.58
<b>HI</b>	43.96	39.73	47.64	31.30	44.21	30.89	34.66
<b>L/B</b>	3.17	3.35	2.80	2.94	2.63	3.30	3.23

The existence of a high level of genetic variation in the analyzed material was indicated by the discrimination of germplasm lines in too many clusters. Significant genetic divergence in the rice content has also been documented by previous workers. The existence of considerable genetic diversity among the germplasm lines examined in the present study showed that this material could serve as a good source for the selection of different parents for hybridization programs aimed at isolating suitable grain yield segregants and other significant characters and that the selection of parents depends primarily on the contribution of the characters. A comparison of the contribution of different characters towards total divergence was estimated based on the ranking method. The contribution of different characters to total divergence is presented in Table 5. Number of spikelets per panicle had maximum contribution (52.17%), followed by number of grains per panicle (27.26%), plant height (9.46%), days to first flowering (4.17%), and days to maturity (2.08%). Hence, number of spikelets per panicle, number of grains per panicle, plant height, days to first flowering, and days to maturity were found to be potential contributors to genetic divergence in the germplasm studied. These results were in agreement with the findings of Archana *et al.* (2018), Behera *et al.* (2018), Ashok *et al.* (2017), Medhabati *et al.* (2013), and Ovung *et al.* (2012) who have also studied diversity in rice genotypes using 21, 38, 64, 32, and 70 genotypes respectively.

**Table 5: Percent contribution of each character towards total genetic divergence**

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Sl.No.	Characters	% Contribution	Times Ranked 1 <sup>st</sup>
1	Days to first flowering	4.17	259
2	Days to 50% flowering	0.19	12
3	Days to maturity	2.08	129
4	Number of effective tillers per plant	0.00	0.00
5	Plant height	9.46	588
6	Panicle length (cm)	0.02	1
7	Number of spikelets per panicle	52.17	3243
8	Number of grains per panicle	27.26	1717
9	Spikelet fertility (%)	1.19	74
10	Grain weight per panicle (g)	0.00	0
11	Grain yield per plant (g)	1.17	73
12	1000 grain weight (g)	0.03	2
13	Grain yield per plot (Kg)	0.00	0
14	Biomass yield per plot (Kg)	0.00	0
15	Harvest index (%)	1.9	118
16	Kernel L/B ratio	0.00	0

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