Biological Forum – An International Journal **13(4): 687-695(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Variability and Divergence Studies for Yield and its related traits in Rice (*Oryza sativa* L.)

S. K. Singh[1], Manoj Kumar S. C.[1], Mounika Korada[1*], Amrutlal Khaire[1], Prasanta Kumar Majhi[1,2], D. K. Singh[1,3] and Jayasudha S.[1]

[1]Department of Genetics and Plant Breeding,
Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, (Uttar Pradesh), India.
[2]Department of Plant Breeding and Genetics,
Odisha University of Agriculture and Technology, RRTTS, Keonjhar, (Odisha), India.
[3]Department of Genetics and Plant Breeding, College of Horticulture,
Banda University of Agriculture and Technology, Banda, (Uttar Pradesh), India.

(Corresponding author: Mounika Korada)*
(Received 04 September 2021, Accepted 08 November, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The amount of genetic variability present in crop germplasm and the knowledge of its nature and magnitude is very important before starting any crop improvement program. In this view, fifty-five rice genotypes were evaluated for studying the genetic parameters (genetic variability, heritability and genetic advance as percent of mean) and genetic divergence for yield contributing characters at three different locations in Eastern Uttar Pradesh, India. The study was conducted during *Kharif* 2020 using Alpha lattice design. The data were collected on 15 quantitative traits. The combined ANOVA revealed the presence of significant variability in experimental material for all the traits under study across all three locations. High GCV and PCV were recorded for traits like grain yield per plot, biomass and grain yield per hectare. High heritability with high genetic advance as percent of mean was reported for plant height, number of productive tillers per plant, filled grains per panicle, grain yield per plot, grain yield per hectare, biomass, harvest index, test weight, and kernel L/B ratio. This suggests that these characters are governed by additive genes in their expression, implying that environmental influence is minimal and that they will respond better to selection. Further, genetic diversity analysis among the 55 rice genotypes using Mahalanobis's D^2 distributed them into eight clusters with cluster I containing the maximum number of genotypes. The highest intra-cluster distance was recorded in cluster VII. The maximum inter-cluster distance was observed between clusters V and VI indicating wider genetic diversity between these clusters, and hence, crosses involving parents belonging to these clusters are likely to produce wide variability and transgressive segregants with high heterotic effects.

Keywords: Genetic Divergence, Heritability, Mahalanobis' D^2, Rice, Variability.

INTRODUCTION

Rice (*Oryza sativa* L.) is an autogamous monocotyledon cereal crop that belongs to the genus *Oryza* of the grass family *Poaceae* (*Graminae*) and has chromosome number 2n=24. It is the staple food for nearly 4 billion people around the world, providing 27% of calories in low- and middle-income countries. Global rice demand is expected to rise from 479 million tons of milled rice in 2014 to 536-551 million tons in 2030, owing to expected population growth, income growth, and a decrease in rice area (IRRI: Rice Today-https://ricecrp.org/importance-of-rice/).

Almost 95% of the rice production happens in Asian countries and nearly half of the global population consumes it. Rice cultivation ranks third in agricultural commodity production, after sugarcane and maize (Priya *et al.*, 2019). Rice is grown on an area of 167.25 million hectares with gross production of 496.22 million tonnes around the world (FAO, 2019). Globally India is the second largest producer of rice after China. In India rice is cultivated on an area of 43.78 million hectares with production and productivity of 118.43 million tons and 2705 kg/ha respectively. In India, Uttar Pradesh stands second with 15.52 million Tonnes production of rice after West Bengal with 15.57 million tonnes (Directorate of Economics and Statistics, 2020).

The genetic improvement of any crop generally requires knowledge of the nature and magnitude of variation in its available germplasm, the relationship between yield and other agronomic characteristics, and the extent to which environmental factors influence the

expression of these traits (Edukondalu *et al.,* 2017). Therefore, studying various genetic parameters *viz*., genetic variability, heritability and genetic advance is of preliminary importance. Genetic variability among the traits is necessary for breeding and in selecting the desirable genotypes. Heritability can be used to assess the degree of transmissibility of desired traits to progenies during the breeding process (Sabesan *et al.,* 2009). The genotypic coefficient of variation coupled with estimates of heritability would provide an accurate picture of the amount of genetic advance to be expected from a selection (Jayasudha *et al.,* 2010).High heritability coupled with high genetic advance would be a more useful tool in predicting the resultant effect in the selection of best genotypes for yield and its components. Previous studies of Sumanth *et al.,* (2017), Behera *et al.,* (2018), Kujur *et al.,* (2019), Rahman *et al.,* (2019) and Panda *et al.,* (2020) and on rice showed the existence of considerable variability among the genotypes and a wide genetic variation in rice populations

Genetic diversity is vital in plant breeding as progeny from divergent parents tend to exhibit superior heterosis and provide a wide-ranging spectrum of variability in segregating generations. Hybridization among different genotypes and handling of their segregants is the most common and effective means of generating variability (Singh *et al.,* 2019). The assessment of genetic diversity between and within groups or clusters is important for the proper selection of parents and for the better search of heterosis (Arunachalam, 1981). The success of genetic diversity results were reported by many scientists. Keeping this in view, the present investigation was carried out to study various genetic parameters and genetic diversity among 55 rice genotypes across three different locations.

MATERIAL AND METHODS

A. Plant material and layout

Fifty-five rice genotypes including five checks *viz.*,HUR-105 (LC-1), BRR Dhan 64, DRR Dhan 48, MTU1010, Sambha Mahsuri were evaluated during *Kharif*-2020 at three locations of Eastern Uttar Pradesh *viz*., 1. Agricultural research farm of Banaras Hindu University, Varanasi2. Bhikaripur, Varanasi district and 3. Rampur, Mirzapur district. The experimental material used in the present study was obtained from IRRI South Asia Hub, Hyderabad, and is presented in Table 1. The field experimentation of this material was conducted using an Alpha Lattice Design with three replications across all three locations. Each replication consists of 5 blocks with 11 plots each. 21 days old seedlings of each genotype were transplanted to the main field with a spacing of 20 x 15 cm between the rows and plants within a row.

All the regular agronomic practices and plant protection measures were followed in all three experimental locations to ensure uniform, healthy and stable crop growth.

Table 1: List of fifty-five rice genotypes used in the present study.

Sr. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	HL19WS-33A-1	20	HL19WS-33A-359	38	HL19WS-33B-224
2	HL19WS-33A-12	21	HL19WS-33A-367	39	HL19WS-33B-225
3	HL19WS-33A-16	22	HL19WS-33A-401	40	HL19WS-33B-239
4	HL19WS-33A-26	23	HL19WS-33A-491	41	HL19WS-33B-246
5	HL19WS-33A-39	24	HL19WS-33A-589	42	HL19WS-33B-249
6	HL19WS-33A-40	25	HL19WS-33A-604	43	HL19WS-33B-252
7	HL19WS-33A-49	26	HL19WS-33A-625	44	HL19WS-33B-317
8	HL19WS-33A-51	27	HL19WS-33A-628	45	HL19WS-33B-324
9	HL19WS-33A-59	28	HL19WS-33B-2	46	HL19WS-33B-359
10	HL19WS-33A-60	29	HL19WS-33B-6	47	HL19WS-33B-361
11	HL19WS-33A-61	30	HL19WS-33B-36	48	HL19WS-33B-369
12	HL19WS-33A-66	31	HL19WS-33B-43	49	HL19WS-33B-405
13	HL19WS-33A-133	32	HL19WS-33B-75	50	HL19WS-33B-439
14	HL19WS-33A-135	33	HL19WS-33B-77		Checks
15	HL19WS-33A-137	34	HL19WS-33B-127	51	Samba Mahsuri
16	HL19WS-33A-139	35	HL19WS-33B-128	52	MTU1010
17	HL19WS-33A-232	36	HL19WS-33B-171	53	BRR Dhan 64
18	HL19WS-33A-332	37	HL19WS-33B-182	54	DRR Dhan 48
19	HL19WS-33A-358			55	HUR 105 (LC-1)

B. Morphological data

Observations were recorded from five randomly selected competitive plants of each genotype in each replication for number of productive tillers per plant, plant height (cm), panicle length (cm), number of filled grains per panicle, spikelets fertility percent, harvest index, 1000-grain weight (g), kernel length (mm), kernel breadth (mm) and kernel L/B ratio. The data on days to 50% flowering, days to maturity, grain yield per plot (kg), grain yield per ha (kg) and biomass per plot (kg) were recorded on a whole plot basis.

C. Statistical analysis

The mean data for all the traits obtained from each replication was subjected to statistical analysis. Combined ANOVA of Alpha lattice design computed to test the significance as suggested by Patterson and Williams, 1976. Genotypic and phenotypic coefficients of variation were calculated by the method given by Burton, 1952 and heritability (h^2) in the broad sense was estimated by the formula specified by Hanson *et al.,* (1956). Genetic advance as percent mean was assessed for each trait under study using the formula stated by Johnson *et al*., 1955. SAS 2009 version was used for computing combined ANOVA of Alpha lattice Design and MS- Excel 2019 for estimating the genetic parameters.

According to Sivasubramanian and Menon (1973), the PCV and GCV are classified as low (<10%), moderate (10-20%), and high (> 20%). The heritability estimates were categorized into low (0 - 30%), moderate (30 - 60%) and high (>60%) as proposed by Robinson *et al*., 1949. GA percent mean values were categorized into low (<10%), moderate (10-20%), and high (> 20%) as given by Johnson (1955).

The analysis of genetic divergence was done using Mahalanobis's D^2 statistic (1936). The grouping of genotypes into different clusters was done using Tocher's method as described by Rao, 1952. The procedure described by Singh and Choudhary (1977) was used to estimate the average intra and inter-cluster distances, cluster means, and contribution of different characters to total divergence. Genetic divergence analysis was done using INDOSTAT version 8.1.

RESULTS AND DISCUSSION

The combined Analysis of Variance (ANOVA) revealed significant differences among the genotypes for all the characters across all three environments, indicating the presence of sufficient amount of genetic variability in the studied material (Table 2). It also showed that significant results existed for environments and genotype x environment, indicating that environments were different and the interaction between genotype and environment was present. However, the variation among blocks within the replication was insignificant.

Table 2. Combined ANOVA table showing mean sum of square for different characters in rice.

Source of Variation / Traits	Environment (E)	Replication	Genotype (G)	Block(rep)	E x G	Residuals
	df=2	df=2	df=54	df=12	df=108	df=316
Days to 50% flowering	739.35**	6.22	354.06**	3.57	18.85**	2.1
Days to maturity	570.79**	8.37*	349.97**	2.67	19.76**	2.76
Plant height	3667.38**	73.38	3315.48**	61.37	100.49**	46.12
No. of productive tillers	40.46**	0.41	14.77**	0.17	4.91**	0.15
Panicle length	0.83	14.11**	31.8**	0.85	4.01**	1.33
No. of Filled grains	5546.61**	165.54	4352.24**	58.6	643.46**	61.08
Spikelet fertility %	916.68**	83.33	463.65**	28.33	60.63**	31.94
Grain Yield per plot	0.5**	0.01*	0.21**	0	0.04**	0
Biomass	6.78**	0.17*	2.48**	0.05	0.39**	0.04
Harvest index	581.25**	7.24	152.61**	2.55	35.71**	3.22
Test Weight	31.09**	0.1	99.68**	0.11	5.87**	0.08
Kernel Length	0.28**	0.01	3.37**	0	0.16**	0
Kernel Breadth	0.56**	0	0.26**	0	0.02**	0
Kernel L/B Ratio	2.94**	0.01*	1.68**	0	0.1**	0
Grain yield per Ha	15299757.7**	249121.7*	6432955.2**	69232.2	1131112**	59622.9

** Significant at 1% probability level * Significant at 5% probability level

A. Genetic Parameters (Variability, Heritability and Genetic Advance)

In the present investigation, the variation among genotypes was estimated as the coefficient of variation. The phenotypic coefficient of variation (PCV) was marginally higher than the genotypic coefficient of variation (GCV) indicating the influence of environment on the expression of these traits in the genotypes (Table 3 and Fig.1). High GCV and PCV were recorded for traits *viz*., grain yield per plot, biomass and grain yield per hectare. The high GCV suggests that direct selection may be effective for such traits. These results are in conformity with those obtained for grain yield per plant and biological yield by Shukla *et al.* (2005) and Singh (2021) and for grain yield per hectare by Islam *et al.* (2015). Moderate PCV and GCV were observed for characters like plant height, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility percent, harvest index, test weight and kernel L/B ratio. These results were in accordance with the research findings of Singh, (2021) for spikelet fertility percent, test weight and kernel L/B ratio, Singh *et al.*, 2021 for plant height, number of productive tillers per plant and Barhate *et al.*, (2021) for number of filled grains per panicle, harvest index. Low PCV and GCV were observed for characters like days to 50% flowering, days to maturity, panicle length (cm), kernel length (mm) and kernel breadth (mm). The low estimates of GCV suggest that direct selection for such traits may be ineffective. The

results were in agreement with the findings of Srujana *et al*., 2017 for 50% flowering, days to maturity, panicle length (cm), and Singh, (2021) for kernel length (mm) and kernel breadth (mm).

Heritability of a genetic character is key in understanding its response to selection. In the present study, the heritability in broad sense varied from 58.37% (spikelet fertility percent) to 99.255% (1000 grain weight). High heritability was reported for all the characters viz., days to 50% flowering, days to maturity, number of productive tillers per plant, plant height (cm), panicle length (cm), number of filled grains per panicle, grain yield per plot (kg), grain yield per ha (kg), biomass per plant (kg), harvest index, 1000-grain weight (g), kernel length (mm), kernel breadth (mm) and kernel L/B ratio except spikelet fertility percent, which showed moderate heritability (Table 3). The results were similar to the research findings of Tuwar *et al.*, 2013, Dhurai *et al.*, 2014, and Keerthiraj *et al*., 2020.

Almost all studied characters had high heritability, suggesting that selecting for such traits based on phenotypic values could be effective. However, selection would be most effective if the character has a high heritability combined with high genetic advance (Johnson *et al*., 1955).

Table 3: Estimates of variability, heritability and genetic advance as percent of mean for grain yield and yield traits in rice.

Traits	Mean	Range		Coefficient of Variation		Heritability (h^2 bs) %	GAM
		Maximum	Minimum	PCV (%)	GCV (%)		
Days 50% flowering	85.46	99.33	71.22	7.34	7.14	94.65	14.31
Days to maturity	109.02	122.89	94.56	5.76	5.56	93.01	11.04
Plant height	118.08	166.29	91.87	17.01	16.01	88.56	31.03
No. of tillers per plant	8.86	12.43	6.28	12.6	11.81	87.9	22.81
Panicle length	23.87	27.32	19.86	8.8	7.36	69.89	12.68
No. of filled grains	108.87	174.5	62.76	19.98	18.65	87.09	35.85
Spikelet fertility %	78.03	89.54	49.29	11.23	8.58	58.37	13.5
Grain yield per plot	0.522	0.9	0.22	27.77	26.47	90.81	51.95
Biomass	2.29	3.52	1.26	22.67	21.02	86	40.16
Harvest index	25.25	35.53	17.56	15.95	14.27	80.13	26.32
Test weight	21.74	29.14	13.9	14.91	14.85	99.25	30.48
Kernel length	6.22	7.92	4.97	9.67	9.61	98.72	19.66
kernel breadth	1.87	2.29	1.52	8.75	8.68	98.48	17.75
Kernel L/B ratio	3.35	4.35	2.37	12.58	12.53	99.16	25.71
Grain yield per Ha	2905.02	4987.04	1206.17	27.73	26.42	0.9081	51.87

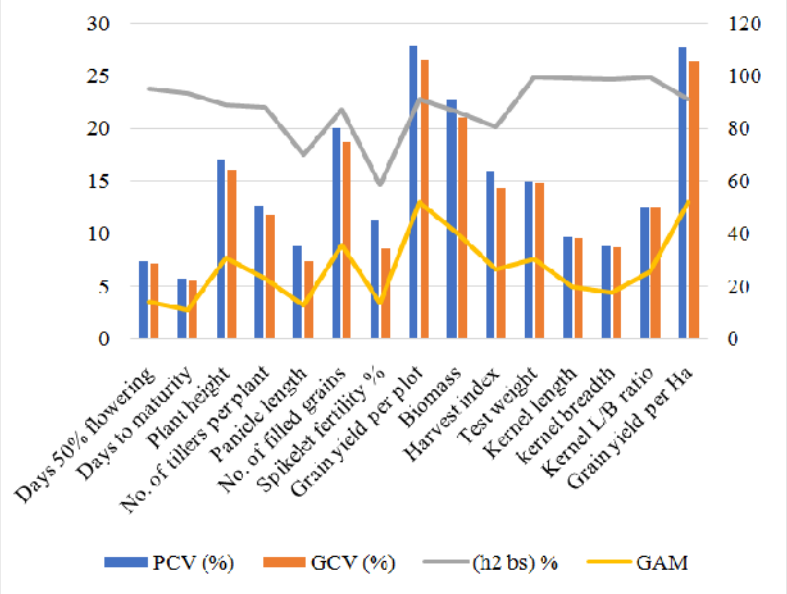

Fig 1. Genetic variability parameters (GCV, PCV, heritability (bs), and GA as % of mean) for 15 morphological traits in rice.

High heritability with high genetic advance as percent of mean was reported for plant height, number of productive tillers per plant, filled grains per panicle, grain yield per plot(g), grain yield per hectare (kg), biomass, harvest index, test weight, and kernel L/B ratio (Table 3). This expression of these characters are governed by additive genes and hence environmental influence would be least, and thus they will respond better to selection. Similar results were found by Singh, (2021) and Singh, (2021). High heritability with moderate genetic advance as percent of mean was observed for traits *viz.*, days to 50% flowering, days to maturity, panicle length, kernel length and kernel breadth. These consequences demonstrated that both additive and non-additive gene action predominate, implying that selection may be ineffective. The results were in accordance with the research findings of Dhurai *et al.*, (2014), Ashok *et al*., (2016) and Khaire *et al.*, (2017).

Genetic Diversity:

Contribution of each character towards total divergence. Pivotal condensation method measured the degree of diversification and determined the relative contribution of all the 15 characters to total divergence and was presented in Table 6 and fig 2. Among all the characters included in the study, plant height showed the highest contribution (33.4%) towards total genetic divergence followed by test weight (15.08%), kernel length (14.01), days to 50% flowering (13.6%), number of filled grains per panicle (8.55%), kernel breadth (3.64%), panicle length (3.1%), spikelet fertility (2.76%) grain yield per plot (2.15%), kernel L/B ratio (1.82%) and biomass (1.48%). The characters like number of tillers per plant (0.34%) and harvest index (0.07%) showed negligible contribution towards total divergence. On the other hand, characters *viz*., days to maturity and grain yield per hectare showed no contribution towards total divergence. The traits *viz.*, plant height, test weight, kernel length, days to 50% flowering and number of filled grains per panicle were the main contributors which accounted for 84.64 % of total genetic divergence.

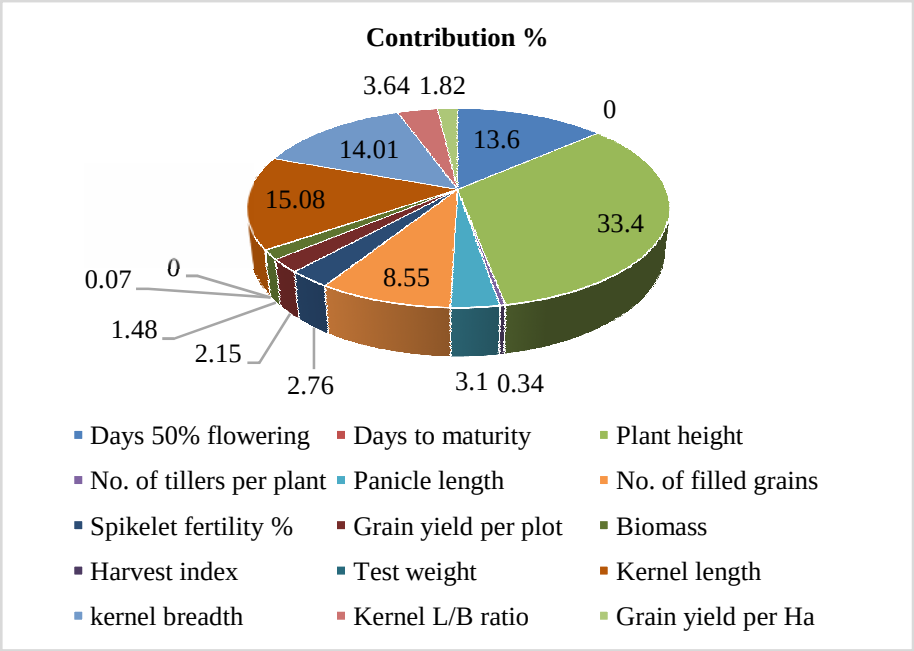

Fig. 2. Percent contribution of each character to the total divergence.

Clustering of genotypes. The fifty-five rice genotypes were grouped into eight different clusters using Tocher's method (Table 4) with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values and the distribution of 55 genotypes into eight clusters is at random. The maximum number of genotypes were grouped into cluster I (16 genotypes). Cluster II had 11 genotypes followed by Cluster VII with 8 genotypes, Cluster III with 7 genotypes and Cluster VI with 2 genotypes. Cluster V and VIII are solitary clusters with a single genotype in each. Kamlesh *et al.*, 2015 grouped 40 genotypes into 8 clusters and Singh *et al.*, 2019 grouped 50 genotypes into 8 clusters using Mahalanobis's D^2 statistic.

Intra and Inter-cluster distances. The average intra and inter-cluster D^2 values within and among the clusters were presented in Table 5 and Fig. 3 and 4. Intra-cluster D^2 values ranged from 0.00 (Cluster V and VIII) to 43.29 (Cluster VII). The high intra-cluster distance in cluster VII indicates the presence of wide genetic diversity among the genotypes present within this cluster. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. The inter-cluster distances were worked out considering 15 characters

and these distances ranged from 20.84 to 108.66. The maximum inter-cluster distance was observed between clusters V and VI (108.66), followed by clusters III and IV (90.54), clusters IV and VI (81.26) and clusters IV and VIII (73.56) suggesting that there is wide genetic diversity between these clusters and crosses can be made between the genotypes of these clusters to obtain desirable transgressive segregants. Similar findings were reported by Priyanka *et al*., (2015) and Mukul *et al*., (2019).

Table 4: Clustering of fifty-five genotypes of rice.

Clusters	No. of genotypes	Name of the genotypes
Cluster I	16	HL19WS-33A-359, HL19WS-33B-171, HUR 105, HL19WS-33B-224, HL19WS-33A-604, HL19WS-33A-625, HL19WS-33A-1, HL19WS-33A-60, HL19WS-33A-358, HL19WS-33B-324, HL19WS-33A-139, HL19WS-33B-317, HL19WS-33B-127, HL19WS-33B-225, HL19WS-33B-249, HL19WS-33A-61
Cluster II	11	HL19WS-33A-49, HL19WS-33B-246, HL19WS-33A-51, HL19WS-33A-332, HL19WS-33A-628, HL19WS-33B-359, HL19WS-33B-239, HL19WS-33A-66, HL19WS-33B-75, HL19WS-33A-491, HL19WS-33A-135
Cluster III	7	HL19WS-33B-36, HL19WS-33B-405, DRR Dhan 48 HL19WS-33B-369, BRR Dhan 64, HL19WS-33A-59, HL19WS-33A-589
Cluster IV	9	HL19WS-33A-40, HL19WS-33A-39, HL19WS-33A-232, HL19WS-33A-26, HL19WS-33B-43, HL19WS-33B-128, HL19WS-33B-77, HL19WS-33B-361, MTU 1010
Cluster V	1	Samba Mahsuri
Cluster VI	2	HL19WS-33A-133, HL19WS-33A-137
Cluster VII	8	HL19WS-33B-2, HL19WS-33B-6, HL19WS-33B-439, HL19WS-33B-182, HL19WS-33B-252, HL19WS-33A-16, HL19WS-33A-12, HL19WS-33A-401
Cluster VIII	1	HL19WS-33A-367

Table 5: Intra and Inter cluster D^2 values among the eight clusters.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	12.01	27.18	26.41	20.84	42.5	73.55	40.55	65.74
Cluster II		16.26	33	33.59	59.21	41.87	31.04	38.92
Cluster III			17.79	42.61	27.86	90.54	42	49.95
Cluster IV				24.9	61.36	81.26	52.15	73.56
Cluster V					0	108.66	71.01	45.48
Cluster VI						5.96	62.69	49.01
Cluster VII							43.29	58.06
Cluster VIII								0

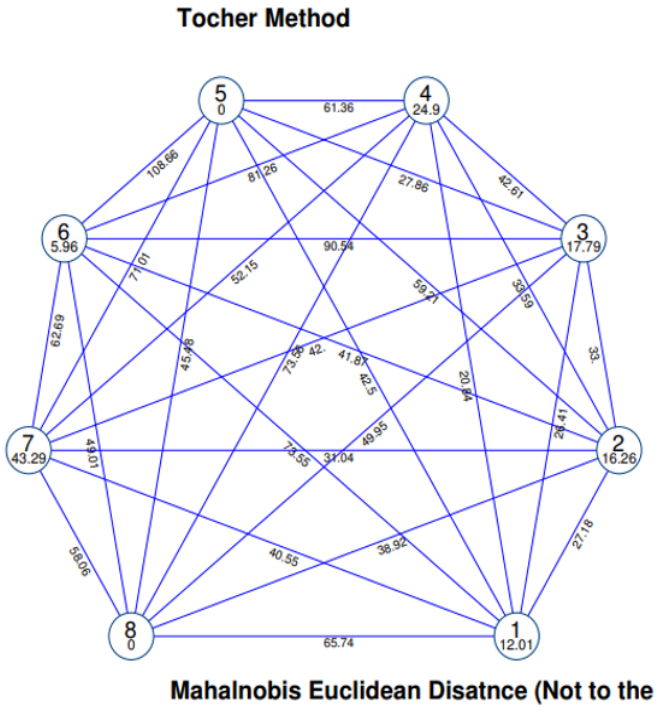

Fig. 3. Cluster diagram representing eight clusters and their intra and inter distance D^2 values.

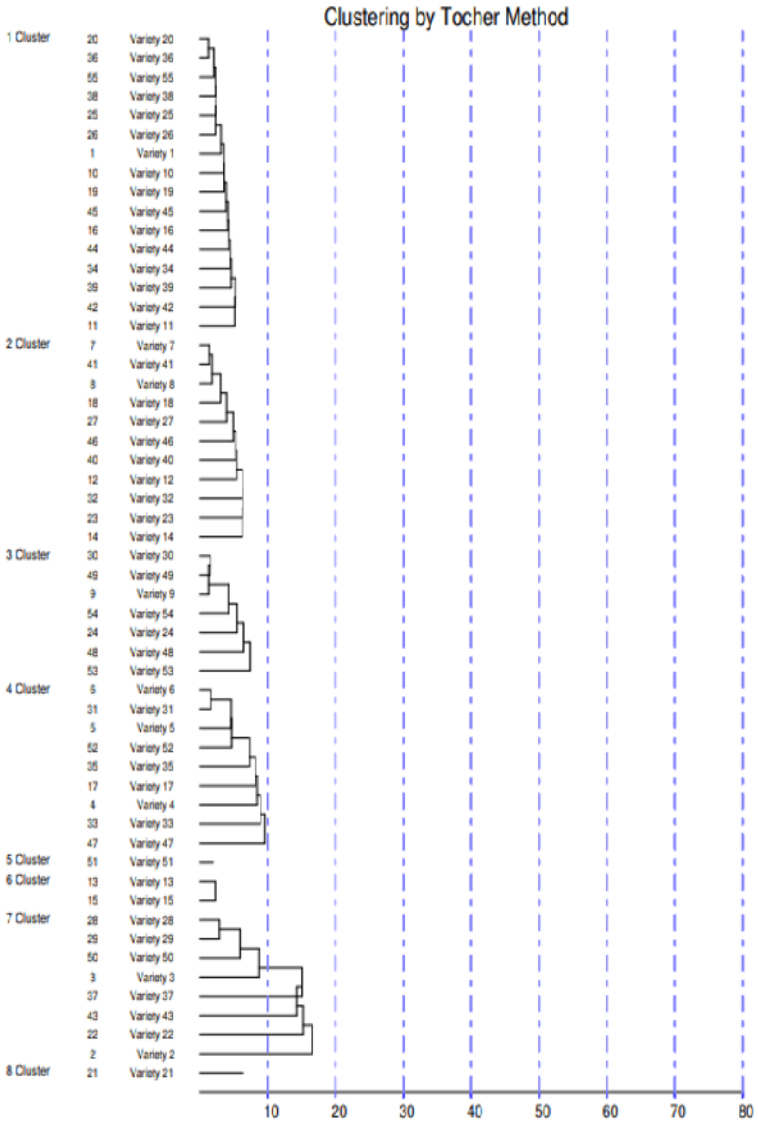

Fig. 4. Dendrogram showing the relationship among the fifty-five genotypes of rice.

Cluster means. Cluster means specifies the average performance of all the genotypes present in a specific cluster. The cluster mean values for 15 characters recorded in the present study are presented in Table 6. The cluster means of Days to 50 percent flowering ranged from 78.76 (Cluster IV) to 98.86 (Cluster VI). For days to maturity, cluster means varied between 102.43 (Cluster IV) to 121.94 (Cluster VI). Number of tillers per plant showed cluster means ranging from 6.33 (Cluster VI) to 11.34 (Cluster VIII). For plant height, cluster means ranged between 97.11 (Cluster V) and 161.11 (Cluster VI). Panicle length showed cluster means ranging from 21.83 (Cluster III) to 25.82 (Cluster IV).

The cluster means of filled grains per panicle ranged from 96.32 (Cluster VI) to 146.6 (Cluster V), spikelet fertility percent ranged from 71.07 (cluster VII) to 84.53 (cluster V), grain yield per plot ranged from 0.39 (cluster VIII) to 0.56 (cluster VI); biomass ranged from 1.96 (cluster III) to 2.81 (cluster VI); harvest index ranged from 22.03 (cluster VI) to 26.37 (cluster IV) and grain yield per hectare 2602.78 (Cluster VII) to 3117.59 (cluster VI). The cluster means for test weight were ranged from 13.9 (Cluster V) to 28.23 (cluster VI), kernel length ranged from 5.18 (Cluster V) to 7.72 (cluster VI), kernel breadth ranged from 1.52 (Cluster V) to 2.07 (Cluster VII) and kernel L/B ratio ranged from 2.81 (Cluster III) to 4.09 (cluster VI). The divergence in quantitative characters were also reported by Subudhi *et al.*, (2008), Parikh *et al.*, (2011), Priyanka *et al.*, (2015), Behera *et al.*, (2018) and Singh *et al.*, (2020). Discrepancies in the results could be attributed to dissimilar sets of genotypes as well as the role of environmental variability, as stated by Barhate *et al.*, (2020). The above results indicated a wide range of mean values between the clusters and these clusters can be exploited in the breeding programs for specific trait improvement.

Table 6: Mean values of eight clusters estimated by Tocher's method from 55 rice genotypes.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Times ranked 1st	contribution %
Days 50% flowering	84.17	85.15	86.76	78.76	96.56	98.56	88.9	96.22	202	13.6
Days to maturity	107.72	108.67	110.24	102.43	120.44	121.94	112.44	119.78	0	0
Plant height	103.47	134.21	108.62	110.18	97.11	161.1	129.9	148.17	496	33.4
No. of tillers per plant	8.84	8.63	9.07	9.74	9.43	6.33	8.34	11.34	5	0.34
Panicle length	23.38	24.49	21.83	23.99	22.42	25.82	25.59	22.39	46	3.1
No. of filled grains	108.97	106.98	127.04	102.06	146.6	96.32	102.1	103.68	127	8.55
Spikelet fertility %	78.91	77.79	78.43	81.86	84.53	81.38	71.07	72.02	41	2.76
Grain yield per plot	0.55	0.55	0.49	0.53	0.51	0.56	0.47	0.39	32	2.15
Biomass	2.16	2.6	1.96	2.27	2.01	2.81	2.39	2.34	22	1.48
Harvest index	26.34	24.33	25.75	26.37	25.85	22.03	23.8	22.06	1	0.07
Grain yield per Ha	3053.86	3043.16	2703.17	2940.12	2843.21	3117.59	2602.78	2156.17	0	0
Test weight	21.94	22.91	19.46	20.94	13.9	28.23	22.81	15.38	224	15.08
Kernel length	6.38	6.24	5.46	6.38	5.18	7.72	6.22	5.69	208	14.01
kernel breadth	1.82	1.92	1.97	1.73	1.52	1.89	2.07	1.61	54	3.64
kernel L/B ratio	3.51	3.28	2.81	3.69	3.42	4.09	3.04	3.53	27	1.82

CONCLUSION

The current study required an interrelationship between yield and other traits among the 55 tested genotypes due to the presence of adequate genetic variability, heritability, and genetic advance. Grain yield per plot, biomass, and grain yield per hectare all had high estimates of GCV, PCV, and heritability, as well as high genetic advance. For a successful breeding program selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. Based on the inter-cluster distances, clusters V and VI are highly divergent followed by clusters III and IV and genotypes included in these clusters can be crossed. However, in addition to genetic distance, *per se* yield and yield contributing traits should be taken into consideration. Taking these factors such as genetic distance and *per se* performance into consideration, genotypes *viz*.,HL19WS-33B-369, DRR Dhan 48, HL19WS-33A-137, BRR Dhan 64, HL19WS-33A-589, HL19WS-33A-133 and Sambha Mahsurican be selected for the use in the breeding programmes as they are present in divergent clusters and have better *per se* performance.

Acknowledgment. The authors thankfully acknowledge IRRI-South Asia Hub, Hyderabad for providing the requisite germplasm and Harvest Plus Project of IRRI funded by IFPRI-CIAT, USA for their support to get this work accomplished.

REFERENCES

Arunachalam, V. (1981). Genetic distance in plant breeding. *Indian Journal of Genetics and Plant Breeding, 41*, 226-236.

Ashok, S., Jyothula, D. P. B., Babu, D. R., & Rao, V. S. (2016). Studies on genetic variability, heritability and genetic advance for yield components and grain quality parameters of rice (*Oryza sativa* L.). *The Andhra Agriculture Journal, 63*(3): 575-579.

Barhate, K. K., Jadhav, M. S., & Bhavsar, V. V. (2021). Genetic variability, heritability and genetic advance in aromatic lines of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, *10*(3), 360-362.

Behera, Biswaranjan, Simanchal Sahu, Rajesh Kumar Kar, and Ritu Kumari Pandey (2018). Studies on genetic variability for some metric traits in slender grain rice genotypes. *Journal of Applied and Natural Science*, *10*(1): 375-378.

Behera, P. P., Singh, S. K., Singh, D. K., Reddy, Y. S., Habde, S., Khaire, A., & Ashrutha, M. A. (2018). Genetic diversity analysis of rice (*Oryza sativa* L.) genotypes with high grain zinc content for yield and yield traits. *Journal of Pharmacognosy and Phytochemistry*, *7*(4), 1319-1323.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceedings of the VI International Grassland Congress, 1952*, 277-283.

DE&S, (2020). https://eands.dacnet.nic.in/PDF/Pocket%202020-%20Final%20web%20file.pdf

Dhurai, S. Y., Bhati, P. K., & Saroj, S. K. (2014). Studies on genetic variability for yield and quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. *The Bioscan*, *9*(2), 745-748.

Edukondalu, B., Reddy, R. V., Rani, S. T., Kumari, C. A., & Soundharya, B. (2017). Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, *6*(10), 2369-2376.

FAO, 2019. https://www.fao.org/publications/sofa/2019/en/

Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. *Agronomy journal*, *48*(6), 268-272.

IRRI-Rice today-https://ricecrp.org/importance-of-rice/

Islam, M. A., Raffi, S. A., Hossain, M. A., & Hasan, A. K. (2015). Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. *Progressive Agriculture*, *26*(1), 26-31.

Jayasudha, S., & Sharma, D. (2010). Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Electronic Journal of Plant Breeding*, *1*(5), 1332-1338.

Johnson, H. W., Robinson, H. F., Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, *47*: 314- 318

Kamlesh, K., Shinde, S. R., & Jagtap, S. M. (2015). Genetic divergence in upland rice (*Oryza sativa* L.). *International Journal of Plant Sciences (Muzaffarnagar)*, *10*(1), 60-63.

Keerthiraj, B., & Biju, S. (2020). Genetic variability, heritability and genetic advance of yield and lodging-related traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, *11*(04), 1093-1098.

Khaire, A. R., Kunkerkar, R. L., Thorat, B. S., Gavai, M. P., & Bhave, S. G. (2017). Studies on genetic variability for yield and yield contributing traits in local rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, *6*(5), 1376-1378.

Kujur, M. J., Koutu, G. K., Krishnan, R. S. R., & Singh, Y. (2019). Genetic variability of agro-morphological traits in traditional varieties of rice (*Oryza sativa* L.) from Madhya Pradesh, India. *International Journal of Chemical Studies*, *6*, 1693-1700.

Mahalanobis, P. C. (1928). A statistical study at Chinese head measurement. *Journal of Asiatic Society*, 25: 301-377

Mukul, S., Singh, A., Singh, P. K., & Singh, S. P. (2019). Estimation of genetic divergence analysis for yield and bacterial leaf blight (BLB) disease resistance in rice (*Oryza sativa* ***L.***). *Journal of Pharmacognosy and Phytochemistry*, *8*(2), 1124-1128.

Panda, D., Sahu, N., Behera, P. K., & Lenka, K. (2020). Genetic variability of panicle architecture in indigenous rice landraces of Koraput region of Eastern Ghats of India for crop improvement. *Physiology and Molecular Biology of Plants*, *26*(10), 1961-1971.

Parikh, M., Motiramani, N. K., Rastogi, N. K., Sarawgi, A. K., & Sharma, B. (2011). Genetic diversity in rice accessions of Madhya Pradesh and Chhattisgarh. *Indian Journal of Plant Genetic Resources*, *24*(2), 218-222.

Patterson, H. D., & Williams, E. R. (1976). A new class of resolvable incomplete block designs. *Biometrika*, *63*(1), 83-92.

Priya, T. R., Nelson, A. R. L. E., Ravichandran, K., & Antony, U. (2019). Nutritional and functional properties of coloured rice varieties of South India: a review. *Journal of Ethnic Foods*, *6*(1), 1-11.

Priyanka, K. (2015). Genetic divergence in Indigenous aromatic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, *6*(4), 1096-1102.

Rahman, A. K. M. H., Islam, M. M., Nadim, M. K. A., Akter, S. E., Alim, S. M. A., & Noor, M. M. A. (2021). Genetic variability analysis of different yield contributing characters of cultivated T. Aman rice (*Oryza sativa*) varieties. *Journal of Bioscience and Agriculture Research*, *27*(01), 2258-2266.

Rao, C. R. (1952). Advanced statistical methods in biometric research. *John Wiley and Sons Inc*., New York. 1952, 236-272.

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy journal*.

Sabesan, T., Suresh, R., & Saravanan, K. (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electronic Journal of Plant Breeding*, *1*(1), 56-59.

Shukla, V., Singh, S., Singh, S. K., & Singh, H. (2005). Estimation of genetic variability, heritability and genetic advance in "new plant type" tropical japonica rice under upland environment. *Agricultural Science Digest*, *25*(3), 207-209.

Singh, A., Ekka, R. E., Sinha, S. K., & Tiwari, J. K. (2020). Genetic variability, heritability and genetic advance for yield contributing traits in aromatic and pigmented rice (*Oryza sativa* L.). *Journal of pharmacognosy and phytochemistry*, *6*, 5-8.

Singh, B. (2021). Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, *10*(8): 1627-1630.

Singh, K. S., Suneetha, Y., Kumar, G. V., Rao, V. S., Raja, D. S., & Srinivas, T. (2021). Variability, correlation and path studies in coloured rice. *International journal of chemical studies*, *8*(4), 2138-2144.

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. *Biometrical methods in quantitative genetic analysis.* Kalyani Publishers, New Delhi, 215-218.

Singh, S. K., Pandey, V., Mounika, K., Singh, D. K., Khaire, A. R., Habde, S., & Majhi, P. K. (2020). Study of genetic divergence in rice (*Oryza sativa* L.) genotypes with high grain zinc using Mahalanobis' D2 analysis. *Electronic Journal of Plant Breeding*, *11*(02), 367-372.

Singh, V., Lal, G. M., & Devi, S. V. (2019). Studies on genetic divergence in rice germplasm (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, *10*(4), 1593-1599.

Siva Subramanian, V. and P. Madhava Menon (1973). Path analysis for yield and yield components of rice. *Madras Agricultural Journal*, *60*: 1217-1221.

Srujana, G., Suresh, B. G., Lavanya, G. R., Ram, B. J., & Sumanth, V. (2017). Studies on Genetic Variability, Heritability and Genetic advance for yield and quality components in rice (*Oryza sativa* L.). *Journal of pharmacognosy and phytochemistry*, *6*(4), 564-566.

Subudhi, H. N., Prasad, D., Bose, L. K., & Swain, D. (2008). Genetic diversity studies in promising lowland rice varieties. *Crop Improvement*, *45*(4), 273-276.

Sumanth, V., Suresh, B. G., Ram, B. J., & Srujana, G. (2017). Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, *6*(4), 1437-1439.

Tuwar, A. K., Singh, S. K., Sharma, A., & Bhati, P. K. (2013). Appraisal of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Biolife*, *1*(3), 84-89.

How to cite this article: Singh, S. K.; Kumar S. C. M.; Korada, M.; Khaire, A.; Majhi, P.K.; Singh, D. K. and Jayasudha, S. (2021). Genetic Variability and Divergence Studies for Yield and its related traits in Rice (*Oryza sativa* L.). *Biological Forum – An International Journal*, *13*(4): 687-695.