Received: 07 Apr 2021 | Revised: 13 Dec 2021 | Accepted: 15 Dec 2021

Electronic Journal of Plant Breeding

Research Article

Exploring variability and genetic diversity among rice genotypes in Eastern Uttar Pradesh

Pratibha Singh, S. K. Singh, Mounika Korada*, Amrutlal Khaire, D. K. Singh, Sonali Vijay Habde, Prasanta Kumar Majhi and Rudresha Naik

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, U.P.-221005, India.
***E-Mail:** monikakorada@gmail.com

Abstract
The genetic improvement of any crop mainly depends on the amount of genetic variability present in the population. To explore this variability, an effort was made to classify, understand the nature and magnitude of genetic variability and diversity among 112 rice genotypes for 16 quantitative traits using Mahalanobis D^2 statistics. Analysis of variance revealed a wide and significant variation for all the 16 traits studied. 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, days to first flowering, days to 50% flowering, and plant height showed high heritability coupled with high genetic advance as per cent of mean suggesting that selection for the improvement of these traits may be rewarding. Cluster analysis indicated that the 112 rice genotypes were grouped into 7 clusters, wherein cluster I had the highest number of genotypes (73) followed by cluster III with 22 genotypes. The maximum inter-cluster distance was recorded between clusters V and VII with a D^2 value of 58981.07, followed by clusters II and V (51875.13). The number of spikelets per panicle (52.17%) and the number of grains per panicle (27.26%) were found to be the most contributing traits towards total genetic diversity. Hence, information on the nature and degree of divergence would help the plant breeder in the selection and hybridization procedure for choosing the right type of parents to improve yield and other traits.

Key words: Genetic diversity, Heritability, Mahalanobis D^2, Rice, Variability.

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, it is very important to improve rice 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 any crop improvement program, to increase productivity breeder needs to maintain a pool of diverse desirable donor parents (Joshi and Barh, 2013). An obvious knowledge of genetic diversity is critical for the productive management and use of genetic tools for rice breeding. Hybridization between desired genotypes followed by selection depends primarily on the selection of parents having genetic divergence for different characters. Multivariate analysis like Mahalanobis D^2 statistic quantifies the degree of divergence in a population at the genotypic level and assess the relative contribution of different components to the total divergence both at the intra-cluster and inter-cluster levels. A high level of productivity in crop plants is obtained only in the presence of greater amounts of variability and genetic diversity

(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.

The D^2 statistic is a valuable tool in quantifying the degree of divergence in a set of populations. Apart from estimating the genetic divergence in the base population, it also helps the breeder to classify the population into distinct clusters for their further use in crop improvement programs. Keeping this in view, an attempt was made in this study to find out the genetic variability and diversity among 112 rice genotypes and their heritability, genetic advance as percent mean which would help in the selection and further improvement of these genotypes.

MATERIALS AND METHODS

The experimental material comprised of 112 rice genotypes obtained from the IRRI AGGRi Alliance project and the experiment was conducted during *Kharif,* 2019 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India, situated at 25 18′N latitudes, 83 03′E longitudes of 87 meters above MSL. The 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 with 4 square meter each plot. Standard agronomic practices and plant protection measures were taken as per the schedule. Observations were recorded on 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 *viz.,* 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 the methodology proposed by Patterson and Williams (1976). The genotypic and phenotypic variances, as well as the genotypic and phenotypic coefficient of variations (GCV and PCV), 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 among the genotypes was estimated using Mahalanobis' D^2 statistics (1936) and the germplasm was grouped into several clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance for all the characters showed a fair and significant difference between the genotypes under study, suggesting the existence of appropriate heterogeneity. 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 the current study, PCV was higher than GCV with a narrow difference between PCV and GCV indicating less influence of environment on the manifestation of these characters. These results were similar to the findings of Dhurai *et al*. (2014), Mishu *et al*. (2016), Pal *et al*. (2016), Bagudam *et al*. (2018), Singh *et al*. (2018) and Kurmanchali *et al*. (2019). 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 Singh *et al*. (2018) and Perween *et al*. (2020).

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 material, high heritability coupled with high genetic advance as per cent of mean was recorded for harvest index (99.60% and 31.48%, respectively), 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 Bagudam *et al*. (2018), Singh *et al*. (2018), Kurmanchali *et al*. (2019), Tiwari *et al*. (2019) and Perween *et al*. (2020). GCV, PCV, heritability in the broad sense (h^2_{bs}) and genetic advance as percent of mean (5%) estimated for yield and quality traits are presented in **Table 1**.

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 in any crop. The multivariate analysis developed by Mahalanobis (1936) is suitable for quantifying the degree of divergence in the available germplasm and grouping the germplasm into different clusters. D^2 statistics

Table 1. Estimates genetic variability parameters for grain yield and yield components in Rice

S.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	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	26.32	33.50	61.70	42.61
11	Grain yield per plant	21.09	29.37	51.60	31.20
12	1000 grain weight	10.88	11.27	93.10	21.63
13	Grain yield per plot	18.72	20.47	83.60	35.25
14	Biomass yield per plot	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

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. 1**). 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 used for the 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 in cluster II, four in cluster ,IV whereas clusters V, VI, and VII contained one genotype each. To study the genetic diversity with regard to grain yield, yield components and quality traits in rice, Srinivas (2018) has classified 37 elite genotypes into 18 clusters with cluster I having the maximum (14) genotypes. Similarly, Singh *et al.* (2019) have classified 22 and 29 genotypes into 6 and 6 clusters, respectively. In the present study, the highest intracluster distance was observed in cluster IV (4602.68) which comprised of four 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 is presented in **Table 3** and diagrammatically represented in **Fig. 2**.

Analysis of cluster means values indicated that 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 noticed in cluster VII. The cluster V grouped genotypes with the highest mean value for the number of spikelets in a panicle, number of grains in a panicle and spikelet fertility per cent and 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 found in cluster II and that for grain weight of a panicle in cluster III. Hence, germplasm included in clusters II, III, V, VI and VII seems to be promising, with various traits under study.

The existence of a high level of genetic diversity in the analyzed material was indicated by the discrimination of germplasm lines in too many clusters. Significant genetic divergence in rice has also been documented by previous workers *viz.,* Awasthi *et al*. (2005); Seetharam *et al.* (2009); Rajesh *et al.* (2010); Dey *et al*. (2018); Devi *et al*. (2019) and Singh *et al.* (2020). 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

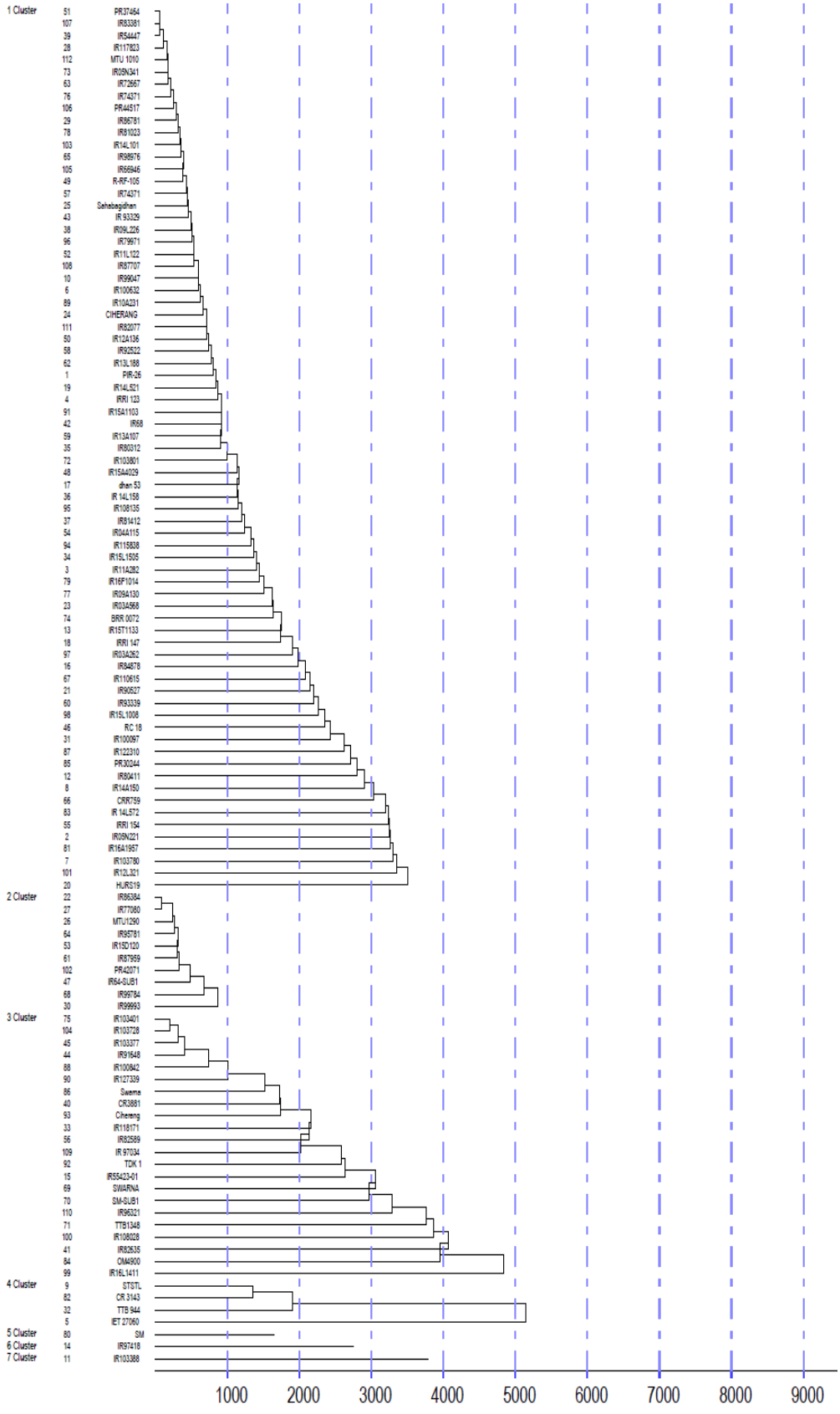

Fig. 1. Dendrogram representing the grouping of 112 rice genotypes by Tocher's Method

Table 2. Grouping of 112 rice germplasm using Mahalanobis' D^2 method

Cluster	Germplasm	Number
I	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-21-12-21-1RGA-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
II	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
III	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 97034-21-2-1-3, TDK 1, IR55423-01, Swarna-Sub1, Samba 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	22
IV	SALT TOL SIN THWE LATT, CR 3143-1-1-1-1-2-1, TTB 944-31-10-1-2, CR 2860-S-B-189-1-1-1 (IET 27060)	4
V	Sambamahsuri	1
VI	IR97418-32-3-1-AJY 1-1	1
VII	IR103388-B-B-2-3	1

Table 3. Average intra and inter-cluster distances among seven clusters

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

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 number of spikelets per panicle had maximum contribution (52.17%) toward total divergence 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 Ovung *et al.* (2012), Medhabati *et al.* (2013), Ashok *et al.* (2017), Archana *et al.* (2018) and Behera *et al.* (2018) who has

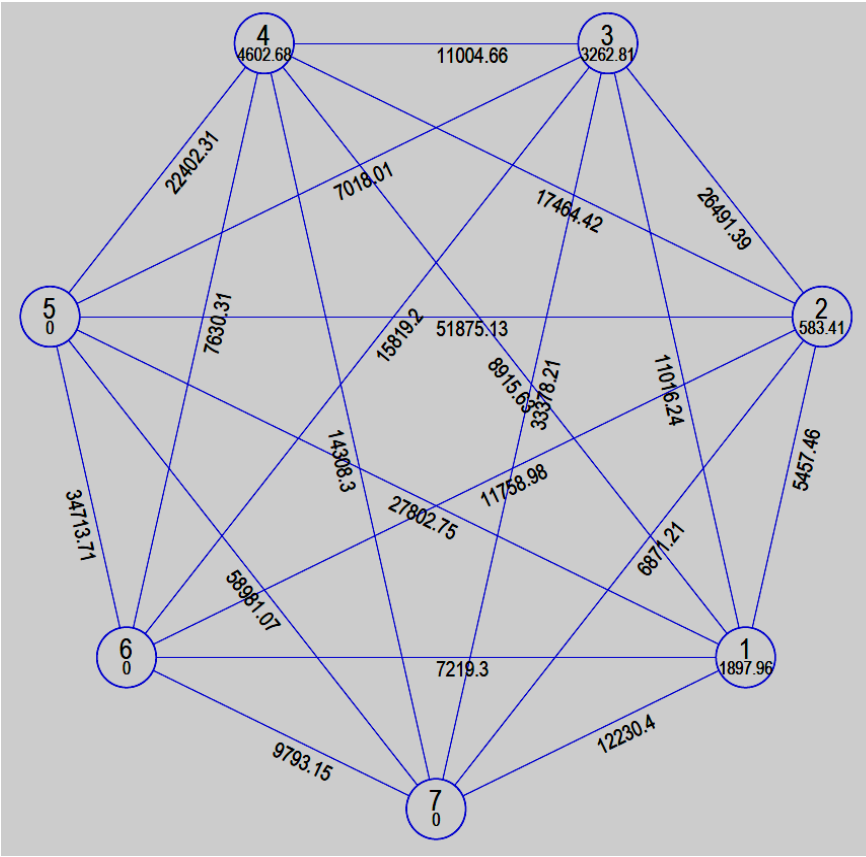

Fig. 2. Cluster diagram depicting intra and inter-cluster distances between rice germplasm lines

Table 4. Mean values of different characters of 112 rice genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
DF	94.21	90.60	104.45	127.58	118.00	102.67	128.67
D_{50}	98.80	94.70	108.50	131.33	122.00	107.67	133.67
DM	127.13	123.60	138.00	160.58	152.00	136.67	162.67
ET	10.79	13.10	10.62	9.33	10.67	11.33	10.67
PH	105.35	98.02	108.78	134.39	91.97	181.67	140.03
PL	25.85	23.73	26.26	25.68	23.93	30.47	22.73
SP	132.29	82.73	196.76	172.67	243.67	131.67	74.67
GP	104.33	63.57	167.38	103.42	215.67	101.67	51.00
SF	78.92	77.02	85.02	61.52	88.45	75.69	68.04
GWP	2.34	1.34	3.34	2.27	2.90	2.20	1.27
GYP	19.99	16.38	22.66	24.50	19.13	22.43	13.60
GW	23.54	23.81	21.84	22.80	15.33	22.80	24.53
GY	1.59	1.32	1.86	1.51	1.67	1.50	1.93
BYP	3.65	3.36	3.92	4.75	3.77	4.84	5.58
HI	0.43	0.39	0.47	0.31	0.44	0.30	0.34
L/B	3.17	3.35	2.80	2.94	2.63	3.30	3.23

DF - Days to first flowering, D_{50} - Days to 50% flowering, DM - Days to maturity, ET - Number of effective tillers per plant, PH - Plant height (cm), PL - Panicle length (cm), SP - Number of spikelets per panicle, GP - Number of grains per panicle, SF - Spikelet fertility (%), GWP - Grain weight per panicle (g), GYP - Grain yield per plant (g), GW - 1000 grain weight (g), GY - Grain yield per plot (kg), BYP - Biomass yield per plot (kg), HI - Harvest index, L/B - Kernel L/B ratio

Table 5. Per cent contribution of each character towards total genetic divergence

S.No.	Characters	% Contribution	Times Ranked 1st
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	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	0.00	0
11	Grain yield per plant	1.17	73
12	1000 grain weight	0.03	2
13	Grain yield per plot	0.00	0
14	Biomass yield per plot	0.00	0
15	Harvest index	1.9	118
16	Kernel L/B ratio	0.00	0

also studied diversity in rice using 21, 38, 64, 32, and 70 genotypes, respectively. The contribution of different characters to total divergence is presented in **Table 5**.

ACKNOWLEDGEMENT

The authors thankfully acknowledge IRRI AGRRi Alliance Project, IRRI, the Philippines for providing the requisite germplasm and financial support to conduct the trial and get this work accomplished.

REFERENCES

Allard, R. W. 1960. Principles of Plant Breeding. *John Wiley and Sonc Inc.*, New York, USA.

Archana, R. S., Rani, M. S., Vardhan, K. V. and Fareeda, G. 2018. Genetic diversity studies among rice (*Oryza sativa*L.) genotypes for grain yield, yield components and nutritional traits in rice. *International Journal of Chemical Studies*, **6**(6): 134-137.

Ashok, S., Jyothula, D. P. B. and Ratnababu, D. 2017. Genetic divergence studies for yield, yield components and grain quality parameters in rice (*Oryza sativa*L.). *Electronic Journal of Plant Breeding,* **8**(4): 1240-1246. [Cross Ref]

Awasthi, L. P., Misra, C. H. and Pandey, V. K. 2005. Genetic divergence in Indian aromatic rice. *Crop Research,* **30**: 199-201.

Bagudam, R., Eswari, K. B., Badri, J. and Rao, P. R. 2018. Variability, heritability and genetic advance for yield and its component traits in NPT core set of rice (*Oryza sativa*L.). *Electronic Journal of Plant Breeding*, **9**(4): 1545-1551. [Cross Ref]

Behera, P. P., Singh, S. K., Singh, D. K., Reddy, Y. S., Habde, S., Khaire, A. and 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. and De Vane, E. H. 1952. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478-481. [Cross Ref]

Devi, A., Kumar, P., Dwivedi, R., Verma, O. P., Singh, P.K. and Dwivedi, D.K. 2017. Gene action, combining ability analysis for yield and yield contributing traits in rice over environment. *Journal of Pharmacognosy and Phytochemistry*, **6**(3):662-671.

Devi, M., Jyothula, D. P. B., Krishnaveni, B. and Rao, V. S. 2019. Genetic divergence studies in rice (*Oryza sativa* L.) hyrids for yield, yield component traits and quality parameters. *Int. J. Curr. Microbiol. App. Sci*, **8**(6): 1577-1583. [Cross Ref]

Dey, R., Singh, S. K., Mounika, K., Kujur, S. N. and Sharma, Y. 2018. Genetic diversity analysis in rice (*Oryza sativa* L.) genotypes. *Int. J. Agri., Envi. And Bio.* Special Issue 849-853.

Dhurai, S. Y., Bhati, P. K. and 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.

Johnson, H.W., Robinson, H. F. and Comstock, R. 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy Journal*, **47**(7): 314-318. [Cross Ref]

Joshi, M. and Barh, B. 2013.Genetic diversity assessment in lentil (*Lens culinaris medikus*) genotypes through ISSR markers. *The Bioscan*, **8**(4): 1529-1532.

Kurmanchali, M., Kurmanchali, N., Kukreti, A., Sihag, N., Chaudhary, H. and Karnwal, M. K. 2019. Study of genetic variability, heritability and genetic advance for various yield attributing and quality traits in basmati rice (*Oryza sativa* L.). *International Journal of Chemical Sciences*, **7**(1): 2486-2489.

Mahalanobis, P. C. 1936. A statistical study of the Chinese head. *Man in India*, **8**: 107-122.

Medhabati, K., Das, K. R., Kumar, M., Rohini, H., Sunitibala, H. and Singh, T. D. 2013. Genetic divergence in indigenous wild and cultivated rice species of Manipur valley. *International Scholarly Research Notices Genetics*, **20**: 6. [Cross Ref]

Mishu, F.M., Rahman, W., Azad, M. A. K., Biswas, B. K., Talukder, A. I., Kayers, O., Islam, R. and Alam, R. 2016. Study on genetic variability and character association of aromatic rice (*Oryza sativa* L.) cultivar. *International Journal of Plant and Soil Science*, **9**(1): 1-8. [Cross Ref]

Ovung, C.Y., Lal, G. M. and Rai, P. K. 2012. Studies on genetic diversity in rice (*Oryza sativa* L.). *Journal of Agricultural Technology*, **8**(3): 1059-1065.

Pal, N., Koutu, G. K. and Tiwari, A. 2016. Genetic variability, correlation and path coefficient studied for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *International Journal of Agriculture Sciences,* **55**(8): 2988-2992.

Patterson, H. D. and Williams, E.R.1976. A new class of resolvable incomplete block designs. *Biometrika,* **63**: 83-90. [Cross Ref]

Perween, S., Kumar, A., Singh, S. P., Satyendra, Kumar, M. and Kumar, R. R. 2020. Genetic variability parameters for yield and yield related traits in rice (*Oryza sativa* L.) under irrigated and drought stress condition. *Int. J. Curr. Microbiol. App. Sci.*, **9**(02): 1137-1143. [Cross Ref]

Rajesh, T., Paramasivam, K. and Thirumeni, S. 2010. Genetic divergence in land races of rice. *Electronic Journal of Plant Breeding*, **1**(2): 199-204.

Rao, C. R. 1952. Advanced statistical methods in biometrical research. *John Wiley and Sons. Ind.*, New York.

Seetharam, K., Thirumeni, S. and Paramasivam, K. 2009. Estimation of genetic diversity in rice (*Oryza sativa* L.) genotypes using SSR markers and morphological characters. *African journal of Biotechnology*, **8**(10).

Singh, S. K., Vennela, P. R., Singh, R., Gayatonde, V. and Singh, D. K. 2018. Studies on character association, path analysis and genetic variabilty in rice (*Oryza sativa* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences,* **7**(5): 2702-2712. [Cross Ref]

Singh, S. K., Pandey, V., Mounika, K., Singh, D. K., Khaire, A. R., Habde, S. and 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. [Cross Ref]

Tiwari, D. N., Tripathi, S. R., Tripathi, M. P., Khatri, N. and Bastola, B. R. 2019. Genetic variability and correlation of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, pp. 9. [Cross Ref]

Tripathi, A., Rajani, B., Ahirwal, R. P., Paroha, S., Sahu, R. and Ranganatha, A. R. G. 2013. Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *The Bioscan*, **8**(4): 1387-1391.