ASSESSMENT OF GENETIC DIVERSITY IN RICE (Oryza sativa L.) GENOTYPES FOR GRAIN YIELD CHARACTERS

ABSTRACT

A set ~~of 55~~of 55 genotypes of rice were evaluated for~~ studying of **“Assessment of**~~Genetic Diversity and~~ in Rice (*Oryza sativa L.)*Genotypes for~~Grain Yield Characters”. The experiment was conducted in a Randomized Block Design with three replications during the *kharif* season, 2021 at Naini Agriculture Institute, Naini. The plant to plant distance was 15 cm and row to row distance was 20 cm. The data were recorded from five randomly selected plants for each genotypes in all the replications for thirteen characters. Analysis of variance showed significant differences among genotypes for all 13 characters indicating that the material has adequate genetic variability to support the breeding programme for improving the grain yield of rice. Out of 55 rice genotypes evaluated for various characters, 5 genotypes were found superior for different characters. These 5 genotypes were found better for more than one character. Among the lines SHUATS DHAN-6 (62.133g) recorded the highest grain yield per hill followed by the genotypes BPT-3291 (51.8g), SHIATS Dhan -2 (51.467g), SIGNET-5455 (50.467g) andSIGNET-5455 (50.4). All these genotypes were significantly higher as compared to the check NDR - 359 (CHECK) (22.67g). High estimate of heritability coupled with high genetic advance as percent of mean was recorded for Grain yield per hill, Biological yield, Number of spikelets per panicle, Harvest Index, Flag leaf length, Number of tillers per ~~hill ,~~hill, Number of panicles per hill , Flag leaf width, Test weight, and Plant height. These traits are governed by additive gene effects and therefore, may be improved through direct selection. Further the characters *viz.*, Biological yield, Harvest Index, Number of tillers per hill, Days to fifty percent flowering, Flag leaf length and Test weight, had the highest direct positive effect and indirect effect (through each other) on grain yield per hill. Thus, selections for these characters will prove~~d~~ efficient for the improvement of grain yield of rice. All the 55 rice genotypes were classified using Mahalanobis D^2 statistics involving 13 quantitative characters of 55 genotypes grouped into 6 clusters In the present study, the highest inter cluster distance observed between cluster IV and cluster V (368.37) followed by cluster II and cluster V (361.04).

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keywords: Rice, Additive gene, Variability, Significance, Diversity, Hybridization

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the genus *Oryza*of *Poaceae* family *Graminae* and is a true diploid with chromosome number 2n = 24. Rice has been cultivated by mankind for more than 10,000 years. The cultivated varieties of *Orzya sativa* grouped into three sub species, indica, japonica and javanica. Where Indica are grown through the tropical and sub-tropical region and japonica varieties are grown throughout the temperate zone and javanica are grown mainly in the part of Indonesia.

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Rice plays an important role in Indian economy being a staple food for two third of the over all population. The nutrient content of rice are 80% carbohydrates, 7-8% protein (The amino acid profile shows that it is rich in glutamic acid and Aspartic acid, highest quality cereal protein being rich in lysine (3.8%), 3%, fiber, iron 1mg and zinc 0.5 mg **(Juliano*et al.*, 1985).** Rice is a short day autogamous crop.

Comment [PCA2]: In terms of global importance where does rice rank
Could also you give a brief summary on the production of rice globally before you narrow down to India

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Rice is the major crop in Uttar Pradesh and is grown in about 5.9 m ha. The cropping intensity is 153%. The state ranks 1" in the country in production in rice. The production is 44.01and productivity of the state is round 2.2t/ha thus it is understood that there is an extreme need to enhance the rice productivity in Uttar Pradesh, which will be achieved only by developing high yielding hybrid varieties **(Agriculture statistics, 2020).**Current population in India is 120 cores by 2025 it will be around 150 cores.So there is need to develop high yielding alternatives like expansion of cultivable land, water and other natural resources would be the major obstacles in rice cultivation **(Yashitola*et al*. 2002).** This emphasises the development of realistic strategies to boost the rice production rapidly through maximum utilization of innovative technologies. Like other crops, rice also exhibiting enough heterosisupto 25% **(Siddiq, 1997).**

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MATERIALS AND METHODS

The present investigation entitled **"Assessment of genetic diversity in Rice (*Oryza sativa* l.) genotypes for grain yield characters"** was made to understand the genetic diversity, variability, heritability, correlation & diversity in rice. The details of the materials used and the methods adopted in the investigation, which was carried out at Department of Genetics and Plant breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini during the *kharif*season of 2021

Experimental materials

The experimental material for present investigation comprised of forty genotypes of rice obtained from Department of Genetics and Plant Breeding, Prayagraj.

Source: Dept. of Genetics and Plant Breeding (SHUATS).

Where was the study conducted?

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How did you collect your data, did you use any descriptors or?

How did you analyse your data, which software, how was clustering done

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Table 1 Analysis of Variance for 13 Characters in Rice 55 Genotypes

Mean Sum of Squares				
S. No	**Characters**	**Replication (d.f=2)**	**Treatment (d.f=54)**	**Error (d.f=108)**

1	Days to fifty percent flowering	17.144	432.266**	5.964
2	Plant height	6.37	441.787**	3.397
3	Flag leaf length	3.58	550.813**	12.344
4	Flag leaf width	7.70	87.474**	5.825
5	Number of tillers per hill	0.001	0.108**	0.005
6	Number of panicles per hill	0.382	17.788**	2.066
7	Panicle length	0.75	16.766**	1.404
8	Days to maturity	0.423	12.217**	1.362
9	Biological yield	488.08	10268.683**	334.943
10	Harvest Index	0.911	46.659**	0.901
11	Number of spikelets per panicle	8.806	980.149**	51.647
12	Test weight	23.416	352.779**	16.8
13	Grain yield per hill	3.497	281.763**	15.318

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**** Significant at P = 0.01 level of significance, * Significant at P = 0.05 level of significance.**

Table 2. Grand mean, variation, heritability and genetic advance for yield contributing characters in 55 rice genotypes

Sl.No.	TRAITS	GCV	PCV	h^2 (Broad Sense) %	Genetic Advancement	Gen.Adv as % of Mean
1	**Days to fifty percent flowering**	11.46	11.70	95.97	24.05	23.14
2	**Plant height**	9.05	9.15	97.72	24.61	18.44
3	**Flag leaf length**	10.53	10.89	93.56	26.69	20.99
4	**Flag leaf width**	13.70	15.09	82.37	9.75	25.62
5	**Number of tillers per hill**	15.36	16.34	88.34	0.35	29.74
6	**Number of panicles per hill**	8.76	10.34	71.72	3.99	15.28
7	**Panicle length**	20.90	23.59	78.47	4.13	38.15
8	**Days to maturity**	18.27	21.44	72.65	3.34	32.09
9	**Biological yield**	26.14	27.43	90.81	112.96	51.33
10	**Harvest Index**	19.77	20.35	94.42	7.81	39.58
11	**Number of spikelets per panicle**	25.20	27.22	85.69	33.55	48.06
12	**Test weight**	21.15	22.68	86.95	20.32	40.63
13	**Grain yield per hill**	27.49	29.77	85.29	17.92	52.31

PCV = Phenotypic coefficient of Variation, GCV = Genotypic coefficient of Variation, h 2 = Heritability in broad sense, GAPM = Genetic advance in per cent of mean

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Table.3Phenotypic correlation among the different traits of rice lines evaluated during *kharif*, 2021

Traits	Genotypic/ phenotypic	Days to fifty percent flowering	Days to maturity	Plant height	Flag leaf length	Flag leaf width	Panicle length	Number of total tillers per hill	Number of panicles	Number of spikelets per panicle	Test weight	Biological yield	Harvest Index	Grain yield per hill
Days to fifty percent flowering	G	1.0000	0.513**	0.0081	0.0057	0.221*	-0.285**	-0.268**	-0.290**	0.172*	-0.466**	0.1322	-0.531**	-0.291**
	P	1.0000	0.492**	-0.0036	-0.0094	0.207*	-0.221*	-0.239*	-0.235*	0.158*	-0.448**	0.1152	-0.485**	-0.267**
Days to maturity	G		1.0000	-0.0372	0.0048	0.175*	-0.0710	-0.388**	-0.373**	0.208*	-0.177*	0.0968	-0.445**	-0.243*
	P		1.0000	-0.0458	0.0014	0.157*	-0.0477	-0.344**	-0.321**	0.199*	-0.166*	0.0863	-0.410**	-0.223*
Plant height	G			1.0000	0.615**	0.1478	0.483**	-0.0430	-0.0540	0.1004	0.415**	0.353**	-0.267**	0.1161
	P			1.0000	0.546**	0.1389	0.370**	-0.0285	-0.0366	0.0911	0.383**	0.321**	-0.232*	0.1110
Flag leaf length	G				1.0000	0.1126	0.251*	0.0971	0.1470	-0.1496	0.238*	0.262**	-0.162*	0.1197
	P				1.0000	0.0669	0.164*	0.0976	0.1183	-0.1108	0.228*	0.247*	-0.154*	0.1092
Flag leaf width	G					1.0000	0.233*	0.1358	-0.0352	0.546**	-0.163*	0.326**	-0.288**	0.0794
	P					1.0000	0.209*	0.1276	-0.0230	0.473**	-0.1469	0.268**	-0.222*	0.0680
Panicle length	G						1.0000	0.0798	0.0285	-0.0833	0.612**	0.230*	-0.0983	0.161*
	P						1.0000	0.0353	-0.0009	-0.0571	0.511**	0.163*	-0.0833	0.0958
Number of total tillers per hill	G							1.0000	0.886**	0.0459	0.0882	0.198*	0.395**	0.459**
	P							1.0000	0.889**	0.0559	0.0766	0.261**	0.346**	0.487**
Number of panicles	G								1.0000	0.0125	0.1086	0.364**	0.367**	0.603**
	P								1.0000	0.0252	0.0882	0.389**	0.307**	0.586**
Number of spikelets per panicle	G									1.0000	-0.385**	0.416**	-0.1503	0.267**
	P									1.0000	-0.338**	0.407**	-0.1389	0.266**
Test weight	G										1.0000	0.0745	0.178*	0.225*
	P										1.0000	0.0676	0.165*	0.202*
Biological yield	G											1.0000	-0.317**	0.675**
	P											1.0000	-0.303**	0.696**
Harvest Index	G												1.0000	0.474**
	P												1.0000	0.454**
Grain yield per hill	G													1.0000
	P													1.0000

****,* Significant 1% and 5% level of significance respectively.**

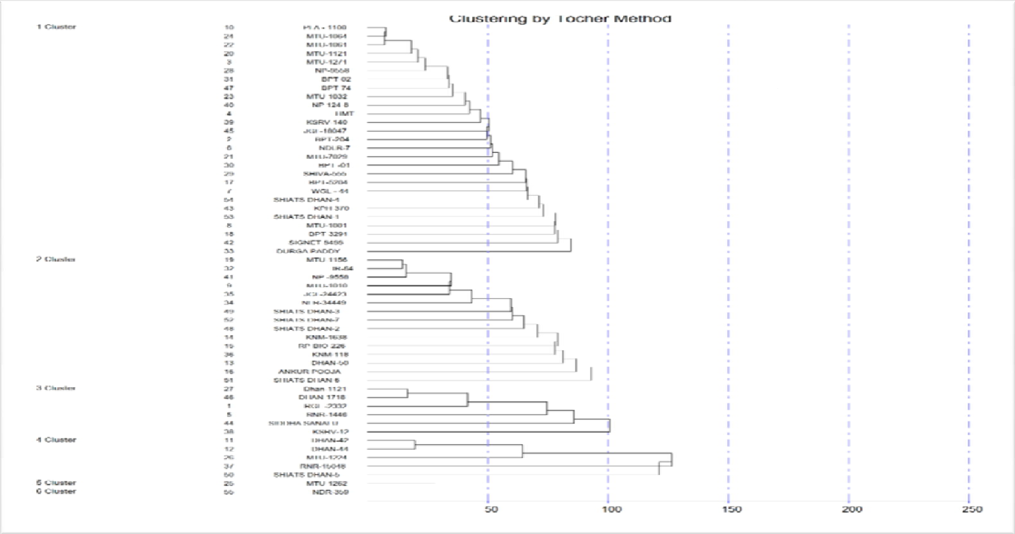


Fig: 1. Dendrogram for 13 traits of 55 genotypes of rice towards genetic divergence bytocher's method.

Table 4. Grouping of 55 rice genotypes into clusters by using Mahalanobis' D^2 method

Cluster Group	No. of genotype	List of genotypes
Cluster 1	27	PLA - 1100, MTU-1064, MTU-1061, MTU-1121, MTU-1271, NP-9558, BPT-02, BPT-74, MTU-1032, NP 124-8, HMT, KSRV-140, JGl-18047, BPT-20'4, NDLR-7, MTU-7029, BPT -01, SHIVA-555, BPT-5204, WGL - 44, SHIATS DHAN-4, KPH-370, SHIATS DHAN-1, MTU-1001, BPT-3291, SIGNET-5455 and DURGA PADDY
Cluster 2	15	MTU-1156, IR-64, NP -9558, MTU-1010, JGl-24423, NLR-34449, SHIATS DHAN-3, SHIATS DHAN-7, SHIATS DHAN-2, KNM-1638, RP-BIO-226, KNM-118, DHAN-50, ANKUR POOJA and SHIATS DHAN-6
Cluster 3	6	Dhan-1121, DHAN-1718, RGL -2332, RNR-1446, SIDDHA SANALU and KSRV-12
Cluster 4	5	DHAN-42, DHAN-44, MTU-1224, RNR-15048 and SHIATS DHAN-5
Cluster 5	1	MTU-1262
Cluster 6	1	NDR-359

Table 5. Average intra and inter-cluster distances among six clusters

Clsuters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	65.32	156.72	119.25	201.57	114.48	132.40
Cluster 2		78.94	166.94	142.00	361.04	164.27
Cluster 3			98.12	274.65	214.73	173.07
Cluster 4				132.46	368.37	194.15
Cluster 5					0.00	238.52
Cluster 6						0.00

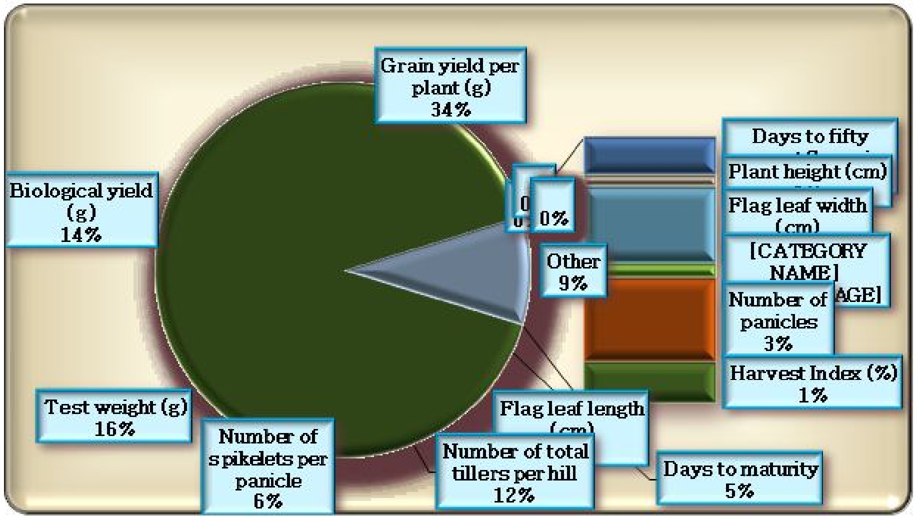
	Cluster Means: Tocher Method											
Clusters	**Days to fifty percent flowering**	**Plant height**	**Flag leaf length**	**Flag leaf width**	**Number of tillers per hill**	**Number of panicles per hill**	**Panicle length**	**Days to maturity**	**Biological yield**	**Harvest Index**	**Number of spikelets per panicle**	**Test weight**
1	109.48	123.6	37.53	1.24	25.58	10.09	9.72	227.00	18.25	67.66	47.79	31.88
2	92.07	127.2	38.42	1.12	27.05	11.53	11.37	190.50	22.36	72.00	54.13	38.31
3	108.73	149.6	42.83	1.12	27.38	10.08	9.94	213.56	24.05	77.64	42.93	33.27
4	99.67	120.3	35.09	1.21	24.72	12.28	11.45	266.49	15.34	67.95	59.93	39.53
5	125.00	120.3	35.94	1.44	24.68	8.47	8.47	292.60	14.00	74.80	25.64	19.13
6	105.00	125.0	35.81	1.80	27.96	19.60	14.00	210.60	23.10	51.50	66.32	33.30

Table 6. Mean values of different characters of 55 rice genotypes

Table 7. Percent contribution of 13 traits for 55 rice genotypes towards genetic divergence

TRAITS	CONTRIBUTION %
Days to fifty percent flowering	1.35
Plant height	4.92
Flag leaf length	0.4
Flag leaf width	3.37
Number of tillers per hill	2.69
Number of panicles per hill	0.54
Panicle length	12.05
Days to maturity	2.96
Biological yield	5.93
Harvest Index	15.96
Number of spikelets per panicle	14.48
Test weight	1.48
Grain yield per hill	33.87

Fig.2Pie chat Per cent contribution of 13 biometrical traits of 55 rice genotypestowards genetic divergence



Results and Discussion

Analysis of Variance for Quantitative Characters of rice (*Oryza sativa* L.)

Analysis of variance for different characters is presented in Table The mean squares due to genotypes showed highly significant differences (α=0.01) for all characters indicating the presence of substantial amount of genetic variability among the rice genotypes.It indicated that there is an ample scope for selection of promising lines from the present gene pool for yield and its component characters. The presence of large amount variability might be due to diverse source of material taken as well as environmental influence affecting the phenotypes. Replications were non-significant for all the characters indicating good homogeneity among replications.The mean values, the coefficient of variation (C.V.), standard error of the mean (SEm±), the critical difference (C.D.) at 5%, range of 55 genotypes for 13 quantitative characters are presented in Table 2 which revealed a wide range of variation for all traits studied.On the basis of mean performance, Rice genotypes SHIATS DHAN- 6 (62.1), MTU-1224 (54.8), SHIATS DHAN -2 (51.4), BPT-3291 (51.8) SIGNET-5455 (50.4) were found to be superior in grain yield.The PCV was higher than their corresponding GCV for all the traits indicating the influence of environment.Siva Subramanian and Menon (1973) : Classified variability as low if coefficient of variation (<10%), moderate (10-20%) and high (>20%).High magnitude of GCV and PCV was recorded for grain yield per hill (29.7), biological yield (27.22), number of spikelets per panicle (27.40)Lowest GCV and PCV was observed at days to maturity (9.15).

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Heritability

Johnson *et al.*, (1955) Classified heritability as low (<30%), medium (30-60%), and high (>60%).High estimates of heritability were recorded for days to maturity (97.7), days to 50% flowering (95.97), test weight (94.4), plant height (93.5),no of spikelets per panicle (90.8).

Genetic Advance

High genetic advance as percent mean was observed for grain yield per hill (52.3), number of spikelets per panicle (51.33), biological yield (48.06), harvest index (40.6),test weight (39.58).

At both genotypic and phenotypic level, biological yield exhibited highly significant positive association with number of tillers per hill, number of panicles, no of spikelets per panicle, harvest index.

Genetic Advance As Percent Mean

The estimation of genetic advance as percent mean is classified as low (<10%), moderate (10 to 20%) and high (>20%) proposed by Johnson *et* al., 1955.

Number of spikelets per panicle (51.332), Test weight (39.585) ,Biological yield (48.069),Harvest Index (40.636), Grain yield per plant (52.312).

Correlation coefficient among yield and its related traits in rice genotypes at phenotypic and genotypic levels

At both genotypic and phenotypic level,biological yield exhibited a highly significant positive association with, number of panicles, number of tillers per hill, harvest index and number of spikelets per panicle that contributes to the grain yield. Positive non significant for days to 50% flowering and days to maturity.

Mahalanobis D^2 analysis

The data collected on 13 yield and yield contributing characters for 54+1(check) genotypes of rice were subjected to genetic divergence by using Mahalanobis D^2 statistic. The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity.

The distribution of 54+1 (check) genotypes into six clusters was by Tocher method at a random with maximum number of genotypes (Twenty seven) for Cluster I in Cluster II, (15) and minimum Cluster III, (5) Cluster IV (1), V (1). The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation.

Intra and Inter cluster Average Divergence (D^2)

The intra cluster values ranged from 0 to132.4 . The maximum intra cluster distance were observed in cluster IV (132.4) followed by cluster III (98.16).The minimum intracluster distance for cluster II,(78.9) I, (65.3) V, VI exhibited zero.

The inter cluster distance varied from 114.4 (between I and V) to 368.3 (between IV and V). The highest inter cluster distance observed between cluster IV and cluster V (368.3) followed by cluster II and V (361.04), cluster V and VI (238.5), The minimum inter cluster distance observed between cluster IV and VI (194.1) and cluster I and V (114.4) Suggesting that selection of two parents from more divergent parents in hybridization programme to produce the better yield traits from the diverse parents and also more of combining ability each other.

Cluster Mean values for quantitative characters of rice genotypes

Mean performance of a cluster is the mean of overall values of individual correlated variables of all genotypes included in that cluster.

Highest cluster mean for grain yield per hill was recorded in cluster IV (39.5) followed by cluster II (38.3), cluster VI (33.3).

Contribution of individual characters towards total divergence

The trait grain yield per hill (34%) had maximum contribution towards to genetic divergence followed by test weight (16%), biological yield (14%), number of total tillers per hill(12%) others (9%).

While selecting parents in hybridization programme genotypes having the more divergence between grain yield per hill have fruitful improvement traits in progenies in selection procedures.

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Your results are not well organized although you have got very good data

Conclusion

From the present investigation it is concluded that analysis of variance showed significant variation to all the characters. Among 55 genotypes SHUATS DHAN – 6 (62.13) genotypes were found to be superior for Grain yield per hill over the check (NDR-359). High to moderate estimates of GCV, PCV, High heritability coupled with high genetic advance as percent mean in the present genotypes was recorded for grain yield/hill, Test Weight and Biological Yield. At both genotypic and phenotypic level biological yield is highly significant and positively correlated with grain yield. Cluster IV and V (368.3), cluster III and IV (274.6) had high inter cluster distances, were most diverse from each other and the genotypes present in these clusters provide a broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes for grain yield improvement in rice genotypes.

REFERENCES

Abigail Seneega, T.V., Gnanamala, R. P., Parameswari, C., Vellaikumar. S. and Priyanka, A. R. (2019) Genetic variability and association studies in F2 generation of rice (*Oryza sativa* L.*). Electronic Journal of Plant Breeding*, **10**(2): 512-517.

Al - Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances in upland cotton cross of interspecific origin. *Agronomy Journal*, 50: 633-637.

Allam, C.R., Jaiswal, H.K., Qamar, A., Venkateshwarlu, C. and Reddy, Y.S. (2015). Variability, heritability and genetic advance studies in some indigenous genotypes of basmati rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **6**(2): 506-511

Arivoli, V., Saravanan, K and Prakash, M. (2007). A Study on D^2 Analysis in Rice. *International Journal of Plant Sciences***, 4**(1): 157-160.

Banumathy, S., Manimaran, R., Sheeba, A., Manivannan, N., Ramya, B., Kumar, D. and Ramasubramanian, G.V. (2010). Genetic Diversity Analysis of Rice Germplasm Lines for Yield Attributing Traits. *Electronic Journal of Plant Breeding*, **1**(4): 500-504.

Bhati P.K., Singh S.K., Dhurai S.Y. and Sharma Amita. (2015). Genetic divergence for quantitative traits in rice germplasm. *Electronic Journal of Plant Breeding*, 6(2): 528-534.

Elayaraja K., Prakash M. and Kumar B.S. (2005). Studies on variability and heritability of rice. *Crop Research*, 5 (21): 248-242.

Hossain M.S., Singh and A.K., Zaman F. (2009). Cooking and eating characteristics of some newly identified inter sub-specific (indica/japonica) rice hybrids. *Science Asia*, 35: 320-325.

Jayasudha S. and 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.E. and Comstock R.E. (1955). Estimate of genetic and environmental variability in rice (*Oryzasativa*.L). *Agronomy Journal* 47: 314-318.

Juliano B.O. (1972). Rice chemistry and technology. *The American Association of cereal chemists.* Inc., Minnesota, USA.

Fisher R.A. (1918). The correlation between relative on the supposition of Mendalian Inheritance. *Trance RoyalSoc., Edinburg.* 52: 399-403.

Mahalabonis P.C. (1928). On the generalized distance in statistics. *Proceedings of Natural Institution Science India.*, 2: 49-55.

Neethu-Francis., Packiaraj D., Geethanjali S. and Hemaprabha K. (2018). Correlation and Path Coefficient Analysis for Yield Contributing Characters in Rice (*Oryza sativa L.*) Cultivars. *International Journal of Current Microbiology and Applied Sciences* 7(6): 2292-2296.

Pratap N., Singh P.K., Shekhar R., Soni S.K. and Mall A.K. (2012). Genetic Variability, Character Association and Diversity Analysis For Economic Traits in Rice (*Oryza sativa L.*) *SAARC J. Agri*., 10(2): 83-94.

Sameera S.K., Prasannarajesh A., Jayalakshmi V., Nirmala P.J and Srinivas T. (2015). Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*.6 (1): 269-273.

Selvaraj I., Nagarajan P., Thiyagarajan K., Bharathi M. and Rabindra R. (2011). Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice(*Oryza sativa* L.). *African Journal of Biotechnology*, 10(17): 3322-3334.

Manne Vinod, Suresh B.G., Lavanya G.R. and Jalandhar Ram B. (2017) Studies on variability, heritability and genetic advance for quantitative characters in exotic rice (*Oryza sativa* L.) Germplasm. *Journal of Pharmacognosy and Phytochemistry* ; (3): 829-831