Genetic diversity analysis for yield and yield components in rice

Amudha K* and Ariharasutharsan G

Department of Rice, Centre for Plant Breeding and Genetics,
Tamil Nadu Agricultural University, Coimbatore-641003
* Corresponding author Email:amudha_pbg@yahoo.com

Abstract

The present investigation was carried out to explore the extent of divergence in 55 rice germplasm accessions for twelve characters during *Kharif*, 2019. In D^2 analysis, the 55 genotypes were grouped into fourteen clusters. The clustering pattern indicated that there was no parallelism between genetic diversity and geographical origin as the genotypes of the same origin were included in different clusters and *vice versa*. The maximum inter cluster distance was found between cluster IX and cluster XIII (1313.049) followed by cluster X and cluster XIII (1152.033), cluster XII and cluster XIII (1039.108), cluster III and cluster XIII (1015.310) and cluster I and cluster XIII (978.369). Genetically distant parents from these clusters could be able to produce higher heterosis in progenies on hybridization. Single plant yield (43.29%) followed by grain length (12.99%), 100 grain weight (12.12%) grain width (11.85%) and days to 50% flowering (11.85%) were the major contributors towards the total genetic divergence among the genotypes studied. Selection could be made based on grain yield per plant, hundred grain weight and days to 50% flowering for the progenies identified.

Introduction

Rice is cultivated in an area of 43.66 million ha with a production of 118.87 million tonnes and a productivity of 2.7 tonnes per hectare (Indiastat, 2020). It contributes to about 40% of the total food grain production. Rice is a source of livelihood for 120-150 million rural households. So, rice is life for Indians as it plays a vital role in diet, economy, employment, culture and history. Even though India had attained self sufficiency in rice, keeping in view the continuously growing population it is estimated that about 140Mt of rice would be required by 2050 to ensure the food and livelihood security of the people. To achieve this, rice production has to be increased by about 1.5Mt/year and the productivity to 3.25t/ha by 2050 (Pathak *et al.,* 2018). It is a challenging task for the rice breeders as yield in rice has attained a plateau. To break the yield barrier in rice, it is imperative to broaden the genetic base of rice cultivars for which existence of genetic variability and diversity in a population is a prerequisite (Allard, 1960). Genetically diverse population would aid in the selection of diverse parents which could be utilized for the development of high yielding rice varieties superior to existing varieties. The germplasm with inherent genetic value and wide variability and diversity would be a potent source for the genetic improvement of rice. Hence, the information on genetic diversity in germplasm collections would immensely help the plant breeder in selection of diverse parents for crossing programmes so as to obtain highly heterotic F_1 and broad spectrum of variability in subsequent segregating generations (Vivekanandan and Subramanian, 1993). Multivariate analysis like Mahalanobis D^2 statistic provides useful tool for measuring the genetic diversity in a given population with respect to different characters considered together. Hence, the present study was undertaken to assess the nature and magnitude of genetic divergence present in rice germplasm for yield, yield attributes and grain characters.

Materials and Methods

The experimental material for the present study comprised of 54 numbers of rice germplasm collection maintained as T numbers at Department of Rice and check CO(R)50. Details of the rice germplasm collections and check used in the present study along with its pedigree details are given in **Table.1** The fifty-five germplasm collections including check were raised in Randomized Block design (RBD) with two replications at Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University and Coimbatore during *Kharif,* 2019. Each genotype was raised in two rows with each row of 3 meters' length. Row to row and plant to plant spacing was maintained at 20 x 20 cm. All the recommended agronomic practices were followed. Data on all yield and yield attributing characters (except days to flowering) *viz.,* plant height, leaf length, leaf width, panicle length, number of tillers per plant, number of productive tillers per plant, 100-grain weight, grain length, grain breadth, L/B ratio and single plant yield were recorded in five competitive plants selected at random for each genotype in each replication. Days to 50 percent flowering was recorded on plot basis. Data recorded for twelve quantitative traits were analyzed using GENRES software. Mahalanobis D^2 analysis (1949) was used for working out the genetic distance between the genotypes whereas grouping of varieties into clusters was done using Tochers method suggested by Rao (1952).

Table. 1 Details of rice germplasm accessions used along with pedigree

S.No	Genotypes	Pedigree	Origin
1.	T15	*Chani Brara*	Indigenous landrace of Travancore
2.	T23	*Safeda*	Exotic collection from central province
3.	T26	*Bhangara Bellu Bhatta*	Indigenous landrace of Mysore
4.	T54	*Ratna Chvdi*	Indigenous landrace of Ganjam,Orissa
5.	T65	Chennangi	Indigenous landrace of Salem, Tamil Nadu
6.	T71	*Vellai Gundu Samba*	Indigenous land race of South Arcot, Tamil Nadu
7.	T73	*Godumani Samba*	Indigenous landrace of South Arcot, Tamil Nadu
8.	T75	*Norungan*	Indigenous landrace of Tamil Nadu
9.	T089	*Chintamani*	Indigenous landrace of Tamil Nadu
10.	T146	*Ayyan Samba*	Indigenous landrace of Gobi, Tamil Nadu
11.	T153	*Nyan* 5	An exotic collection from Burma
12.	T181	*Arupatham Vellai*	Indigenous landrace of Tirunelveli
13.	T186	Seevan Samba	Indigenous landrace of Tirunelveli
14.	T209	*Bobbili Ganti*	Indigenous landrace of Vizakapattinam
15.	T227	*Vayan hill paddy*	Indigenous landrace of Malabar
16.	T261	*Mangam Samba*	Indigenous landrace of South Arcot
17.	T268	*Myosan*	Exotic collection from Burma
18.	T271	*Kukka Nyan B.60*	Exotic collection from Burma
19.	T272	*Kukka Nyan 1*	Exotic collection from Burma
20.	T273	*Kunwah B.61*	Exotic collection from Burma
21.	T275	*Naseingale –C. 27*	Exotic collection from Burma
22.	T277	*Matawaka –C. 89*	Exotic collection from Burma

S.No	Genotypes	Pedigree	Origin
23.	T279	*Palak E.19*	Exotic collection from Burma
24.	T307	*Matawaka –C.* 100	Exotic collection from Burma
25.	T309	*Lawangai*	Indigenous collection from north West frontier provinces
26.	T311	Double grain paddy	Indigenous landrace from Pune
27.	T317	*Periavellai Red rice*	Exotic collection from Ceylon
28.	T341	*Poongar*	Indigenous collection from Tamil Nadu
29.	T355	*Nallakonamani*	Indigenous collection from Vizhakapattinam
30.	T356	*Dasaradhinu* an indigenous collection from Ganjam, Orissa	Indigenous collection from Ganjam, Orissa
31.	T374	*Varigarudan Samba*	Indigenous landrace of Tamil Nadu
32.	T378	*Forhina*	Exotic collection from USA
33.	T420	*Vellai Kuruvai*	Indigenous landrace of Tamil Nadu
34.	T422	*Rangoon Samba*	Indigenous landrace of Tamil Nadu
35.	T432	*Thogai Samba*	Indigenous landrace of Tamil Nadu
36.	T433	*Maranel*	Indigenous landrace of Tamil Nadu
37.	T541	*Karthigai Samba*	Indigenous landrace of Tamil Nadu
38.	T542	*Sirumani*	Indigenous landrace of Tamil Nadu
39.	T549	*Alther Samba*	Indigenous landrace of Tamil Nadu
40.	T710	*White Amon*	Indigenous landrace from Assam
41.	T716	*Parichak*	Indigenous landrace from Assam
42.	T722	*Lead rice*	Exotic collection from USA
43.	T730	*Larly-Wreight* an exotic collection from Italy	*Exotic collection from Italy*
44.	T761	*V.Vulgariskom Eat164 F*	Exotic collection from Russia
45.	T777	*Seeraga Samba*	Indigenous landrace of Tamil Nadu
46.	T810	A29-16	Exotic collection from Mudon
47.	T812	*Thulasi Vasanai Seeraga Samba*	Indigenous landrace of Tamil Nadu
48.	T854	*Karajano*	Exotic collection from West Africa
49.	T872	*Thengaipoo Samba*	Indigenous landrace of Tamil Nadu
50.	T1001	*Poyongchao*	Exotic collection from China
51.	T1022	*Kothamalli* Samba	Indigenous landrace of Tamil Nadu
52.	T1067	*Thooyamalli*	Indigenous landrace of Tamil Nadu
53.	T1071	*Salem 3*	Indigenous landrace of Tamil Nadu
54.	T1092	*Muthuvellai*	Indigenous landrace of Tamil Nadu
Check			
55.	CO(R)50	CO 43/ADT 38	India

Results and Discussion

The analysis of variance for 12 quantitative characters revealed highly significant differences among the genotypes for all the characters studied (**Table 2**). The results indicated the existence of variation among the genotypes for all the characters under study. Fifty-five genotypes were clustered into 14 clusters based on minimum D^2 values and confirmation of tentative grouping by Tocher's method. Out of fourteen major clusters, cluster XI was the widest with 14 number of genotypes followed by cluster IX (9), clusters XII& XIII (4), cluster XIV (5) and cluster I(3) . Clusters II, Cluster III, Cluster IV, Cluster V, Cluster VI, Cluster VII, VIII and cluster X had the minimum number of 2 genotypes each. Grouping of 55 genotypes in to fourteen clusters itself indicates that the genetic material is divergent enough. The germplasm material used in the present study may serve as a novel source for the selection of the diverse parents for hybridization programmes aimed at isolating desirable segregants for grain yield and other important characters. Presence of substantial amount of genetic divergence in the rice germplasm was earlier reported by Sri Lakshmi *et al.* (2021); Rukmini Devi *et al.,* (2020) and Vishnu Bridha Devi *et al.* (2018).

Distribution of genotypes into various clusters was observed to be at random (**Table 3**). Genotypes originated from same or diverse eco-geographical region were present in different clusters as well as in same cluster. This is in conformity with the report of Kumar *et al.,* (2020). This random grouping may be attributed to the interchange breeding material over locations followed by intensive selection both by natural and human selection for diverse and adaptable gene complexes resulting in genetic drift and consequently increased genetic diversity (Arunachalam and Ram, 1967).

Table. 2 Analysis of variance for grain yield & its component traits and grain characters in rice germplasm

S. No	Source	df	PH	DFF	LL	LW	NT/Plt	ET/Plt	PL	100 GW	GL	GW	L/B ratio	SPY
1.	Repli-cation	1	MSS											
			1.1659	0.4614	2.5943	0.0508	5.1072	5.8069	2.8027	0.0038	0.0005	0.0002	0.0283	4.6715
2.	Geno-type	54	159.6065**	103.0579**	27.5750**	0.1678**	30.6794**	33.3847**	37.0025**	0.2160**	0.237 **	0.0022**	0.5124**	163.5362**
3.	Error	54	12.4773	0.7600	1.0380	0.0113	1.6598	7.8301	2.8855	0.0046	0.0004	0.0001	0.0274	3.4523

PH-Plant height; DFF-Days to 50% flowering; LL-Leaf length; LW-leaf width; NT/Plt Number of tillers per plant; ET/Plt-Number of productive tillers per plant; PL-Panicle length; 100GW-100 grain weight; GL-Grain length; GW-Grain width; L/B ratio-Length/Breadth ratio,100GW-100 grain weight; SPY-Single plant yield *, ** Significant at 1% and 5% levels, respectively

Table. 3 Constitution of D^2 clusters for 55 genotypes of rice

Cluster No.	Number of genotypes	Name of the genotypes
I	3	T15, T422, T590
II	2	T432, T722
III	2	T209, T272
IV	2	T268, T307
V	2	T378, T710
VI	2	T186, T317
VII	2	T181, T273
VIII	2	T341, T1022
IX	9	T23, T26, T54, T65, T71, T75, T73, T374, T854
X	2	T311, T541
XI	14	T146, T153, T227, T261, T271, T275, T279, T309, T355, T356, T420, T433, T542, T1071
XII	4	T1067, T549, T716, T1001
XIII	4	T809, T730, T761, T777
XIV	5	T1092, CO(R)50, T810, T812, T872

Narrow range of genetic variability will be exhibited by the genotypes grouped within a cluster whereas genotypes included in different clusters will show wider variability. The maximum inter cluster distance was found between cluster IX and cluster XIII (1313.049) followed by cluster X and cluster XIII (1152.033), cluster XII and cluster XIII (1039.108), cluster III and cluster XIII (1015.310) and cluster I and cluster XIII (978.369). Greater the genetic distance between two clusters wider the genetic diversity among the genotypes of these clusters. Generally, it is assumed that cross combinations involving the parents belonging to most divergent clusters will manifest maximum amount of heterosis. So, in recombination breeding programme selection of highly divergent superior genotypes from the genetically distant clusters would be of great use in order to get desirable transgressive segregants. Hence, hybridization between the genotypes of cluster IX (T23, T26, T54, T65, T71, T75, T73, T374, T854), cluster X (T311, T541), cluster XII (T1067, T549, T716, T1001), cluster III (T209, T272) with genotypes of cluster XIII (T809, T730, T761, T777) are expected to produce highly heterotic F_1 and broad spectrum of variability in subsequent segregating generations enabling further selection and improvement (Rukmini Devi *et al.,* 2020). The minimum inter cluster distance was observed between cluster IV and VII (67.812) followed by cluster II and cluster VI (82.332), cluster VI and cluster VII (89.089), cluster I and cluster V (110.739), cluster II and cluster VII (111.768) and cluster V and cluster VIII (115.61). So, the genotypes included in them were closely related. The maximum intra cluster distance was exhibited by cluster XIV (852.674) followed by clusters XII (727.193), XI(684.01) , XIII (627.188) and IX (563.403). The minimum intra cluster distance was exhibited by cluster II (35.681) (**Table 4**). To maintain relatively broad genetic base, selection of parents from genetically homogeneous clusters should be strictly avoided. Parallel findings were reported by Nirosha *et al.,* (2016); Mamta Kumari *et al.,* (2016) and Lahari *et al.,* (2017).

Cluster mean analysis revealed wide range of variation for all the traits studied (**Tables 5a&b**). Cluster mean for days to 50% flowering was lowest for cluster X (94.750) and hence germplasm lines in this cluster may be used as a donor for earliness in rice breeding programmes. The highest cluster mean value for leaf length (36.443 cm) and leaf width (1.406cm) was observed in cluster VII and cluster XIV respectively. Hence the genotypes in these clusters would be useful for the improvement of physiological efficiency through hybridization. Regarding number of tillers and productive tillers per plant, cluster III (21.750) had the highest cluster mean value so the germplasm accessions present in this cluster may be used as a donor for the introgression of profuse tillering habit in to the desirable genotypes. Genetic improvement for panicle length could be achieved through hybridization using genotypes possessing long droopy panicles present in clusters IX and XIV due to its highest cluster mean (24.167) for this trait. Genotypes in cluster V (2.320) with high test weight could be excellent donors for the development of bold grain rice varieties. High yielding genotypes can be developed by using elite genotypes present in cluster IV (27.600) as donors in crossing programme. Genotypes with all the desirable traits were not present in any one of the clusters which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Similar kind of results were reported in rice by Muthuramu and Sakthivel (2018); Ranjith *et al., (*2018) and Kavurikalpana *et al.*, (2018). Thus according to the breeding objectives, trait specific lines can be picked out from different clusters and involved in hybridization programs for improvement of the character.

Table 4. Average intra-(in bold) and inter-cluster D² distances

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**195.512**	209.165	208.984	535.499	110.739	233.551	411.57	162.197	372.785	127.288	591.790	484.86	978.369	642.725
II		**35.681**	218.546	194.17	217.325	82.332	111.768	134.667	433.217	266.668	366.796	348.730	607.200	425.767
III			**36.85**	283.063	293.746	135.446	262.597	275.542	339.784	152.814	481.279.	540.214	1015.310	528.521
IV				**41.265**	649.751	132.739	67.812	478.449	627.475	568.258	390.953	546.731	713.966	430.703
V					**42.700**	281.895	476.134	115.61	396.471	146.052	644.427	456.66	933.162	706.054
VI						**45.175**	89.089	242.845	379.066	267.818	363.008	373.328	667.009	389.643
VII							**54.017**	341.83	565.555	488.907	362.573	436.227	576.254	391.314
VIII								**57.370**	479.482	174.564	530.560	494.228	701.059	592.232
IX									**563.403**	332.594	762.520	662.177	1313.049	793.155
X										**65.879**	632.169	568.470	1152.033	666.668
XI											**684.01**	711.902	897.179	686.973
XII												**727.193**	1039.108	748.351
XIII													**627.188**	915.583
XIV														**852.674**

Table.5a Cluster mean values of rice genotypes for different yield & yield contributing traits and grain characters

| Clusters	Plant height (cm)	Days to 50% flowering (days)	Leaf length (cm)	leaf width (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)
I	93.417	99.167	31.472	1.133	15.528	15.388	21.862
II	95.750	105.000	26.558	1.068	17.625	16.750	22.877
III	90.330	95.500	31.667	1.158	21.750	21.750	22.300
IV	94.583	104.000	31.658	1.260	12.500	12.500	22.458
V	89.585	101.500	29.975	1.217	13.415	12.458	23.000
VI	92.750	102.750	30.458	1.132	16.500	15.250	21.210
VII	92.080	106.500	36.443	1.233	20.417	20.417	24.083
VIII	80.750	101.500	29.608	1.100	13.585	12.417	21.208
IX	88.343	98.167	30.306	1.317	14.463	12.092	24.167
X	83.210	94.750	29.540	1.257	12.500	12.000	21.085
XI	97.738	103.250	32.024	1.297	16.095	15.136	22.607
XII	90.646	107.125	30.171	1.268	15.792	14.416	22.874
XIII	96.250	111.125	36.296	1.335	18.855	17.584	23.667
XIV	89.167	104.000	36.434	1.406	16.667	16.300	24.167

Table.5b Cluster mean values of rice genotypes for different yield & yield contributing traits and grain characters

Clusters	100 grain weight (g)	Grain length (mm)	Grain width (mm)	Length/Breadth ratio	Single plant yield (g)
I	**2.298**	8.12	3.00	2.707	16.200
II	2.243	7.67	3.00	2.557	24.150
III	1.857	6.83	3.00	2.275	18.575
IV	1.773	6.15	3.00	2.055	27.600
V	2.320	8.92	3.00	2.973	12.100
VI	2.090	6.65	2.95	2.287	16.900
VII	1.977	7.00	3.00	2.330	22.075
VIII	2.215	8.57	2.88	2.950	24.175
IX	2.172	7.32	3.11	2.375	14.444
X	2.278	7.58	3.00	2.528	21.150
XI	2.010	7.02	2.94	2.385	24.839
XII	2.280	8.17	3.25	2.557	15.113
XIII	2.079	7.16	2.16	3.474	21.563
XIV	2.078	6.62	2.79	2.673	23.670

Table. 6 Percentage contribution of each character to total genetic divergence

S.No.	Characters	No. of first rank	Percent contribution
1	Single plant yield	643	43.29
2	Grain length	193	12.99
3	100 grain weight	180	12.12
4	Days to 50% flowering	176	11.85
5	Grain width	176	11.85
6	Grain Length/Width ratio	52	3.50
7	Panicle length	41	2.76
8	Plant height	10	0.67
9	Leaf length	7	0.47
10	Leaf width	3	0.20
11	Number of tillers per plant	2	0.13
12	Number of productive tillers per plant	2	0.13
	TOTAL	**1485**	**100**
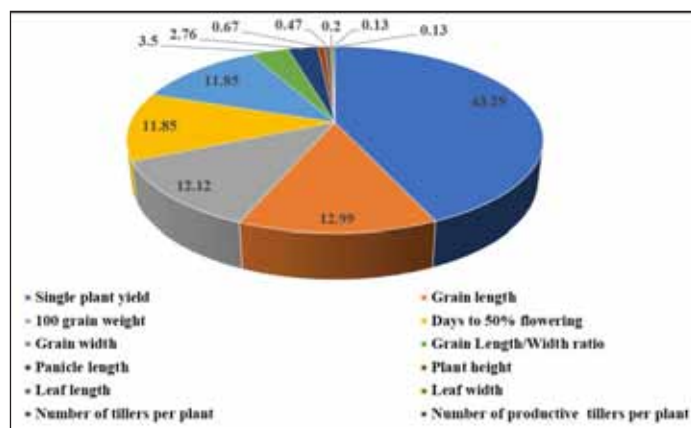
Figure 1: Percentage of contribution of each character to total genetic divergence

From the relative contribution of individual traits towards the divergence, it was found that the maximum contributing trait for divergence was single plant yield (43.29%) followed by grain length (12.99%), 100 grain weight (12.12%) grain width (11.85%) and days to 50% flowering (11.85%). Least contribution (0.13%) towards divergence was by number of tillers and productive tillers per plant (**Table 6**) and (**Figure 1**). These observations were in agreement with report of Kumari *et al.* (2018) and Rashmi *et al.* (2017) for days to 50% flowering; Sowmiya and Venkatesan (2017) for hundred grain weight and grain yield per plant and Vennila *et al.* (2011) for grain length. Hence, during selection of parents for hybridization and selection in the segregating populations traits like grain yield per plant, grain length, grain width, hundred grain weight and days to 50% flowering should be given importance.

References

Allard RW. 1960. Principles of Plant Breeding. John Wiley and Sons Inc., New York. 485.

Arunachalam V and Ram J. 1967. Geographical diversity in relation to genetic divergence in cultivated sorghum. *Indian Journal of Genetics and Plant Breeding*, 27:369-380

Kavurikalpana Thirumeni S and Shashidhara N. 2018. Genetic divergence analysis for quantitative traits in rice (*Oryza sativa* L.). *International Journal of Agriculture, Environment and Biotechnology,* 11(3): 469-473

Kumar Saurabh Singh, Suneetha Y, Vinay Kumar G, Srinivasa Rao V, Sandeep Raja and Srinivas DT. 2020. Genetic divergence studies for yield and quality traits in coloured rice. *Journal of Pharmacognosy and Phytochemistry,* 9(4):1234-1240.

Kumari S, Singh PK, Bisen P, Loitongbam B, Rai VP and Sinha B. 2018. Genetic diversity analysis of rice (*Oryza sativa* L.) germplasm through morphological markers. *International Journal of Agriculture, Environment and Biotechnology,* pp. 953-957(Special Issue).

Lahari P, Dushyanthakumar BM and Raghavendra P. 2017. Genetic diversity for grain yield and its components in rice (*Oryza sativa* L.) genotypes under submergence. *Electronic Journal of Plant Breeding,* 5(1): 67-70

Mahalanobis P. 1949. Historical note on the D²-statistics, appendix I. anthropological survey of United Provinces, 1941: a statistical study.

Mamta Kumari G, Babu S and Patel NB. 2016. Genetic diversity analysis of rice (*Oryza sativa* L.) germplasm under aerobic condition. *Bangladesh Journal of Botany,* 45(3): 727-732

Muthuramu S and Sakthivel S. 2018. Genetic diversity analysis for yield traits in upland rice (*Oryza sativa* L.) *Journal of Rice Research*, 10(1): 40-43.

Nirosha R, Thippeswamy S, Ravindrababu V, Reddy VR and Spandana B. 2016. Genetic diversity analysis of zinc, iron, grain protein content and yield components in rice. *Electronic Journal of Plant Breeding,* 7(2): 371-377.

Pathak H, Samal P and Shahid M. 2018. Revitalizing rice systems for enhancing productivity, profitability and climate resilience. pp. 1-17. **In**. Rice Research for Enhancing Productivity, Profitability and Climate Resilience (eds. Pathak, H., Nayak, A.K., Jena, M., Singh, O.N., Samal, P. and Sharma, S.G.). ICAR-National Rice Research Institute, Cuttack, Odisha, India.

Ranjith P, Sahu S, Dash K, Bastia DN and Pradhan BD. 2018. Genetic diversity studies in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, (2):2529-2531.

Rao CR. Advanced statistical methods in biometrical research. John Wiley and sons. New York 1952, 236- 272.

Rashmi D, Bisen P, Saha S, Loitongbam B, Singh S and Singh PK . 2017. Genetic diversity analysis in rice (*Oryza sativa L.*) accessions using SSR markers. *International Journal of Agriculture, Environment & Biotechnology,* 10(4): 457-467.

Rukmini Devi K, Venkanna V, Hari Y, Satish Chandra B, Lingaiah N, Rajendra Prasad K. 2020. Studies on genetic diversity and variability for yield and quality traits in promising germplasm lines in rice (*Oryza sativa L.*) *The Pharma Innovation Journal*, 2020;9(1):391-39.

Sowmiya, C.A. and Venkatesan, M. 2017. Studies on genetic diverity in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Science, 6*(9): 1749-1756.

Sri Lakshmi M, Suneetha Y and Srinivas T. 2021. Genetic diversity analysis for grain yield and yield components in rice. *International Journal of Chemical Studies*, 9(1): 1386-1389.

Vennila S, Anbuselvam Y and Palaniraja K. 2011. Research Notes D^2 analysis of rice germplasm for some quantitative and quality traits. *Electronic Journal of Plant Breeding*, 2(3):392-403.

Vishnu Brindha Devi G, Arumugachamy S and Amudha K. 2018. Determination of genetic divergence based on biometrical traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,* 9(4): 1557-1562.

Vivekananda P and Sukanya subramaniyan. 1993. Genetic divergence in rainfed rice. *Oryza,* 30: 60-62.