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GENETIC DIVERSITY ANALYSIS IN SOME LOW LAND RICE LANDRACES USING AGRO-MORPHOLOGICAL TRAITS

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ABSTRACT

Forty four landraces of lowland rice were assessed for genetic diversity using D^2 statistics based on various grain yielding parameters. Significant variability was found among the traits studied. Eight diverse clusters were made to set them into groups. The pattern of distribution of genotypes from different eco-geographic regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The maximum inter-cluster distance was observed between cluster III and IV (1033.15), followed by clusters II and VIII (935.07). Maximum intra-cluster distance was observed in cluster IV (731.01). Divergence analysis revealed significant variation among the parental lines for all the agro-morphological traits. Cluster analysis showed that superior cultivars like 'Kanakchur' from cluster IV; cv. 'FR13A', 'Jaladhi2', 'Matla' and 'Purni' from cluster III; cv. 'Latisail', 'Pimpu Dibasa', 'Jeeringa Samba' and 'Shib Chato' from cluster II; and cv. 'ARC11210', 'Kumar Gore', 'NC678', 'Sada Mota' and 'Kantaranga' from cluster VI may be taken in hybridization program, based on the genetic distance, relative contribution of characters towards total divergence and yield potential of genotypes. The characters *viz*., days to 50% flowering, plant height, panicle weight and number of grains panicle^{-1} contributed maximum towards the divergence among genotypes taken for this study. So, allelic diversity among the genotypes and the concerned traits taken for this experiment should be taken into consideration while framing a rice breeding programme.

Keywords: Cluster mean, D^2 analysis, lowland rice, panicle yield

INTRODUCTION

Rice [*Oryza sativa* L.] (2n = 24) is main staple food crop feeding billions of people in the world and serves as a major sources of nutrition to its consumers. Rice provides 23% of the global human per capita protein (IRRI, 2002). On the basis of mean grain yield per hectare, rice crop produces more food energy and protein than wheat and maize crops. Rice supports more people per unit land area than other staple crops (Lu and Chang, 1980). Genetic improvement of any crop depends mainly upon the amount of genetic variability present in the population (Mishra *et al*., 2003; Chakravorty and Ghosh, 2013). Diversity of parents is much emphasized in crossing programmes because the crosses between the genotypes with maximum genetic divergence are likely to yield the desirable recombinants. Genetic variability is more in populations from diversified environments than the populations from homogenous ecological regions (Chaturvedi and Maurya, 2005).

Rainfed lowland is an ecosystem which is constrained by excess water and uncontrolled flooding. It also experiences drought depending upon the rainfall and its distribution. About 25% of rice lands are under this ecosystem producing an average yield of 1-2 t ha^{-1}. Crop production in this ecosystem is governed by a number of physical and biological constraints, including submergence and drought. However, this ecosystem is suitable for crop diversification (Ram *et al*., 2002). Diversity of flood-prone environments renders germplasm improvement for submergence tolerance coupled with high productivity more challenging and difficult (Ram *et.al*., 2002). The study of genetic divergence among the plant materials is a vital tool for choosing efficient parents for crop improvement. The divergence studies on landraces of West Bengal state of India have previously been undertaken (Chakravorty and Ghosh, 2011, 2012) which revealed that genetic divergence can occur without geographic separation through disruptive selection as well. Further, 51 rice landraces of Gangetic alluvial zone of south Bengal were categorized into 11 clusters. There is good scope to bring about the genetic improvement in rice through hybridization and selection by crossing accessions from different clusters. The nature and magnitude of genetic divergence helps the plant breeders in choosing right parents for breeding programme meant for high heterotic expression in F_1s and broad spectrum of variability in subsequent generations (Ramkrishna Prasad *et al.*, 2018; Shruti *et al*., 2019). The present study was aimed to assess the nature and degree of genetic divergence among some lowland rice collected from different agro-climatic zones of West Bengal, Orissa, and Uttar Pradesh states of India, and Bangladesh so that the generated information can be exploited for future varietal improvement programme of lowland rice.

MATERIALS AND METHODS

Forty four cultivars of traditional lowland rice were collected from the gene bank of Rice Research Station, Chinsurah, West Bengal (India) during *kharif* season and were grown at the Instructional Farm of Zonal Adaptive Research Station, Krishnagar, Nadia, West Bengal for three consecutive years of 2021-2023 (23˚24´N latitude and 88˚31´E longitude with an altitude of 9.75 m) to carry out. the present study. Of the lowland rice, 33 cultivars were collected from West Bengal [10 (Doi Muri, Kodalpasa, Ketokijota, Kantaranga, Gerua Muri, Pimpu Dibasa, Tulasi Amrit, Purni, Pimpu Dibasa, Khejurchori, and Ajan) from Midnapore (W), 9 cultivars (Kanakchur, Kumar Gore, Gheus, Mete, Jala Kamini, Raj Jhingasail, Rupsail, Jaladhi 2, and Matla) from 24-Parganas South, 2 cultivsrs (Gopalbhog, and Shib Chato) from Midnapore (N), 2 cultivars (Narashinghajata, and Patnai) from Midnapore (E), 2 cultivars (Tulaipanji, and Kalonunia) from West Dinajpur, 2 cultivars (Gobindobhog, and Badsa Bhog) from Burdwan, 2 cultivars (Kalamkathi 147, and Jhingasail) from Bankura, 2 cultivars (Kalojira, and Nigersail) from Jalpaiguri, 1 cultivar (Sadamota) from Parganas North, and 1 cultivar (Nc 678) from Murshidabad], 4 cultivars (ARC 6157, ARC 11210, ARC 6631, and ARC6136) from Assam, 3 cultivars (Chini Kappor-A, Chini Kappor-B, and Jeeriga Samba) from Uttar Pradesh, 3 cultivars (Fr 13a, Sr 26b, and Fr 43b) from Orissa, and 1 cultivar (Latisail) from Bangladesh.

The experiment was conducted on a soil having slight acidic pH, with low soluble salts (EC 0.15 dS m^{-1}**)**, medium organic carbon content (0.57%), Total N (0.056 in kg ha^{-1}), medium in available P (25.28 kg ha^{-1}) and K (148.77 kg ha^{-1}). The landrace materials were grown in a completely randomized block design with treatment replicated three times. Each entry was transplanted (45 days old seedling) in a plot of 6 m^2 with a plot spacing of 20 cm x 15 cm. A random sample of five competitive plants was used for observations on different traits under study. Nutrients (N: P_2O_5: K_2O) @ 40:20:20 kg ha^{-1} were applied (ICAR; Sagar *et al.*, 2024) During the crop period the water depth of the field was 40-50 cm. The panicle characters observed in undergoing the experiment were panicle length, number of nodes $panicle^{-1}$, number of primary branches $panicle^{-1}$, number of secondary branches $panicle^{-1}$, number of spikelets on primary branches $panicle^{-1}$, number of spikelets on secondary branches $panicle^{-1}$, number of spikelets $panicle^{-1}$, number of grains on primary branches $panicle^{-1}$, number of grains on secondary branches $panicle^{-1}$, fertility % of spikelets on primary branches panicle^{-1}, fertility % of spikelets on secondary branches panicle^{-1}, fertility % of spikelets panicle^{-1}, grain length, grain breadth, grain length/breadth ratio, grain thickness, kernel length, kernel breadth, kernel length/breadth ratio, kernel thickness, 100 grain weight, 100 kernel weight and panicle yield. Mahalanobis's D^2 statistics and grouping of the genotypes into clusters was carried out following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Genetic diversity of genotypes

A significant difference among the 44 traditional rice cultivars was observed for all 23 quantitative characters, thereby revealing the presence of high variability among the genotypes for all the traits (Table 1). Denoting the quite diverse material (Table 2), the D^2 values of genotypes started from 78.93 and extended upto 1033.15. As per genetic distance, the traditional rice cultivars were segregated into 8 clusters (Table 2). Cluster-VII, the largest cluster, comprised of 10 genotypes, followed by cluster-III with 8 genotypes, cluster V with 7 genotypes and cluster I with 6 genotypes,

Table 1: Estimation of statistical and genetic parameters of agro-morphological traits for different lowland of rice

S. No.	Traits	Mean ± S.E.	Range	GCV	PCV	h^2 (heritability)	GA (% of mean)	CV%
1	Panicle length	26.86 ± 0.99*	23.2-30.8*	7.00	8.33	70.53	12.11	4.52
2	Nodes panicle^{-1} (No.)	8.51 ± 0.69*	6.3-11.0	9.81	13.99	49.21	14.19	9.97
3	Pr. branches panicle^{-1} (No.)	12.09±0.82*	8.6-14.9	12.79	15.30	69.91	22.04	8.39
4	Sec. branches panicle^{-1}(No.)	39.42±5.27*	20.2-65.4	25.00	29.90	69.95	43.09	16.39
5	Spikelets on Pr. branches panicle^{-1} (No.)	72.03±6.03*	51.4-98.3	13.68	17.10	63.98	22.55	10.26
6	Spikelets on Sec. branches panicle^{-1} (No.)	136.24±20.5*	47.5-282.3	35.51	40.01	78.77	64.93	18.43
7	Spikelets panicle^{-1} (No.)	208.07±22.8*	108.2-346.9	24.03	27.53	76.17	43.21	13.44
8	Grains on Pr. branches panicle^{-1} (No.)	64.61±6.22*	42.0-85.6	13.84	18.19	57.90	21.70	11.80
9	Grains on Sec. branches panicle^{-1} (No.)	104.54±16.1*	40.0-223.1	38.23	42.66	80.31	70.59	18.92
10	Spikelet fertility on Pr. branches panicle^{-1} (%)	89.76±4.28*	79.3-95.8	2.73	7.13	14.68	2.16	6.58
11	Spikelet fertility on Sec. branches panicle^{-1} (%)	77.22±6.24*	41.5-95.0	13.67	16.88	65.63	22.82	9.89
12	Spikelet fertility panicle^{-1} (%)	81.98±4.15*	55.7-93.8	9.71	11.53	70.98	16.87	6.21
13	Grain length (mm)	8.15±0.28*	6.0-11.0$^{@}$	14.90	15.50	92.41	29.52	4.27
14	Grain breadth (mm)	2.83±0.06*	1.9-3.7$^{@}$	17.85	18.05	97.77	36.37	2.69
15	Grain length/breadth	2.93±0.11*	2.2-4.2$^{@}$	18.49	19.16	93.22	36.80	4.98
16	Grain thickness (mm)	2.00±0.05*	1.6-2.4	11.24	11.68	92.70	22.31	3.15
17	Kernel length (mm)	5.71±0.14*	4.1-8.0$^{@}$	15.56	15.87	96.24	31.46	3.07
18	Kernel breadth (mm)	2.41±0.05*	1.7-3.2$^{@}$	17.73	17.95	97.48	36.06	2.85
19	Kernel length/breadth	2.41±0.08*	1.8-3.4$^{@}$	19.63	20.13	95.14	39.45	4.43
20	Kernel thickness (mm)	1.78±0.04*	1.5-2.3	11.54	11.97	92.96	22.94	3.17
21	1000 grain weight (g)	2.37±0.007*	1.1-3.6$^{\$}$	32.68	32.68	99.99	67.32	0.37
22	1000 kernel weight (g)	1.84±0.02*	0.8-2.8$^{\$}$	33.12	33.15	99.80	68.17	1.50
23	Panicle yield (t ha^{-1})	3.915±0.36*	1.8-7.2	32.07	34.04	88.80	62.27	11.39

Note: Pr. = Primary; Sec. = Secondary; # - cm, @ - mm, $ - g, * indicates significant at 5% level

Table 2: Average inter- and intra-cluster D^2 values among eleven clusters in 44 traditional rice cultivar

Cluster	Genotypes in each cluster									
	No.	Names of the genotypes	I	II	III	IV	V	VI	VII	VIII
I	6	ARC6613, ARC6136, Gehus, Mete, Ajan, and FR43B	78.9							
II	4	Latisail, Pimpudibasa, Jeeriga Samba, and Shib Chato	393.8	97.9						
III	8	FR13A, Jaladhi2, Matla, ARC6157, SR26B, Purni, Jalakamini, and Patnai	458.2	499.0	155.3					
IV	1	Kanakchur	307.3	643.9	1033.1	731.0				
V	7	Tulaipanji, Gopalbhog, Kalonunia, Gobindobhog, Kalojira, Doimuri, and Badsabhog	400.5	626.8	366.1	151.7	370.2			
VI	4	Nigersail, Jhingasail, Raj Jhingasail, and Tulsi amrit	834.1	509.6	437.3	544.0	296.7	675.0		
VII	10	ARC11210, Kumargore, NC678, Sadamota, Kantaranga, GeruaMuri, Narashingjata, Khajurchoti, Kodalpasa, and Ketokajata	322.0	772.5	661.0	786.3	578.3	297.6	438.7	
VIII	4	Kalamkathi147, Rupsail, Chini Kappor-A, and Chini Kappor-B	225.0	935.1	198.8	545.3	831.1	140.4	448.8	409.2

Diagonal figures indicate intra-cluster values

respectively. The cluster II, VI and VIII comprised 4 genotypes each. Cluster IV had only1 genotype. The clustering pattern revealed that the genotypes collected from same geographic origin were distributed in different clusters. Similar findings of non-correspondence of genetic divergence with geographic diversity were reported earlier in rice (Vivekanandan and Subramanian, 1993; Rahman *et al*., 1997; Shanmugasundaram *et al*., 2000). The genetic drift and selection in environment could be the reason for greater diversity than geographic distances (Cui *et al*., 2021). The intra-cluster average D^2 values ranged from 78.93 to 731.01 (Table 2). Intra-cluster distance refers to the average distance between data points within the same cluster. The smaller the intra-cluster distance, the more similar and tightly packed the data points are within the cluster. The high intra-cluster distance indicates the presence of wide genetic diversity among the genotypes (Tejaswini *et al*., 2016).

Intra- and inter-cluster divergence

The maximum intra-cluster distance was observed in cluster IV (731.01), indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce more desirable breeding materials for achieving maximum genetic distance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines (Rahman *et al*., 1997). Therefore, genotypes from cluster IV should be given emphasis while selection of parents for hybridization programme since most of the elite breeding cultivars were included in this cluster.

Inter-cluster value was maximum (1033.15) between cluster III and IV, followed by 935.07 (between cluster II and VIII), 834.1 (between cluster I and VI), 831.09 (between cluster V and VIII) and 786.35 (between cluster VI and VIII) (Table 2). It study revealed that the test genotypes are genetically diverse and may give rise to high heterotic response (Arunkumar and Narayanan, 2023). Similar results were also reported by Satish and Senapati (2017) and Vadigeri *et al*. (2021). The genotypes included in these cluster have the greater divergence and hence the crossing between the genotypes in these clusters were expected to give desirable recombinants. Hence, inter-mating between the genotypes in these clusters (III, IV, II, VIII, I and VI) were expected to give more transgressive segregants in future generations. The lowest inter- cluster value was 140.43 (between cluster VI and VIII) indicated close relationship among the genotypes included in these clusters.

Cluster mean

All the traits under study exhibited a wide range of variation in cluster mean values (Table 3). Keeping in view, the output data, it was maintained that cluster V had highest panicle yield plant^{-1}

(4.13) and second highest number of grains on primary branches panicle^{-1} (71.55) and grain thickness value (2.04). In this experiment cluster mean with respect to panicle yield plant^{-1} varied from 3.70 to 4.13. Cluster I had the highest number of spikelets on primary branches panicle^{-1} (90.05), number of grains on primary branches panicle^{-1} (72.0) and number of secondary branches panicle^{-1} (41.3). Cluster II had highest fertility percentage of spikelets on primary branches panicle^{-1} (97.44), kernel length (6.01) and 1000 grain weight (2.37). Besides, cluster II had second highest value in number of primary branches panicle^{-1} (12.63), number of spikelets on secondary branches panicle^{-1} (141.34) and grain breadth (2.90). Cluster III had highest number of nodes panicle^{-1} (8.97), number of spikelets on secondary branches panicle^{-1} (146.02), number of spikelets panicle^{-1} (231.54), number of grains on secondary branches panicle^{-1} (120.05); whereas, this cluster had second highest value in number spikelets on primary branches panicle^{-1} (89.53), fertility percentage of spikelets on primary branches panicle^{-1} (89.26), kernel length (5.81), kernel length/breadth ratio (2.5) and panicle yield (3.99). Cluster IV had highest grain length (8.89), grain thickness (2.09) and kernel thickness (1.81). It had second highest value in panicle length (26.80). Cluster VI had highest panicle length (27.16) and 1000 grain weight (2.37). It had second highest value in fertility percentage of spikelets on primary branches panicle^{-1} (96.07), kernel breadth (2.44), kernel thickness (1.80) and 1000 kernel weight (1.94). Cluster VII had highest value in fertility percentage of spikelets panicle^{-1} (90.05), grain breadth (2.95), kernel breadth (2.46), kernel kength/breadth ratio (3.43) and 1000 kernel weight (1.97). It had second highest value in number of spikelets panicle^{-1} Cluster VIII had highest value in number of number of primary branches panicle^{-1} (12.830 and grain length/breadth ratio (2.97). It had second highest value in number of grains on secondary branches panicle^{-1} (111.76), fertility percentage of spikelets on primary branches panicle^{-1} (81.06) and kernel

Table 3: Cluster means and percent contribution to the genetic divergence of 23 characters

S. No.	Traits/ clusters	I	II	III	IV	V	VI	VII	VIII	CV (%)	PC (%)
1	Panicle length (cm)	25.36	26.55	25.39	26.80	26.03	27.16	25.89	26.55	4.71	1.02
2	Nodes panicle^{-1} (No.)	8.11	6.08	8.79	7.61	7.33	8.05	6.55	8.19	9.45	3.24
3	Primary branches panicle^{-1} (No.)	11.90	12.63	12.05	11.55	11.70	11.54	12.09	12.83	8.61	3.96
4	Secondary branches panicle^{-1} (No.)	41.30	39.55	36.50	40.09	39.78	38.63	39.54	40.01	16.09	6.53
5	Spikelets on primary branches panicle^{-1} (No.)	90.05	77.61	89.53	71.53	75.99	83.33	76.11	70.09	11.12	6.02
6	Spikelets on secondary branches panicle^{-1} (No.)	129.44	141.34	146.02	139.28	130.09	138.55	140.31	129.99	48.32	9.56
7	Spikelets panicle^{-1} (No.)	201.67	205.11	231.54	206.23	199.67	209.78	220.09	206.41	14.09	10.37
8	Grains on primary branches panicle^{-1} (No.)	72.00	69.81	65.43	69.90	71.55	66.12	61.77	64.36	11.05	4.32
9	Grains on secondary branches panicle^{-1} (No.)	109.54	108.31	120.05	111.44	105.09	100.76	109.53	111.76	19.31	3.55
10	Spikelet fertility on primary branches panicle^{-1} (%)	83.09	97.44	89.26	87.60	80.09	96.07	88.83	85.41	8.88	4.19
11	Spikelet fertility on secondary branches panicle^{-1} (%)	70.09	77.12	83.00	71.32	71.98	75.66	80.23	81.06	9.79	11.67
12	Spikelet fertility panicle^{-1} (%)	83.70	84.90	89.09	81.56	88.76	88.73	90.05	88.87	6.70	7.18
13	Grain length (mm)	8.32	8.15	8.06	8.89	8.65	8.23	8.83	8.15	4.19	2.95
14	Grain breadth (mm)	2.79	2.90	2.83	2.88	2.79	2.71	2.95	2.86	2.71	2.17
15	Grain length/breadth	2.92	2.90	2.84	2.93	2.89	2.84	2.94	2.97	5.01	3.02
16	Grain thickness (mm)	2.00	2.01	2.01	2.09	2.04	2.00	2.02	2.00	3.20	1.67
17	Kernel length (mm)	5.33	6.01	5.81	5.63	5.70	5.76	5.23	5.19	3.09	1.98
18	Kernel breadth (mm)	2,33	2.39	2.42	2.40	2.42	2.44	2.46	2.44	2.93	1.19
19	Kernel length/breadth	2.40	2.41	2.50	2.39	2.36	2.40	3.43	2.47	4.44	2.55
20	Kernel thickness (mm)	1.77	1.73	1.79	1.81	1.78	1.80	1.77	1.78	3.19	0.71
21	1000 grain weight (g)	2.35	2.37	2.33	2.35	2.33	2.37	2.36	2.34	0.35	3.30
22	1000 kernel weight (g)	1.79	1.88	1.84	1.89	1.79	1.94	1.97	1.85	1.50	1.51
23	Panicle yield (t ha^{-1})	3.72	3.97	3.99	3.70	4.13	3.95	3.95	3.93	11.55	7.34

breadth (2.44). The greater distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the clusters having maximum inter-cluster distance can be selected for crop improvement programme.

Contribution of the characters towards genetic divergence

The divergence pattern has revealed that the characters *viz*., fertility percentage of spikelets panicle^{-1}, number of grains on primary branches panicle^{-1}, number of spikelets on secondary branches panicle^{-1}, panicle yield, grain length and number of secondary branches number of grains on primary branches panicle^{-1} depicted maximum divergence (Table 3) and were supposed to contribute a lot in rice improvement programme. Hence taking these characters in consideration will prove very beneficial for heterosis breeding in lowland rice to select divergent parent. A number of workers like Kulsum *et al*. (2013), Debsharma *et al*. (2023) and Saivenkat *et al*. (2024) upheld the relative importance of some of those characters in inter varietal divergence in rice.

The present investigation proposes the use of parental lines selected from cluster IV (Kanakchur) for grain length, grain thickness, kernel thickness and panicle length, cluster III (e.g. FR13A, Jaladhi2, Matla, Purni, etc.) for the number of nodes panicle^{-1}, number of spikelets on secondary branches panicle^{-1}, number of spikelets panicle^{-1}, number of grains on secondary branches panicle^{-1}, fertility percentage of spikelets on secondary branches panicle^{-1}, cluster II (e.g. Latisail, Pimpu Dibasa, Jeeringa Samba and Shib Chato) for fertility percentage of spikelets on primary branches panicle^{-1}, kernel length 1000 grain weight and cluster VI (e.g. ARC11210, Kumar gore, NC678, Sada Mota, Kantaranga) for panicle length, 1000-grain weight in a hybridization programme, finding out the importance of genetic distance, relative contribution of characters towards total divergence and yield potential of genotypes.

The races collected from separate geographic regions exhibited genetic differences among divergent populations which apparently appears to involve silent mutations, thereby appear responsible for morphological and physiological changes leading to reproductive isolation, either due to novel adaptations via selection or due to genetic drift. The 44 land races were distributed into 8 clusters with high inter-cluster distance (1033.15 between cluster III and IV) and intra-cluster distance (731.01, in cluster IV) revealed the significance of this study.

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REFERENCES

Arunkumar, P. and Narayanan, R. 2023. Estimation of genetic diversity for grain yield and its components traits in rice (*Oryza sativa* L.) under coastal saline condition. *Mysore Journal of Agricultural Science*, **57**(3): 88-96.

Chakravorty, A. and Ghosh, P.D. 2012. Genetic divergence in landraces of rice (*O. sativa* L.) of West Bengal. *Journal of Crop and Weed*, **8**(2): 25-28.

Chakravorty, A. and Ghosh, P.D. 2013. Estimation of variability, diversity and correlation studies with respect to different agro-morphological traits in traditional rice (*O. sativa* L.) of West Bengal, India. *Oryza.* **50**(2): 127-131.

Chaturvedi, H.P. and Maurya, D.M. 2005. Genetic divergence analysis in rice (*Oryza sativa* L.). *Advances in Plant Science*, **18**(1): 349-353.

Cui, D., Tang, C., Lu, H., Li, J., Ma, X., Han, B., Yang, Y., Dong, C., Zhang, F., Dai, L. and Han, L. 2021. Genetic differentiation and restricted gene flow in rice landraces from Ynnan, China: Effects of isolation by distance and isolation by environment. *Rice*, **14**(54): 1-14.

Debsharma, S.K., Md, A.S., Md, H.A., Maniruzzaman, S., Roy, P.R., Brestic, M., Gaber, A. and Hossain, A. 2023. Harnessing on genetic variability and diversity of rice (*Oryza sativa* L.) genotypes based on quantitative and qualitative traits for desirable crossing materials. *Genes*, **14**(1): 10 [*https://doi.org/10.3390/genes14010010*].

IRRI. 2002. *Rice Almanac* (3rd edn.). International Rice Research Institute, Manila, Philippines.

Kulsum, U., Siddque, A., Hasan, J. and Begum, F. 2013. Genetic diversity in some selected rice genotypes (*Oryza sativa* L.). *Bangladesh Journal of Agriculture*, **38**: 63-72.

Lu, J.J. and Chang, T.T. 1980. Rice in its temporal and spatial perspectives. pp. 1-75. **In:** *Rice: Production and Utilization* (ed. B.S. Luh), AVI Publishing Co., Westport, Conn, USA.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of the National Institute of Sciences, India*. **2**: 49-55.

Mishra, L.K., Sarawagi, A.K. and Mishra, R.K. 2003. Genetic diversity for agromorphological and quality traits in rice (*O. sativa* L.). *Advances in Plant Science*, **16**(1): 287-293.

Murty, B.R. and Arunachalam, V. 1966. The nature of genetic divergence divergence in relation to breeding system in some crop plants. *Indian Journal of Genetics*, **26**: 188-198.

Pradhan, S.K. and Mani, S.C. 2005. Genetic diversity in basmati rice. *Oryza*, **42**: 150-152.

Rahman, M., Acharya, B., Shukla, S.N. and Pande, K. 1997. Genetic divergence in low land rice germplasm. *Oryza*, **34**: 209-212.

Ram, P.C., Singh, B.B., Singh, A.K., Ram, P., Sing, P.N., Singh, H.P., Boamfa, E.I., Harren, F.J.M., Santosha, E., Jackson, M.B., Setter, T.L., Reuss, J., Wade, L.J., Singh, V.P. and Singh, R.K. 2002. Physiological basis of submergence tolerance in rainfed lowland rice: prospects for germplasm improvement through marker aided breeding. *Field Crop Research*, **76**: 131-152.

Ramkrishna Prasad, K., Suneetha, Y. and Srinivas, T. 2018. Genetic diversity studies in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **9**(4): 1335-1341.

Rao, C.R. 1952. *Advance Statistical Method for Biometrical Research.* John Wiley & Sons, New York, USA.

Sagar, L., Maitra, S., Singh, S. and Sairam, M. 2024. Advanced strategies for optimization of primary nutrients requirement in rice - A review. *Plant Science Today*, **11**(1): 353-365.

Saivenkat, K.S., Sekhar, M.R., Vemireddy, L.R., Umar, S.N. and Bommisetty, R. 2024. Multivariate analysis of rice indigenous germplasm for identification of high yield potential genotypes based on yield and its attributes. *Genetic Resources and Crop Evolution*, **71**: 1-17.

Satish, V. and Senapati, B.K. 2017. Study of genetic diversity in some newly developed rice genotypes. *International Journal of Current Microbiology and Applied Sciences*, **6**(10): 2693-2698.

Shanmugadundaram, P., Souframanien, J. and Sadasivan, S. 2000. Genetic divergence among rice varieties released from paddy breeding station, Coimbatore, India. *Oryza*, **37**(3): 225-228.

Shruti, K., Balakrishan, B., Senguttuvel, P. and Hari Prasad, A.S. 2019. Evaluation of genetic diversity of parental lines for development of heterotic groups in hybrid rice (*Oryza sativa* L.). *Journal of Plant Biochemistry and Biotechnology*, **29**(4): 236-252.

Tejaswini K.L.Y., Manukonda, S., Ramana Rao, P.V., Ravi Kumar, B.N.V.S.R., Mohammad, L.A. and Raju, S.K. 2016. Cluster analysis studies in rice (*Oryza sativa* L.) suing wards minimum variance method. *Journal of Agricultural and Crop Research*, **4**(9): 129-139.

Vadigeri, P., Diwan, J.R., Mahantashivayogayya, Kulkarni, V. and Pramesh, D. 2021. Genetic diversity studies of rice genotypes for yield related traits. *Acta Botanica*, **9**(3): 1-7. [*https://dx.doi.org/10.3897ACTA2021.V09.164*].

Zahin, M., Hasan, S., Aqil, F., Khan, M.S., Husain, F.M. and Ahmad, I. 2010. Screening of certain medicinal plants from India for their anti-quorum sensing activity. *Indian journal of Experimental Biology*, **48**(12): 1219-1224.