www.ThePharmaJournal.com

The Pharma Innovation

Bhagyasri Majhi
P.G Student, Section of Genetics
and Plant Breeding, S.G. College
of Agriculture and Research
Station (IGKV, Raipur),
Kumhrawand, Jagdalpur,
Bastar, Chhattisgarh, India

Sonali Kar
Scientist, Section of Genetics and
Plant Breeding, S.G. College of
Agriculture and Research
Station (IGKV, Raipur),
Kumhrawand, Jagdalpur,
Bastar, India

Multivariate analysis of lowland rice (*Oryza sativa* L.) genotypes for high yielding attributes

Bhagyasri Majhi and Sonali Kar

Abstract
Multivariate analysis has been used frequently for genetic diversity analysis in rice by plant breeders which aids in study the characteristics of the genotypes separately and make a trade-off among the characteristics to arrive most suitable variety. The current study was held on 64 rice genotypes including 4 checks at Instructional cum Research Farm, Section of Genetics and Plant Breeding, S. G. College of Agriculture and Research Station, Jagdalpur during kharif *2022*. In order to evaluate genetic diversity as well as character associations, 17 yield-attributing traits among genotypes were exposed to a multivariate analytic method called cluster analysis. ANOVA revealed that all characters under study were significant for variability. Using hierarchical cluster analysis, the dendrogram divided 64 rice genotypes into seven clusters. Cluster V recorded greatest intra-cluster distance recorded, while clusters V and IV recorded greatest inter-cluster distance. Cluster IV with 3 genotypes, *viz.*, BNKR 121, MSN-119 and KHP-14 exhibited highest mean performance for grain yield followed by days to 50% flowering, plant height, flag leaf length and flag leaf width. The most genotypes were included in Cluster VII, which also had the highest cluster means for harvest index, grain width, and kernel width. As a result, genotypes grouped in clusters IV and VII with high yield potentiality should be prioritized. These genotypes were found to suitable genotypes for lowland ecology. Further, these promising genotypes could be recommended for varietal development.

Keywords: Rice, analysis of variance, multivariate analysis and genetic diversity

Introduction
Rice is one of the world's most important crops, with a wide geographic range reaching from 50°N to 35°S, and anticipated to be the most vulnerable crop to climate change in future (Mohanty *et al*., 2013) [7]. It is an autogamous, short-day cereal crop that belongs to the Poaceae family, order Cyperales, and class Monocotyledon. It is a member of the *Oryzae* genus, which includes 25 species out of which two species: *Oryza sativa* and *Oryza glaberrima* (2n = 24) are widely produced at global level, with the rest being wild species.

During *kharif* 2021, total rice cultivated in the world was 165.65 MH, with the production of 515.08 Mmt and productivity of 4620 kg ha⁻¹ (Anonymous, 2022 a) [1]. India is the world's second-largest producer and consumer of rice, accounting for 20% of total global rice output. In India, total rice produced on 45 MH, with rice output anticipated at 127.93 Mt and productivity of 2713 kg ha⁻¹ in 2021-22 (Anonymous, 2022 b) [2].

The presence of genetic variation among genotypes is critical to the success of plant breeding experiments. When it involves choosing the proper sort of parents for a hybridization programme, it's far the maximum essential device for a plant breeder. The expertise on diversity and genetic distance among groups of genotypes allows to choose parental genotypes for hybridization programs and to decide the extent of genetic divergence amongst lowland rice genotypes using multivariate analysis.

Materials and Methods
The current study was held at the Instructional cum Research Farm of S.G. College of Agriculture and Research Station at Kumhrawand located in Jagdalpur, Bastar (C.G.) during *Kharif* 2022. The required material for the experiment comprised of total 64 genotypes of rice along with 4 checks namely Swarna (NC), PA 6444 (HC), NDR 8002 (ZC) and Jal dubi (LC) were included for comparative studies with two replications in Randomized Block Design. The plants were spaced 20 cm apart in rows and 10 cm apart between them. Gross Plot Size and Net Plot Size of 2 m x 5 m = 10 m² and 1.6 m x 4.8 m = 7.68 m² respectively were used to sow the crop.

Corresponding Author:
Bhagyasri Majhi
P.G Student, Section of Genetics
and Plant Breeding, S.G. College
of Agriculture and Research
Station (IGKV, Raipur),
Kumhrawand, Jagdalpur,
Bastar, Chhattisgarh, India

Observations were recorded for Quantitative characters i.e., plant height (cm), days to 50% flowering, no. of effective tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), test weight (g), number of filled grains per panicle, biological yield (kg), harvest index (%) and grain yield (q/ha) along with quality characters like kernel length, kernel breadth, kernel L:B ratio, grain length, grain width, grain L:B ratio, on 5 random plants of each replication have been estimated according to the standard procedures given by IIRR, Hyderabad. Genetic diversity analysis was carried out following the D^2 statistics given by Mahalanobis (1936) [5].

Results and Discussion
The ANOVA demonstrated that all of the traits under consideration were significant for variability. The 64 genotypes were classified into seven clusters (Table 1). Cluster VII consisted of 21 genotypes and found to be the largest cluster followed by, Cluster III consisted of 14 genotypes, cluster I consisted 10 genotypes, cluster II consisted 8 genotypes, cluster VI consisted 5 genotypes and cluster IV and cluster V consisted 3 genotypes each, which represents high level of genetic divergence among the experimented material and which can be exploited to develop genotypes with economically important traits and can be used in a hybridization programme. These findings were similar with Tripathi *et al.*, (2017) [8], Ashok *et al.* (2017) [3], and Mandal *et al.* (2022) [6].

Among the 7 clusters, greatest intra-cluster distance recorded for cluster V (3.205) indicating the similarities among genotypes *viz.*, CRHR 163, HUR 22-5, RP 6460-C3-206. Followed by cluster VII (3.151), cluster III (3.112), cluster I (3.061), cluster VI (3.038) cluster II (2.951) and cluster IV (2.592). Highest inter cluster distance recorded between cluster V and cluster IV (7.586) indicating that genotypes present in that cluster had considerable genetic distance among themselves and indicates the greater divergence between these clusters, followed by cluster VII and V (6.933). The intra and inter cluster distances were presented in Table 2. Dendrogram of 64 rice genotypes are showed in Fig.1. As a result, the hybridization programs might employ genotypes from these clusters that are genetically diverse. These crosses

would result in high heterotic F_1 lines, and the recombinants could achieve broad spectrum variability in advance generation.

Cluster mean performances for all the traits were presented in Table 3. Cluster mean values were found to have a vast range among the genotypes under study, which implies the existence of variation amon them. Cluster IV with 3 genotypes, exhibited highest mean performance for the characters like plant height (131.63), days to 50% flowering (129.33), flag leaf length (37.08), grain yield (52.18) and flag leaf width (1.95). Whereas, cluster VI with 5 genotypes, exhibited highest mean performance for the characters like panicle length (27.87), number of effective tillers per plant (8.81), number of filled grains per panicle (198.70) and grain L:B ratio (3.76). Cluster V with 3 genotypes, exhibited highest mean performance for the characters like grain length (10.36), kernel length (7.47) and kernel L:B ratio (3.54). Cluster VII with 21 genotypes, exhibited highest mean performance for the characters like harvest index (49.45), grain width (3.19) and kernel width (2.61). Cluster II with 8 genotypes, exhibited highest mean performance for the character biological yield (11.75) and cluster III with 14 genotypes, exhibited highest mean performance for the character test weight (25.13). The findings demonstrate that genotypes with high values for a specific trait can be selected from clusters IV and VI. But primarily from cluster IV, which had the greatest mean values for the most of the attributes. Furthermore, if used as a criterion for hybridization in genotypes of that cluster, characters with high cluster means will lead to better outcomes, while improving those traits.

The majority of studies have used the Mahalanobis D^2 statistic for multivariate analysis in crop species to determine genetic divergence among them. According to Vennela *et al.* (2017) [9] and Bhati *et al.* (2015) [4], this approach is effective for examining genetic divergence in rice genotypes.

The contribution of each character to genetic divergence is displayed in Table 4. Biological yield had highest contribution 8.44% towards genetic diversity followed by harvest index had contribution of 7.72% and flag leaf width contributed 7.35%.

Table 1: Grouping of genotypes into 7 clusters on the basis of D^2 analysis

Clusters	No. of genotypes	Genotypes
I	10	BRR 0150, NVSR 762, RP 6528-RMS-13-29-34-83, RR 5346, CR 3856-44-22-2-1-11-4-5-5, WGL 1601, RP 5285-154-64-2-2-2-1, MTU 1349, RIL-SM5, RP 6354-5-76-39-80.
II	8	AD 18158, Pusa 5159-1-2-1-1-1-4, BRR 2110 ACK 20001, MTU 1400, OR 2748, MTU 1398, CR 3984-1-5-4-3-2.
III	14	R 2404-346-1-164-1, NDR 2022-6, CR 4206-17-4-2-2, RP 6195-MC, NDR 8002, CR 4426-4-1-1-1, BRR 0225, CR 4421-10-2-2-1, PA 6444, NVSR 796, RIL-SM 2-2-2, NLR 3747, CRHR 166, CRHR 702.
IV	3	BNKR 121, MSN-119, KHP-14.
V	3	CRHR 163, HUR 22-5, RP 6460-C3-206.
VI	5	KNM 12469, KNM 12472, BPT 3272, RP 6703-SP-M-KS-67-11-2-7-1-9-5, P .3333.
VII	21	CR 3895-1-4-5-1-1, CRL 145-4-1, Bangabandhu-1 Plus, CR 4427-3-2-1-1-2-1, MTU 1399, MEPH-173, CR 4354-3-2-1-2-1, HURS 22-2, CRL 146-35-1, Swarna, RP 6702-SP-M-SS-99-99-5-6-10-3-4-1, CR 3988-6-3-1-1, AD 18084, VNR-233, CR 3562-2-1-1-1-1-1, Pusa 5315-2-5-1-62-1-3-4, KNM 12488, CR 4350-7-5-1-17, RP 6704-MS-SS-166-3-1-5-6-4-7, R 2370-496-1-278-1, Jaldubi.

Table 2: Estimation of intra (diagonal and bold) and inter cluster distances among 7 clusters

Clusters	I	II	III	IV	V	VI	VII
I	3.061						
II	3.483	2.951					
III	3.666	4.042	3.112				
IV	4.969	4.146	4.231	2.592			
V	4.232	6.441	5.133	7.586	3.205		
VI	3.911	4.151	5.048	4.676	6.708	3.038	
VII	4.242	2.944	3.349	4.557	6.933	5.339	3.151

**Table 3:** Cluster mean performance of yield and yield attributing characters

Clusters		DFF	PH	NET	PL	FLL	FLW	NFGP	BY	TW	HI	GL	GW	GL: B	KL	KW	KL: B	GY
I	Mean	110.20	105.07	6.75	23.27	26.86	1.60	151.50	8.93	20.91	42.70	8.23	2.61	3.24	6.22	1.99	3.15	37.96
	± SE	5.82	10.52	1.57	1.95	2.65	0.08	38.35	0.99	4.42	6.57	0.73	0.38	0.67	0.60	0.15	0.41	6.53
II	Mean	123.75	99.58	8.31	23.05	29.79	1.79	169.69	11.75	23.72	38.52	7.64	2.87	2.68	5.91	2.27	2.64	45.38
	± SE	6.64	9.01	1.36	3.60	2.74	0.18	31.29	1.39	3.44	4.33	0.77	0.20	0.36	0.67	0.40	0.30	8.18
III	Mean	113.75	114.26	8.35	27.74	32.13	1.69	161.57	9.30	25.13	48.50	9.64	3.07	3.15	7.24	2.55	2.86	44.64
	± SE	10.27	9.13	2.39	2.90	2.96	0.18	36.10	1.08	3.86	5.73	0.64	0.11	0.24	0.74	0.25	0.33	5.69
IV	Mean	129.33	131.63	8.25	19.83	37.08	1.95	169.67	11.46	22.56	45.95	8.74	2.79	3.14	7.10	2.18	3.31	52.18
	± SE	2.52	8.76	1.98	3.10	5.42	0.06	24.34	1.15	2.88	5.93	0.76	0.26	0.20	0.82	0.49	0.35	4.84
V	Mean	105.50	90.43	6.65	24.30	25.18	1.08	175.50	7.46	21.87	37.47	10.36	3.08	3.46	7.47	2.12	3.54	27.73
	± SE	8.67	4.18	1.13	2.85	2.65	0.31	63.62	1.28	1.55	7.09	0.57	0.58	0.79	0.78	0.12	0.43	5.83
VI	Mean	123.50	119.16	8.81	27.87	31.51	1.73	198.70	11.14	17.29	37.45	8.03	2.14	3.76	5.71	1.79	3.19	41.62
	± SE	4.46	14.06	2.74	4.52	3.57	0.30	21.20	1.14	0.43	7.77	0.46	0.14	0.31	0.56	0.18	0.15	9.75
VII	Mean	115.14	113.90	8.72	24.62	32.53	1.75	182.71	9.85	24.02	49.45	7.58	3.19	2.39	5.83	2.61	2.27	48.49
	± SE	6.53	11.86	1.95	2.72	4.97	0.19	24.82	1.47	3.99	5.91	0.48	0.32	0.22	0.32	0.31	0.28	7.98

Note: Data in the bold digits represents the highest mean values recorded for particular traits.
Key words: DFF=Days to 50% flowering; PH=Plant height; NET= Number of effective tillers; PL=Panicle length; FLL=Flag leaf length; FLW=Flag leaf width; NFGP=Number of filled grains per panicle; BY=Biological yield; TW=Test weight; HI=Harvest index; GL=Grain length; GW=Grain width; GL:B= Grain L:B ratio; KL=Kernel length; KW=Kernel width; KL:B= Kernel L:B ratio; GY=Grain yield.

Table 4: Contribution of yield and yield attributing characters towards genetic diversity

S. No.	Characters	Contribution %
1.	Days to 50% flowering	6.26
2.	Plant height (cm)	4.05
3.	Number of effective tillers per plant	6.35
4.	Panicle length (cm)	4.84
5.	Flag leaf length (cm)	4.22
6.	Flag leaf breadth (cm)	7.35
7.	Number of filled grains per panicle	7.23
8.	Biological yield (kg)	8.44
9.	Test weight (g)	6.87
10.	Harvest index (%)	7.72
11.	Grain length (mm)	5.87
12.	Grain breadth (mm)	6.27
13.	Grain L:B ratio	5.39
14.	Kernel length (mm)	2.95
15.	Kernel breadth (mm)	5.20
16.	Kernel L:B ratio	6.42
17.	Grain yield per hectare (q/ha)	4.57
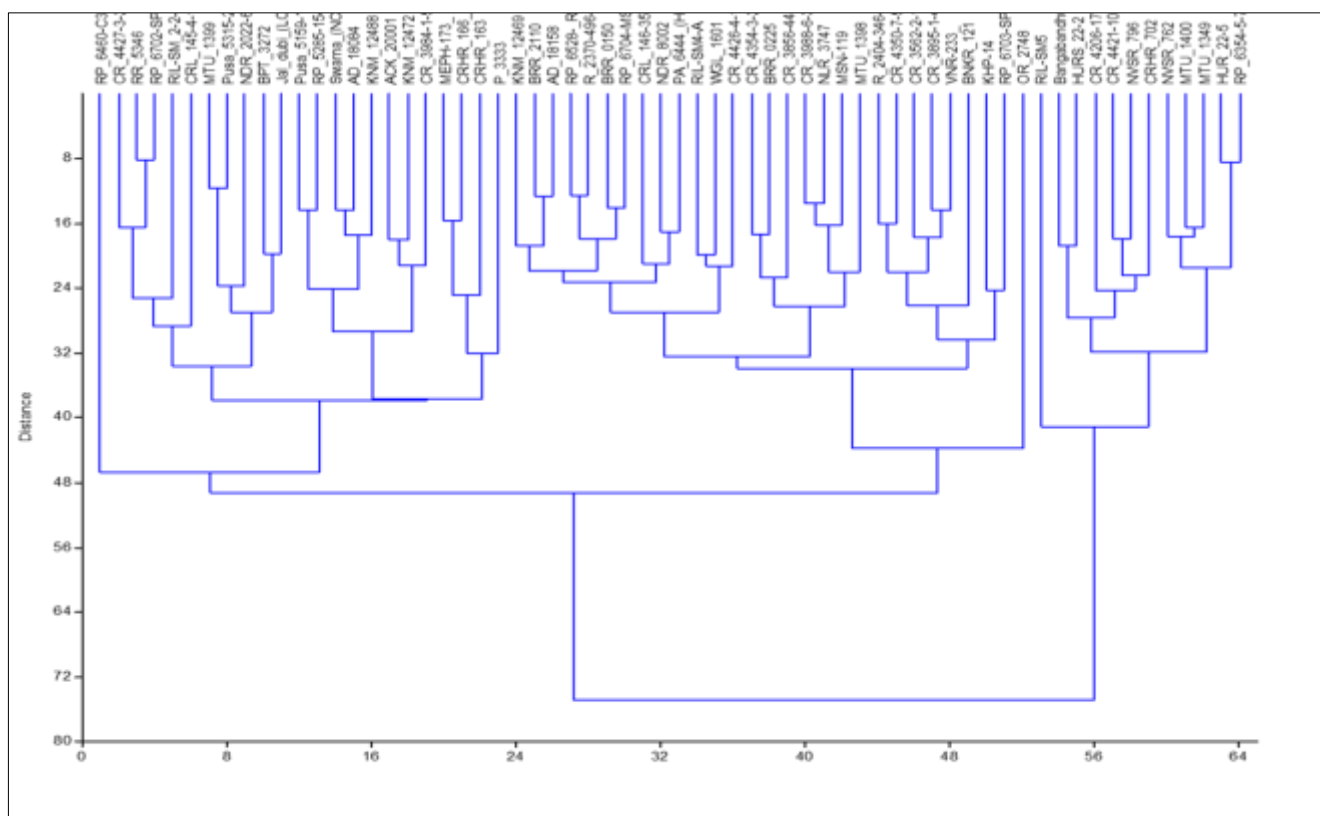
Fig 1: Dendrogram representing cluster pattern of 64 rice genotypes

Conclusions

Analysis of variance showed that all of the studied traits varied significantly across all 64 genotypes (i.e., at 1% level of significance). The presence of high significant values revealed that all the characters had high variability. Cluster analysis revealed that Cluster IV with 3 genotypes, *viz.*, BNKR 121, MSN-119 and KHP-14 exhibited highest mean performance for the characters like grain yield, plant height, flag leaf length, days to 50% flowering and flag leaf width. These genotypes were found to suitable genotypes for lowland ecology. Further, these promising genotypes can be used in future breeding program.

Acknowledgement

Reference

1. Anonymous. World Agricultural Production, Foreign Agricultural Service, United States Department of Agriculture, Washington, D.C., United States; c2022a Sept. p. 38.
2. Anonymous. Annual Report, Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture & Farmers Welfare, Govt. of India, New Delhi; c2022b Aug. p. 8.
3. Ashok S, Jyothula DPB, Ratnababu D. Genetic divergence studies for yield, yield components and grain quality parameters in rice (*Oryza sativa* L.). Electron. J. of Plant Breed., 2017;8(4):1240-1246.
4. Bhati PK, Singh SK, Dhurai SY, Sharma A. Genetic divergence for quantitative traits in rice germplasm. Electron. J. of Plant Breed. 2015;6(2):528-53.
5. Mahalanobis PC, On the generalized distance in statistics. Proc. Natl. Inst. Sci. (India). 1936;12:49- 55.
6. Mandal RK, Singh UK, Kumar R. Genetic divergence analysis in rice (*Oryza sativa* L.) under low land condition. The Pharma Innovation J. 2022;11(7):2205-2208.
7. Mohanty S, Wassmann R, Nelson A, Moya P, Jagadish SVK. Rice and climate change: Significance for food security and vulnerability. International Rice Research Institute; c2013. p. 14.
8. Tripathi A, Kumar S, Singh MK, Kumar A and Karnwal MK. Phenotypic assessment of rice (*Oryza sativa* L.) genotypes for genetic variability and varietal diversity under direct seeded condition. J Appl. Nat. Sci. 2017;9(1):6-9.
9. Vennela PR, Singh SK, Singh R, Gayatonde V, Singh DK. Genetic divergence Studies in Rice (*Oryza sativa* L.) for Yield and Yield Related Traits. Int. J of Plant Research. 2017;30:191-195.