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ASSESSMENT OF GENETIC VARIABILITY, GENETIC DIVERGENCE AND CORRELATION AMONG YIELD AND YIELD-RELATED TRAITS IN RICE (*Oryza sativa* L.)

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ABSTRACT

The increase in rice (*Oryza sativa* L.) productivity relies on the efficient use of the genetic variability found in traditional germplasm. During Kharif 2024, a field study was undertaken at ITM University in Gwalior to evaluate genetic variability, heritability, trait associations, and genetic divergence across 46 rice genotypes. The genotypes were analysed using a Randomized Block Design (RBD) with three replications for ten yield-related characteristics. The analysis of variance showed highly significant differences among all the genotypes for the traits examined. The high GCV and PCV values for grain yield per plant, panicle length, productive tillers, and spikelets per panicle indicated substantial genetic variability and potential for selection. High genetic advance pointed to the predominance of additive gene action, which supports effective phenotypic selection. Correlation analysis indicated a significant positive relationship between grain yield, panicle length, and the number of productive tillers. In contrast, days to 50% flowering was negatively associated, indicating the advantage of early flowering genotypes under the studied conditions. Cluster analysis using D² segregated the genotypes into non-overlapping clusters and suggested making hybrids by inter-cluster divergence exploiting genetic distance between distant groups. The results revealed substantial genetic diversity among indigenous rice landraces and identified key factors influencing yield, while also identifying divergent parental lines among high-yielding rice cultivars. Several genotypes exhibited a significant yield performance, which can be explored as breeding material. Burma Black and Akhanibora showed maximum inter-cluster divergence and may serve as promising parents for hybridization programmes.

Keywords: *Oryza sativa* L.; genetic variability; heritability; genetic divergence; grain yield.

Introduction

The genus *Oryza* belongs to the Poaceae family and constitutes one of the major cereal crops and acts as a primary food source for a major portion of the world's population. Rice possesses a diploid number of chromosomes $2n = 2x = 24$, and the grain contains approximately 77-80% of starch. India is one of the largest producers and leading exporters of rice around the world, with a yearly production of nearly 135 million tonnes cultivated on a total area of about 44 million hectares. Central India, especially Madhya Pradesh, is among the most prominent regions for rice cultivation. Rice cultivation in Madhya Pradesh covers nearly 2.0 million hectares, with a production of about

5.2 million tonnes and an average yield of 2.6 t ha^{-1} (Food and Agriculture Organization, 2023; Ministry of Agriculture and Farmers Welfare, 2023; Directorate of Economics and Statistics, 2023). Previous studies show the significance of genetic variability in any plant selection process (Johnson *et al.*, 1955; Burton and DeVane, 1953). Knowledge of the correlation between grain yield and its component traits is vital in selection processes. Recent studies have also emphasized the importance of variability, heritability, and correlation analysis in rice breeding programmes for improving yield and related traits (Debsharma *et al.*, 2023; Shajan *et al.*, 2024; Nivedha *et al.*, 2024; Pathak *et al.*, 2024).

Assessment of genetic variability parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance for important economic characters, is an absolute necessity in breeding programmes (Burton and DeVane, 1953). Genetic variability and diversity are the basis of any good breeding and selection programme, while heritability and genetic advance can help us understand more about inheritance and selection efficiency. It is extremely important to determine genetic variability and diversity in order to efficiently utilize the available gene pool. The application of various types of genotypes under changing climatic conditions and rising food demands has made it absolutely necessary. Increasing food demand along with climate variability has further increased the need to utilize diverse rice genotypes in breeding programmes (Venkateshwarlu *et al.*, 2022; Calayugan *et al.*, 2024).

Thus, this study has been carried out on genetic variability, heritability, correlation and genetic divergence amongst rice varieties obtained from irrigated upland environments of Madhya Pradesh.

Materials and Methods

Experimental Site

This study was carried out during *Kharif* 2024 at Crop Research Centre-I, Department of Genetics and Plant Breeding, ITM University, Gwalior, Madhya Pradesh, India.

Experimental Material

In this experiment, 46 rice genotypes were used, consisting of 40 germplasm lines along with six check varieties, namely Pusa-2090, PRH-10, Jaya, Pusa-44, IR-64, and PS-5. The germplasm lines used in the experiment were obtained from the Department of Genetics and Plant Breeding, ITM University, Gwalior, Madhya Pradesh.

Experimental Design

This experiment was conducted following a Randomized Block Design (RBD) in three replications. Each genotype was grown in plots measuring 1.2 m × 1.8 m with 30 cm row-to-row and 20 cm plant-to-plant spacing. Ten quantitative traits were recorded from ten competitive plants per plot from each genotype. The mean of ten randomly selected plants per plot was used for analysis. The standard agronomic practices were followed throughout the experiment.

Traits Recorded

Observations were recorded for days to 50% flowering, days to maturity, plant height (cm), flag leaf

length (cm), number of productive tillers per plant, panicle length (cm), panicle weight (g), number of spikelets per panicle, 1000-grain weight (g), and grain yield per plant (g).

Statistical Analysis

Statistical analysis was conducted using analysis of variance (ANOVA) as outlined by Panse and Sukhatme (1985) to evaluate the significance of differences among genotypes. Both genotypic and phenotypic variances, as well as broad-sense heritability, genetic advance, and genetic advance expressed as a percentage of the mean (GAM), were calculated following the methodology presented by Johnson *et al.* (1955). The genotypic (GCV) and phenotypic (PCV) coefficients of variation were determined based on the approach described by Burton and DeVane (1953). Correlation coefficients at both genotypic and phenotypic levels were computed using the technique outlined by Singh and Choudhary (1977). The genetic divergence among different genotypes was assessed using Mahalanobis D^2 statistics (Mahalanobis, 1936), with clustering executed according to Tocher's method as detailed by Rao (1952).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance revealed highly significant differences among the 46 rice genotypes for all the quantitative traits studied. Significant genotype mean sum of squares were observed for days to 50% flowering (91.74**), days to maturity (107.67**), plant height (250.23**), flag leaf length (69.85**), number of productive tillers per plant (3.04**), panicle length (73.51**), number of spikelets per panicle (4129.47**), panicle weight (0.55**), 1000-grain weight (8.45**) and grain yield per plant (89.65**). The analysis of variance is presented in Table 1.

The wide variation observed for days to 50% flowering and days to maturity indicates the presence of early and late flowering genotypes which could provide breeding material needed to create rice varieties. Paramanik *et al.* (2025) also found significant variation within rice genotypes when evaluating different environments for flowering. In regards to growth-related traits, all genotypes showed a statistically significant difference between plant height and flag leaf length. Likewise, Kalpande *et al.* (2024) and Madishetty *et al.* (2023) found greater variability amongst genotypes when examining multiple growth traits within rice genotype, particularly with trait plant height.

Similarly, panicle weight and 1000-grain weight also exhibited significant levels of variability among available genotypes, providing a good opportunity for successful selection. Nivedha *et al.* (2024) also found substantial variability between genotypes in terms of yield and yield-related traits. Previous researchers such

as Kavitha *et al.* (2022) also reported significant levels of variability between genotypes in terms of grain yield and yield-related traits. Overall, the findings suggest that most of the observed variation is genetic in nature, indicating good scope for selection and improvement of important traits.

Table 1 : Analysis of variance (ANOVA) among 46 rice genotypes for 10 quantitative traits

Source	Mean Sum of Squares (MSS)		
	Replication	Genotype	Error
	2	45	90
Days to 50% flowering	29.88	91.74**	9.64
Days to maturity	5.01	107.67**	12.93
Plant height	20.65	250.23**	6.54
Flag leaf length	0.55	69.85**	3.26
Number of productive tillers per plant	0.01	3.04**	0.03
Panicle length	0.25	73.51**	0.38
Number of spikelets per panicle	34.97	4129.47**	27.5
Panicle weight	0.02	0.55**	0.004
1000-grain weight	0.7	8.45**	0.4
Grain yield	0.89	89.65**	0.24

Note: * significant at 5%; ** significant at 1% level.

Coefficients of variation for genotype (GCV) and phenotype (PCV)

The presence of exploitable genetic variability was indicated by the high variability of traits including grain yield per plant (27.3% and 27.4%), panicle length (18.8% and 18.9%), number of spikelets per panicle (17.9% and 18.1%), and number of productive tillers per plant (14.1% and 14.4%). Moderate variability was shown by the GCV and PCV values of characteristics including plant height (8.8% and 9.3%) and flag leaf length (9.7% and 10.4%). Conversely, low GCV and PCV values were found in days to 50% flowering (4.8% and 5.6%), days to maturity (4.1% and 4.9%), 1000-grain weight (6.4% and 6.9%), and panicle weight (5.0% and 5.5%).

High GCV and PCV values for panicle length, productive tillers and spikelets per panicle indicated strong genetic variability and high selection potential. Pathak *et al.* (2024) noted similar potential for finding genetically based variability in their rice germplasm. The small differences between GCV and PCV values for most traits indicated relatively low environmental influence on trait expression. The moderate amount of variability in plant height and flag leaf length demonstrates that these traits indicate good scope for improvement through selection. Days to 50% flowering, days to maturity, 1000-grain weight and panicle weight all had low levels of GCV and PCV, indicating comparatively less variability than any of

the other traits in this study. These findings agree with Singh *et al.* (2023) and Kavitha *et al.* (2022) who also reported wide genetic variability and favourable trait associations among rice genotypes, signifying good scope for genetic improvement through selection and hybridization.

Heritability (broad sense)

Heritability estimates ranged from 70.1% for days to maturity to 99.2% for grain yield per plant. Strong genetic control over trait expression was demonstrated by the high heritability of grain yield per plant (99.2%), panicle length (98.5%), number of spikelets per panicle (98.0%), and number of productive tillers per plant (96.9%). Plant height (92.6%), 1000-grain weight (87.1%), flag leaf length (87.2%), panicle weight (79.8%), days to 50% flowering (73.9%), and days to maturity (70.1%) were also found to have high heritability. The extent of variability along with estimates of genotypic and phenotypic coefficient of variation, broad-sense heritability, genetic advance and genetic advance expressed as percentage of mean are presented in Table 2.

In the present study, most traits exhibited high heritability, indicating the predominance of genetic factors over environmental influence. Earlier studies by Reddy *et al.* (2021), also observed high heritability for grain yield and important yield contributing traits in rice genotypes. Very high heritability estimates were recorded for grain yield per plant, panicle length,

spikelets per panicle and productive tillers per plant, suggesting that improvement of these traits through direct selection would be effective. Pradhan *et al.*

(2020) also reported comparable variability patterns and found high heritability estimates for several quantitative characters in rice.

Table 2 : Estimates of variability parameters for yield and yield component traits in rice genotypes

S. No.	Traits	Coefficient of Variation		h^2 (bs) %	Genetic Advance	Genetic advance as % of mean
		GCV (%)	PCV (%)			
1	Days to 50% flowering	4.8	5.6	73.9	9.3	8.5
2	Days to maturity	4.1	4.9	70.1	9.8	7.2
3	Number of productive tillers per plant	14.1	14.4	96.9	2.0	28.7
4	Plant height	8.8	9.3	92.6	17.9	17.5
5	1000-grain weight	6.4	6.9	87.1	3.1	12.3
6	Flag leaf length	9.7	10.4	87.2	9.1	18.7
7	Panicle length	18.8	18.9	98.5	10.1	38.4
8	Number of spikelets per panicle	17.9	18.1	98	75.4	36.6
9	Panicle weight	5.0	5.5	79.8	0.2	9.1
10	Grain yield	27.3	27.4	99.2	11.2	56.1

High heritability was also observed for plant height, 1000-grain weight, flag leaf length, panicle weight, days to 50% flowering and days to maturity, which indicated strong genetic control over these characters. Traits with high heritability are generally considered more stable across environments and therefore useful in crop improvement programmes. Comparable observations were made by Kumar *et al.* (2023) who suggested that traits with high heritability can be effectively used in rice improvement and selection programmes.

Genetic advance

Genetic advance showed noticeable variation among the traits studied. The high genetic advance for spikelets per panicle indicates strong additive gene action and wide genetic variability among genotypes. Relatively higher values were also observed for plant height (17.9), grain yield per plant (11.2), panicle length (10.1), and days to maturity (9.8). Moderate values were recorded for days to 50% flowering (9.3), flag leaf length (9.1), and 1000-grain weight (3.1). In contrast, lower values were observed for number of productive tillers per plant (2.0) and panicle weight (0.2), indicating comparatively limited improvement through direct selection.

The high genetic advance was observed for spikelets per panicle, indicating the presence of sufficient variability and the important role of additive gene action in controlling this trait. High genetic advance was also recorded for plant height, grain yield per plant, panicle length and days to maturity, suggesting that these characters can be effectively

improved through selection. Comparable findings were earlier reported by Suresh *et al.* (2022) in rice genotypes. Moderate genetic advance was observed for days to 50% flowering, flag leaf length and 1000-grain weight, which indicated moderate scope for improvement through breeding and selection. Yadav *et al.* (2021) reported analogous results, further confirming the strong influence of yield-contributing traits such as panicle length and productive tillers on grain yield in rice. In contrast, productive tillers per plant and panicle weight exhibited low genetic advance, suggesting comparatively less possibility of improvement through direct selection. The low genetic advance for these traits may be due to the influence of non-additive gene action and environmental effects. The findings of Kavitha *et al.* (2022) also support the present results and highlighted the usefulness of traits with high genetic advance in rice improvement programmes.

Correlation Coefficient Analysis

Genotypic correlations were generally higher than phenotypic correlations, indicating strong genetic relationships among traits with relatively lower environmental influence. Similar observations were recorded by Sharma *et al.* (2021), who reported stronger genotypic correlations than phenotypic correlations for most quantitative traits.

At the genotypic level, panicle length (0.83) and the number of productive tillers per plant (0.43) significantly positively correlated with grain yield per plant, suggesting that these characteristics are important for increasing output. Similar conclusions

were drawn by Chaudhary *et al.* (2022), who suggested that productive tillers and panicle length can be used as effective selection criteria in rice breeding. Days to 50% flowering showed a significant negative correlation (-0.33), indicating that early flowering genotypes may be advantageous. Grain yield and the number of productive tillers per plant were positively correlated with panicle length. Similar findings were reported by Nivedha *et al.* (2024), who observed

positive associations of grain yield with productive tillers and panicle length. Days to 50% flowering showed negative associations with plant height and 1000-grain weight but positive correlations with trait days to maturity. In general, the majority of correlations were more noticeable at the genotypic than the phenotypic level. The genotypic correlation coefficients among grain yield and its component traits are presented in Table 3.

Table 3 : Genotypic correlation coefficient estimates for yield and variables that contribute to yield.

Traits	DFF	DM	NPTP	PH	TGW	FLL	PL	NSPP	PW	GY
DFF		0.99**	0.1449	-0.3553*	-0.3723*	-0.1967	-0.2554	-0.0466	-0.1199	-0.3328*
DM			0.1985	-0.2947*	-0.4346**	-0.1386	-0.2008	-0.1341	-0.0432	-0.2537
NPTP				-0.0447	-0.1128	0.0839	0.4258**	-0.0811	0.1635	0.4265**
PH					0.489**	0.2496	-0.0873	0.2382	0.012	-0.0095
TGW						0.1344	0.1954	0.2271	0.0086	0.107
FLL							-0.1252	0.104	0.1166	0.0792
PL								0.2147	0.155	0.8295**
NSPP									-0.1381	0.2321
PW										0.1568
GY										

Note: DFF stands for days to 50% flowering, DM for days to maturity, NPTP for the number of productive tillers per plant, PH for plant height, TGW for 1000-grain weight, FLL for flag leaf length, PL for panicle length, NSPP for the number of spikelets per panicle, PW for panicle weight, and GY for grain yield (g plant⁻¹).

At phenotypic level, Grain yield on a plant basis had a significant positive correlation with panicle length (0.82), productive tillers per plant (0.42), and spikelets per panicle (0.23). Further support was provided by Rao *et al.* (2020), who observed positive and stable associations among yield and yield contributing traits in rice genotypes. On the other hand, grain yield negatively correlated with days to 50% flowering and days to maturity, suggesting that late flowering could lead to poor yields. Similar results were also reported by Patel *et al.* (2022), who found

strong positive correlations among grain yield and major yield contributing traits in rice.

The relationship between panicle length and yield as well as other traits that contribute to yield was positively stable across environments. These results are consistent with Meena *et al.* (2023), who highlighted the importance of panicle length and spikelets per panicle in grain yield improvement. Generally, the pattern of phenotypic correlation was similar to genotypic correlation but was relatively weaker. The phenotypic correlation coefficients among grain yield and its component traits are presented in Table 4.

Table 4 : Estimates of phenotypic correlation coefficients for yield and yield-contributing traits in rice genotypes

Traits	DFF	DM	NPTP	PH	TGW	FLL	PL	NSPP	PW	GY
DFF		0.743**	0.1165	-0.2774**	-0.2812**	-0.1396	-0.2098*	-0.0429	-0.1202	-0.2807**
DM			0.1623	-0.2578**	-0.3659**	-0.1057	-0.1691*	-0.1089	-0.0632	-0.2059*
NPTP				-0.0427	-0.1059	0.0715	0.417**	-0.0764	0.1383	0.4188**
PH					0.4505**	0.2232**	-0.0849	0.2266**	-0.0098	-0.0133
TGW						0.1284	0.1825*	0.2139*	-0.008	0.1006
FLL							-0.1099	0.0933	0.0906	0.0744
PL								0.2135*	0.123	0.8191**
NSPP									-0.1164	0.2287**
PW										0.136
GY										

Note: DFF- days to 50% flowering; DM- days to maturity; NPTP- number of productive tillers per plant; PH- plant height; TGW- 1000-grain weight; FLL- flag leaf length; PL- panicle length; NSPP- number of spikelets per panicle; PW- panicle weight and GY- grain yield (g plant⁻¹)

Genetic Divergence Analysis

Based on Mahalanobis D^2 analysis, the 46 rice genotypes were classified into four distinct clusters, as shown in Table 5. Among them, Cluster I contained the highest number of genotypes (39), suggesting limited divergence within cultivated material, followed by Cluster II (5 genotypes), while Clusters III and IV each consisted of a single genotype, indicating unique genetic lines. The distribution of genotypes into clusters indicates that most of the genotypes share a common genetic background, whereas the single-genotype clusters represent unique and diverse lines. The results are consistent with the findings of Sarkar *et al.* (2021), who observed substantial genetic diversity and distinct cluster formation among rice genotypes using Mahalanobis D^2 analysis.

Table 5 : Cluster-wise distribution of 46 rice genotypes

Cluster No.	Number of genotypes	Name of Genotypes
I	39	Dubraj, Ashanliya, Langalmuthi, Baigan Manjira, Shikote, 1847, Pokhrabara, Lal Boro, Lal basmati, Adanchilpa, Kalojira, Sial-bhomra, Borshlaxmi, Gumbaho, Joldyapa, Pusa-2090, PRH-10, Jaya, Pusa-44, Paru, 1886, P-2070, PS-5, Matla, Bhutmuri, Molliphulo, Lalchalmota, Siuli, Bishnu Bogh, Radhe emo, Radha Tilak, Ramjira, Black, Putikhali, Jugol, Ambhamohar, 1121, Sita Bogh, pateni
II	5	1885, Raj jhing, Matidhan, Mohanbogh, IR-64
III	1	Burma black
IV	1	Akhanibora

There is variability among the rice genotypes, as seen by the distinct differences in mean values between the clusters for every attribute examined. Cluster I showed comparatively lower mean performance, while Cluster II reported relatively higher mean values for grain yield and other yield-related attributes. Equivalent results were made by Tripathi *et al.* (2023), who found that solitary clusters represented highly diverse genotypes useful for hybridization programmes. The cluster diagram for 46 rice genotypes is presented in Fig. 1. The average intra- and inter-cluster distances among the clusters are presented in Table 6.

Table 6 : Average intra- and inter-cluster distances (D^2) among rice genotypes

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	482.54	1017.30	3334.62	887.26
Cluster II		261.67	1342.59	834.23
Cluster III			0.00	2033.03
Cluster IV				0.00

Because of their distinct genetic makeup, clusters III and IV, which each have a single genotype, also showed notable mean values for a few attributes. Comparable results were observed by Thakur *et al.* (2020), who emphasized that genetically distant clusters with superior mean performance can be effectively utilized in rice breeding programmes. Overall, the variations in cluster mean values show that genotypes varied greatly in terms of yield and associated attributes. Crosses involving genetically distant parents such as Burma Black (Cluster III) and Akhanibora (Cluster IV) with high-performing genotypes from Cluster II may generate superior transgressive segregants. Table 7 provides cluster mean values for yield and associated attributes. Selection of parents with high inter-cluster distance and complementary traits is expected to enhance recombination and improve grain yield in segregating generations.

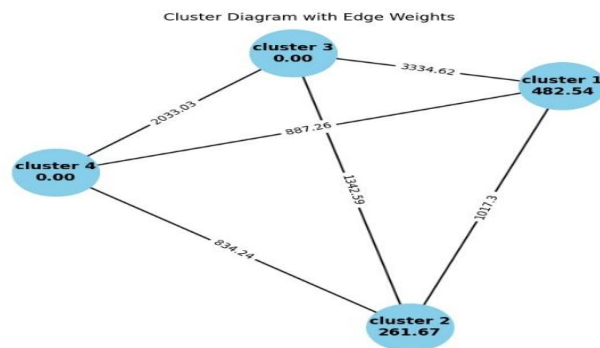


Fig. 1 : Cluster diagram showing genetic divergence among 46 rice genotypes.

Table 7 : Cluster mean values for yield and yield-contributing traits

Trait	Cluster I	Cluster II	Cluster III	Cluster IV
DFF	109.59	103.3	103.34	104.3
DM	136.6	133.7	129.88	133
NPTP	6.97	8.7	7.3	8.3
PH	101.84	113.8	97.86	117.4
TGW	25.59	25.3	25.84	23.9
FLL	48.31	55.3	47.28	48.3
PL	25.10	32.50	33.74	30.0
NSPP	202.86	237.7	204.52	308.7
PW	2.54	2.6	2.7	2.5
GY	18.45	28.24	26.94	22.6

Note: DFF stands for days to 50% flowering; DM for days to maturity; NPTP for number of productive tillers per plant; PH for plant height; TGW for 1000-grain weight; FLL for flag leaf length; PL for panicle length; NSPP for number of spikelets per panicle; PW for panicle weight; and GY for grain yield (g plant⁻¹)

Conclusion

The present study revealed significant genetic variability among 46 rice genotypes for yield and its contributing traits, indicating strong potential for

genetic improvement through selection. High heritability coupled with high genetic advance for grain yield, panicle length, and spikelets per panicle confirms the predominance of additive gene action, making these traits reliable selection criteria in breeding programmes. Correlation analysis highlighted panicle length and productive tillers per plant as key yield determinants, while early flowering genotypes showed a yield advantage under the studied environment. D² clustering revealed significant genetic divergence among genotypes, with Burma Black (Cluster III) and Akhanibora (Cluster IV) identified as highly divergent parental lines. The study suggests that hybridization between genetically distant clusters, particularly involving high-yielding and diverse genotypes, can generate superior recombinants. These findings provide a practical breeding framework for improving grain yield and developing high-performing rice varieties adapted to irrigated conditions of Madhya Pradesh.

References

- Food and Agriculture Organization (FAO). (2023). *Rice market monitor*. FAO, Rome, Italy.
- Ministry of Agriculture and Farmers Welfare. (2023). *Agricultural statistics at a glance 2023*. Government of India, New Delhi, India.
- Directorate of Economics and Statistics. (2023). *State-wise crop production statistics*. Government of India, New Delhi, India.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**, 314–318.
- Burton, G.W. and DeVane, E. H. (1953). Estimating heritability in tall fescue. *Agronomy Journal*, **45**, 478–481.
- Debsharma, S. K., Ali, M. H., Roy, P. R., Brestic, M., Gaber, A. and Hossain, A. (2023). Harnessing genetic variability and diversity of rice genotypes. *Genes*, **14**, 10.
- Shajan, K. T., Lal, G. M. and Bara, B. M. (2024). Evaluation of genetic variability, correlation and path analysis in rice. *Annals of Agricultural Research*, **45**, 112–118.
- Nivedha, R., Manonmani, S., Kalaimagal, T., Raveendran, M. and Kavitha, S. (2024). Assessing genetic diversity of rice using morphological and molecular markers. *Rice*, **17**, 17.
- Pathak, V., Prasuna, C. H., Umakanth, B., Surekha, K., Subbarao, L. V. and Padmavathi, G. (2024). Genetic variability and association analysis in rice. *Indian Journal of Agricultural Sciences*, **94**, 786–790.
- Venkateshwarlu, C., Kole, P. C., Paul, P. J., Singh, A. K. and Kumar, A. (2022). Genetic variability in drought tolerant rice lines. *Frontiers in Plant Science*, **13**, 814774.
- Calayugan, M.I.C., Hore, T.K., Palanog, A.D. & Swamy, B.P.M.(2024). Deciphering the genetic basis of agronomic and yield traits in rice. *Scientific Reports*, **14**, 18024.
- Panse, V. G. and Sukhatme, P. S. (1985). *Statistical methods for agricultural workers* (4th ed.). ICAR, New Delhi, India.
- Singh, R. K. and Chaudhary, B. D. (1977). Variance and covariance analysis. In *Biometrical methods in quantitative genetic analysis* (pp. 39–68). Kalyani Publishers.
- Mahalanobis, P. C. (1936). On generalized distance in statistics. *Proceedings of the National Institute of Sciences of India*, **2**, 49–55.
- Rao, C. R. (1952). *Advanced statistical methods in biometric research*. Wiley, New York, USA.
- Paramanik, S., Rao, M. S., Rashmi, K., Panda, K. K. and Chakraborty, A. (2025). Studies on genetic variability, heritability and genetic advance for quantitative traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **14**, 1527–1537.
- Kalpande, P. S., Meshram, M. and Borkar, V. (2024). Genetic variability, correlation and path coefficient analysis in early transplanted rice genotypes. *International Journal of Plant and Soil Science*, **36**, 128–134.
- Madishetty, A. R., Lal, G. M. and Adarsh, K. (2023). Genetic variability and correlation studies for yield and yield related traits in rice (*Oryza sativa* L.). *International Journal of Plant and Soil Science*, **35**, 1165–1176.
- Kavitha, S., Kumar, P. and Ramesh, T. (2022). Genetic variability and correlation studies in rice genotypes. *Electronic Journal of Plant Breeding*, **13**, 95–102.
- Singh, R. K., Patel, S. K., Sharma, A. and Verma, O. P. (2023). Genetic variability and correlation in rice genotypes. *Biological Forum—An International Journal*, **15**, 210–216.
- Reddy, B. R., Kumar, S. S. and Rao, V. S. (2021). Genetic diversity in rice genotypes. *Andhra Agricultural Journal*, **68**, 356–362.
- Pradhan, S. K., Das, S. R. and Patnaik, R. K. (2020). Genetic variability in rice germplasm. *International Journal of Current Microbiology and Applied Sciences*, **9**, 2500–2507.
- Kumar, A., Singh, R. K. and Sharma, V. (2023). Heritability and genetic advance in rice. *International Journal of Environment and Climate Change*, **13**, 980–987.
- Suresh, B., Reddy, P. N. and Kumar, G. P. (2022). Genetic divergence in rice. *Oryza*, **59**, 214–220.
- Yadav, S. K., Patel, R. K. and Verma, O. P. (2021). Genetic variability in rice. *Journal of Pharmacognosy and Phytochemistry*, **10**, 178–183.
- Sharma, R. K., Yadav, P. and Kumar, S. (2021). Genetic association in rice. *Biological Forum – An International Journal*, **13**, 421–427.
- Chaudhary, H. K., Kumar, A. and Singh, P. (2022). Correlation studies in rice. *Electronic Journal of Plant Breeding*, **13**, 410–417.
- Rao, P. S., Reddy, B. R. and Kumar, A. (2020). Correlation analysis in rice. *Journal of Pharmacognosy and Phytochemistry*, **9**, 1220–1225.
- Patel, D. K., Sharma, A. and Singh, P. K. (2022). Correlation studies in rice. *The Pharma Innovation Journal*, **11**, 1560–1565.
- Meena, R. K., Sharma, V. and Singh, A. (2023). Path coefficient analysis in rice. *International Journal of Environment and Climate Change*, **13**, 550–557.
- Sarkar, S., Das, B. and Roy, A. (2021). Genetic divergence in rice. *Oryza*, **58**, 512–519.
- Tripathi, A. K., Verma, O. P. and Singh, P. K. (2023). Genetic diversity in rice. *Biological Forum – An International Journal*, **15**, 890–897.
- Thakur, A. K., Sharma, R. K. and Verma, S. (2020). Cluster analysis in rice. *International Journal of Current Microbiology and Applied Sciences*, **9**, 3100–3108.