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EVALUATION OF GENETIC DIVERSITY AND YIELD-RELATED TRAITS IN RICE (*Oryza sativa* L.) GENOTYPES THROUGH PATH COEFFICIENT ANALYSIS AND MAHALANOBIS' D²

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ABSTRACT

Rice (*Oryza sativa* L.), a self-pollinated annual cereal crop ($2n = 24$) belonging to the family Poaceae, is one of the world's most important staple foods and is extensively cultivated across tropical and subtropical regions. The present investigation was conducted during the *Kharif* 2022 season at the Agricultural Research Farm, Hirapuri Colony, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, India. A total of thirteen promising rice germplasm lines were evaluated under field conditions to investigate genetic variation and the association among grain yield and related traits. The experiment was carried out to assess trait relationships using path coefficient analysis and Mahalanobis' D² to identify key yield-contributing characters and promising genotypes for use in rice improvement programmes. Path coefficient analysis indicated that biological yield per plant exerted the highest positive direct effect on grain yield per plant, suggesting that this trait should be given greater emphasis during selection for yield improvement. Based on Mahalanobis' D² analysis, the thirteen rice genotypes were grouped into three distinct clusters, reflecting the extent of genetic divergence among the experimental materials. Cluster I was the largest, comprising six genotypes, followed by Cluster II with four genotypes and Cluster III with three genotypes. Among the clusters, Cluster I exhibited the greatest intra-cluster distance, whereas comparatively lower intra-cluster distances were observed in Clusters III and II. The relatively higher intra-cluster distance in Cluster I indicates the presence of greater genetic variability among its constituent genotypes, highlighting their potential value for parent selection in hybridization programmes aimed at broadening the genetic base and improving grain yield.

Keywords : Rice, Variability, Genotypic Path, Phenotypic Path, Mahalanobis' D².

Introduction

Rice (*Oryza sativa* L.) is one of the world's most significant cereal crops and serves as the principal staple food for more than half of the global population. It is a self-pollinated annual cereal species possessing a diploid chromosome number of $2n = 24$. At present, rice is cultivated in over 100 countries, with Asian nations contributing nearly 90% of the global production and consumption. Among these, India, China, Indonesia, Bangladesh, Vietnam, and Thailand

are the major rice-producing and consuming countries. India occupies a leading position in global rice cultivation by having the largest area under rice cultivation and making a substantial contribution to worldwide production. The crop plays a vital role in ensuring food security, creating employment opportunities, and sustaining the livelihoods of millions of farming families across the world. Rice is cultivated under diverse agroecosystems, including irrigated, rainfed lowland, upland, deep-water, and

coastal environments. Its successful cultivation requires favorable climatic conditions characterized by warm temperatures, sufficient water availability, and fertile soils for optimal growth and productivity. Over the past few decades, remarkable improvements in rice productivity have been achieved through advances in plant breeding, improved crop management practices, efficient irrigation systems, and effective crop protection measures. In addition to being the primary source of carbohydrates, rice provides appreciable amounts of proteins, vitamins, minerals, and dietary energy, contributing nearly 20% of the total caloric intake of the global population. Besides its nutritional importance, rice also has considerable economic value through domestic marketing, international trade, export earnings, and various industrial applications. Path coefficient analysis is a widely used statistical technique in breeding that helps elucidate the complex relationships among yield and its associated traits by separating correlation coefficients into their direct and indirect components. As grain yield is a polygenic trait governed by numerous interdependent morphological, physiological, and agronomic characteristics, correlation analysis alone is often insufficient to determine the actual contribution of individual traits to yield improvement. By quantifying the direct and indirect influences of different characters, path coefficient analysis enables breeders to identify traits that have genuine causal effects on grain yield and to distinguish them from those whose associations arise through other variables. Such information is essential for designing effective selection strategies and enhancing the efficiency of breeding programmes. In rice, traits including the number of productive tillers per plant, panicle length, grains per panicle, filled grains per panicle, thousand-grain weight, and harvest index have consistently been identified as having strong positive direct effects on grain yield. Therefore, path coefficient analysis serves as a valuable tool for selecting superior genotypes and supports the development of high-yielding, stable, and widely adaptable rice cultivars. Mahalanobis' D^2 analysis is an effective multivariate statistical method extensively employed in breeding to evaluate the extent of genetic divergence among genotypes using multiple quantitative traits simultaneously. It enables the grouping of genotypes into distinct clusters based on their genetic similarities and differences, thereby assisting breeders in selecting diverse parents for hybridization programmes. Crosses involving genetically divergent parents are more likely to produce greater heterosis and desirable transgressive segregants, making D^2 analysis an essential tool in parent selection. Furthermore, the technique provides

comprehensive information on intra- and inter-cluster distances, cluster mean performance, and the relative contribution of individual traits to overall genetic divergence, helping to identify the major characters responsible for genetic variability. The analysis also facilitates the effective characterization, conservation, and utilization of rice germplasm resources, thereby enhancing the efficiency of crop improvement programmes. Hence, Mahalanobis' D^2 analysis plays a pivotal role in developing high-yielding, genetically diverse, and broadly adapted rice cultivars through the strategic exploitation of available genetic variation. Therefore, the present investigation was undertaken to Evaluation of Genetic Diversity and Yield-Related Traits in Rice (*Oryza sativa* L.) Through Path Coefficient Analysis and Mahalanobis' D^2 . The results of this study are expected to facilitate the identification of superior genotypes and key selection traits for enhancing grain yield, thereby contributing to the development of improved rice cultivars.

Materials and Methods

The field experiment was conducted during the *Kharif* 2022 growing season at the Agricultural Research Farm, Hirapuri Colony, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, India. A total of thirteen promising rice (*Oryza sativa* L.) germplasm lines were selected for evaluation to investigate the relationships among yield and its component traits. Seedlings of all genotypes were initially raised in a nursery, with sowing carried out on 22 June 2022, and were subsequently transplanted to the experimental field on 4 July 2022. The trial was laid out with three replications, and each genotype was planted in rows measuring 1.5 m in length. While maintaining a spacing of 20 cm $\times$ 15 cm between rows and plants to ensure uniform crop establishment and minimize interplant competition. All recommended agronomic and crop management practices, including irrigation, nutrient management, weed control, and plant protection measures, were uniformly implemented throughout the cropping period to provide optimum growing conditions. The study was undertaken to evaluate the association among yield-related traits and to characterize the genetic variation present in the experimental material using correlation and principal component analyses. The findings were intended to identify the most influential traits contributing to grain yield and to recognize promising genotypes that could serve as valuable genetic resources for future rice improvement programmes.

Results and Discussion

Path-coefficient analysis

Grain yield is a complex quantitative trait governed by the combined action of numerous genes and is strongly influenced by its associated component characters. Consequently, selection for higher grain yield often results in simultaneous changes in other correlated traits, while improvement in these component traits may also influence yield performance. To obtain a clearer understanding of the contribution of individual characters, the genotypic correlation coefficients were partitioned into their direct and indirect effects using path coefficient analysis. This approach provides a more precise assessment of the causal relationships among agronomic traits and facilitates the identification of characters that can be effectively utilized as selection criteria for grain yield improvement. The results of the path coefficient analysis are presented in Tables-1 & 2, where the correlation coefficients of the eleven yield-related traits were decomposed into their respective direct and indirect effects on grain yield per plant, thereby revealing the relative importance of each trait in determining overall yield performance.

Phenotypic path coefficient analysis with grain yield/plant

The direct effect of days to 50% flowering on grain yield per plant was seen positive (0.3414) (Table-1). It showed positive indirect effect on grain yield per plant via plant height (0.4598), panicle length (0.0598) and grain length breadth ratio (0.0414). Days to 50% flowering (0.3089), plant height (0.4464), effective tillers per plant (0.0106), panicle length (0.0262), and grain length to breadth ratio (0.0491) all showed positive indirect effects with days to maturity. Plant height had a positive direct effect on grain yield per plant (0.6071). However, it demonstrated a favorable indirect influence on grain yield per plant via days to 50% flowering (0.2585), panicle length (0.1243), grains per panicle (0.0718), grain breadth (0.0235), and grain length breadth ratio (0.0479). The impact of 1000 grains on days to 50% flowering (0.0972), plant height (0.2898), the number of effective tillers per plant (0.0145), the length of the panicle (0.943), the number of grains per panicle (0.1074) and the breadth of the grain (0.1037) all indicated positive indirect effects on grain production per plant. The number of effective tillers per plant had a positive direct impact on the amount of grain produced per plant (0.2641). However, it demonstrated a favorable indirect impact on grain yield per plant through grains per panicle (0.0909), grain length (0.0317) and grain width (0.0479). The

panicle length had a positive direct effect on plant-level grain yield (0.2570). The number of days to 50% flowering (0.0794), plant height (0.2937), grains per panicle (0.0706), grain breadth (0.0025) and grain length breadth ratio (0.0533) all indicated positive indirect effects on grain yield per plant. The number of grains per panicle had a positive direct impact on grain yield per plant (0.4325). However, it had a favorable indirect impact on plant height (0.1007), effective tillers per plant (0.0555), panicle length (0.419), grain length (0.0710), grain breadth (0.0710), and grain yield per plant (0.743) as well as on days to maturity (0.2093) and effective tillers per plant (0.1007). Grain length with days to 50% flowering (0.1475), plant height (0.4041), panicle length (0.1451), grain breadth (0.0189), and grain length breadth ratio (0.0731) indicated a positive indirect effect on grain yield per plant. The direct impact of grain breadth on plant yield was favorable (0.1830). However, it demonstrated a favorable indirect influence on grain yield per plant through days to maturity (0.1261), plant height (0.0780), effective tillers per plant (0.691), panicle length (0.0035) and grains per panicle (0.1678).

Genotypic path coefficient analysis with grain yield/plant

The trait Grain yield per plant showed a positive direct correlation with days to 50% flowering (0.3802). It demonstrated a favorable indirect impact on grain yield per plant through plant height (0.2553), panicle length (0.0690), and grain length breadth ratio (0.0880) (Table-2). Days to maturity demonstrated a favorable indirect influence on grain yield per plant via days to 50% flowering (0.3513), plant height (0.2462), effective tillers per plant (0.0108), panicle length (0.0301), and grain length breadth ratio (0.1070). The effect of plant height on grain yield per plant was direct favorable (0.3319). The number of days to 50% flowering (0.2925), the length of the panicle (0.1425), the total number of grains in the panicle (0.0923), and the grain length to breadth ratio (0.0982). The impact of 1000 grain weight favorable indirect influence on grain yield per plant via days to 50% flowering (0.1102), plant height (0.1588), effective tillers per plant (0.0155), panicle length (0.1080), grains per panicle (0.1372), and grain yield per plant (0.084). Number of effective tillers per plant had a favorable direct impact on grains yield per plant (0.2641). The plant height (0.0102), total number of grains per panicle (0.1258), and grain yield per plant (0.246) all indicated a positive indirect effect on grain yield per plant. The panicle length was direct effect on grain yield per plant was favorable (0.2936). The number of days to 50% flowering (0.0893), plant height (0.1611),

grains per panicle (0.0903), grain length-to-breadth ratio (0.1104), and grain yield per plant (0.363) all exhibited a positive indirect effect on the amount of grain produced per plant. Grain yield per plant was positively impacted directly (0.5504) from total number of grains per panicle. While it had a favorable indirect impact on plant height (0.056), effective tillers per plant (0.603), panicle length (0.481), days to maturity (0.1905), and grain yield per plant (0.813) as well as on these other variables. The grain length breadth ratio had direct effect on grain yield per plant was favorable (0.3300). While it demonstrated a favorable indirect impact on grain output per plant through plant height (0.0988), days to 50% flowering (0.1013), 1000 grain weight (0.1461), panicle length (0.0982), and grain length breadth ratio (0.3300). Similar findings have also been found by Faysal *et al.* (2022); Jangala *et al.* (2022); Kulsum *et al.* (2022) and Ali *et al.* (2026).

Genetic divergence (D^2 Statistics)

Grouping of the genotypes into clusters

13 rice genotypes were categorized into three clusters in the current study using Mahalanobis D^2 statistics. In Fig. 2 and Table 3, the Torchers method's

clustering pattern is presented. The distribution of genotypes into different clusters shows that variations in adaption, selection pressure, and environmental conditions may be to blame for the genetic diversity observed among genotypes with the same geographic origin.

Intra and Inter Cluster Distance

In terms of intra-cluster distance (Table-4), cluster I has the greatest value of 2.437, followed by cluster III (2.252) and cluster II (1.955). Large genetic diversity among the clusters' genotypes is shown by the highest intra cluster distance. While, Cluster III and II had the greatest inter-cluster separation (4.472), followed by cluster II and I (3.851), while cluster III and I had the smallest inter-cluster separation (3.803).

The highest value of the inter-cluster distance denotes a high degree of genetic diversity and may be used in rice hybridization programs to increase grain yield, whereas the lowest value of the inter-cluster distance revealed that the genotypes of these clusters had a close relationship and thus could not be used in hybridization programs. Similar findings have also been made by Thakare *et al.* (2025); Thang *et al.* (2022), and Vennila *et al.* (2022).

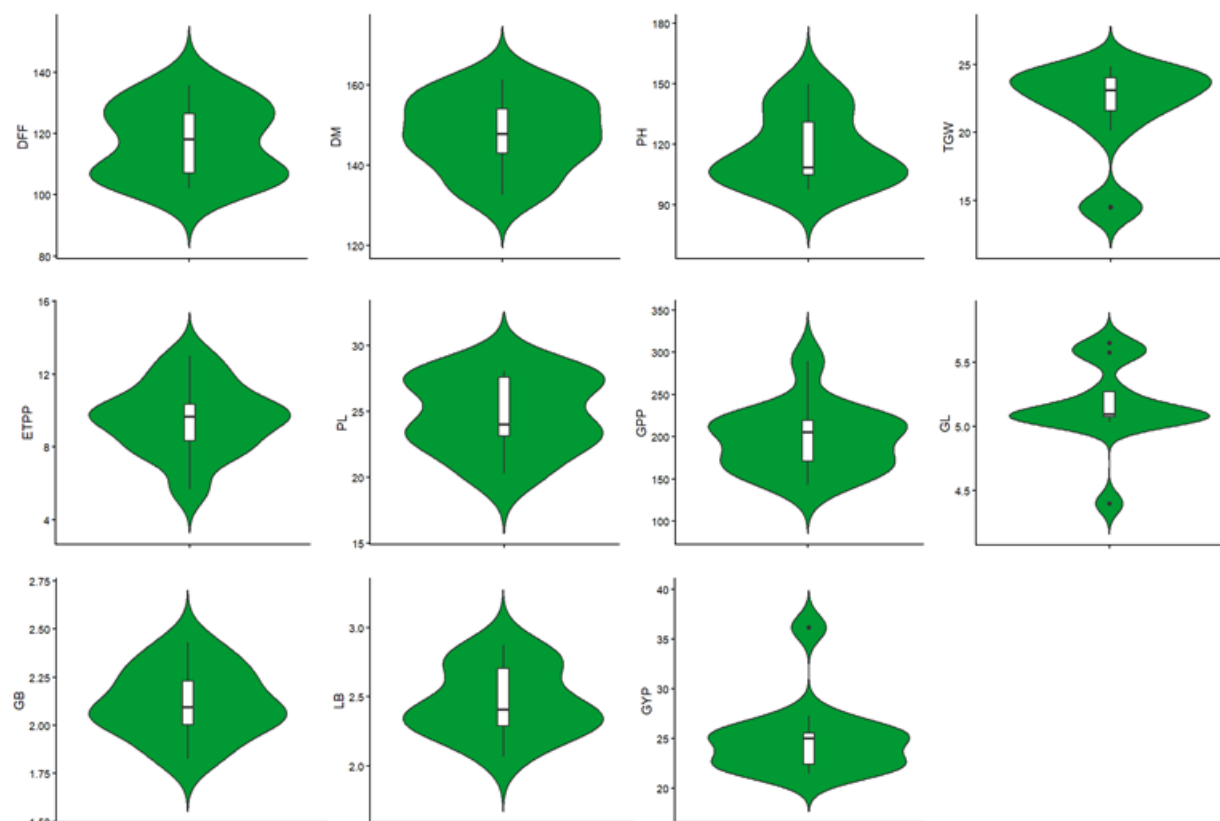


Fig. 1 : Violin plot for variability in field condition. Where, DFF, Days to 50% flowering; DM, Days to maturity; PH, Plant height; TGW, 1000-grain weight; ETPP, Effective tillers per plant; PL, Panicle length; GPP, Grain per panicle; GL, Grain length; GB, Grain breadth; LB, Grain length: breadth ratio; GYP, Grain yield per plant.

Table 1 : Phenotypic path with grain Yield/plant:

Characters	DFF	DM	PH (cm)	1000 GW (g)	ETPP	PL (cm)	Grains / panicle	GL[L] (mm)	GB[B] (mm)	L/B	GY/P(g)
DFF	0.3414	-0.9492	0.4598	-0.0931	-0.0194	0.0598	-0.0450	-0.1240	-0.0067	0.0414	-0.335*
DM	0.3089	-1.0489	0.4464	-0.0234	0.0106	0.0262	-0.0863	-0.0846	-0.0220	0.0491	-0.424**
PH(cm)	0.2585	-0.7713	0.6071	-0.1561	-0.0217	0.1243	0.0718	-0.1910	0.0235	0.0479	-0.007
1000 GW(g)	0.0972	-0.0752	0.2898	-0.3270	0.0145	0.0943	0.1074	-0.1852	0.1037	-0.0379	0.082
ETPP	-0.0251	-0.0422	-0.0498	-0.0180	0.2641	-0.0389	0.0909	0.0317	0.0479	-0.0441	0.217
PL(cm)	0.0794	-0.1070	0.2937	-0.1200	-0.0400	0.2570	0.0706	-0.1621	0.0025	0.0533	0.327*
Grains/panicle	-0.0355	0.2093	0.1007	-0.0812	0.0555	0.0419	0.4325	0.0182	0.0710	-0.0698	0.743**
GL[L](mm)	0.1475	-0.3094	0.4041	-0.2110	-0.0292	0.1451	-0.0275	-0.2870	0.0189	0.0731	-0.075
GB[B](mm)	-0.0125	0.1261	0.0780	-0.1852	0.0691	0.0035	0.1678	-0.0297	0.1830	-0.1201	0.280
L/B	0.0844	-0.3075	0.1739	0.0740	-0.0697	0.0819	-0.1803	-0.1253	-0.1313	0.1673	-0.233

Residual effect = 0.203

*, ** significant at 5% and 1% level, respectively

Table 2 : Genotypic path with grain Yield/plant:

Characters	DFF	DM	PH (cm)	1000 GW (g)	ETPP	PL (cm)	Grains / panicle	GL[L] (mm)	GB[B] (mm)	L/B	GY/P(g)
DFF	0.3802	-0.8749	0.2553	-0.1757	-0.0175	0.0690	-0.0571	-0.0211	-0.0180	0.0880	-0.372*
DM	0.3513	-0.9469	0.2462	-0.0451	0.0108	0.0301	-0.1107	-0.0153	-0.0824	0.1070	-0.455**
PH(cm)	0.2925	-0.7025	0.3319	-0.2902	-0.0228	0.1425	0.0923	-0.0327	0.0815	0.0982	-0.009
1000 GW(g)	0.1102	-0.0705	0.1588	-0.6062	0.0155	0.1080	0.1372	-0.0319	0.3426	-0.0795	0.084
ETPP	-0.0252	-0.0387	-0.0286	-0.0355	0.2641	-0.0498	0.1258	0.0064	0.1210	-0.0932	0.246
PL(cm)	0.0893	-0.0972	0.1611	-0.2230	-0.0448	0.2936	0.0903	-0.0279	0.0111	0.1104	0.363*
Grains/panicle	-0.0394	0.1905	0.0556	-0.1511	0.0603	0.0481	0.5504	0.0034	0.2395	-0.1449	0.813**
GL[L](mm)	0.1822	-0.3298	0.2466	-0.4399	-0.0383	0.1861	-0.0427	-0.0440	0.1068	0.1567	-0.016
GB[B](mm)	-0.0145	0.1655	0.0573	-0.4405	0.0678	0.0069	0.2796	-0.0100	0.4715	-0.2662	0.317*
L/B	0.1013	-0.3071	0.0988	0.1461	-0.0746	0.0982	-0.2416	-0.0209	-0.3803	0.3300	-0.250

Residual Effect = 0.077

*, ** significant at 5% and 1% level, respectively

Table 3 : Clustering pattern of 13 rice genotypes into clusters according to Mahalanobis D² statistics.

Clusters	No of genotypes	Genotypes
I	6	1 2 3 4 6 8
II	4	7 9 12 13
III	3	5 10 11

Table 4 : Average intra and inter-cluster values among three clusters from 13 rice genotypes.

Clusters	I	II	III
I	2.437		
II	3.851	1.955	
III	3.803	4.472	2.252

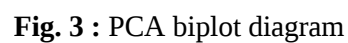
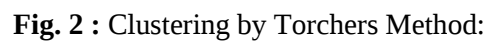


Table 5 : Cluster means Mahalanobis.

Clusters		DFF	DM	PH (cm)	1000 GW (g)	ETPP	PL (cm)	Grains/ panicle	GL[L] (mm)	GB[B] (mm)	L/B	GY/P (g)
I	Mean	112.39	144.33	103.17	19.39	8.89	23.42	178.00	4.97	2.02	2.49	23.71
	SE±	10.04	5.75	3.94	3.91	1.76	2.91	26.69	0.28	0.15	0.20	1.85
II	Mean	130.58	158.08	140.92	23.58	9.08	26.58	192.25	5.47	2.10	2.62	23.53
	SE±	5.16	3.04	7.85	1.22	1.77	2.17	30.67	0.25	0.13	0.26	1.80
III	Mean	109.78	141.89	115.00	24.04	11.56	25.10	244.11	5.14	2.34	2.20	29.49
	SE±	7.24	10.96	5.86	0.87	1.71	2.57	39.52	0.12	0.10	0.12	5.90

Conclusion

Path coefficient analysis indicated that biological yield per plant exerted the highest positive direct effect on grain yield per plant, suggesting that this trait should be given greater emphasis during selection for yield improvement. Based on Mahalanobis' D² analysis, the thirteen rice genotypes were grouped into three distinct clusters, reflecting the extent of genetic divergence among the experimental materials. Cluster I was the largest, comprising six genotypes, followed by Cluster II with four genotypes and Cluster III with three genotypes. Among the clusters, Cluster I exhibited the greatest intra-cluster distance, whereas comparatively lower intra-cluster distances were observed in Clusters III and II. The relatively higher intra-cluster distance in Cluster I indicates the presence of greater genetic variability among its constituent genotypes, highlighting their potential value for parent selection in hybridization programmes aimed at broadening the genetic base and improving grain yield.

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References

- Ali, Z., Naeem, M., Rafiq, I., Rehman, A., Ahmad, S., Alwutayd, K. M., ... Iqbal, R. (2026). Evaluation of genetic diversity, yield, and its associated traits in rice (*Oryza sativa* L.) genotypes. *Plant Molecular Biology Reporter*, **44**(1), 1–13.
- Faysal, A. S. M., Ali, L., Azam, M. G., Sarker, U., Ercisli, S., Golokhvast, K. S. and Marc, R. A. (2022). Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. *Plants*, **11**(21), 2952.
- Jangala, D. J., Amudha, K., Geetha, S. and Uma, D. (2022). Studies on genetic diversity, correlation and path analysis in rice germplasm. *Electronic Journal of Plant Breeding*, **13**(2), 655.
- Kulsum, U., Sarker, U. and Rasul, M. G. (2022). Genetic variability, heritability and interrelationship in salt-tolerant lines of T. Aman rice. *Genetika*, **54**(2), 761–776.
- Thakare, V. V., Lal, G. M. and Bara, B. M. (2025). Assessment of genetic divergence using D² analysis in rice (*Oryza sativa* L.) germplasm. *New Horizons of Science, Technology and Culture*, **5**, 87–107.
- Thang, N. B. (2022). Genetic divergence of cultivated rice varieties in North Vietnam for grain quality traits using D² cluster analysis. *Vietnam Journal of Agricultural Sciences*, **5**(2), 1435–1444.
- Vennila, S., Desika, J., Suganthi, S. and Bhuvaneswari, R. (2022). Genetic diversity in released and traditional rice (*Oryza sativa* L.) varieties of Tamil Nadu using D² statistics. *Indian Journal of Natural Sciences*, **13**(74), 47835–47840.