Genetic Diversity of South Indian Rice (*Oryza sativa* L.) Genotypes based on Yield and its Components

Gokul M.[1], N.B. John Kingsly[1], G. Ashwin Bernald[1], J. Lydia Pramitha[1] and S. Praveena Katharine[2]*
[1]Division of Genetics and Plant Breeding, School of Agricultural Sciences,
Karunya Institute of Technology and Sciences, Coimbatore (Tamil Nadu), India.
[2]Division of Soil Science and Agricultural Chemistry, School of Agricultural Sciences,
Karunya Institute of Technology and Sciences, Coimbatore (Tamil Nadu), India.

(Corresponding author: John Kingsly)*

ABSTRACT: Rice serves as the primary dietary component for over 50% of the global population. In order to accommodate the increasing needs of an expanding population, it is imperative to enhance yield levels. The generation of variability is significant in order to enhance yield and facilitate the development of breeding programmes. A total of sixty high yielding rice cultivars were subjected to a comprehensive investigation of genetic variability across eleven distinct traits. The plant height, number of productive tillers, grain breadth, and grain length showed high GCV, PCV, Heritability as well as GAM. The genetic diversity of 60 genotypes was evaluated using D^2 statistics, followed by their categorization into eight clusters utilising R packages. Among the eight clusters under consideration, it was observed that Cluster I encompassed a total of 20 distinct genotypes, while Cluster III comprises 17 distinct genotypes. The observed clustering patterns of the Sornamasuri and karuppukavuni genotypes indicate a notable level of genetic diversity within the examined population. Among the eight clusters, it was observed that the Cluster VII and Cluster V exhibit the highest inter-cluster distance. Clusters VII and V exhibit a noteworthy degree of genetic diversity, as evidenced by the observed differences between these two clusters. Based on the observations derived from the diversity experiment, it has been ascertained that specific characteristics display notable variations across various genotypes. The aforementioned characteristics include 1000 grain weight, days to 50% flowering, the number of productive tillers and single plant yield.

Keywords: Rice, D^2 statistics, heritability, variability, genetic diversity.

INTRODUCTION

Rice possesses significant agricultural significance within the Indian context, owing to its widespread cultivation across diverse ecologies and its manifestation of a wide range of phonological traits and yield fluctuations. The diminishing land area suitable for rice cultivation can be attributed to the rapid expansion of the human population, the adverse impacts of climate change, and shifting societal preferences. The observed phenomenon continues to endure despite the simultaneous rise in rice consumption, a variable that exhibits a direct correlation with the expanding global populace. Based on the findings of Nakano *et al.* (2023), it has been determined that the present global rice consumption is approximately 600 million metric tons. Nevertheless, based on projections, it is anticipated that the global demand for rice will experience a substantial surge, reaching an estimated quantity of approximately 758 million metric tons by the year 2025.

To fulfil the increasing demand of consumers, it is critically necessary to develop new rice cultivars with high yields, resilience to both biotic and abiotic stresses, and good grain quality. There is an urgent need for the development of novel rice cultivars that possess high yield potential, resilience against both biotic and abiotic stresses, and superior grain quality in order to effectively address future consumer demands (Umadevi *et al.*, 2019). Traditional rice varieties are renowned for their capacity to thrive in a wide range of conditions, enabling them to effectively navigate fluctuating climates and act as repositories of genes that confer resistance to pests and diseases. Consequently, the utilization of conventional rice cultivars emerges as the optimal and ecologically sound approach for the development of climate-resilient rice varieties that exhibit resistance to significant biotic and abiotic stresses (Thuy *et al.*, 2023). According to N.I. Vavilov, South Asia holds considerable importance as a primary origin and diverse reservoir of rice. The region has remarkable diversity in terms of qualitative and quantitative features, as well as the sources of resistance to a wide range of biotic and abiotic stresses. As a consequence of the rigorous selection conducted by plant breeders to emphasize a limited set of

characteristics, notably yield, and the utilization of a restricted pool of progenitors in breeding initiatives subsequent to the Green Revolution in the mid-1960s, the existing diversity has been further diminished, resulting in a reduced quantity of high-yielding cultivars that have supplanted numerous landraces. The aforementioned process has ultimately led to a reduction in crop diversity, rendering the crop more vulnerable to a range of biotic and abiotic stress (Salunkhe *et al*., 2023).

According to this study, the main factors that contributed to the genetic divergence between the genotypes were single plant yield, grain length, 1000 grain weight, grain width, and days to 50% flowering. Therefore, selection efforts could be concentrated on these traits to increase grain yield. In light of these results, the current study was carried out to evaluate the type and degree of genetic divergence present in rice germplasm for yield, yield attributes, and grain characteristics. It also examined the important relationships between the traits examined by correlation and path (Chandra *et al*., 2023).

Multivariate statistical tools have been extensively used to summarize and describe the inherent variability among crop genotypes. Principal Component Analysis (PCA), cluster analysis, and diversity analysis are examples of multivariate statistical tools. Mahalanobis D^2 statistics, which are based on generalized distance, are useful for determining the degree of genetic divergence at the genotypic level (Mahalanobis, 1936). The degree of genetic measures, including ANOVA,

broad sense heritability, genetic gain, phenotypic and genotypic variances and Phenotypic and Genotypic Coefficients of Variations (PCV and GCV), helps determine the best selection strategies to use for enhancing particular traits. The tools listed above are useful for comprehending the variety of characters found in the genotypes and their application in subsequent breeding programs. As a result, the goals of this study were to evaluate the genetic diversity, genotype grouping based on variations, and per cent contribution between the traits.

MATERIALS AND METHODS

The experiment was conducted with sixty rice genotypes collected from different parts of South India. They were evaluated at Karunya Institute of Technology and Sciences, Coimbatore during summer 2023. The genotypes were raised in a Randomized Block Design (RBD) with three replications under a spacing of 20 × 20 cm by implementing the recommended packages of agricultural practices.

RESULTS AND DISCUSSION

The genetic variability present in any crop species is the primary resource for choosing the best-performing lines from a diverse collection of germplasm lines and afterwards assessing the level of variability caused for the attributes of interest. In this study, the analysis of variance revealed the presence of significant differences among the genotypes for all eleven traits (Table 1).

Table 1: Analysis of variance for eleven traits.

Sr. No.	Traits	Mean sum of square		
		Replication	Genotype	Error
1.	Plant height	644.33	1609.51***	594.15
2.	Days to 50% flowering	0	913.77***	0
3.	Number of tillers per plant	0.33	8.6707***	1.29
4.	Number of Productive tillers	0.3	3.11607***	1.08
5.	Leaf length	9.28	295.52***	3.19
6.	Leaf width	0.03	0.116177***	0.01
7.	Panicle length	2.36	6.0719***	1.27
8.	Grain length	0.04	2.17533***	0.09
9.	Grain breadth	0.01	0.66875***	0.04
10.	1000 grain weight	0.03	93.181***	0.06
11.	Single plant yield	0.55	227.254***	0.41

***Significant at 0.1 %

The Phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV) for all eleven traits. This indicates that the influence of the environment of these traits were at a lower level. Higher PV as well as GV was recorded for plant height, days to 50% flowering, number of tillers per plant, number of productive tillers, panicle length, leaf length, leaf breadth, grain length, grain breadth, 1000 grain weight, single plant yield. The highest difference between the PCV and GCV was

observed in the plant height and the least difference between the PCV and GCV was observed in the 1000 grain weight (Table 3). The results suggest that there is an environmental impact on the phenotypic manifestation of these characteristics, implying that utilising selection methods based on these traits may be a feasible strategy for improving rice yield in breeding initiatives. The reports of Devi *et al.* (2020) supports the above findings.

Table 2: Genetic variability parameters for eleven traits.

Sr. No.	Traits	EV	GV	PV	ECV	GCV	PCV	H	GA	GAM
1.	Plant height	594.15	338.45	932.60	20.80	15.70	26.06	36.29	22.83	19.48
2.	Days to 50% flowering	0.00	304.59	304.59	0.00	19.82	19.82	100.00	35.96	40.83
3.	Number of tillers per plant	1.29	2.46	3.75	5.27	7.30	9.00	65.69	2.62	12.18
4.	Number of productive tillers	1.08	0.68	1.76	8.37	6.63	10.68	38.52	1.05	8.47
5.	Leaf length	3.19	97.44	100.63	5.16	28.52	28.98	96.83	20.01	57.81
6.	Leaf width	0.01	0.04	0.04	8.06	16.40	18.27	80.63	0.35	30.34
7.	Panicle length	1.27	1.60	2.87	4.71	5.28	7.71	55.80	1.95	8.14
8.	Grain length	0.09	0.69	0.79	3.83	10.45	11.13	88.14	1.61	20.20
9.	Grain breadth	0.04	0.21	0.25	6.58	16.00	17.30	85.57	0.88	30.48
10.	1000 grain weight	0.06	31.04	31.10	1.12	25.75	25.78	99.81	11.47	53.00
11.	Single plant yield	0.41	75.61	76.03	1.81	24.48	24.54	99.46	17.86	50.29

EV- Environmental Variance, GV- Genotypic Variance, PV- Phenotypic Variance, ECV- Environmental Coefficient of Variance, GCV- Genotypic Coefficient of Variance, PCV- Phenotypic Coefficient of Variance, H- Heritability, GA- Genetic Advance, GAM- Genetic Advance as percentage Mean.

Heritability quantifies the degree of genetic transmission of traits from parents to their offspring and can be utilized as a predictive measure for genetic advance. The sole focus lies on the dependability of the phenotypic value in order to attain an elevated breeding value throughout the course of the selection process. In the present study all eleven traits ranged 100 to 36.29 per cent. Among the eleven traits highest heritability was observed in days to 50% flowering (100) followed by 1000 grain weight (99.81), single plant yield (99.46), Leaf length (96.83), Grain breadth (8.55), Grain length (88.14), Leaf width (80.63), Number of tillers per plant (65.69), Panicle length (55.80), Number of Productive tillers (38.52) and Plant height (36.29). The genetic parameter of variability revealed that days to 50% flowering and thousand grain weight having high mean, high heritability and high genetic advance as percentage of mean among all traits (Tiwari *et al*., 2021). The elevated heritability percentage observed for these traits implies that the influence of environmental factors on their phenotypic manifestation was relatively minimal. Consequently, it is feasible to employ uncomplicated selection techniques that leverage the substantial heritability of these traits in order to improve yield.

The heritability of a trait is determined by the collective influence of both additive and non-additive genetic factors. However, the practical utility of this phenomenon cannot be fully realized unless it is substantiated by genetic advance. The study of genetic advance provides valuable insights into the nature of gene action, particularly in relation to quantitative traits. Among the eleven traits highest Genetic advance was observed in days to 50% flowering (35.95), followed by Plant height (22.83), Leaf length (20.00), Single plant yield (17.86), 1000 grain weight (11.46), Number of tillers per plant (2.61), Panicle length (1.94), Grain length (1.61), Number of productive tillers (1.05), Grain breadth (0.87) and Leaf width (0.35) (Table 2). The utilization of the parameter "genetic advance as a percentage of mean" is deemed to be a more dependable measure compared to the sole consideration of "genetic advance." The highest genetic

advance as percentage of mean was Leaf length (57.80) followed by 1000 grain weight (53.00), Single plant yield (50.28), days to 50% flowering (40.83), Grain breadth (30.47), Leaf width (30.34), similar results recorded for harvest index by Sravani *et al.* (2022); and Grain length (20.20), Plant height (19.48), Number of tillers per plant (12.18); whereas the lowest genetic advance as a percentage of mean was observed in Number of productive tillers (8.47), Panicle length (8.13). The observed high genetic advance suggests that there is a significant influence of additive gene action. Therefore, the implementation of a selection process that prioritizes the aforementioned traits exhibiting substantial genetic advance would yield highly favourable outcomes. Consequently, the genotypes identified through this process can be utilized as a foundational lineage within the varietal development program.

A. Genetic divergence
D^2 statistics were used to assess the genetic diversity of 60 genotypes, which were then classified into eight clusters using R packages. Out of eight clusters, Cluster I and III feature 20 and 17 genotypes respectively (Table 6), indicating that crossing among genotypes in this cluster may result in transgressive sergeants, Clusters VI and VIII exhibit a singular genotype within each cluster. The observation of a solitary genotype in clusters VI and VIII suggests that it exhibits greater genetic divergence compared to the other genotypes. Consequently, it would be advisable to engage in crossbreeding with genotypes originating from distinct clusters in order to achieve heterosis for specific traits of interest. Cluster means of different traits were given in the (Table 3). Cluster I has the lowest mean other the Single plant yield, Plant height, Leaf length, Panicle length, Cluster II has the lower mean value for Leaf width, Grain breadth, Grain length, Cluster III has the highest mean value for Plant height, days to 50% flowering, Leaf length, Cluster IV has the highest mean value of Plant height, Leaf length, Panicle length, Cluster V has the highest mean value for days to 50% flowering, Plant height, Single plant yield, Cluster VI

has the highest mean value for Plant height, days to 50% flowering, Single plant yield, Panicle length, Cluster VII has the highest mean value for Plant height, days to 50% flowering, Single plant yield, 1000 grain weight, Cluster VIII highest mean value for days to 50% flowering, Plant height, Single plant yield.

Similarly, days to 50% flowering, plant height and number of seeds per panicle were attained as the major contributors for genetic diversity by Kumari *et al.* (2018); Rashmi *et al.* (2018); Amudha and Ariharasutharsan (2021).
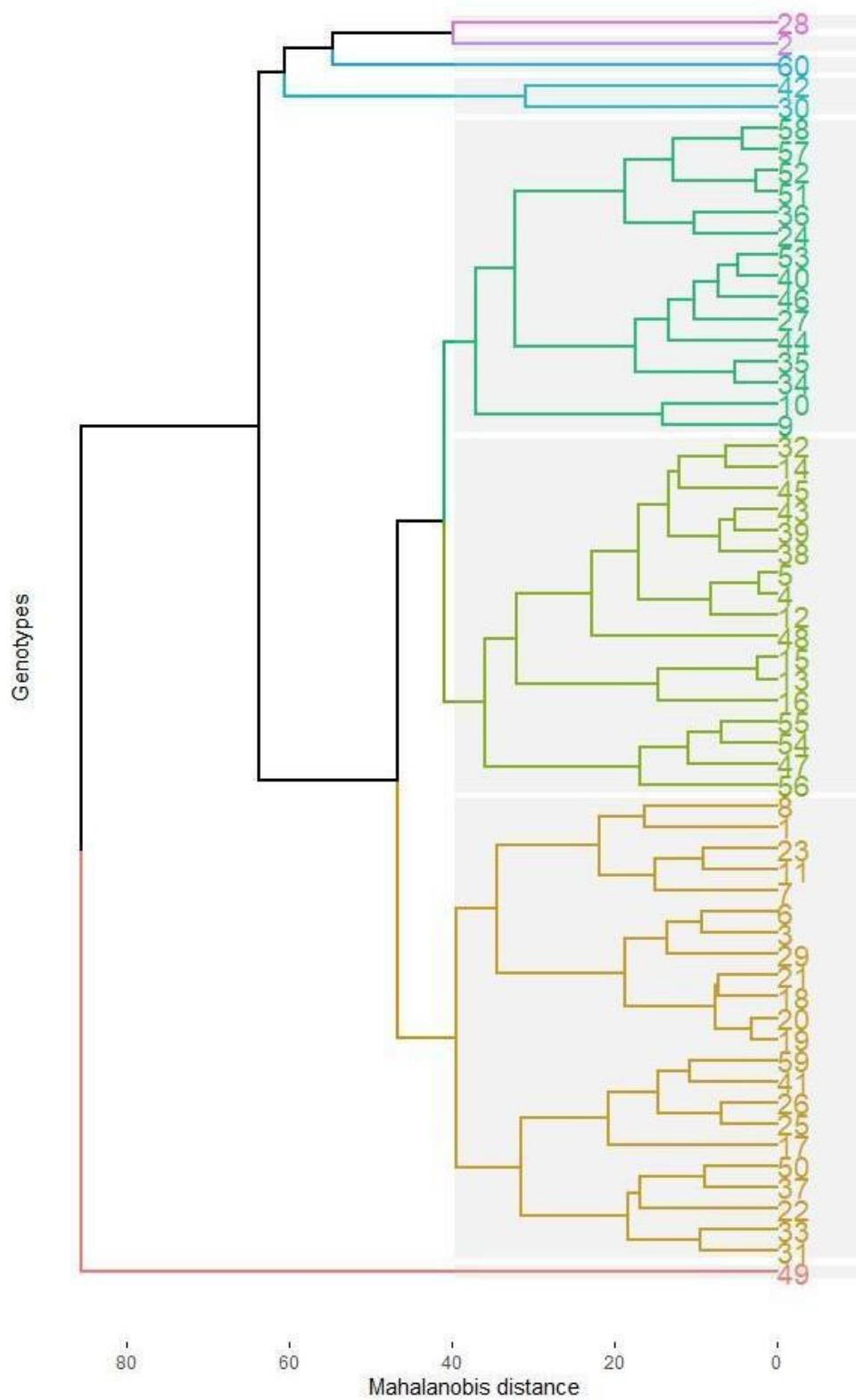

Fig. 1. Cluster dendrogram for sixty genotypes.

Table 3: Estimates of cluster means of eleven traits to diversity.

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
PH	113.85	100.15	120.24	114.75	107.90	142.31	163.75	80.86
DFF	86.50	78.50	85.12	77.80	110.83	118.00	93.33	108.00
NT	21.28	19.00	22.05	21.13	22.24	23.00	20.63	22.11
NPT	12.23	11.78	12.50	12.47	11.91	12.89	12.41	18.78
LL	31.34	26.78	34.14	35.89	36.89	73.53	41.67	37.40
LW	1.18	0.95	1.12	1.25	1.16	0.87	1.09	1.10
PL	23.84	19.91	25.00	23.16	23.95	22.96	23.99	24.21
GL	8.30	5.70	7.81	7.88	8.58	8.57	7.17	7.80
GB	2.67	2.27	2.82	3.32	3.26	3.60	2.59	2.43
1000 GW	22.46	14.03	17.91	24.15	25.73	26.74	27.06	12.46
SPY	34.68	22.85	29.77	43.79	36.99	48.73	42.58	49.90

PH- Plant Height, DFF- Days to 50% Flowering, NT- Number of Tillers per plant, NPT- Number of Productive Tillers, LL- Leaf Length, LW- Leaf Width, PL- Panicle Length, GL- Grain Length, GB- Grain Breadth, 1000 GW- 1000 Grain Weight, SPY- Single Plant Yield.

Based on the findings, it can be assumed that cluster I primarily comprises early maturing varieties characterized by a relatively low average for yield contributing traits. Conversely, cluster V predominantly consists of late maturing landraces exhibiting a high average for yield contributing traits. Cluster VI and cluster VIII have zero inter cluster distance. Cluster I, cluster II, cluster III, cluster VII has the maximum intercluster distance. Cluster VII has the maximum intercluster distance (34.9), Cluster V has the maximum intercluster distance (25.39) (Table 4). To mitigate the adverse associations between yield and its corresponding attributes, it is plausible to utilize these genotypes within breeding initiatives to establish parental crosses involving the most diverse and closely related groups.

Table 4: Inter and Intra cluster distance between each cluster based on D^2 values.

Cluster	C1	C2	C3	C4	C5	C6	C7	C8
C1	33.07	53.96	39.99	39.60	38.71	50.70	51.24	64.44
C2		31.23	56.40	51.99	52.84	51.77	57.47	81.93
C3			33.30	36.22	39.05	42.91	50.41	60.54
C4				25.39	42.98	46.27	52.62	63.18
C5					27.20	40.10	61.19	72.13
C6						0.00	45.93	57.73
C7							34.90	77.31
C8								0.00

In addition to the phenomenon of divergence, it is imperative to consider the performance of genotypes and characters that exhibit the greatest contribution to said divergence, as they appear to hold advantageous potential for the enhancement of crops. Genetic diversity was evaluated by conducting Mahalanobis D^2 analysis on data collected for eleven yield and yield attributing traits in a sample of 60 genotypes. Among all the eleven traits, number of tiller exhibited the maximum contribution (17.06) towards the diversity by taking the first rank for 302 times followed by Leaf width (14.12% ranked first for 250 times), Panicle length (12.14% ranked first for 215 times), Single plant yield (11.299% ranked first for 200 times), days to 50% flowering (10.28% ranked first for 182 times), 1000 grain weight (9.774% ranked first for 173 times), Grain breadth (8.98% ranked first for 159 times), Grain length (7.17% ranked first for 127 times), Plant height (3.72% ranked first for 66 times), Leaf length (3.44% ranked first for 61 times), Number of productive tillers (1.97% ranked first for 35 times) (Table 5). The Mahalanobis D^2 statistic has been widely utilized by numerous researchers in the field of multivariate analysis. This includes its application in assessing the extent of differentiation within agricultural germplasm collections and various varieties.

Table 5: Relative contribution of eleven traits to genetic diversity in 60 selected varieties of rice.

Percent contribution		
	Rank	Percentage (%)
PH	66	3.729
DFF	182	10.282
NT	302	17.062
NPT	35	1.977
LL	61	3.446
LW	250	14.124
PL	215	12.147
GL	127	7.175
GB	159	8.983
1000 GW	173	9.774
SPY	200	11.299

PH- Plant Height, DFF- Days to 50% Flowering, NT- Number of Tillers per plant, NPT- Number of Productive Tillers, LL- Leaf Length, LW- Leaf Width, PL- Panicle Length, GL- Grain Length, GB- Grain Breadth, 1000 GW- 1000 Grain Weight, SPY- Single Plant Yield.

Table 6: Distribution of genotypes into different clusters.

Cluster	Genotypes
1	Chinnar 20, ADT 38, Anna 4, ASD 19, CO 53, Ezhome-3, Ezhome-4, Jaiva, KAU Maithilla, Kothamalli samba, Pokali, Naveen, Milagu samba, Nujvara, Ponni, Rakthashali, Chithiraikar, Sivapukavuni, Thanga samba.
2	ADT 37, VGD 1.
3	ADT 39, ADT 45, ADT 53, CO 51, CO 52, CO 54, CO 55, Ezhome-1, Seeraga samba, Kamdan Samba, Kullakar, Lavanya, Mapilli samba, TKM 13, TKM 15, TRY 4, Vellakar.
4	Annaikomban, Arumpathamkuruvai, ASD 16, Karunguravai, Norugan, Puluthikar, Raja samba, TKM 9, TPS 3, TPS 5.
5	CR1009 Sub 1, Green Chinnar, Kalabatti, Kolan Samba, Kuliadichan, Vellathondai.
6	Karuppukavuni.
7	Kichidi samba, Pongar, TRY 3.
8	Sonamasuri.

CONCLUSIONS

From the present study, it was concluded that the Plant height, Number of productive tillers, Grain breadth, Grain length showed high GCV, PCV, heritability as well as GAM. Hence, these traits should be taken into consideration at the time of selecting the genotypes for enhancing the yield. The observed clustering patterns of the Sornamasuri and karuppukavuni genotypes indicate a notable level of genetic diversity within the examined population. Among the eight clusters, it is observed that Cluster VII and Cluster V exhibit the highest inter-cluster distance. Clusters VII and V exhibit a noteworthy degree of genetic diversity, as evidenced by the observed differences between these two clusters Based on the results obtained from the diversity studies, it has been noted that specific characteristics, namely 1000 grain weight, days to 50 % flowering, and the number of productive tillers, display noteworthy variations among the genotypes. The aforementioned characteristics have been discerned as pivotal factors that contribute significantly to the overall genetic variability that is observed.

FUTURE SCOPE

Based on results of present investigation the genotypes included in this study are used for future breeding processes .Future research may focus on breeding high yielding rice varieties by important traits such as number of productive tillers, days to 50% flowering, single plant and panicle length. Further investigation of the background genes and genetic mechanisms responsible for the characters identified can provide valuable insights. Consequently, the present investigation can be utilized to discern the variables that contribute to the variability and select the cultivars to serve as donors for the augmentation of traits in subsequent breeding endeavours.

REFERENCES

Amudha, K. and Ariharasutharsan, G. (2021). Genetic variability and interrelationship analysis of quantitative traits in Rice (*Oryza sativa* L.) germplasm. *Applied Biological Research*, *22*(3), 293-299.

Chandra, B. S., Hari, Y., Devi, K. R., Venkanna, V., Prasad, K. R., Kumar, R. S. and Reddy, R. U. (2023). Character Association and Path Analysis Studies for Grain Yield, its components and Gall Midge incidence in Rice (*Oryza sativa* L.). *Biological Forum–An International Journal*, *15*(8), 28-31.

Devi, R. K., Chandra, B. S., Hari, Y., Prasad, K. R., Lingaiah, N. and Rao, P. J. M. (2020). Genetic divergence and variability studies for yield and quality traits in elite rice (*Oryza sativa* L.) genotypes. *Caribbean Journal of Science and Technology, 39*(18), 29-43.

Kumari, S., Singh, P. K., Bisen, P., Loitongbam, B., Rai, V. P. and Sinha, B. (2018). Genetic diversity analysis of rice (*Oryza sativa* L.) germplasm through morphological markers. *International Journal of Agriculture, Environment and Bioresearch,* 953-957.

Nakano, H., Tanaka, R., Guan, S. and Ohdan, H. (2023). Predicting rice grain yield using normalized difference vegetation index from UAV and Green Seeker. *Crop and Environment*, *2*(2), 59-65.

Rashmi, D., Saha, S., Bisen, P. and Singh, P. K. (2018). Assessment of Character Contribution to the Divergence in Rice (*Oryza sativa* L.) Germplasm. *Indian Journal of Plant Genetic Resources, 32*(1), 54-58.

Salunkhe, H., Kumar, A., Krishna, B., Talekar, N. and Pawar, P. (2023). Genetic Diversity and Principal Component Analysis for Yield and its component Trait in Rice. *Biological Forum–An International Journal*, *15*(5), 102-107.

Sravani, B., Anuradha, C., Sundaram, R. M., Supriya, K., Gandhi, N. and Fiyaz, R. A. (2022). Genetic Variability, Heritability and Genetic Advance in 3K Rice (*Oryza sativa* L.) Genotypes. *International Journal of Environment and Climate Change*, *12*(11), 2259-2265.

Thuy, N. P., Nhu, T. T. T., Trai, N. N., Nhu, N. K., Thao, N. H. X., Phong, V. T. and Luan, N. T. (2023). Genetic variability for micronutrients under an aerobic condition in local landraces of rice from different agro-ecological regions of Karnataka, India. *Biodiversitas Journal of Biological Diversity*, *24*(1), 1-10.

Tiwari, S., Koutu, G. K. and Pathak, N. (2021). Diversity Analysis of Grain Attributes in Restorer Lines of Rice (*Oryzae sativa* L). *Biological Forum–An International Journal*, *13*(2), 386-392.

Umadevi, M., Shanthi, P. and Saraswathi, R. (2019). Characterization of rice landraces of Tamil Nadu by multivariate analysis. *Electronic Journal of Plant Breeding*, *10*(3), 1185-1193.