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Genetic variability and diversity in rice (*Oryza sativa* L.) landraces of Nagaland

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ABSTRACT

Rice is the principal food crop of Nagaland and plays a major role in tradition and culture of the ethnic tribes of the state. Leveraging the genetic variability present within the indigenous rice germplasm is necessary for further improvement of them. Hence, the present study was aimed to evaluate the genetic variability, genetic divergence and trait association of grain yield and its attributes in 22 rice landraces from the foot hills of Nagaland. Observations were recorded for eight yield-contributing traits. Analysis of variance revealed significant variation for all the parameters under study. High genotypic and phenotypic coefficient of variation was recorded for number of effective tillers and grain yield per hectare. While remaining yield traits showed medium to low range variation. In the present study, all yield and yield-related traits displayed high heritability. High heritability along with a high genetic advance as percentage of the mean was observed for plant height, number of effective tillers, panicle length, number of grains per plant and grain yield per hectare. Grain yield per hectare exhibited positive and significant correlations with plant height, number of effective tillers, and spikelet fertility, while days to 50 per cent flowering exhibited negative significant association with grain yield at both genotypic and phenotypic levels. All yield traits under study displayed significant positive correlations and positive direct effects to grain yield per hectare except days to 50 per cent flowering at both genotypic and phenotypic levels. The twenty-two genotypes were grouped into six clusters based on the relative magnitudes of D^2 values using Tocher's method. The present study suggested that the genotypes Boyoh, Ereima, Nyari, Rukhatang, Thevuru, Maso Tsuk, and Kemeny as the potential parents for hybridization programme to obtain desirable segregants.

Key words: Rice landraces, Variability, D^2 analysis, Correlation and Path analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important staple cereal crops and is cultivated in 114 countries under diverse environmental conditions (Balakrishnan *et al.,* 2024). It forms an important food source for over 3.5 billion people contributing more than 20 *per cent* of total dietary calories. About 90 *per cent* of rice is produced and consumed in Asia. In India, rice is cultivated in a 43.79 million-hectare area with a production of 116.42 million tonnes in the year 2022-23 (Ratnam *et al.,* 2024). In Nagaland, a good number of local varieties and landraces with high genetic variability are maintained by the tribal farmers, which offer scope for further improvement through selection in spite of their low yield potential (Roy *et al.,* 2024). The improvement of these locally adapted genotypes for grain yield and quality attributing traits will reduce the pressure of increasing the land area under rice cultivation in Nagaland (Verma *et al.,* 2021). Nagaland has the richest pockets of rice germplasm in valleys as well as in hilly areas. The landraces of rice exhibit large variations in morphology, thus signifying the vast genetic diversity among the cultivars (Lalrindiki *et al,* 2024.). Assessment of genetic variation and diversity will create a benchmark for further improving of the local landraces of rice in Nagaland.

Grain yield is a complex trait contributed by various component traits and possesses low heritability. Therefore, selection for yield *per se* is ineffective due to its complex nature and, thus, indirect selection for yield attributing traits is more effective (Biswas *et al.,* 2024). Variability is the prerequisite for selection to be effective. The extent of phenotypic variability which is due to genotype governs the heritability. Heritability on the other hand indicates the extent to which trait variation is genetically determined (Krishnan *et al.,* 2024). For effective selection, traits not only possess high heritability but also high genetic advance. Correlation analysis helps in understanding the interrelationship of different

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traits and thus provides basis of formulating selection scheme. Path coefficient analysis further refines this by partitioning correlation coefficients into direct and indirect effects, providing deeper insight into trait relationships (Biswas *et al.,* 2024).

Rice holds a significant place in the traditions of Nagaland's ethnic tribes and is deeply embedded in their cultural practices. The diverse rice landraces in Nagaland exhibit extensive phenotypic variation, adapting well to the wide-ranging hill environments. This diversity highlights the importance of identifying elite and novel variants that are well-suited to different agroclimatic conditions, offering valuable resources for future breeding efforts. In this study 22 rice landraces grown in the foothills of Nagaland, were characterised and subjected to variability and diversity studies. The information obtained from the study would be helpful for breeders for undertaking rice improvement programme in the foothills of Nagaland. .

MATERIALS AND METHODS

Experiment location and Plant material

The study was conducted during the *Kharif* season-2023, at the Research Farm of the Department of Genetics and Plant Breeding, School of Agricultural Science, Nagaland University, Medziphema, India. A total of 22 rice landraces collected from various parts of Nagaland were used in the study and are presented in Table 5.

Experimental design and field layout

The study employed a randomized complete block design (RCBD) with three replications. Within each replication, there were twenty-two plots measuring 3m x 3m, spaced at intervals of 50 cm. Plant spacing within rows was 15 cm, while row spacing was 20 cm. Recommended agricultural practices were followed to raise the crop.

Data collection

A total of eight quantitative characters on 22 rice landraces genotypes were considered for experimentation. These characteristics were chosen based on descriptions and guidelines provided by PPV & FR in 2001 (DUS). For each characteristic, data were gathered from five randomly sampled plants from each genotype and in each replication. The eight quantitative traits under the investigation were *viz.*, day to 50 *per cent* flowering (DF), days of maturity (DM), Plant height (PH), number of effective tillers per hill (TPH), Panicle length (PL), number of grains per plant (GP), Spikelet fertility (SF) and Grain yield per hectare (GYPH).

Statistical analysis

An analysis of variance (ANOVA) was conducted using the OPSTAT open-source software to evaluate the data. The phenotypic, genotypic, and environmental coefficients of variation were calculated following the methods outlined by Burton and De Vane (1953). Heritability estimations were derived according to Allard (1960). The potential genetic advance through selection was calculated based on the approach by Johnson *et al.,* (1955). Phenotypic and genotypic correlation coefficients were determined as suggested by Al-Jibouri *et al.,* (1958). The partitioning of the genotypic correlation coefficients into direct and indirect effects was done using the method proposed by Dewey and Lu (1959). Genetic diversity was estimated using D^2 statistic (Mahalanobis, 1936). The genetic distance ('D') between clusters was derived by taking the square root of the average D^2 values. Genotypes were grouped into clusters using Tocher's method based on the ascending order of their D^2 following Singh and Choudhury (1985).

RESULTS AND DISCUSSION

Analysis of variance

The results of the analysis of variance for the eight quantitative traits under investigation are presented in Table 1. The results indicated significant variation ($P < 0.05$) among the genotypes for all the traits suggesting presence of substantial amount of genetic variation among the evaluated genotypes. Comparable findings were also observed in studies conducted by Demeke *et al.,* (2023) and Asante *et al.,* (2019).

Genetic Parameters of Variation

The success of crop breeding relies heavily on the genetic variability present in the population and the heritability of the traits. To select desirable traits for trait modeling, a plant

Table 1: Analysis of variance for eight characters in 22 genotypes of rice

Source of variance	Mean square		
	Replications	Genotypes	Error
Degree of freedom	2	21	42
Days to 50% flowering	97.059	193.900**	0.344
Days to maturity	59.066	358.801**	0.313
Plant height	80.01	1697.463**	0.239
No. of effective tillers	2.871	6.870**	0.046
Panicle length	34.911	23.472**	0.161
No. of grain per plant	44.492	1760.152**	0.122
Spikelet fertility	71.225	68.312**	0.289
Grain Yield per hectare	5.353	2.429**	0.043

breeder must analyze the genetic variation within the existing population (Gupta *et al.,* 2020). The genetic variance components for yield and yield-related traits are presented in Table 2. The results of the present study revealed that the phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all the traits. This might be due to influence of environmental effect. High genotypic and phenotypic coefficients of variation (greater than 20%) were observed for number of effective tillers and grain yield per hectare. This indicated that simple selection would be effective for these traits. Similar findings were also reported in other studies by Debsharma *et al.,* (2022) Sanku *et al.,* (2022) and Kangkana Thakur *et al.* (2025).

Table 2: Genetic parameters of yield and its related traits in 22 genotypes of rice

Coefficient of variation				
Character	GCV %	PCV %	Heritability (Broad sence) %	Genetic advance as % of mean
Days to 50% flowering	8.953	8.961	99.81	18.427
Days to maturity	9.098	9.102	99.9	18.734
Plant height	16.284	16.285	99.8	33.543
Number of effective tillers	23.307	23.385	99.3	47.853
Panicle length	10.35	10.386	99.33	21.248
Number of grain per plant	17.32	17.321	99.99	35.678
Spikelet fertility	5.331	5.343	99.6	10.959
Grain yield per hectare	23.34	23.55	98.22	47.653

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation

Mere presence of genetic variation may not indicate the effectiveness of selection unless the heritability and genetic advance are not known. In the present study, all yield and yield-related traits displayed high heritability (>60%), indicating a strong correlation between phenotypic and genotypic values. However, the success of selection depends not only on heritability but also on genetic advance (Debsharma *et al.,* 2022). High heritability along with a high genetic advance as percentage of the mean was observed for plant height, number. of effective tillers, panicle length, number of grains per plant and grain yield per hectare. It could be inferred that these traits predominantly exhibited additive gene action, suggesting that simple selection methods could effectively improve them. High heritability along with medium genetic advance as percentage of the mean, was observed for days to flowering, maturity and spikelet fertility. These findings are supported by the observations made earlier by Srujana *et al.,* (2017), Thuy *et al.,* (2023), Deivanai *et al.,* (2025), H.M. Sachin Kumar *et al.,* (2025) and Islam *et al.,* (2025).

Correlation Studies:

Understanding the strength of the association between yield and its contributing traits is necessaryl for planning an effective selection program. The correlation coefficients (both genotypic and phenotypic) for grain yield and yield traits are presented in Table 3. Grain yield per hectare exhibited positive and significant correlations with plant height, number of effective tillers and spikelet fertility, while days to 50 *per cent* flowering exhibited negative significant correlation with grain yield at both genotypic and phenotypic levels. This suggests that these traits are genetically linked or share common genetic factors contributing to yield. The strong correlations observed at both genotypic and phenotypic levels indicate that selecting these traits could effectively improve seed yield. Similar findings on the correlation of these traits with seed yield were also reported by Srujana *et al.,* (2017) and Thuy *et al.,* (2023).

Table 3: Genotypic and Phenotypic correlation of eight yield traits in 22 rice genotypes

	Characters	Days to 50% flowering	Days to maturity	Plant height	Number of effective tillers	Panicle length	Number of grain per plant	Spikelet fertility	Yield per hectare	
Genotypic correlation	Days to 50% flowering	1	0.479*	-0.331	-0.591**	-0.352*	-0.2637	-0.209	-0.366*	Phenotypic correlation
	Days to maturity	0.479*	1	-0.27	-0.358	-0.765**	-0.463*	-0.203	-0.123	
	Plant height	-0.331	-0.27	1	0.593**	0.201	0.144	0.388*	0.457*	
	No. of effective tillers	-0.591**	-0.358	0.593**	1	0.1967	-0.099	0.441*	0.503**	
	Panicle length	-0.352*	-0.765**	0.201	0.1967	1	0.295	-0.065	0.033	
	No. grain per panicle	-0.2637	-0.463*	0.144	-0.099	0.295	1	0.002	0.022	
	spikelet fertility	-0.209	-0.203	0.388*	0.441*	-0.065	0.002	1	0.454**	
	Grain yield per hectare	-0.366*	-0.123	0.457*	0.503**	0.033	0.022	0.454**	1	

*** = Significate at 1% level, *= Significate at 5% level*

Path coefficient analysis

Path coefficient analysis was conducted at the genotypic level to differentiate the direct and indirect effects of various yield-contributing traits, as presented in Table 4. The traits, *viz*., plant height, number of effective tillers and spikelet fertility under study displayed significant positive correlations and positive direct effects to grain yield per hectare. Therefore, emphasis should be placed on selecting these traits to obtain improvement on grain yield. These findings are consistent with of the observations of Gupta *et al.,* (2020). The residual effect was estimated at 0.7873, indicating that the traits studied do not fully account for the variability observed, suggesting that additional relevant characters may exist outside those currently investigated. Similar results were reported by Girma *et al.,* (2018) and Sadimantara *et al.,* (2021).

Table 4: Direct and indirect effects of yield components on seed yield at genotypic level in 22 rice genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers	Panicle length	Number of grain per plant	Spikelet fertility	r_g with Yield per hectare
Days to 50% flowering	-0.1866	-0.0894	0.0619	0.1103	0.0658	0.0492	0.0391	-0.3664
Days to maturity	0.1040	0.2171	-0.0586	-0.0779	-0.1661	-0.1007	-0.0442	-0.1236
Plant height	-0.0645	-0.0526	0.1945	0.1155	0.0392	0.0281	0.0756	0.4571
No. of effective tillers	-0.1283	-0.0778	0.1288	0.2169	0.0427	-0.0217	0.0958	0.5037
Panicle length	-0.0221	-0.0480	0.0127	0.0123	0.0628	0.0185	-0.0041	0.0337
No. of grain per plant	-0.0076	-0.0133	0.0041	-0.0029	0.0085	0.0287	0.0000	0.0022
Spikelet fertility	-0.0614	-0.0595	0.1137	0.1293	-0.0191	0.0000	0.2926	0.4549

RESIDUAL EFFECT = 0.7873

Genetic Divergence Analysis

In the present study genetic divergence among the 22 rice genotypes of Nagaland was studied using Mahalanobis' D² statistic. This method determines the statistical distance between the genotypes and based on which a hierchial classification of genotypes can be obtained by following different clustering methods. In the present investigation clustering was done by Tocher's method. These clusters assist plant breeders in identifying genetically diverse parents within the population (Rajappa *et al.,* 2024). The current study aims to pinpoint genetically diversified parents for hybridization programs. The twenty-two genotypes were grouped into six clusters based on the relative magnitudes of D² values using Tocher's method. Among these clusters, Cluster I contained the highest number of genotypes (14), followed by Cluster III, which included four genotypes. Clusters II, IV, V and VI each contained a single genotype. The distribution of genotypes across the four clusters is presented in Table 5, representing a high degree of genetic divergence among the genotypes.

Table 5: Clustering pattern of 22 rice genotypes on the basis of Tocher's method

Cluster	No. of genotypes in Cluster	List of Genotypes
Cluster 1	14	Aongsho, Malanken, Bhalum - I, Manabe, Manen Tsuk, Chali Yoh, Doulong, Moro Etyo, Hyung Yoh, Samro Yoh, Semmeki, Koyapvu Tsuk, Shangya, Lamjet
Cluster 2	1	Engcha Yoh
Cluster 3	4	Kemenya, Rukhatang, Maso Tsuk, Thevuru
Cluster 4	1	Nyari
Cluster 5	1	Ereima
Cluster 6	1	Boyoh

In D^2 analysis, cluster distance indicates the diversity between clusters. The inter-cluster distances measure the relatedness and genetic relationships among genotypes across different groups. Average intra and inter- cluster distances among the six clusters in rice landraces is presented in Table 6. In this study, cluster IV and VI exhibited the largest average inter-cluster distance of 366.49 followed by cluster II and IV (295.69), cluster III and IV (281.52) and Cluster V and VI (211.67). A greater inter-cluster distance suggests that the genotypes within these clusters are more diverse. Conversely, a smaller inter-cluster distance indicates a closer relationship among the genotypes in those clusters, typically reflecting similar gene complexes (Padmakumar *et al.,* 2024).

Table 6: Average intra and inter- cluster incidents among four clusters in 22 rice genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	85.07	118.15	140.41	231.57	167.45	213.5
Cluster 2		0	200.81	295.69	170.14	108.54
Cluster 3			83.84	126.54	127.2	281.52
Cluster 4				0	180.61	366.49
Cluster 5					0	211.67
Cluster 6						0

The maximum inter-cluster distance points to significant diversity among the genotypes across the groups (Singh *et al.,* 2024). The promising genotypes identified in these clusters could serve as potential parents for breeding. Crosses between genotypes from distinct clusters are believed to have the highest potential for producing beneficial recombinants, which can enhance yield component traits (Singh *et al.,* 2024). Based on the clustering pattern in the present study suggests the genotypes Boyoh, Ereima, Nyari, Rukhatang, Thevuru, Maso Tsuk, and Kemeny were identified as potential parents and suitable candidates for hybridization programme. Geographic distribution significantly influences genetic divergence and relationships among the genotypes across different environments (Rao and Chaturvedi, 2024). Geographic factors can lead to the development of unique genotypes with specific adaptations, resulting in diverse clusters and varying distances between them (Rao and Chaturvedi, 2024).

Table 7: Cluster wise mean value of eight characters in 22 rice genotypes

	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers	Panicle length	No. of grain per plant	Spikelet fertility	Yield per hectare
Cluster 1	87.85	117.13	158.06	6.75	27.58	145.35	89.49	4.00
Cluster 2	81.87	109.27	139.07	7.40	30.37	171.60	89.10	3.30
Cluster 3	97.52	125.87	135.33	6.60	24.85	113.56	91.98	3.48
Cluster 4	82.33	143.73	114.73	6.10	22.83	87.20	86.83	4.23
Cluster 5	101.10	126.67	95.63	3.93	29.90	130.57	81.93	3.80
Cluster 6	88.53	120.30	109.77	4.10	23.87	198.10	86.30	2.83

Cluster mean values are presented in Table 7. Among the clusters, Cluster VI exhibited the highest mean value for the number of grains per plant (198.10), with a lower value of yield per hectare (2.83 tons). Cluster IV, with the highest yield per hectare (4.23 tons), was also promising, despite showing moderate values for other traits. Clusters I and IV are ideal due to their respective high mean plant heights (158.06 cm and 143.73 cm). Thus, Clusters IV and VI

Table 8: Contribution of each character of 22 rice genotypes towards the divergence

. No.	Source	Contribution %
1	Days to 50% flowering	0.87%
2	Days to maturity	3.90%
3	Plant height	32.03%
4	Number of effective tillers	0.43%
5	Panicle length	0.00%
6	Number of grain per panicle	60.17%
7	Spikelet fertility	2.60%
8	Yield per hectare	0.00%

appeared to be significant for selection of parents for inclusion in hybridization programme to obtain desirable segregants. The character plant height (32.03%) and number of grains per panicle (60.17%) contributed maximum towards the divergence (Table 8).

CONCLUSION

In the present study, traits *viz.*, plant height, number of effective tillers, panicle length, number of grains per plant and grain yield per ha exhibited high heritability coupled with high genetic advance suggesting selection based on these traits would be effective for improving grain yield. Plant height, number of effective tillers and spikelet fertility under study displayed significant positive correlations and positive direct effects to grain yield per hectare. Therefore, emphasis should be placed on selecting these traits to obtain improvement on grain yield. The genotypes viz., Boyoh, Nyari, Ereima, Kemenya, Rukhatang, Maso Tsuk, and Thevuru exhibited the highest number of productive tillers per plant, longer panicles, a higher percentage of spikelet fertility, and high yield. However, these genotypes also showed high inter-cluster distance indicating their genetic divergence. Therefore, they are considered as divergent genotypes and are recommended for use in heterosis breeding programs.

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