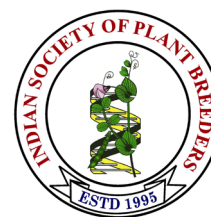


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## Research Note

### Genetic diversity of upland rice genotypes of Nagaland based on root and shoot morphological characteristics

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#### Abstract

Upland rice is a staple food with abundant genetic diversity that needs to be explored and studied. The present study is the first of its kind in the Nagaland region, where 28 upland local genotypes were evaluated for genetic diversity, with special reference to root characteristics. Root dry weight, root fresh weight, root volume, and root-to-shoot ratio were found to significantly contribute to genetic diversity among root traits. In contrast, grain yield per plant, days to 50% flowering, and plant height are key traits responsible for genetic diversity among the shoot traits. Four clusters were formed, among which Cluster-2 and Cluster-4 were the most distinct and Cluster-4 had the maximum number of genotypes. Genotypes Chahashye, Chishoghi, Sulijak, Taposen Youli and Manen (Red) SARS-5 showed greater diversity than the other genotypes. Cluster-1 showed the maximum contribution of one character, i.e., the root length (MRL), and Cluster-2 showed the maximum contribution of four characters, viz. root dry weight, the root-to-shoot ratio, plant height and the number of days to 50% flowering. Cluster 3 showed the maximum contribution of three characteristics viz., number of days to maturity, panicle length, and number of panicles per plant. Cluster 4 showed the maximum contribution of six characteristics, mostly yield-related traits, such as root volume, number of tillers per plant, number of effective spikelets per panicle, 1000-grain weight, shoot length, and grain yield per plant. This study revealed that the genotypes in Cluster-4 has the greatest potential and could be exploited through hybridization programs for yield improvement and drought stress breeding.

**Keywords:** Rice, Nagaland genotypes, PCA, Genetic diversity, Yield improvement.

Rice (*Oryza sativa* L.) is a semi-aquatic annual herbaceous grass of the family Poaceae with a diploid chromosome number of  $2n=24$ . It is a significant grain crop worldwide. It exhibits significant adaptability and is cultivated in diverse environments ranging from wetlands to drylands. Upland rice refers to rice grown in non-flooded, rainfed fields, which contrasts with paddy or lowland rice, which is typically cultivated under water-logged conditions.

It is also known as autumn rice since it is directly sown in dry circumstances from May–June and harvested from

September to early October. Upland rice covers over 18 million hectares worldwide, with South Asia accounting for approximately 42% (Taridala *et al.*, 2018). Nearly 85% of the country's upland rice (5.2 million hectares) is grown in Eastern India (Gairola *et al.*, 2024).

Eastern India has the greatest coverage and is distinguished by direct seeding and minimum input utilization. Rice is an important crop in Nagaland. Unlike other systems, the output in uplands has remained low for several decades, at approximately 1–2 tonnes per

hectare. Upland rice, which is grown by smallholder farmers, is the least productive rice production system. The majority of the entire land under rice in the state is located in the low-productivity category. The state is devoid of high and medium productivity categories. As it relies on antiquated cultivars and lacks modern irrigation technology, Nagaland's rice yields are dismally low. According to the Nagaland Statistical Handbook 2023, the productivity of upland rice in Nagaland is 1.98 tonnes per hectare. The importance of preserving rice genotype cultivated by indigenous communities in Nagaland is emphasized because of their cultural importance and contribution to genetic diversity, which is crucial for future food security.

Upland rice production is a prominent agricultural activity in Nagaland, supporting a large amount of the population's livelihood. This practice is linked to the cultural and culinary choices of the Naga people and helps to maintain the genetic variety of rice genotype in the region (Roy *et al.*, 2023).

Upland rice has an abundance of undiscovered genetic resources. These genetic variations are critical for developing rice varieties, particularly in the midst of climate change and water scarcity (Lyu *et al.*, 2014). Several studies have been conducted on the genetic diversity of upland rice in Eastern India, highlighting the wide range of genetic cultivars. Vanlalsanga and Singh (2019) reported a high level of gene diversity in upland rice genotype from Mizoram, Northeast India, with significant genetic divergence among populations. Similarly, Li *et al.* (2023) explored the genetic diversity of Shanlan upland rice, revealing a significant number of alleles (164 alleles) detected via SSR markers, indicating rich genetic diversity among upland rice cultivars in Southeast Asia and southern China, potentially including regions of Eastern India. Nilthong *et al.* (2020) corroborated these findings with evidence of substantial genetic variability in highland rice cultivars in northern Thailand.

Thanh *et al.* (1999) reported considerable heterogeneity in root shape among upland rice. Uga *et al.* (2009) investigated the genetic diversity of root anatomical and morphological properties across different cultivated rice varieties and reported differential genetic diversity in terms of root characteristics across the japonica and indica groups. In contrast, Gowda *et al.* (2011) reviewed the genetic variation in the response of rice roots to drought, emphasizing the necessity of identifying important root features for improving drought resistance.

Root system architecture plays a central role in drought adaptation. Lynch (2013) proposed the ideotype concept "steep, cheap, and deep" to describe efficient root traits that optimize water and nitrogen acquisition in low-input systems. While this model was proposed for maize, its principles apply to upland rice, which similarly experiences

water stress under rainfed conditions. Research on rice genetic diversity, particularly concerning root traits, is difficult and hence limited.

Previous studies (Singh and Changkija, 2016; Lalhruaitluangi *et al.*, 2022) have focused primarily on shoot-based traits of indigenous upland rice genotype while identifying high-yielding genotypes. However, none have investigated root characteristics in the context of Nagaland's genetic resources. This study is the first to evaluate 28 improved upland genotypes from Nagaland with specific reference to root traits such as root dry weight, root fresh weight, root volume, and root-to-shoot ratio, all of which contributed significantly to genetic divergence among genotypes. In comparison, shoot traits like grain yield per plant, days to 50% flowering, and plant height were also key contributors. These findings provide a foundation for future breeding programs aiming to select for yield-enhancing and stress-resilient traits simultaneously.

**Experimental material and layout:** Twenty-eight upland rice genotype (genotypes) from Nagaland, as listed in **Table 1**, were used for this study based on their ecological relevance and representativeness of the region's upland rice diversity. This number was carefully chosen to balance genetic breadth with practical manageability, ensuring meaningful diversity analysis without compromising statistical power under field constraints. The experiment was conducted during the *Kharif* season of 2023–2024 at the research farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema Campus (20°45'43"N latitude and 93°53'04"E longitude). Seeds were procured from the State Agricultural Research Station (SARS), Mokokchung, and maintained by the department. Due to logistical limitations such as restricted land availability and resource constraints, the study was designed with two replications using a Completely Randomised Block Design (CRBD). Each plot measured 5.0 × 4.0 m and consisted of 3 rows with 4 PVC pipes per row (12 plants per plot), with uniform spacing of 50 × 50 cm. Although two replications were employed due to land and logistical constraints, field variability was minimised through uniform cultivation practices. Additionally, robust multivariate statistical tools—such as Mahalanobis D<sup>2</sup> distance, PCA, and clustering algorithms—were used to enhance the detection of trait-based diversity and ensure the reliability of results despite limited replication.

Observations were recorded on 10 randomly selected plants per plot to evaluate fifteen morphological traits in a stage-wise manner based on the crop's growth phases. During the vegetative stage, the traits recorded included number of tillers per plant (NTP), shoot length (SL), plant height (PH), Maximum root length (MRL), root volume (RV), root fresh weight (RFW), root dry weight (RDW), and root-to-shoot ratio (RSR). At the reproductive

| Genotypes            | Code Given | Place of collection                                              |
|----------------------|------------|------------------------------------------------------------------|
| Pfukhi Lha           | 1          | State Agricultural Research Station (SARS), Mokokchung, Nagaland |
| Sulijak              | 2          | SARS Mokokchung                                                  |
| Moya Chali           | 3          | SARS Mokokchung                                                  |
| Moyatsak             | 4          | SARS Mokokchung                                                  |
| Chishoghi            | 5          | SARS Mokokchung                                                  |
| Thangmo Red          | 6          | SARS Mokokchung                                                  |
| Thangmo White        | 7          | SARS Mokokchung                                                  |
| Chahashye            | 8          | SARS Mokokchung                                                  |
| Taposen Youli        | 9          | SARS Mokokchung                                                  |
| Kedayishefe          | 10         | SARS Mokokchung                                                  |
| Shyekenyii           | 11         | SARS Mokokchung                                                  |
| Amusu                | 12         | SARS Mokokchung                                                  |
| Rosho Lha            | 13         | SARS Mokokchung                                                  |
| Manen (Red) SARS-5   | 14         | SARS Mokokchung                                                  |
| Thupfu Lha           | 15         | SARS Mokokchung                                                  |
| Tungo                | 16         | SARS Mokokchung                                                  |
| Ngoni                | 17         | SARS Mokokchung                                                  |
| Sangmangtsuk SARS-1  | 18         | SARS Mokokchung                                                  |
| Ongpangsuk           | 19         | SARS Mokokchung                                                  |
| Korean Tsuk          | 20         | SARS Mokokchung                                                  |
| Apuapa SARS-1        | 21         | SARS Mokokchung                                                  |
| RCM-9                | 22         | SARS Mokokchung                                                  |
| Toungmiki            | 23         | SARS Mokokchung                                                  |
| Yarba SARS-3         | 24         | SARS Mokokchung                                                  |
| Chali                | 25         | SARS Mokokchung                                                  |
| Kezie SARS-94        | 26         | SARS Mokokchung                                                  |
| Tsushvuri            | 27         | SARS Mokokchung                                                  |
| Longkhum Tsuk SARS-2 | 28         | SARS Mokokchung                                                  |

stage, number of days to 50% flowering (DTF), number of panicles per plant (NPPP), panicle length (PL), and effective number of spikelets per panicle (ESPP) were measured. Finally, at the maturity stage, data were collected for days to maturity (DM), 1000-grain weight (GW), and grain yield per plant (GYPP).

Principal component analysis (PCA) was carried out in the R studio package version 4.3.1 of 2023, followed by cluster analysis and, finally, diversity studies via  $D^2$  statistics. The ggplot 2 and facto extra packages were used to plot graphs wherever needed. The elbow method was used to determine the number of clusters. The Euclidean distance matrix was used to measure cluster separation, whereas the Mahalanobis distance matrix was used to account for the data distribution and percentage contribution of traits.

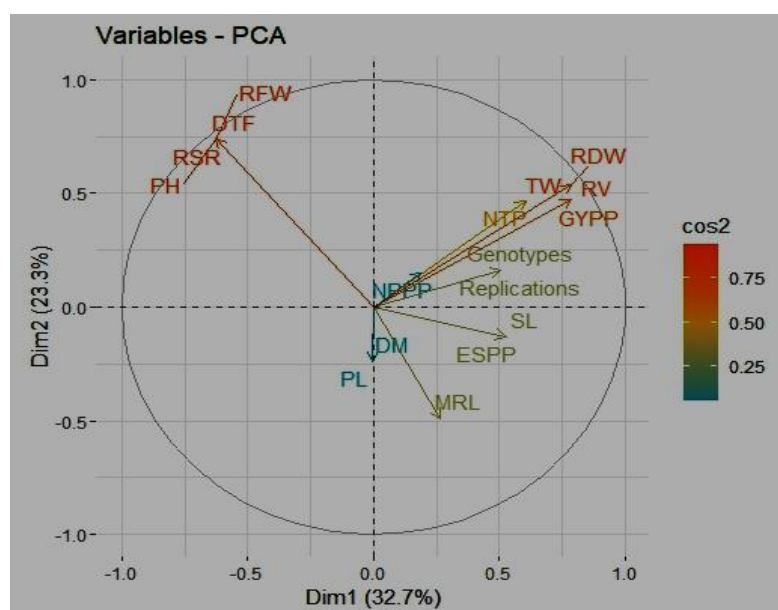
Associations between the characteristics under investigation: These association studies reveal key findings that could be useful for further analysis and interpretation for diversity. **Tables 2 and 3** present the

results of association studies of various characteristics. These association studies play crucial roles in diversity analysis, as reported by Ali *et al.* (2024). Correlation guides trait prioritization for targeted breeding efforts. As mentioned in **Table 2**, the characteristics contributing to genetic diversity were correlated, and their possible implications along with explanations are provided. This correlation also plays a significant role in PCA for accounting for significant variance and thus helps in clustering.

*Exploring trait associations and their contributions to genotypic variation via PCA:* Eigenvalues greater than 1.0 ensure that each component explains more variance than a single original variable. Therefore, PC1, PC2, PC3 and PC4 have eigenvalues greater than 1.0. PC1 has the highest eigenvalue (5.42), which captures most of the variability, followed by PC2 (4.08) and PC3 (2.36). However, PC4 (1.79) contributes less to the overall variance loading, indicating how strongly a variable contributes to a specific principal component.

**Table 2. The correlation of characters and their implications**

| Characters            | Correlation                                                                                                                                                                                                           | Implications                                                                                                                                                                        |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Grain yield per plant | Positively correlated with Root dry weight, Root fresh weight, Number of tillers per plant, Effective spikelet's, 1000-grain weight and Number of panicles per plant whereas negatively correlated with Plant height. | These traits had significant contribution to diversity as supported by the finding in Fig-1. So very crucial for breeding and hybridization programmes.                             |
| Panicle Length        | Positively correlated with Maximum root length and negatively with Root dry weight.                                                                                                                                   | This relationship could be advantageous for nutrient acquisition while it implies heavier roots may lead to shorter panicles due to resource allocation during stress situation.    |
| Days to 50% flowering | Negatively correlated with Maximum root length, Plant height and Shoot length.                                                                                                                                        | Longer root tends to flower earlier whereas taller plants may allocate more resources to stem growth and delay flowering. Therefore, shorter shoot may prioritize flowering sooner. |
| Plant height          | Positively with Maximum root length and negatively with Root dry weight, Number of tiller per plant, Effective spikelet's per panicle, 1000-grain weight, Days to 50% flowering and Grain yield per plant.            | Plant height being a significant contributor to diversity as evident from Fig-1. However, increased PH reduces yield-attributing traits.                                            |

**Fig 1. A biplot analysis of different rice genotypes**

The PC1 component captures the most variability in the data, as it alone explains 61% of the total variance. The traits with high positive values were Root fresh weight and Days to 50% flowering, and the negative values were Root volume and Root dry weight, which significantly influence PC1. In PC2, traits such as RFW and PH had the highest positive values, whereas traits such as Maximum root length, Days to maturity and Panicle length presented high negative values. However, PC1 and PC2 explained 76% of the variability.

PCA is carried out to identify key traits that contributed most significantly to the overall variability observed in the genotypes. The first two principal components (Dim1 and Dim2), which collectively explain 56% of the variance in the data (**Fig.1**). Dim1 accounts for 32.7% of the variability, whereas Dim2 explains 23.3%. Root dry weight, Root fresh weight, Root volume and Root shoot ratio significantly contribute to genetic diversity among root traits, whereas Grain yield per plant, Days to 50 % flowering and Plant height are key traits responsible

Table 3. Correlation between various traits of upland rice genotypes

|      | MRL     | RV     | RFW    | RDW    | RSR     | NTP     | PH      | ESPP     | DM     | TW      | DTF     | SL      | PL      | NPPP     | GYPP     |
|------|---------|--------|--------|--------|---------|---------|---------|----------|--------|---------|---------|---------|---------|----------|----------|
| MRL  | 1       | 0.09   | -0.36  | -0.15  | -0.02   | -0.31   | 0.47*   | -0.394*  | 0.246  | -0.189  |         | -0.219  | 0.453*  | 0.101    | -0.217   |
| RV   | 0.09    | 1      | 0.53** | 0.54** | -0.01   | 0.54**  | -0.086  | 0.523**  | -0.099 | 0.229   | -0.196  | 0.207   | -0.029  | 0.360    | 0.258    |
| RFW  | 0.36    | 0.53** | 1      | 0.91** | 0.38*   | 0.65**  | -0.350  | 0.694**  | 0.077  | 0.504** | 0.067   | 0.299   | -0.318  | 0.159    | 0.495**  |
| RDW  | -0.15   | 0.54** | 0.91** | 1      | 0.42*   | 0.602** | -0.456* | 0.597**  | 0.058  | 0.638** | -0.028  | 0.222   | -0.377* | 0.237    | 0.667**  |
| RSR  | -0.02   | -0.10  | 0.38*  | 0.42*  | 1       | -0.45*  | 0.099   | -0.075   | -0.154 | -0.198  | 0.072   | -0.596* | 0.031   | 0.263    | -0.155   |
| NTP  | -0.31   | 0.54** | 0.65** | 0.60** | -0.45*  | 1       | -0.450* | 0.680**  | -0.061 | 0.581** | 0.047   | 0.394*  | -0.285  | 0.546**  | 0.765**  |
| PH   | 0.47*   | -0.08  | -0.35  | -0.45* | 0.09    | -0.45*  | 1       | -0.589** | -0.085 |         | -0.423* | -0.132  | 0.367   | -0.253   | -0.797** |
| ESPP | -0.39*  | 0.52** | 0.69** | 0.59** | -0.07   | 0.68**  |         | 1        | 0.139  | 0.588** | 0.349   | 0.248   | 0.028   | 0.381*   | 0.445*   |
| DM   | 0.24    | -0.09  | 0.07   | 0.05   | -0.15   | -0.06   | -0.085  | 0.139    | 1      | 0.141   | -0.317  | 0.163   | -0.208  | 0.034    | 0.101    |
| TW   | -0.18   | 0.22   | 0.50** | 0.63** | -0.19   | 0.58**  |         | 0.588**  | 0.141  | 1       | -0.135  | 0.359   | -0.263  | 0.227    | 0.989**  |
| DTF  | -0.53** | -0.19  | 0.06   | -0.02  | 0.07    | 0.04    | -0.423* | 0.349    | -0.317 | -0.135  | 1       | -0.398* | -0.026  | -0.054   | -0.171   |
| SL   | -0.21   | 0.20   | 0.29   | 0.22   | -0.59** | 0.39*   | -0.132  | 0.248    | 0.163  | 0.359   | -0.398* | 1       | -0.077  | -0.513** | 0.312    |
| PL   | 0.45*   | -0.02  | -0.31  | -0.37  | 0.03    | -0.28   | 0.367   | 0.028    | -0.208 | -0.263  | -0.026  | -0.077  | 1       | 0.103    | -0.198   |
| NPPP | 0.10    | 0.36   | 0.15   | 0.23   | 0.26    | 0.54**  | -0.253  | 0.381*   | 0.034  | 0.227   | -0.054  |         | 0.103   | 1        | 0.527**  |
| GYPP | -0.21   | 0.25   | 0.49** | 0.66** | -0.15   | 0.76**  |         | 0.445*   | 0.101  | 0.989** | -0.171  | 0.312   | -0.198  | 0.527**  | 1        |

Significant positive correlation

Significant negative correlation

MRL = Maximum root length, RV = Root volume, RDW = Root dry weight, RSR = Root-to-shoot ratio, NTP = Number of tillers per plant, PH = Plant height, ESPP = Effective spikelets per panicle, DM = Days to maturity, TW = 1000-grain weight, DTF = Days to 50% flowering, SL = Shoot length, NPPP = Number of panicles per plant, GYPP = Grain yield per plant.

for genetic diversity among shoot traits. The traits viz., GYPP, DTF and PH were identified as significant traits contributing to genetic diversity among shoot traits in upland rice. The importance of panicle-related traits in genotypic divergence is further validated by Saraswathi *et al.* (2012), who reported that 100-grain weight alone contributed 57.65% to the total genetic divergence among 125 advanced rice breeding lines using Mahalanobis  $D^2$  analysis. These traits are influenced by genetic variability, as evidenced by studies on rice genotypes in upland environments (Jambhulkar and Bose, 2014; Kumar *et al.*, 2022). These root properties are connected and significantly associated with each other, demonstrating their importance in the genetic diversity of upland rice, especially in terms of drought resistance (Thanh *et al.*, 1999). Agronomic variables such as grain yield per plant, days to 50% flowering and plant height show genetic variability in upland rice. These characteristics are critical to rice productivity and adaptability in upland ecosystems (Kumar *et al.*, 2024).

The traits, such as Root dry weight, Root volume, 1000-grain weight, Grain yield per plant and Number of tillers per plant, were positively related, indicating that a shared genetic basis with favourable alleles for one trait may also carry favourable alleles for the other.

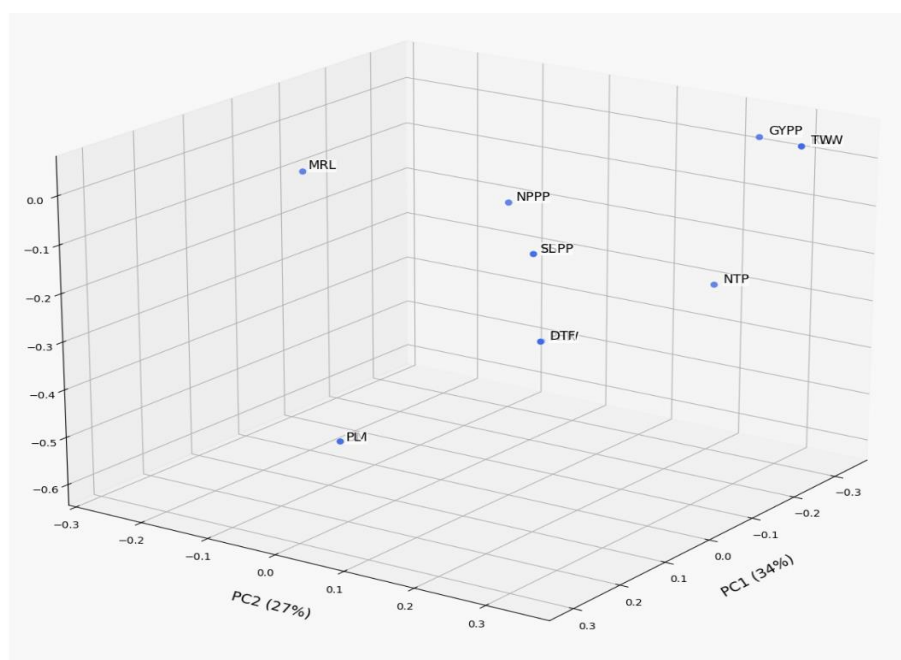
**Clustering Upland Rice: Understanding Genetic Diversity:** Cluster analysis helps to identify groups (clusters) of similar rice genotypes on the basis of their trait profiles. Clusters highlight genotypes with distinct trait combinations and guide the selection of diverse parents for hybridization, ensuring a broader genetic base.

Breeding programs can prioritize specific clusters for desired traits (e.g., yield, stress tolerance). In this study, four optimal numbers of clusters were formed using the elbow method. The inter cluster distances are provided in **Fig. 3**. However, the dendrogram containing various genotypes in the four clusters is depicted in **Fig-4**.

As shown in **Fig. 3**, Cluster-1 and Cluster-4 were found to be moderately close. Similarly, Cluster-2 and Cluster-3 were relatively closer than the other pairs. However, Cluster-2 and Cluster-4 were the most distant, followed by Cluster-3 and Cluster-4. The blue color in the heatmap indicates low distances (clusters are similar or close), whereas red indicates high distances (clusters are dissimilar or distant). Clusters with low distances are more similar.

Although molecular markers like SSR and SNP are widely used in genetic diversity studies, the present research focused on morphological and physiological traits, particularly root traits, due to their direct relevance in drought-prone, rainfed upland rice environments. Traits such as Root dry weight, Root volume and Root fresh weight provide phenotypic insights into drought tolerance, which is critical for improving productivity in Nagaland's upland systems. The absence of molecular data is acknowledged; however, this study aimed to capture field-applicable diversity patterns under actual agronomic conditions.

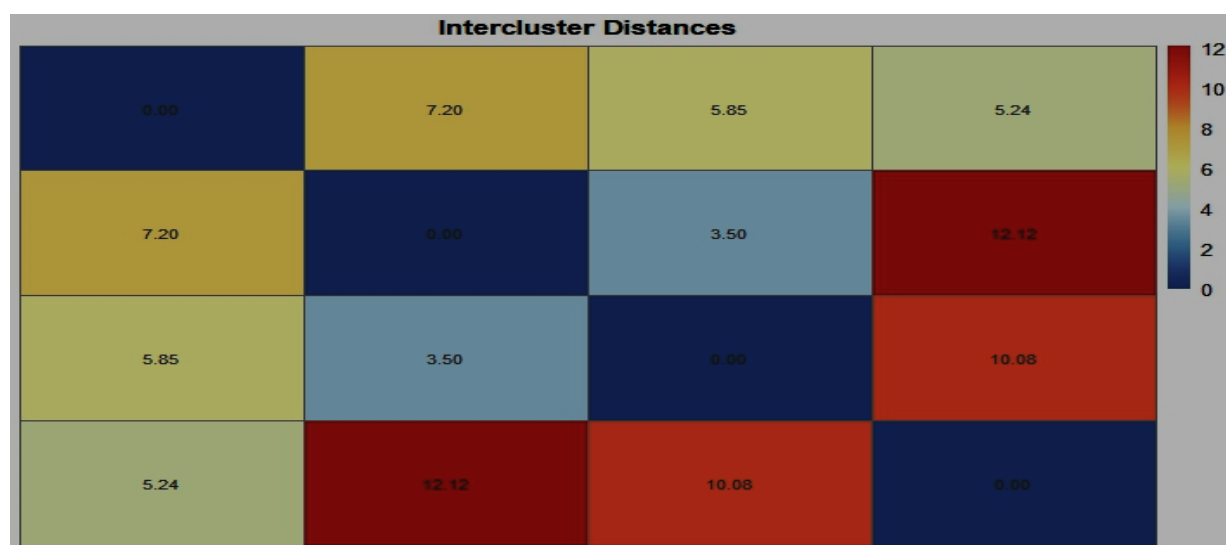
These clusters may share common genetic traits or characteristics, so similar clusters were merged for focused trait improvement (e.g., Cluster-1 and Cluster-3).



**Fig. 2. A 3D PCA loadings plot of different traits**

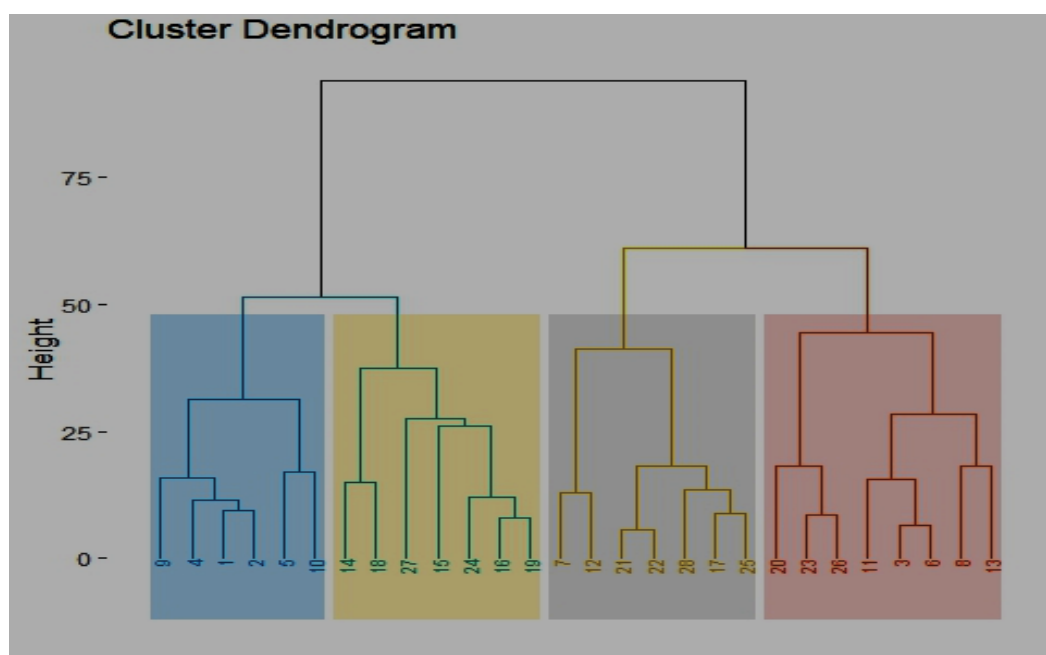
**Table 4. PCA Loadings and Eigenvalues for rice genotypes for various characters**

| Variables                           | PC1    | PC2    | PC3    | PC4    |
|-------------------------------------|--------|--------|--------|--------|
| Maximum root length                 | -0.086 | -0.267 | -0.093 | 0.271  |
| Root volume                         | -0.334 | 0.307  | 0.020  | 0.084  |
| Root fresh weight                   | 0.304  | 0.343  | -0.125 | -0.052 |
| Root dry weight                     | -0.334 | 0.307  | 0.020  | 0.084  |
| Root shoot ratio                    | 0.304  | 0.343  | -0.125 | -0.052 |
| Number of tillers per plant         | -0.234 | 0.247  | -0.249 | 0.090  |
| Plant height                        | 0.304  | 0.343  | -0.125 | -0.052 |
| Effective spikelets per panicle     | -0.253 | -0.030 | -0.268 | -0.499 |
| Days to maturity                    | 0.018  | -0.140 | -0.598 | 0.185  |
| 1000 grain weight                   | -0.334 | 0.307  | 0.020  | 0.084  |
| Days to 50% flowering               | 0.302  | 0.343  | -0.125 | -0.052 |
| Shoot length                        | -0.253 | -0.030 | -0.268 | -0.499 |
| Panicle length                      | 0.018  | -0.140 | -0.598 | 0.185  |
| Number of panicles per plant        | -0.053 | 0.064  | -0.060 | 0.550  |
| Grain yield per plant               | -0.314 | 0.259  | 0.034  | 0.119  |
| Eigenvalue                          | 5.42   | 4.08   | 2.36   | 1.79   |
| Proportion of variability explained | 34%    | 61%    | 76%    | 87%    |

**Fig 3. Inter cluster heatmap of rice genotypes (in order of Clusters 1, 2, 3 and 4).**

These clusters have consistent trait patterns (low intracluster distance), which represent stable genotypes. These can serve as parents for specific environments or stress conditions. Clusters with high distances are distinct. These clusters represent diverse genetic backgrounds; thus, exploring unique traits (e.g., Cluster-2 and Cluster-4) within these distinct clusters could be more beneficial. Validation through multi-location field trials and hybrid performance studies is essential before any concrete breeding recommendations can be made.

In **Fig. 4**, the dendrogram visually represents the hierarchical clustering of 28 genotypes. Each leaf node corresponds to an individual genotype. The coloured branches represent distinct clusters formed during the analysis, where genotypes within the same cluster are genetically more similar to each other. Clusters that are positioned closer together on the dendrogram indicate a higher degree of genetic similarity, while those farther apart reflect greater genetic divergence. Based on the clustering analysis, the genotypes were grouped into



**Fig. 4. Hierarchical cluster grouping of 28 genotypes into four clusters from left to right (in order of clusters 2, 3, 1 and 4)**

four distinct clusters. Cluster 1 consisted of Thangmo White, Amusu, Apuapa SARS-1, RCM-9, Longkhum Tsuk SARS-2, Ngoni, and Chali, which exhibited close genetic similarity among themselves. Cluster 2 included the genotypes Taposen Youli, Moyatsak, Pfukhi Lha, Sulijak, Chishoghi, and Kedavishefe, forming a moderately distinct group with shared traits. In Cluster 3, the genotypes Manen (Red) SARS-5, Sangmangsuk SARS-1, Tsushvuri, Thupfu Lha, Yarba SARS-3, Tungo, and Ongpangsuk were grouped together, indicating a separate pattern of genetic relationship. Finally, Cluster 4, which contained the highest number of genotypes, comprised Korean Tsuk, Toungmiki, Kezie SARS-94, Shyekenyii, Moya Chali, Thangmo Red, Chahashye, and Rosho Lha, reflecting a broad range of genetic variability within this group.

**Principal component analysis (PCA):** An analysis of the diversity among the 28 rice genotypes is presented in **Fig. 5 and Fig. 2**. Principal Component 1 (PC1) on the horizontal axis explains 32.7% of the total variability, while Principal Component 2 (PC2) on the vertical axis accounts for 23.3%. Genotypes Chahashye, Chishoghi, Sulijak, Taposen Youli, Manen (Red) SARS-5, and Tsushvuri exhibit greater diversity, as they are located farther from the origin in the scatter plot. These distant genotypes contribute significantly to overall genetic variability due to their extreme trait expression. Similar trait-based diversity in rice has also been reported through multivariate approaches by Pushpa *et al.* (2022) and Arunkumar *et al.* (2022).

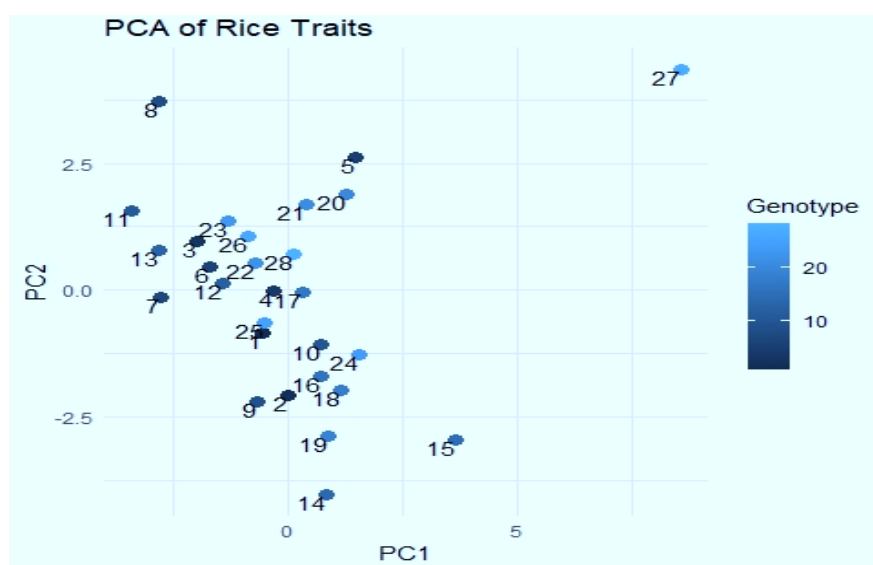
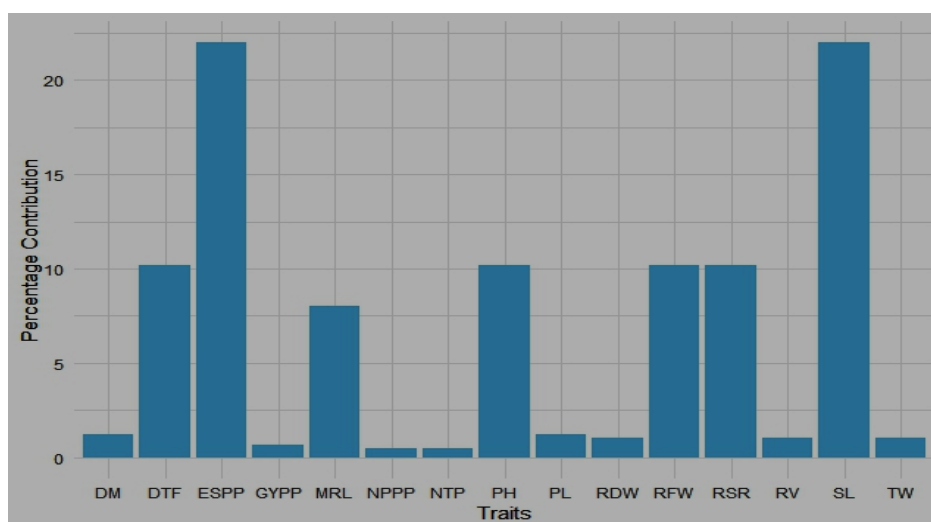
In the scatter plot, each data point represents a genotype and is colour-coded along a gradient. Light blue denotes lower trait values, whereas dark blue indicates higher or more extreme values along this scale. Genotypes such as Chahashye, Chishoghi, Moya Chali, Thangmo Red, Thangmo White, Moyatsak, Pfukhi Lha, Kedavishefe, Taposen Youli, and Sulijak appear in darker shades, suggesting they possess more favourable or extreme trait combinations. Conversely, lighter shades represent genotypes with fewer extreme trait expressions. Breeding programs can prioritize genotypes with specific colour intensities depending on their selection objectives and breeding goals.

**Relative contribution of traits to clusters via  $D^2$  statistics:** Cluster 1 showed the highest contribution from a single trait, namely mean root length. Clusters exhibiting dominance of specific traits, such as Cluster 1, can be effectively utilized for targeted breeding objectives. Cluster 2 had the maximum contribution from four traits: root dry weight, root to shoot ratio, plant height, and days to 50 percent flowering. Cluster 3 exhibited the highest contribution from three traits: days to maturity, panicle length, and number of panicles per plant. Cluster 4 contributed most to six traits, including root volume, number of tillers per plant, effective spikelet per panicle, 1000-grain weight, shoot length, and grain yield per plant, which are primarily associated with yield potential. Clusters like Cluster 4, which show diverse and yield-oriented trait contributions, serve as excellent candidates for hybridization. Crosses between genotypes from different clusters can exploit

**Table 5. Characters contribution to clusters**

| Clu-ster | MRL   | RV    | RDW    | RSR    | NTP   | PH     | ESPP  | DM    | TW    | DTF    | SL    | PL    | NPPP | GYPP  |
|----------|-------|-------|--------|--------|-------|--------|-------|-------|-------|--------|-------|-------|------|-------|
| 1        | 67.59 | 15.43 | 106.50 | 106.55 | 15.52 | 106.55 | 87.65 | 19.18 | 15.43 | 106.55 | 87.65 | 19.18 | 3.67 | 4.10  |
| 2        | 61.46 | 15.94 | 117.42 | 117.42 | 15.71 | 117.42 | 76.13 | 16.91 | 15.94 | 117.42 | 76.13 | 16.91 | 4.15 | 4.26  |
| 3        | 66.93 | 15.93 | 116.56 | 116.56 | 17.04 | 116.56 | 85.58 | 21.04 | 15.93 | 116.56 | 85.58 | 21.04 | 5.56 | 4.70  |
| 4        | 66.00 | 25.62 | 106.67 | 106.67 | 20.80 | 106.67 | 95.25 | 18.06 | 25.62 | 106.67 | 95.25 | 18.06 | 4.50 | 10.60 |

MRL = Maximum root length, RV = Root volume, RDW = Root dry weight, RSR = Root-to-shoot ratio, NTP = Number of tillers per plant, PH = Plant height, ESPP = Effective spikelet per panicle, DM = Days to maturity, TW = 1000-grain weight, DTF = Days to 50% flowering, SL = Shoot length, PL = Panicle length, NPPP = Number of panicles per plant, GYPP = Grain yield per plant.

**Fig. 5. PCA scatter plot highlighting trait variability among upland rice genotypes****Fig.6. Percentage contributions of various traits via D<sup>2</sup> statistics.**

DM = Days to maturity, DTF = Days to 50% flowering, ESPP = Effective spikelets per panicle, GYPP = Grain yield per plant, MRL = Mean root length, NPPP = Number of panicles per plant, NTP = Number of tillers per plant, PH = Plant height, PL = Panicle length, RDW = Root dry weight, RFW = Root fresh weight, RSR = Root-to-shoot ratio, RV = Root volume, SL = Shoot length, TW = 1000-grain weight.

heterosis and create new combinations of desirable traits. Among all the traits studied, effective spikelet per panicle and shoot length contributed the most to genetic diversity, followed by root fresh weight, root to shoot ratio, plant height, and days to 50 percent flowering. In contrast, traits such as mean root length, 1000-grain weight, and days to maturity showed moderate contributions to diversity. However, grain yield per plant, number of panicles per plant, and number of tillers per plant contributed the least to overall diversity.

The number of effective spikelet per panicle directly influences grain yield, as more spikelet suggest a higher potential grain count, which enhances overall productivity. Shoot length is another important trait, as it is strongly associated with seedling vigour. Vigorous seedlings tend to establish quickly and compete effectively with weeds—an especially critical factor for direct-seeded upland rice. Given that upland rice often faces water stress, root traits such as root fresh weight and root to shoot ratio play a vital role in promoting early establishment under moisture-limited conditions.

The significant contribution of root dry weight, root fresh weight, and root volume to genetic diversity aligns with the ideotype theory proposed by Lynch in 2013, which emphasizes the importance of deeper and more efficient root systems as breeding targets for drought-resilient rice cultivars.

The findings from this study suggest that rice breeders should give priority to traits with strong contributions to diversity—particularly effective spikelet per panicle and shoot length—for yield improvement. Strategic trait combinations, such as high effective spikelet per panicle for yield potential, combined with drought-adaptive root traits like root fresh weight and root to shoot ratio, as well as grain yield per plant and number of panicles per plant, could help stabilize yields across variable environments. Although grain yield per plant and number of panicles per plant showed limited variation, this could be due to their close linkage with plant resource allocation mechanisms, as plants naturally balance energy between reproductive output and metabolic maintenance. These traits may show convergence under strong selection pressure in breeding programs that emphasize yield, reducing their variability in the population.

This study is the first to evaluate the genetic diversity of 28 upland rice genotypes from Nagaland based on detailed root and shoot morphological characteristics under rainfed conditions. Root traits—specifically root dry weight, root fresh weight, root volume, and root-to-shoot ratio—were identified as major contributors to genetic divergence, while shoot traits such as grain yield per plant, days to 50 percent flowering, and plant height also played significant roles. These results are consistent with previous findings that emphasize the relevance of combining shoot and root traits in upland rice improvement programs

(Chagas *et al.*, 2025). Principal component and cluster analyses grouped the genotypes into four distinct clusters. Cluster 4 stood out with the highest number of genotypes and showed strong contributions from six yield-associated traits. Genotypes such as Chahashye, Chishoghi, Sulijak, Taposen Youli, and Manen (Red) SARS-5 exhibited greater trait variability, making them promising candidates for breeding programs focused on broadening the genetic base.

Effective spikelets per panicle and shoot length emerged as key selection targets for improving grain yield and adaptability. The significant role of root traits in genetic divergence supports the ideotype framework for drought-resilient upland rice cultivars. Similar conclusions were drawn by Marimuthu *et al.* (2023) in their assessment of genetic variability and selection indices in rice. Overall, this study provides a practical foundation for hybridization strategies that exploit heterosis between divergent clusters, particularly Cluster 2 and Cluster 4.

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