Diversity of Upland Rice (*Oryza sativa* L.) Genotypes in Myanmar

ABSTRACT

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| --- |
| The experiment was carried out to evaluate the genetic diversity of upland rice genotypes. The 83 upland rice genotypes (*Oryza sativa* L.) were grown from June 2023 to November 2023 at the Seed Bank Research field for phenotypic characters and the grain quality test was conducted from December 2023 to May 2024, at Seed bank and Rice Research Center under Department of Agricultural Research (DAR), Yezin, Myanmar. The diversity of 83 upland rice genotypes was assessed through 67 phenotypic characters. A moderate diversity index (0.60) was observed and the genotypes were grouped into six clusters. Clusters I and II each consisted of only one genotype (1.2%) whereas Cluster III had three genotypes (3.6%). Cluster IV contained two genotypes (2.4%), and Cluster V comprised 12 genotypes (14.5%). The maximum number of 64 genotypes (77.1%) was observed in Cluster VI. Kauk Hnyin Saba of cluster I and IR - 71524-26-2-1 of cluster II should be preserved to prevent genetic losses as there were no genetically similar genotype within the cluster.The distinct characteristics observed within these clusters provide valuable opportunities and potential for varietal improvement program in upland rice.  |

*Keywords*: *Upland rice, genetic diversity, cluster analysis, power marker*

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the staple foods for more than half of the world’s human population. Approximately 90% of the world’s rice is grown and consumed in Asia, while 50% of the population depends on rice for food (Tenorio et al., 2013). Myanmar, located in Southeast Asia, is an agricultural country, and its national economy is based on the agricultural sector. Myanmar's major rice ecosystems include rainfed lowland rice, irrigated lowland rice, deep water rice, and upland rice. The rice sown area is 7.09 million hectares with a national average yield of 3.95 metric tons per hectare (MOALI, 2023). Upland rice cultivars have been traditionally cultivated by minority people mainly in mountain areas of Southeast Asia (Oka, 2012). In general, lower rice yields occur throughout the growing season when there is less. It is totally dependent on rainfall distribution and quantities of rainfall are crucial. Abiotic stresses significantly impact growth, yield, and productivity, posing a threat to food security (Veronica, 2024). Upland rice plays a vital role in supporting food security and livelihoods, particularly in rainfed and marginal environments. Upland rice's resilience and adaptability make it a promising crop for diverse agroecosystems, especially in regions facing water scarcity and the impacts of climate change (Emily, 2024). The majority of traditional highland rice types have tall, low tillering, non-shattering panicles, deep roots, slender grain, somewhat early maturity, and generally more resistant to blast disease and drought (Ono, 1971).

Genetic diversity encompasses diversity between species, populations within one species, and individuals within one population. Before the identification of diverse parents in plant breeding programs, breeders and biotechnologists used a multitude of techniques for the characterization of the germplasm to know the genetic diversity (Salgotra, and Chauhan, 2023). Genetic variability is important to take advantage of genetic diversity in crop species to create new rice cultivars that are very stable and able to withstand adverse environments and biotic conditions (Gana, 2013). Plant breeders use genetic diversity to develop new cultivars with improved agronomics, such as higher yield, biotic and abiotic stress tolerance, and to improve the nutritional quality of foods for a growing world population (Swarup et al., 2021). This study was conducted to evaluate the genetic diversity in upland rice genotypes for the maximum utilization of the genetic resources and proper selection of parents.

2. Material and Methods

The 83 upland rice genotypes conserved in the Seed Bank (Table 1) were sown from June 2023 to November 2023 at the Seed Bank Research field for phenotypic characters and the grain quality test was conducted from December 2023 to May 2024, at Seed bank and Rice Research Center under Department of Agricultural Research (DAR), Yezin, Myanmar. Each genotype was sown in 5 rows of 3 m length with a spacing of 25 cm between rows and 25 cm between plants. Cultural practices were done as necessary. The 67 characters of each genotype were collected from five randomly selected plants per plot, using the descriptors for wild and cultivated rice (*Oryza* spp.) established by Biodiversity International, the International Rice Research Institute (IRRI), and WARDA (2007).

**Table 1. List of eighty three upland rice accessions used in this study**

|  |  |  |  |
| --- | --- | --- | --- |
| **No** | **Accession no.** | **Genotypes** | **Sources** |
| 1 | 009875 | WAB-99-14 |  IRRI |
| 2 | 009876 | IR-43 | IRRI |
| 3 | 009877 | WABSOKA | IRRI |
| 4 | 009878 | TOX-1889-4-101-1-1-2 | IRRI |
| 5 | 009879 | IDSA- 69 | IRRI |
| 6 | 009880 | IDSA-11 | IRRI |
| 7 | 009881 | PR- 26406-24-B-B-3 | IRRI |
| 8 | 009882 | WAB-8801-1-38-18-3-P1-HB | IRRI |
| 9 | 009883 |  IR-65258-13-1-B | IRRI |
| 10 | 009917 |  IR-45 | IRRI |
| 11 | 009980 | ROJOMENA | IRRI |
| 12 | 009981 | ITA-329 | IRRI |
| 13 | 010073 | Yn- 2793(Yar 2/ Yadanar) | Myanmar |
| 14 | 010075 | IDSA-64 | IRRI |
| 15 | 010077 | OR-79-21 | IRRI |
| 16 | 010078 | IR-30731-B-4-B-2-4-3 | IRRI |
| 17 | 010079 | PR-272-18-832 | IRRI |
| 18 | 010081 | IR-72768-15-1-1 | IRRI |
| 19 | 010082 | IR-74371-70-1-1 | IRRI |
| 20 | 010083 | IR-75502-24-1-1-B | IRRI |
| 21 | 010084 | IR-74301-54-1-1 | IRRI |
| 22 | 010085 | IR-26417-8-B-B-3 | IRRI |
| 23 | 010094 | FAROX-315-3-2-3-2 | IRRI |

**Table 1. (Continued)**

|  |  |  |  |
| --- | --- | --- | --- |
| **No.** | **Accession no.** | **Genotypes** | **Sources** |
| 24 | 010176 | WAB-128-B-B-2-HB | IRRI |
| 25 | 011036 | WAB-99-2-1 | IRRI |
| 26 | 010178 | WAB- 470- B- A4 | IRRI |
| 27 | 010179 | PR-23722-20 (NSICRC-11) | IRRI |
| 28 | 010180 | WAB -32- 59 | IRRI |
| 29 | 010210 | IR-71524-26-2-1 | IRRI |
| 30 | 010211 | IR-71525-13-2-1 | IRRI |
| 31 | 010212 | IR-70758-17-2-1 | IRRI |
| 32 | 010214 | B-5592-5-ST- 31- 11 | IRRI |
| 33 | 010215 | RR-180-1 | IRRI |
| 34 | 010216 | IR-75518-18-1-2-B | IRRI |
| 35 | 010552 | WAB-340-B-B-2-H2 | IRRI |
| 36 | 010553 | WAB-470- B-A5 | IRRI |
| 37 | 010555 | Kauk Hnyin Nga Cheik | Rakhine |
| 38 | 010999 | Aha Thu Thu Kaung | Kengtaung/ Shan |
| 39 | 011034 | IRAT-156 | IRRI |
| 40 | 011035 | WAB - 272-B-B-H1 | IRRI |
| 41 | 000542 | Taung Ya Saba | Homalin/ Sagaing |
| 42 | 002234 | Nan Hue Khun Ni | Rice Section DAR |
| 43 | 002907 | Kauk Kyauk Pauk | Rice Section DAR |
| 44 | 003186 | Naung Tu Ni | Rice Section DAR |
| 45 | 003280 | Kauk Pwa Phyu | Magwe |
| 46 | 003730 | Ral Leng | Falam/ Chin |
| 47 | 003731 | Ngehi Lut | Falam/ Chin |
| 48 | 003732 | Ngau Tah Cawn | Falam/ Chin |
| 49 | 003733 | Sen Berh | Falam/ Chin |
| 50 | 006079 | Khao Kyaine | Nawng Khio/ Shan |
| 51 | 006080 | Kauk Hnyin Saba | Nawng Khio/ Shan |
| 52 | 006081 | Nga Cheik | Nawng Khio/ Shan |
| 53 | 006419 | Khao Tan | Hsipaw/ Shan |
| 54 | 007257 | Baw Ei Le | Loikaw/ Kayah |
| 55 | 007429 | Bu Bell Du | Loikaw/ Kayah |
| 56 | 008386 | Khaw Lone | Putao/ Kachin |
| 57 | 008547 | Kone Myint -2 | Kyaukme/Shan |
| 58 | 008549 | Kauk Hnyin Nga Cheik | Kyaukme/Shan |
| 59 | 008553 | Khao Hpai | Nawng Khio/ Shan |
| 60 | 008554 | Khao Hauk-1 | Nawng Khio/ Shan |
| 61 | 008557 | Khao Kan Par | Nawng Khio/ Shan |
| 62 | 008559 | Khao Chal | Kunlon / Shan |
| 63 | 008563 | Khao Awut -1 | Kukai /Shan |
| 64 | 008566 | Khao Long | Nawng Khio/ Shan |
| 65 | 008568 | Khao Hauk-2 | Kyaukme/Shan |
| 66 | 008551 | Yout Bokt | Chin |
| 67 | 011661 | Su Sein | Matupi / Chin |
| 68 | 011673 | Yunlu -3 | China |
| 69 | 011674 | Yunlun- 31 | China |
| 70 | 011675 | Yunlun -33 | China |
| 71 | 011676 | IR-71525-B- 2-1 | Hton Bo Farm / Shan |
| 72 | 011677 | Mote Soe Ma Kyway Kyae-1 | Shan South |
| 73 | 011678 | Kyae Myee | Shan South |

**Table 1. (Continued)**

|  |  |  |  |
| --- | --- | --- | --- |
| **No.** | **Accession no.** | **Genotypes** | **Sources** |
| 74 | 011917 | Bu Sue / Vi Sue-2 | Naungtaya/ Shan |
| 75 | 011918 | Pu Nan Pun-4 | Pinglaung / Shan |
| 76 | 011919 | Khao Kham Hwan -4 | Pinglaung / Shan |
| 77 | 011920 | Bu Sue-10 | Naungtaya/ Shan |
| 78 | 011921 | Moke Soe Ma Kyway Kyae-2 | Shan South |
| 79 | 011922 | Khao Pu Maw-2 | Aungban/Shan |
| 80 | 011923 | Bu Sue-3 | Pindaya / Shan |
| 81 | 011924 | Vi Ta Thi-1 | Naungtaya/ Shan |
| 82 | 011925 | Bu Sue/ Vi Sue-8 | Panglpong / Shan |
| 83 | 011926 | Khao Kham Hwan-3 | Naungtaya/ Shan |

**2.2 Statistical Analysis**

The morphological data were analyzed using Power Marker (version 3.25). The distance matrix was generated using the Euclidean Distance Coefficient, and it was used as input for clustering using the unweighted pair group of arithmetic means (UPGMA) method. The dendrogram was shaped using MEGA-11 imbedded in the Power Marker program. The Shannon-Weaver diversity index (H′) (Shannon and Weaver, 1948) of germplasm accessions was calculated based on phenotypic frequency using the standardized Shannon-Weaver diversity index formula:

The Shannon - Weaver diversity index (H′) as presented was estimated using

$$-\sum\_{i=1}^{n}Pi\*Log\_{2}\left(Pi\right)=a\_{0}+\sum\_{n=1}^{\infty }\left(a\_{n}\cos(\frac{nπx}{L})+b\_{n}\sin(\frac{nπx}{L})\right)(Pi)$$

H' =

Pi = the proportion of the total number of entire belonging to the i classes

 characters state,

 N = the number of phenotypic classes for a character

3. results and discussion

**3.1 Diversity of 83 upland ice genotypes**

The diversity of 83 upland rice genotypes was analyzed based on 67 characters and the Shannon-Weaver diversity index (H') was used to evaluate the diversity of the upland rice genotypes, categorized as maximum (H' = 1.00), high (H' = 0.76 - 0.99), moderate (H' = 0.46 - 0.75) and low (H' = 0.01 - 0.45). Among the characters, leaf blade attitude and ligule shape were observed as invariant characters (Table 2). Specifically, all genotypes exhibited an erect leaf blade attitude and a two-cleft ligule shape. Upright leaves improve light perception, photosynthetic efficiency, ventilation, and stress resistance in dense canopy, enabling dense planting and increasing grain yield for cereal crop **(**Cao, Zhong, Wang & Shen, 2022).

Low diversity was observed in 23 characters, namely coleoptile anthocyanin coloration, basal leaf sheath color, leaf sheath anthocyanin coloration, leaf blade anthocyanin coloration, leaf blade pubescence, auricle color, ligule color, stigma color, apiculus lemma color (late stage), lemma and palea color (early and late stages), lemma and palea pubescence, culm habit, node color, internode color, awn distribution, awn length, awn color, panicle attitude of the main axis, panicle attitude of branches, lemma anthocyanin coloration of the keel, sterile lemma color, and pericarp color. These characters were dominated by a single phenotypic state in each case, with frequency distributions ranging from 66.3 % to 98.8 % across the genotypes. As a result, the phenotypic characters showed low diversity indices, ranging from 0.09 to 0.45 and the average diversity index was 0.25.

Moderate diversity was observed in thirteen phenotypic characters, including collar color, flag leaf attitude (early and late), lemma color of the apiculus (early), culm lodging, culm strength, panicle exsertion, panicle length (cm), lemma shape of the apiculus, spikelet fertility, caryopsis shape, gel consistency and grain elongation ratio with diversity indices ranging from 0.47 to 0.72. Among the upland rice genotypes, the caryopsis was predominantly spindle-shape in 44.6 % of the genotypes, long spindle-shape in 37.3 % and the semi-round type in 18.1 %. The apiculus shape of the lemma was predominantly pointed, occurring in 81.9 % of the genotypes. Most of the upland rice genotypes exhibited a low gel consistency, which was the predominant state in 72.3 % of upland rice genotypes and also showed a moderate diversity index (0.71). The grain elongation ratio also showed moderate diversity of 0.64 and 97.6 % of the genotypes displaying a ratio greater than one. This character is a key indicator of desirable rice quality. Kernel elongation is a physical process influenced by various factors such as genotypes, aging temperature, water uptake, amylose content and gelatinization temperature (Golam & Prodhan, 2013). The average moderate diversity index was 0.59.

The high diversity was noticed in 29 characters of upland rice genotypes, viz., seedling height, leaf blade length, leaf blade width, flag leaf length, flag leaf width, ligule length, culm length, culm diameter of basal internode, culm number, days to 50 % flowering , plant height, spikelet number per panicle, number of panicles per hills, panicle secondary branching, panicle threshability, grain length, grain width, grain length width ratio, longer sterile lemma length, shorter sterile lemma length, caryopsis length, caryopsis width, 100 seed weight, filled grain, harvest index, yield per plant, amylose content(%), gelatinization temperature and aroma in high diversity with an average index of 0.85. The panicle threshability was observed with high diversity index (0.88) and 57.8 % of the upland rice genotypes were difficult in panicle threshability. Upland rice genotypes often exhibit difficult panicle threshability due to a combination of genetic traits and environmental adaptation. Overall, the average diversity index for all phenotypic characters was 0.60, indicating moderate diversity among the 83 upland rice genotypes.

**Table 2.The predominant state, distribution (%) and Shannon-Weaver diversity indices (H′) for each character in the entire genotypes**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characters** | **Predominant State** | **Distribution %** | **State Observed** | **H' Index** |
| **Invariant** |  |  |  |   |
| Leaf blade attitude | Erect | 100 | 1 | 0 |
| Ligule shape | 2- cleft | 100 | 3 | 0 |
| **Low diversity** | **H'=0.01-0.45** |
| Coleoptile anthocyanin coloration | Absent | 95.2 | 0 | 0.11 |
| Basal leaf sheath colour | Green | 86.7 | 1 | 0.36 |
| Leaf sheath anthocyanin color | Absent | 86.7 | 0 | 0.24 |
| Leaf blade: anthocyanin coloration | Absent | 96.4 | 0 | 0.14 |
| Leaf blade pubescence | Intermediate | 98.8 | 2 | 0.09 |
| Auricle color | Whitish | 97.6 | 1 | 0.09 |
| Ligule color | Whitish | 94 | 1 | 0.18 |
| Stigma color | White | 94 | 1 | 0.14 |
| Lemma color of apiculus (late) | Straw | 71.7 | 2 | 0.42 |
| Lemma and palea color (early) | Yellowish green | 66.3 | 9 | 0.45 |

**Table 2. (Continued)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characters** | **Predominant State** | **Distribution %** | **State Observed** | **H' Index** |
| **Moderate diversity** | **H'=0.46-0.75** |
| Flag leaf attitude (late) | Horizontal | 47 | 5 | 0.58 |
| Lemma color of apiculus (early) | Green | 59.1 | 4 | 0.58 |
| Culm lodging | Intermediate | 63.9 | 5 | 0.52 |
| Culm strength | Intermediate | 60.2 | 5 | 0.51 |
| Panicle exsertion | Moderately well exserted | 54.2 | 7 | 0.48 |
| Panicle length (cm) | 25-30 | 48.2 | 3 | 0.72 |
| Lemma shape of apiculus | Pointed | 81.9 | 1 | 0.68 |
| Spikelet fertility | Fertile | 59 | 4 | 0.63 |
| Caryopsis shape | Spindle-shaped | 44.6 | 4 | 0.64 |
| Gel consistency(mm) | Low (26-40) | 72.3 | 5 | 0.71 |
| Grain elongation ratio(mm) | 1-1.2 | 97.6 | 1 | 0.64 |
| **High diversity** | **H'=0.76-0.99** |
| Seedling height (cm) | High (21-30) | 61.4 | 3 | 0.9 |
| Leaf blade length (cm) | Intermediate | 62.7 | 2 | 0.87 |
| Leaf blade width (cm) | Intermediate | 92.8 | 2 | 0.84 |
| Flag leaf length (cm) | Intermediate | 78.3 | 2 | 0.88 |
| Flag leaf width (cm) | Intermediate | 92.8 | 2 | 0.85 |
| Ligule length (cm) | Intermediate | 49.4 | 2 | 0.85 |
| Culm length (cm) | Short to intermediate | 31.3 | 3 | 0.87 |
| Culm, diameter at basal internode (cm)  | 2.0-3.0 | 79.5 | 2 | 0.83 |
| Culm number | Intermediate | 68.7 | 2 | 0.86 |
| Days of 50 % flowering | 101-120 | 60.2 | 3 | 0.87 |
| Plant height (cm) | 101-140 | 53 | 2 | 0.88 |
| Spikelet number per panicle | 150-200 | 43.4 | 3 | 0.87 |
| Number of panicle per hills | 10-20 | 67.5 | 2 | 0.85 |
| Panicle secondary branching | Absent | 56.6 | 0 | 0.98 |
| Panicle threshability | Difficult | 43.4 | 1 | 0.88 |
| Grain length (mm) | 81-100 | 75.9 | 2 | 0.88 |
| Grain width (mm) | 26-30 | 49.4 | 2 | 0.89 |
| Grain length-width ratio  | 2.5-3.5 | 51.8 | 2 | 0.87 |
| Longer sterile lemma length (mm) | 2.0-3.0 | 54.2 | 2 | 0.81 |
| Shorter sterile lemma length (mm) | < 2.0 | 67.5 | 1 | 0.81 |
| Caryopsis length (mm) | 2.0-2.5 | 44.6 | 2 | 0.78 |

**Table 2 (Continued)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characters** | **Predominant State** | **Distribution %** | **State Observed** | **H' Index** |
| **High diversity** | **H'=0.76-0.99** |
| Caryopsis width (mm) | 2.0-2.5 | 57.8 | 2 | 0.86 |
| 100 seed weight (g ) | 2.0-2.5 | 66.3 | 1 | 0.80 |
| Filled grain (%) | 70-90 | 69.9 | 3 | 0.81 |
| Harvest Index | 0.4-0.5 | 36.1 | 3 | 0.85 |
| Yield plant**-**1 (g) | 30-50 | 48.2 | 2 | 0.85 |
| Amylose content (%) | Intermediate | 42.2 | 3 | 0.82 |
| (21-25) |
| Gelatinization temperature ( ̊C) | Intermediate | 41 | 2 | 0.84 |
| (70-74ºC) |
| Aroma | Non- aromatic | 48.2 | 0 | 0.82 |
| **Average diversity** |   |  |  | **0.60** |

**3.2 Cluster analysis of the 83 upland rice genotypes**

A dendrogram of the 83 upland rice genotypes was developed based on 67 characters (Figure 1) and the genotypes were grouped into six clusters (Table 3).

Clusters I and II each consisted of only one accession (1.2%).In cluster I, there was only one genotype (Kauk Hnyin Saba), which had distinct characters, including anthocyanin coloration of coleoptile, auricle color, collar color, ligule color, a purple furrow on the green-colored lemma and palea (early), anthocyanin coloration on the node and internode and variable purple coloration of the pericarp. This genotype showed the highest mean values for several important agronomic characters, such as leaf blade length, ligule length, days to 50 % flowering, culm length, culm diameter at the basal internode, plant height and caryopsis length, compared to accessions of other clusters (Table 3). Chhaya and Sharma, (2023) reported the plant height was wide adaptation over different environment.

The only one genotype (IR-71524-26-2-1) of cluster II (Figure 1), showed the highest mean value for seedling height, flag leaf attitude (early and late), flag leaf length, panicle length, spikelet number per panicle, caryopsis shape, awn length, filled grain and harvest index and rice grain quality character was found to be low gelatinization temperature and moderate aroma of rice. Aroma plays an important role in consumers’ preference and market value. Verma and Srivastav, (2018) reported that the aroma is affected by many factors, such as genetic background, environmental conditions and storage in rice. It should be maintained for prevention of genetic losses as no similar genotypes were found in Clusters I and II. The two genotypes (2.4 %) Bu Bell Du and Sen Berh constituted of cluster III having the highest mean value for leaf blade width, flag leaf width, yield per plant, intermediate amylose content, and high gelatinization temperature. Cluster IV consisted of three genotypes (3.6 %) such as Baw Ei Le, WAB-470-B-A5, and Yunlu-3 (Figure 1), which had the maximum mean value of number of panicles per hill. Cluster V consisted of 12 genotypes (14.5 %), namely Mote Soe Ma Kyway Kyae-1, Bu Sue / Vi Sue-2, Bu Sue-10, Khao Awut-1, Mote Soe Ma Kyway Kyae-2, Bu Sue-3, Khao Pu Maw-2, Vi Ta Thi-1, Bu Sue / Vi Sue-8, Khao Kham Hwan-3, Khao Chal, and Khao Long (Figure 1). This cluster showed the maximum value for grain width, caryopsis width, pericarp color and the lowest mean value was awn length

 Cluster VI consisted of the 64 genotypes, such as IR-75502-24-1-1-B, Nan Hue Khun Ni, IR-65258-13-1-B, WAB-470-B-A5, IR-30731-B-4-B-2-4-3 and ROJOMENA, etc (Figure 1). It exhibited the highest mean value for grain length, grain-length-to-width ratio, longer sterile lemma length, shorter sterile lemma length, caryopsis shape and 100-seed weight whereas it exhibited the lowest value of three characters such as leaf blade length, culm length and plant height (Table 4). Among characters, no variation was observed in leaf blade attitude and all were found to be erect. Similarly, no variation was observed in ligule shape as all were 2-cleft. These results showed that the large variability will help rice breeders in selecting the appropriate genotypes for future breeding programs.

**Cluster I (one accession)**



 0.10

**Cluster II (one accession)**

**Cluster III (Three accessions)**

**Cluster IV (Two accessions)**

**Cluster V (Twelve accessions)**

**Cluster VI (Sixty-four accessions)**

**Figure 1. A dendrogram generated through 67 characters using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA)**

**I**

**Table 3. Cluster memberships of 83 upland rice genotypes based on qualitative and quantitative characters**

|  |  |  |  |
| --- | --- | --- | --- |
| **Clusters** | **No of accessions** | **Proportion (%)** | **Genotypes** |
| I | 1 | 1.2 | Kauk Hnyin Saba |
| II | 1 | 1.2 | IR- 71524-26-2-1 |
| III | 3 | 3.6 | Baw Ei Le, WAB-470-B-A5, Yunlu-3 |
| IV | 2 | 2.4 | Bu Bell Du, Sen Berh |
| V | 12 | 14.5 | Mote Soe Ma Kyway Kyae-1, Bu Sue / Vi Sue -2, Bu Sue - 10, Khao Awut -1, Mote Soe Ma Kyway Kyae -2, Bu Sue -3, Khao Pu Maw -2, Vi Ta Thi -1, Bu Sue / Vi Sue -8, Khao Kham Hwan -3, Khao Chal, Khao Long |
| VI | 64 | 77.1 | IR-75502-24-1-1-B, Nan Hue Khun Ni, IR- 65258-13-1-B, WAB-470-B-A5, IR-30731-B-4-B-2-4-3, ROJOMENA, IRAT-156, FAROX-315-3-2-3-2, Khao Kyaine, IDSA-69, IR-71525-13-2-1, Ngau Tah Cawn, WAB-470-B-A4, Taung Ya Saba, IDSA-64, IR-72768-15-1-1, Khao Tan, Kauk Hnyin Nga Cheik-2, Yunlun-33, Yunlun - 31, WABSOKA, WAB-272-B-B-H1,WAB-99-2-1, Yout Bokt, IR-45, Kauk Kyauk Pauk, Naung Tu Ni, Aha Thu Thu Kaung, Kyae Myee, ITA-329, Yn-2793 (Yar 2 / Yadanar), PR-23722-20 (NSICRC-11), WAB-32-59, Kauk Pwa Phyu, Khaw Lone, Kone Myint -2, Su Sein, WAB-340-B-B-2-H2, RR-180-1, IDSA -11, Ral Leng, IR-43, OR-79-21, Khao Kham Hwan - 4, Pu Nan Pun -4, IR - 74371- 70-1-1, IR-26417-8-B-B-3, IR -74301-54-1-1, WAB-8801-1-38-18-3-P1-HB, B-5592-5-ST-31-11, IR-70758-17-2-1, PR-26406-24-B-B-3,IR-71525-B-2-1, WAB- 128-B-B-2-HB, Kauk Hnyin Nga Cheik-1, WAB-99-14, IR- 75518-18-1-2-B, Ngehi Lut, PR -272-18-832, Khao Hauk -1, Khao Hpai, Khao Hauk -2, Khao Kan Par, Nga Cheik |

**Table 4. Cluster mean of each character in the upland rice genotypes**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Cluster I** | **Cluster II** | **Cluster III** | **Cluster IV** | **Cluster V** | **Cluster VI** |
| Coleoptile: anthocyanin coloration | 3.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.1 |
| Seedling height (cm) | 27.7 | 28.7 | 19.9 | 18.1 | 19.9 | 21.6 |
| Basal leaf sheath color  | 2.0 | 1.0 | 2.7 | 1.0 | 1.2 | 1.1 |
| Leaf sheath color  | 3.0 | 0.0 | 3.7 | 0.0 | 0.0 | 0.3 |

**Table 4. (Continued)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Cluster I** | **Cluster II** | **Cluster III** | **Cluster IV** | **Cluster V** | **Cluster VI** |
| Leaf blade color  | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Leaf blade attitude  | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Leaf blade pubescence | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 |
| Auricle color  | 3.0 | 1.0 | 2.0 | 1.0 | 1.0 | 1.0 |
| Collar color | 3.0 | 1.0 | 3.3 | 1.5 | 1.8 | 1.9 |
| Ligule color | 3.0 | 1.0 | 2.0 | 1.0 | 1.0 | 1.1 |
| Ligule shape | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 |
| Leaf blade length (cm)  | 60.8 | 60.5 | 48.8 | 50.8 | 49.8 | 45.9 |
| Leaf blade width (cm) | 1.2 | 0.9 | 1.4 | 1.5 | 1.3 | 1.3 |
| Flag leaf attitude (early) | 3.0 | 1.0 | 3.0 | 3.0 | 4.0 | 3.3 |
| Flag leaf attitude (late) | 5.0 | 1.0 | 4.3 | 5.0 | 5.8 | 4.2 |
| Flag leaf length (cm) | 34.1 | 47.0 | 36.5 | 38.3 | 36.1 | 35.1 |
| Flag leaf width (cm)  | 1.4 | 1.3 | 1.6 | 1.7 | 1.6 | 1.5 |
| Ligule length (cm) | 2.7 | 2.2 | 2.1 | 1.9 | 2.2 | 2.1 |
| Culm length (cm) | 140.3 | 132.8 | 100.6 | 99.9 | 102.7 | 99.3 |
| Culm, diameter at basal internode (cm) | 2.7 | 2.3 | 2.2 | 1.9 | 2.3 | 2.3 |
| Stigma color | 5.0 | 1.0 | 3.7 | 3.0 | 1.3 | 1.0 |
| Culm number | 7.4 | 15.6 | 18.8 | 18.6 | 21.8 | 15.9 |
| Plant height (cm) | 173.3 | 160.9 | 125.4 | 125.7 | 130.2 | 120.3 |
| Days to 50 % flowering | 112.0 | 90.0 | 98.9 | 109.0 | 91.6 | 96.0 |
| Panicle length (cm) | 27.7 | 28.0 | 25.8 | 25.9 | 25.9 | 25.4 |
| Number of panicle per hills | 7.4 | 15.6 | 17.9 | 17.7 | 20.5 | 15.7 |
| Lemma color of apiculus (early) | 7.0 | 2.0 | 8.0 | 7.0 | 6.1 | 4.2 |
| Lemma color of apiculus (late) | 8.0 | 2.0 | 7.0 | 7.5 | 6.4 | 2.5 |
| lemma and palea color (early) | 14.0 | 9.0 | 7.7 | 1.1 | 8.6 | 8.3 |
| Lemma and palea color (late) | 7.0 | 3.0 | 5.3 | 7.0 | 3.7 | 2.4 |
| Lemma and palea pubescence | 4.0 | 4.0 | 4.0 | 4.0 | 3.8 | 3.6 |
| Culm habit | 3.0 | 3.0 | 3.0 | 3.0 | 3.7 | 3.4 |
| Culm lodging resistance | 5.0 | 1.0 | 5.0 | 5.0 | 4.3 | 5.0 |

 **Table 4. (Continued)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Cluster I** | **Cluster II** | **Cluster III** | **Cluster IV** | **Cluster V** | **Cluster VI** |
| Culm strength  | 5.0 | 1.0 | 5.0 | 4.0 | 3.5 | 4.3 |
| Awn distribution  | 1.0 | 1.0 | 0.0 | 1.5 | 0.0 | 0.3 |
| Awn color | 6.0 | 1.0 | 0.0 | 3.0 | 0.0 | 0.2 |
| Panicle attitude of main axis  | 4.0 | 3.0 | 3.3 | 3.0 | 3.0 | 3.0 |
| Panicle attitude of branches  | 5.0 | 5.0 | 4.3 | 3.0 | 3.0 | 3.2 |
| Panicle secondary branches  | 1.0 | 2.0 | 1.7 | 1.5 | 2.0 | 1.3 |
| Panicle exsertion  | 9.0 | 9.0 | 7.0 | 5.0 | 8.7 | 6.8 |
| Node color  | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Internode color  | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Lemma anthocyanin coloration of keel  | 0.0 | 0.0 | 0.0 | 5.0 | 0.8 | 0.2 |
| Lemma shape of apiculus  | 1.0 | 1.0 | 1.0 | 1.0 | 1.8 | 1.1 |
| Panicle threshability  | 2.0 | 1.0 | 1.3 | 3.0 | 1.8 | 1.9 |
| Spikelet fertility  | 5.0 | 5.0 | 3.7 | 4.0 | 3.2 | 4.2 |
| Sterile lemma color  | 4.0 | 1.0 | 1.0 | 3.0 | 2.0 | 1.0 |
| Grain length (mm)  | 8.2 | 8.5 | 8.4 | 8.2 | 7.7 | 9.2 |
| Grain width (mm) | 2.9 | 2.9 | 3.1 | 3.2 | 3.2 | 2.7 |
| Grain length-width ratio (mm) | 2.9 | 2.9 | 2.8 | 2.6 | 2.4 | 3.4 |
| Spikelet number per panicle | 138.8 | 163.4 | 156.3 | 158.4 | 154.5 | 156.1 |
| Longer sterile lemma length (mm) | 1.5 | 2.0 | 2.1 | 1.9 | 1.9 | 2.3 |
| Shorter sterile lemma length (mm) | 1.2 | 2.0 | 1.9 | 1.8 | 1.7 | 2.2 |
| Caryopsis length (mm) | 7.1 | 5.7 | 6.1 | 5.9 | 5.7 | 6.7 |
| Caryopsis width (mm) | 2.3 | 2.4 | 2.7 | 2.8 | 2.9 | 2.4 |
| Caryopsis shape | 4.0 | 2.0 | 4.0 | 3.0 | 2.8 | 4.3 |
| Pericarp color  | 6.0 | 1.0 | 1.0 | 1.0 | 5.0 | 1.7 |
| Awn length (mm) | 0.5 | 0.9 | 0.1 | 0.2 | 0.0 | 0.1 |
| 100 seed weight (g)  | 2.3 | 2.1 | 2.4 | 2.4 | 2.3 | 2.5 |
| Filled grain (%) | 72.5 | 94.6 | 77.9 | 84.0 | 64.4 | 85.2 |
| Harvest Index | 0.3 | 0.5 | 0.3 | 0.4 | 0.2 | 0.4 |
| Yield plant-1(g) | 22.3 | 51.1 | 52.4 | 60.5 | 46.3 | 50.5 |
| Amylose content (%) | 9.0 | 7.8 | 20.1 | 20.5 | 20.1 | 19.8 |
| Gel consistency (mm) | 71.7 | 67.3 | 39.7 | 32.5 | 45.5 | 39.5 |
| Gelatinization temperature( ºC) | 6.0 | 7.0 | 4.7 | 3.0 | 4.9 | 4.3 |
| Grain elongation ratio  | 1.1 | 1.2 | 1.1 | 1.1 | 1.1 | 1.1 |
| Aroma | 1.0 | 2.0 | 1.0 | 1.0 | 0.4 | 0.6 |

4. Conclusion

In this study, 83 upland rice genotypes were characterized to assess their diversity among them. Diversity indices ranged from 0.00 to 0.98 in the observed phenotypes. High diversity index value (0.98) was exhibited by panicle secondary branching followed by seedling height and grain width, indicating that these characters are highly variable among the genotypes. The low diversity index value (0.09) was exhibited by auricle color, leaf blade pubescence, anthocyanin coloration of node and internode color. The leaf blade attitude and ligule shape were observed as invariant characters. The average diversity index for all phenotypic characters was 0.60, indicating moderate diversity among the 83 upland rice genotypes. The genotypes were grouped into six clusters. Cluster I and II each consisted of only one genotype (1.2%) and these accessions should be preserved to prevent genetic losses because there was no similar genotypes within cluster**.** Cluster III had three genotypes (3.6%) whereas cluster IV contained two genotypes (2.4%). Cluster V comprised 12 genotypes (14.5%). The maximum number of 64 genotypes (77.1%) was observed in Cluster VI. Kauk Hnyin Saba of cluster I and IR - 71524-26-2-1 of cluster II should be preserved to prevent genetic losses as there were no genetically similar genotype within the cluster. The distinct characteristics identified in each cluster may provide valuable information for selecting genotypes with specific desirable traits for use in upland rice breeding programs.

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1.

2.

3.

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Competing interests

Authors have declared that no competing interests exist.

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