

## MORPHOLOGICAL DIVERSITY OF SIXTEEN SRI LANKAN TRADITIONAL RICE ACCESSIONS EVALUATED UNDER GREENHOUSE CONDITIONS

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### ABSTRACT

Discovering new genetic resources for desirable morphological characteristics from traditional rice gene pool is essential as there is a limited variation in the existing improved rice cultivars. The present study was carried out to evaluate the morphological diversity of sixteen randomly selected traditional rice accessions. Their morphological characteristics were evaluated at greenhouse conditions at Faculty of Agriculture, University of Ruhuna in *Yala* season, 2016. The greenhouse experiment was carried out according to the randomized complete block design with four replicates. Observations were collected on 8 morphological traits and data were analyzed by factor analysis and cluster analysis using SPSS. Rice accessions were classified according to, Standard Evaluation System of International rice research institute (IRRI) and it was found that sixteen rice accessions were categorized into three different groups according to the plant height (tall, intermediate and semi-dwarf) and two different groups according to the tillering ability (very low tillering, low tillering). According to principle component analysis followed by the Ward linkage analysis and hierarchical dendrogram, evaluated rice accessions were classified into four distinct clusters at rescaled cluster distance 7.5. The tested rice accessions have been dispersed in all the four quadrants of in two-dimensional scatter plot diagram. This reveals the great diversity exists within the Sri Lankan traditional rice accessions even in a random sample. The findings of the present study can be utilized for the further research purposes or breeding programs in rice improvement.

Keywords: Greenhouse experiment, Morphological characteristics, Sri Lanka, Traditional rice

### INTRODUCTION

Rice is an important cereal crop that provides food for more than half of the world population (Sasaki and Burr, 2000). Morphological evaluation is a preliminary step to estimate the variability and association among cultivars though several other tools are also used broadly (Smith *et al.*, 1991). That's why the establishment of a successful crop improvement programme is very much vital to find out the morphological variability of existing cultivars within the country.

In the low-lying rain-fed areas of tropical Asia, paddy fields are unavoidably subjected to un-

predictable water depths. Grain yield decreases with increasing water level. Under such circumstances, intermediate height (110-130 cm) is considered as desirable over dwarf height (90-110 cm). But taller plants are more susceptible to lodging and less responsive to Nitrogen. Intermediate and tall varieties tend to lodge at a close spacing while short and lodging resistant varieties give the highest yield at close spacing (Yoshida, 1981). However, the morphological character that has given high yield is a short, stiff culm that gives lodging resistance (Shigemura, 1966; Chandler, 1968). Changes in morphological characters of rice varieties that are available commercially, indicate that varieties have been chosen for shorter plant height, higher tillering

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ability, and more erect leaves.

Rice is the staple food of Sri Lanka and it is cultivated mostly as a wetland crop in almost all districts. The total land allocated for paddy is estimated to be nearly 792,000 hectares (Central bank, 2018). Sri Lankan agricultural sector contributes to the GDP by 6.9 % and major contribution for the GDP comes from the paddy sector. More than 1.8 million farmer families in Sri Lanka depend on paddy cultivation (Central Bank, 2014). They had produced 2383 metricktons of rice in 2017.

Reintroduction and improvement of traditional rice varieties chosen through mass selection have been reported in various countries (Almekinders and Elings, 2001; Gyawali *et al.*, 2007). The rice germplasm is a rich pool of constructive genes that rice breeders can harness for rice improvement programmes. Genetic variability exists among germplasm leaving a broad capacity for crop improvements. Information on the genetic diversity within and among closely related crop varieties is crucial for a rational use of genetic resources. It helps to screen germplasm and can also be used to forecast potential genetic gains (Singh *et al.*, 2015).

Ikeda and Vaughan (1991) have reported that *O. sativa* varieties which have been cultivated in Sri Lanka from ancient time to 1960s' are known as traditional rice varieties. Sri Lanka has been considered as one of the secondary diversity centers for rice genetic resources. Pri-

yangani *et al.* (2008) has reported that Sri Lanka possesses about two thousands of traditional rice cultivars. These cultivars have distinct morphological characters differ from each other as well as different from modern rice cultivars (Priyangani *et al.*, 2008; Amarasinghe *et al.*, 2012; Ranawake *et al.*, 2014a; Ranawake *et al.*, 2014b).

Even though new improved varieties produce comparatively higher yields, consumer preference is higher for traditional rice varieties owed to their medicinal properties. Additionally, traditional rice varieties are famous due to its high fibre content (Wickramasinghe and Noda, 2008). International Rice Research Institute (IRRI), Philippines identified Sri Lanka as one of the main geographical origins of many valuable traits in rice (IRRI, 2009).

## MATERIALS AND METHODS

Some Sri Lankan traditional rice accessions collected from Plant Genetic Resources Centre, Gannoruwa (PGRC), Sri Lanka were used for the study (Table 1). The experiment was carried out in greenhouse conditions during 2016 *Yala* season. Dormancy broken, surface sterilized rice seeds were germinated and maintained in nursery beds. Ten days old seedlings were transplanted in pots (40 cm \* 30 cm) under greenhouse conditions at the Faculty of Agriculture, University of Ruhuna, Mapalana, Sri Lanka. The experiment was carried out according to Randomized complete block design (RCBD) with three replicates (4 pots per replicate) and three plants for each pot (spacing 15

**Table 1: Traditional rice accessions used for the study.**

PGRC* accession number	Accession name	PGRC accession Number	Accession name
3472	<i>Hatada Wee</i>	4171	<i>Rathal</i>
3493	<i>Hondarawala</i>	4402	<i>Haththe pas Dawase Wee</i>
3573	<i>Pokkali</i>	4576	<i>Pokuru Samba</i>
3652	<i>BurumaThawalu</i>	4724	<i>Goda El Wee</i>
3724	<i>GodaHeenati</i>	4945	<i>Mada El</i>
3735	<i>WelHandiran</i>	5488	<i>Kalukanda</i>
4087	<i>KaluHeenati</i>	5522	<i>Mada El</i>
4162	<i>Pokuru Wee</i>	8499	<i>Hondarawala</i>

\*PGRC = Plant Genetic Resource Center, Gannoruwa, Peradeniya, Sri Lanka

cm \* 15cm). The basal dressing was applied before planting and the top dressing was applied (Basal dressing = Urea 50 Kg/ha, TSP 62.5 Kg/ha, MOP 50 Kg/ha; Top Dressing = Urea 37.5 Kg/ha) two times at two weeks after planting and eight weeks after planting. Data were collected on, plant height (cm), number of tillers per plant, days to 50% flowering, number of fertile tillers per plant, 100-grain weight (g), seed length (mm), seed width (mm), days to maturity, yield per plant and panicle length (cm).

Data were collected according to the Standard Evaluation System (SES) for rice (IRRI, 2013) which describes as follows;

1. Days to flowering- From the date of seeding to 80% heading date
2. Plant height (cm)- Actual measurement from soil surface to tip of the tallest panicle, excluding awns
3. Number of total tillers/plant- Tillers at the maturity stage
4. Number of fertile tillers/plant- Number of panicle bearing tillers/plant
5. Panicle length(cm) - from panicle base to tip
6. 100 grain weight(g)- Hundred grains counted from 10 plants of each replicates
7. Seed length (mm) - longitudinal dimension measured from 10 well-developed grains as the distance from the base of the lowermost sterile lemma to the tip (apiculus) of the lemma or pales, whichever is longer. In the case of awned varieties, length is measured to a point comparable to the tip of the apiculum
8. Seed width (mm)- dorsi-ventral diameter measured from 10 grains as the distance across the lemma and the palea at the widest point
9. Days to maturity - The date on which 80 % of the grains on the panicles are fully ripened.

Sri Lankan traditional rice accessions were grouped according to Standard Evaluation System (IRRI, 2013). Rice plants were classified as semi-dwarf (lowland: less than 110

cm; upland: less than 90cm), intermediate (lowland: 110-130 cm; upland (90-125 cm) and tall (lowland: more than 130 cm; upland: more than 125 cm) accessions according to the height. Tillering ability was determined as very high (more than 25 tillers/plant), good (20/25 tillers/plant), medium (10-19 tillers/plant), low (5-9 tillers/plant) and very low (less than 5 tillers/plant). Traditional rice accessions were grouped by considering days to flowering (Sri Lankan classification) as short duration (105-124 days), medium duration (125-140 days) and late duration (141- 160 days).

Data were subjected to statistical analysis using IBM SPSS 20 statistical software (SPSS Inc, 2011). Morphological diversity among selected traditional rice accessions was identified using principle component analysis (PCA). It was used to determine the optimum number of clusters (Thompson *et al.*, 2003). Ward linkage dendrogram was constructed using cluster analysis in order to obtain morphological relationship among traditional rice accessions (Zapico *et al.*, 2010). The standardized mean values of each morphological characteristic were statistically analyzed using SAS. PCA, cluster analysis and Ward linkage dendrogram were used to study the patterns of the morphological diversity in traditional rice cultivar as described by Mooi and Sarstedt (2011).

## RESULTS AND DISCUSSION

### Grouping traditional rice accessions according to standard evaluation system

International rice research institute has developed guidelines to categorize rice cultivars into diverse groups (IRRI, 2013). The developed standard evaluation system (SES) helps to rice researchers all over the world to separate rice cultivars into standard define groups. Several numbers of parameters such as plant height, the number of total tillers per plant, the number of fertile tillers per plant, days to flowering, filled grain percentage is considered to be group rice accessions in SES.

### Grouping of traditional rice accessions according to plant height

According to the SES of IRRI (IRRI, 2013), selected traditional rice accessions were categorized as semi-dwarf, intermediate and tall as given in Table 2. Out of 16 rice accessions, 14 rice accessions were semi-dwarf (<110 cm), 1 rice accession was intermediate (110-130 cm) and 1 rice accession was tall (> 130 cm).

Significantly highest plant height was recorded in *Wel Handiran-3735* and had an mean value of 131.2 cm. The shortest rice accession *Rathal-4171*, recorded 80.4 cm for plant height (Table 2). Plant height is a major attribute which contributes to the grain yield of rice (Yadav *et al.*, 2011). But increased plant height prone to lodging and reduce the grain yield, quality of production and mechanical harvesting efficiency in rice (Weber and Fehr, 1966; Kono, 1995).

### Grouping traditional rice accessions according to tillering ability

Considering the tillering ability, traditional rice accessions were grouped according to the IRRI, SES as given in Table 3. About 62.5% of the tested traditional rice accessions pro-

duced 5-9 tillers per plant. Significantly higher number of tillers were recorded by the traditional rice accessions *Kalu Heenati-4087*, *Pokuru wee-4162* and *Haththe Pas Dawase Weewhich* were around 9 tillers per plant on average (Table 3). About 37.5% evaluated traditional rice accessions recorded less than 5 tillers per plant which showed very low tillering ability. The lowest number of tillers per plant was recorded in *Hondarawala-3493*, *Mada El-5522* and *Rathal* had a value of 3 tillers per plant. None of the traditional rice accession belonged to medium (10-19 tillers/plant), good (20-25 tillers/plant) or very high (more than 25 tillers/plant) tillering categories.

Development of inbred rice cultivars with new plant architecture has been already identified as one of the opportunities in future rice improvement programmes (Rajapakse *et al.*, 2000). For that reason, the identification of morphological characteristics such as plant height, number of tillers and number of fertile tillers are vital to change the plant architecture of rice. Therefore, the results obtained from the present study with other morphological data can be broadly applicable for crop improvement in future.

**Table 2: Grouping traditional rice accessions according to plant height using IRRI, SES (IRRI, 2013)**

Plant type	PGRC accession number	Accession name	Mean plant height (cm)
Semi- dwarf (<110 cm)	3472	<i>Hatada Wee</i>	106.1 <sup>bc</sup>
	3573	<i>Pokkali</i>	99.1 <sup>bcd</sup>
	3652	<i>Buruma Thawalu</i>	99.6 <sup>bcd</sup>
	3724	<i>Goda Heenati</i>	102.1 <sup>bc</sup>
	4087	<i>Kalu Heenati</i>	103.5 <sup>bc</sup>
	4162	<i>Pokuru Wee</i>	92 <sup>ecd</sup>
	4171	<i>Rathal</i>	80.4 <sup>e</sup>
	4402	<i>Haththe Pas Dawase Wee</i>	101.9 <sup>bc</sup>
	4576	<i>Pokuru Samba</i>	83.1 <sup>ed</sup>
	4724	<i>Goda El Wee</i>	81.6 <sup>e</sup>
	4945	<i>Mada El</i>	79.8 <sup>e</sup>
	5488	<i>Kalukanda</i>	102 <sup>bc</sup>
	5522	<i>Mada El</i>	78.5 <sup>e</sup>
	8499	<i>Hondarawala</i>	102.8 <sup>bc</sup>
Intermediate (110-130 cm)	3493	<i>Hondarawala</i>	116.4 <sup>ab</sup>
Tall (>130 cm)	3735	<i>Wel Handiran</i>	131.2 <sup>a</sup>

DMRT groups of each treatment are indicated in superscripts. Means with the same letters are not significantly different (P<0.05).

### Grouping of traditional rice accessions according to days to flowering

According to the Sri Lankan classification for days to flowering (Personal communication, Department of Agriculture), tested traditional rice accessions were grouped as shown in Table 4.

About 19 % of tested rice accessions completed 50 % flowering within <50 days while

37.5% of rice accessions took 75-99 days for the same. About 44 % of rice accessions completed 50 % flowering within a period of 100-124 days. The shortest days to flowering (44 days) was recorded by Mada El-5522. Pokuru Wee-4162 recorded the significantly highest days to flowering with 113 days (Table 4 and 5).

All the other recorded morphological charac-

**Table 3: Grouping of traditional rice accessions according to number of total tillers per plant using IRRI, SES (IRRI, 2013)**

Tillering ability	PGRC accession number	Accession name	Mean number of total tillers/plant
Very low tillering (<5 tillers/plant)	3493	<i>Hondarawala</i>	3 <sup>c</sup>
	4171	<i>Rathal</i>	3 <sup>e</sup>
	4724	<i>Goda El Wee</i>	4 <sup>ed</sup>
	4945	<i>Mada El</i>	4 <sup>ed</sup>
	5488	<i>Kalukanda</i>	4 <sup>ed</sup>
	5522	<i>Mada El</i>	3 <sup>e</sup>
Low tillering (5-9 tillers/plant)	3472	<i>Hatada Wee</i>	5 <sup>cde</sup>
	3573	<i>Pokkali</i>	7 <sup>bcd</sup>
	3652	<i>BurumaThawalu</i>	7 <sup>bcd</sup>
	3724	<i>GodaHeenati</i>	6 <sup>bcd</sup>
	3735	<i>WelHandiran</i>	8 <sup>ab</sup>
	4087	<i>KaluHeenati</i>	9 <sup>a</sup>
	4162	<i>Pokuru Wee</i>	9 <sup>a</sup>
	4402	<i>Haththe Pas Dawase Wee</i>	9 <sup>a</sup>
	4576	<i>Pokuru Samba</i>	6 <sup>bcd</sup>
	8499	<i>Hondarawala</i>	6 <sup>bcd</sup>

DMRT groups of each treatment are indicated in superscripts. Means with the same letters are not significantly different (P<0.05).

**Table 4: Grouping traditional rice accessions according to days to flowering using Sri Lankan classification (Department of Agriculture, Sri Lanka)**

Classification	PGRC accession number	Accession name	Days to flowering
<50days	5522	<i>Mada El</i>	44 <sup>g</sup>
	4945	<i>Mada El</i>	45 <sup>g</sup>
	5488	<i>Kalukanda</i>	49 <sup>g</sup>
75-99 days	4402	<i>Haththe Pas Dawase Wee</i>	72 <sup>f</sup>
	3735	<i>Wel Handiran</i>	80 <sup>de</sup>
	4087	<i>Kalu Heenati</i>	81 <sup>de</sup>
	4724	<i>Goda El Wee</i>	82 <sup>de</sup>
	4576	<i>Pokuru Samba</i>	84 <sup>de</sup>
	3573	<i>Pokkali</i>	91 <sup>c</sup>
	4171	<i>Rathal</i>	93 <sup>c</sup>
100-124 days	3652	<i>Buruma Thawalu</i>	100 <sup>c</sup>
	3472	<i>Hatada Wee</i>	104 <sup>b</sup> 105 <sup>b</sup>
	34938499	<i>Hondarawala</i>	106 <sup>b</sup>
	3724	<i>Hondarawala</i>	77 <sup>ef</sup>
	4162	<i>Goda Heenati</i>	113 <sup>a</sup>
		<i>Pokuru Wee</i>	

DMRT groups of each treatment are indicated in superscripts. Means with the same letters are not significantly different (P<0.05).

teristics are shown in Table 5.

**Construction of Ward linkage dendrogram using Principle Component Analysis (PCA), factor analysis and cluster analysis to demonstrate the diversity of traditional rice accessions**

The PCA was carried out for the analysis of morphological characteristics of 16 traditional rice accessions (Table 5). Eigenvalue, percentage of variance and cumulative Eigenvalues of morphological characteristics of evaluated traditional rice accessions are shown in Table 6.

Among 9 principle components, two principle components (PCs) described more than one Eigenvalue and explained about 73.33 % cumulative variability of the morphological characteristics. These two PCs 1 and 2 described variability of 41.2 % and 32.03 %, respectively. Based on the rotated component matrix, the evaluated morphological characteristics were grouped according to their designated components (Table 7). Among the tested morphological characteristics, days to flowering, plant height, number of total tillers, number of fertile tillers and days to maturity were described by PC 1 while, hundred grain weight, grain width and grain length were described by PC 2.

The output of PCA was described by cluster analysis using Ward's linkage. All the tested traditional rice accessions were clustered into four morphologically distinct clusters at the rescaled cluster distance of 7.5 (Figure 1, Table 8). At the rescaled cluster distance of 25, two distinct clusters were resulted due to the wide diversity among evaluated traditional rice accessions.

The morphologically similar traditional rice accessions were included into the same clusters by considering the agronomic characteristics. Morphological traits can be used successfully to characterization of rice accessions (Tehrim *et al.*, 2012). Results of the present

**Table 5: Morphological characteristics of sixteen traditional rice accessions**

PGRC accession number	Accession name	DF (days)	PH (cm)	NIT	NFT	PL (cm)	HGW (g)	GW (mm)	GL (mm)	M (days)
3472	<i>Hatada Wee</i>	104 <sup>b</sup>	106.1 <sup>bc</sup>	5 <sup>cde</sup>	3 <sup>de</sup>	24.9 <sup>ab</sup>	1.9417 <sup>f</sup>	2.844 <sup>cdef</sup>	6.014 <sup>f</sup>	134 <sup>b</sup>
3493	<i>Hondarawala</i>	105 <sup>b</sup>	116.4 <sup>ab</sup>	3 <sup>e</sup>	3 <sup>d</sup>	22.27 <sup>abc</sup>	3.0157 <sup>b</sup>	3.209 <sup>a</sup>	8.085 <sup>bc</sup>	135 <sup>b</sup>
3573	<i>Pokkali</i>	91 <sup>c</sup>	99.1 <sup>bcd</sup>	7 <sup>bcd</sup>	5 <sup>bc</sup>	24.67 <sup>ab</sup>	2.431 <sup>de</sup>	2.505 <sup>egf</sup>	8.011 <sup>cdef</sup>	121 <sup>c</sup>
3652	<i>BurumaThawalu</i>	100 <sup>c</sup>	99.6 <sup>bcd</sup>	7 <sup>abc</sup>	5 <sup>ab</sup>	25.3 <sup>ab</sup>	2.4217 <sup>de</sup>	2.868 <sup>cdef</sup>	8.313 <sup>abc</sup>	130 <sup>c</sup>
3724	<i>GodaHeenati</i>	77 <sup>ef</sup>	102.1 <sup>bc</sup>	6 <sup>bcd</sup>	5 <sup>bc</sup>	24.53 <sup>ab</sup>	2.3263 <sup>e</sup>	2.829 <sup>cde</sup>	8 <sup>dc</sup>	107 <sup>ef</sup>
3735	<i>WelHandiran</i>	80 <sup>de</sup>	131.2 <sup>a</sup>	8 <sup>ab</sup>	5 <sup>bc</sup>	22.23 <sup>abc</sup>	2.736 <sup>c</sup>	2.734 <sup>cdef</sup>	7.609 <sup>fg</sup>	110 <sup>ed</sup>
4087	<i>KaluHeenati</i>	81 <sup>de</sup>	103.5 <sup>bc</sup>	9 <sup>a</sup>	7 <sup>a</sup>	21.63 <sup>abc</sup>	3.246 <sup>a</sup>	2.992 <sup>abcd</sup>	7.928 <sup>def</sup>	111 <sup>ed</sup>
4162	<i>Pokuru Wee</i>	113 <sup>a</sup>	92 <sup>ecd</sup>	9 <sup>a</sup>	7 <sup>a</sup>	25.3 <sup>ab</sup>	1.3803 <sup>g</sup>	2.397 <sup>g</sup>	6.403 <sup>h</sup>	143 <sup>a</sup>
4171	<i>Rathal</i>	93 <sup>c</sup>	80.4 <sup>e</sup>	4 <sup>ed</sup>	3 <sup>d</sup>	26.2 <sup>a</sup>	1.4393 <sup>g</sup>	2.25 <sup>h</sup>	6.718 <sup>h</sup>	123 <sup>c</sup>
4402	<i>Haththe pas Dawase Wee</i>	72 <sup>f</sup>	101.9 <sup>bc</sup>	9 <sup>a</sup>	5 <sup>ab</sup>	20.7 <sup>bc</sup>	2.44 <sup>de</sup>	2.865 <sup>cde</sup>	7.669 <sup>ef</sup>	102 <sup>f</sup>
4576	<i>Pokuru Samba</i>	84 <sup>d</sup>	83.1 <sup>ed</sup>	6 <sup>bcd</sup>	3 <sup>dc</sup>	23.3 <sup>ab</sup>	1.5897 <sup>g</sup>	2.497 <sup>fg</sup>	6.276 <sup>i</sup>	114 <sup>d</sup>
4724	<i>Goda El Wee</i>	82 <sup>c</sup>	81.6 <sup>e</sup>	4 <sup>ed</sup>	2 <sup>d</sup>	23.87 <sup>ab</sup>	2.040 <sup>f</sup>	2.67 <sup>ef</sup>	7.294 <sup>g</sup>	124 <sup>c</sup>
4945	<i>Mada El</i>	45 <sup>g</sup>	79.8 <sup>e</sup>	4 <sup>ed</sup>	2 <sup>d</sup>	23.83 <sup>ab</sup>	2.4217 <sup>de</sup>	2.759 <sup>cde</sup>	8.559 <sup>ab</sup>	75 <sup>g</sup>
5488	<i>Kalukanda</i>	49 <sup>g</sup>	102 <sup>bc</sup>	4 <sup>ed</sup>	2 <sup>d</sup>	21.56 <sup>abc</sup>	2.611 <sup>cd</sup>	2.905 <sup>abc</sup>	8.181 <sup>abc</sup>	79 <sup>g</sup>
5522	<i>Mada El</i>	44 <sup>g</sup>	78.5 <sup>e</sup>	3 <sup>e</sup>	2 <sup>d</sup>	15.23 <sup>d</sup>	2.745 <sup>c</sup>	2.917 <sup>bcd</sup>	8.28 <sup>bcd</sup>	74 <sup>g</sup>
8499	<i>Hondarawala</i>	106 <sup>b</sup>	102.8 <sup>bc</sup>	6 <sup>bcd</sup>	5 <sup>ab</sup>	17.9 <sup>dc</sup>	2.6513 <sup>cd</sup>	3.21 <sup>ab</sup>	8.547 <sup>a</sup>	136 <sup>b</sup>

DMRT groups of each parameter are indicated in superscripts. Means with the same letter within the same column are not significantly different (P<0.05). DF: Days to 50% flowering, PH: plant height, NIT: Number of total tillers per plant NIT, Number of fertile tillers per plant, PL: Panicle length, HGW: Hundred grain weight, GW: Grain width, GL: Grain length, M: Days to maturity

study revealed that all the evaluated traditional rice accessions possess a considerable range of morphological variation.

According to Ali *et al.* (2000), cluster analysis has a remarkable effectiveness and capability to identify accessions with the highest level of similarity. Suriyagoda *et al.* (2011) have also revealed a wide variability of rice accessions using cluster analysis. The dendro-

**Table 6: Eigen value, percentage of variance and cumulative Eigenvalues of morphological characteristics of evaluated traditional rice accessions**

Principle component	Eigenvalue	% of variance	Cumulative %
1	3.716	41.289	41.289
2	2.884	32.039	73.328
3	0.983	10.921	84.250
4	0.619	6.881	91.131
5	0.497	5.527	96.658
6	0.156	1.731	98.389
7	0.087	0.968	99.357
8	0.055	0.609	99.966
9	0.003	0.034	100.000

Extraction method was PCA

**Table 7: Rotated component matrix<sup>a</sup> extracted from PCA**

Variables	Component	
	1	2
DF	<b>.849</b>	-.291
PH	<b>.631</b>	.473
NTT	<b>.786</b>	-.034
NFT	<b>.873</b>	.057
PL	.276	<b>-.709</b>
HGW	.034	<b>.959</b>
GW	.076	<b>.880</b>
GL	-.174	<b>.815</b>
M	<b>.853</b>	-.294

Rotation Method: Varimax with Kaiser Normalization.

a. Rotation converged in 3 iterations.

**Table 8: Clustering of traditional rice accessions**

Cluster number	Traditional rice accessions
<b>Cluster 1</b>	<i>Buruma Thawalu-3652, Goda Heenati-3724, Pokkali-3572, Wel Handiran-3735, Haththe Pas Dawase Wee-4402</i>
<b>Cluster 2</b>	<i>Kalu Heenati-4087, Hondarawala-8499, Hondarawala-3493</i>
<b>Cluster 3</b>	<i>Mada El-4945, Kalukanda-488, Mada El-5522</i>
<b>Cluster 4</b>	<i>Rathal-4171, Pokuru Samba-4576, Goda El Wee-4724, Hatada Wee-3472, Pokuru Wee-4162</i>

gram acquired from the present study also provide evidence for that in terms of similarity existing among traditional rice accessions. However, Singh and Rachie (1985) have reported that the genetic make-up of seed, environment and field management practices also influence the morphology of a crop.

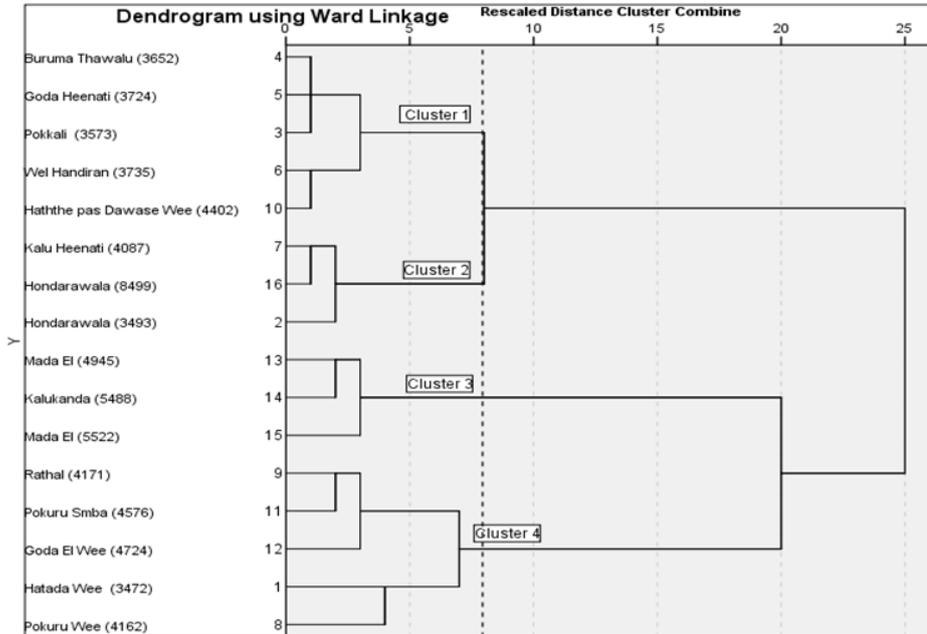
Cluster 1 and cluster 4 contain five each traditional rice accessions while cluster 2 and 3 comprise three each rice accession (Table 8). Cluster 1 contains semi-dwarf rice accessions except for *WelHandiran-3735* and all accessions were low tillering which produced 6-9 tillers per plant. Among clustered rice accessions, 60 % of the accessions took 100-102 days for 50% flowering.

Cluster 2 contains three rice accessions and both Hodarawala accessions are semi-dwarf and *Hondarawala-8499* and *Hondarawala-3493* clustered together in cluster 2 and both started flowering between 100-124 days. Most probably these two accessions would be duplicated. A proper genetic study should be carried out to confirm it. *Mada El-4945* and *Mada El-5522* which have the same accession name were included into cluster 3. Cluster 3 rice accessions were early flowering, (50-74 days) and classified as semi-dwarf. All the tested rice accessions clustered in cluster 4 were semi-dwarf and 60% of rice accessions took 75-99 days to 50 % flowering. *Hatada Wee-3472* and *Pokuru Wee-4162* took 100-124 days to 50 % flowering.

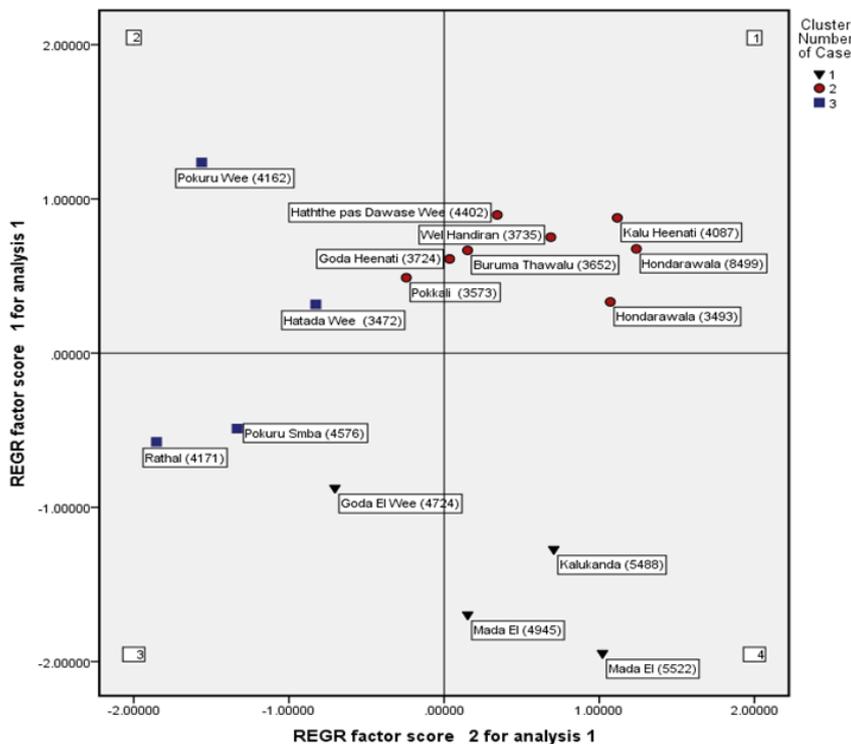
The two-dimensional scatter plot diagram (Figure 3) consisted of four quadrants illustrates the distribution of 16 traditional rice accessions according to the diversity of their

morphological characteristics. The traditional rice accessions belonged to cluster 1 (except *Pokkali-3573*) and cluster 2 have been included into the first quadrant of the 2D scatter plot

diagram. *Pokkali-3573* from cluster 1 and *Hatada Wee-3472*, *Pokuru Wee-4162* which are from cluster 4 have been included into the second quadrant. The third quadrant consisted



**Figure 1: Cluster analysis showing the diversity among traditional rice accessions based on nine morphological characteristics. Dashed line indicates the rescaled distance where clusters were identified.**



**Figure 2: Two-dimensional (2D) scatter plot diagram representing the clusters of traditional rice accessions. 1, 2, 3 and 4 represent the first, second, third and fourth quadrants respectively.**

of Rathal-4171, Pokuru Samba-4576 and Goda El Wee-4724 which belonged to cluster 4. The all traditional rice accessions belonged to cluster 3, namely Mada El-4945, Mada El-5522 and Kalukanda-5488 have been included into the fourth quadrant (Figure 2, Table 8). Since 16 traditional rice accessions have been shown a good distribution among all the four quadrants, the diversity of tested traditional rice accessions is wide.

Although diversity of traditional rice accessions can be studied in this method, Li *et al.* (2006) has highlighted that because of environment consequences, phenotypic values may not be an ideal method for grouping rice accessions. Much improved genetic studies and molecular markers should be used for an accurate diversity analysis.

## CONCLUSION

Considerable range of morphological variation has been found in evaluated traditional rice accessions. Rice accessions were included into three different groups according to plant height (tall, intermediate and semi-dwarf), two different groups according to tillering ability (very low tillering, low tillering) and three groups according to days to 50 % flowering. According to the Ward linkage dendrogram, evaluated rice accessions were belonged to four distinct clusters at rescaled cluster distance 7.5 and described two principle components. In two-dimensional scatter plot diagram, tested rice accessions have been dispersed in all quadrants. PGRC contained some accessions which showed duplications and need to confirm it through proper molecular techniques. The study can be utilized for rice improvement programs.

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