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Assessment of Morphological Characters of Selected Traditional Sri Lankan Rice Varieties (*Oryza sativa* L.)

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Abstract: Rice is the major food for more than half of the world population. Sri Lankan traditional rice varieties have a high genetic diversity and hence, a huge potential for important characters. A morphological study is the initial step towards genetic characterization. This study was aimed to evaluate the variability of selected Sri Lankan traditional rice varieties with respect to morphological characters. Seeds of 24 varieties and IR64 were selected for this study. A pot experiment with Complete Randomized Design (CRD) was used and five replicates were prepared. Fifteen characters were measured using standards published by IRRI. Principal component analysis (PCA) and single linkage cluster analysis were performed. Selected rice varieties were grouped into 5 clusters at 15 minimum distance level. Cluster I comprises twenty one varieties and other four clusters comprise single variety each. Varieties including Goda heenati, Thawalu, Al wee, Goda el wee, Pachchaperumal, Godamanel, Goda wee, Kottiyaran, Kara el, Batapola el, Pokkali, Hetada wee, Moddai karuppan, Vannam villai, Kalu heenaty, Sudu heenaty, Pola el, Kalu bala wee, Kahatawalu, Dahanala and Niyan wee were clustered in one cluster showing high homology. IR64, Gonabaru, Rathl and Ma wee were clustered in different clusters indicating their significant difference from cluster I. First five principle components (PCs) were significant and they accounted for 79 % of total variation. Selected varieties have a significant difference according to clustering pattern. Significant descriptors of PC1 to PC5 can be used to differentiate selected varieties.

Keywords: Morphological characters, Multivariate analysis, Traditional rice

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1. Introduction

Rice continues to be important as a cereal crop which provides more than half of the world dietary energy supply. It is the major staple food for the majority of the people in developing countries where the economy is based on Agriculture. Though the demand for rice has increased during the last decade, production has affected due to reasons like unfavorable weather, decrease of cultivating area and low prices in the market (FAO, 2016). Rice harbor a high genetic diversity and a set of important characters which make it potent to face the challenges brought by unfavorable conditions in the environment. Although it is difficult to gauge the exact rice genotype diversity, it is estimated to be around 140,000 (FAO, 2003). There are more than 40,000 genes mapped in the rice genome. Though the functions of most genes are unknown (IRRI, n. d.).

Out of the south Asian countries, Sri Lanka has a great contribution to the global rice production as it is one of the top twenty rice producing countries per capita (FAO, 2015).

There is a great diversity of the Sri Lankan rice germplasm including improved varieties and traditional varieties which are grown in the fields of lowland and upland. Records in Genbank indicate about 4,000 accessions including wild relatives, land races and old cultivars (FAO, 2007). The majority of the fields are occupied with improved varieties and traditional varieties are grown in a limited area. Due to consumer demand in the recent years, traditional varieties have received an attention as they have beneficial characters such as medicinal and nutritional quality of seeds and environmental stress tolerance capabilities. Information on such characters is needed in genetic improvement programs such as breeding and genetic engineering in order to achieve the target of producing better varieties. Though there are no available scientific evidence about such characters. Therefore, there is a great need of morphological characterization of Sri Lankan traditional rice varieties. This study was aimed to evaluate the variability of selected Sri Lankan traditional rice varieties with respect to vegetative and reproductive characteristics.

2. Materials and Methods 2.1 Selection of Plant Materials

Seeds of twenty four traditional rice varieties and IR64 were selected for the study, based on the knowledge available on their important characters. Seeds of selected varieties (Table 1) were obtained from Plant Genetic Resource center, Gannoruwa, Peradeniya, Sri Lanka.

2.2 Experimental Design and Data Collection

Plants of each variety were grown in pots with surface soil (3.5 kg) which were obtained from a paddy field. Two plants were grown in a pot and five replicates were prepared from each variety. Plants were grown in well watered condition and supplemented with Urea, Triple super phosphate and Murate of potash as recommended by Department of Agriculture, Sri Lanka (Fertilizer usage in paddy cultivation, 2010).

SN	Rice Accession No	Rice Variety	SN	Rice Accession No	Rice Variety
1	3724	Goda Heenaty	14	3762	Vannam villai
2	4203	Thawalu	15	4705	Rathal
3	4024	Al wee	16	3200	Kalu heenaty
4	4724	Goda el wee	17	4126	Ma Wee
5	3408	Pachchaperumal	18	2088	Sudu heenaty
6	4045	Godamanel	19	4915	Pola el
7	3919	Godawee	20	3158	Kalu bala wee
8	3263	Kottiyaran	21	5476	Kahatawalu
9	3242	Kara el	22	3540	Dahanala
10	2105	Batapola el	23	3543	Gonabaru
11	3573	Pokkali	24	4909	Niyan wee
12	3326	Hetada wee	25	2280	IR64
13	3388	Moddai karuppan			

 Table 1: Selected Rice Varieties for the Characterization

Fifteen morphological and yield characteristics were used for the characterization of plants. They were leaf length, leaf width, length of ligule, length of auricle, culm circumference, number of tillers, number of productive tillers, length of panicle, days for 90 % emergence, number of days for 90 % maturity, spikelet fertility, grain length, grain width, grain thickness and weight of 100 grains. Selected rice accessions were characterized using standard evaluation system (IRRI, 2002) and Descriptors for rice, Oryza sativa L (IRRI, 1980). Selected morphological characters were measured using the above mentioned guides and data were analyzed by multivariate analyzing tools.

2.3 Data Analysis

Principal component analysis (PCA) was carried out to assess the variation of the selected morphological characters. Selected rice accessions were grouped based on the variability of the selected morphological characters by performing single linkage cluster analysis. Multivariate analyzing tools provided by IBM SPSS 16.0 statistical software were used for the analysis.

3. Results and Discussions 3.1 Cluster Analysis

Rice varieties were grouped into 5 significant clusters at 15 minimum distance between clusters (Figure 1). Rice varieties were clustered as cluster I comprising twenty one varieties (Goda heenati, Thawalu, Al wee, Goda el wee, Pachchaperumal, Godamanel, Goda wee, Kottiyaran, Kara el, Batapola el, Pokkali, Hetada wee, Moddai karuppan, Vannam villai, Kalu heenaty, Sudu heenaty, Pola el, Kalu bala wee, Kahatawalu, Dahanala and *Niyan wee*) and other four clusters II, III, IV and V comprising single variety each. Clustering of twenty one varieties into one cluster (cluster I) shows the homology of the varieties with respect to measured characters.



Figure 1 Dendogram Resulted from Single linkage Analysis

Clustering of IR64, *Gonabaru, Rathal* and *Ma wee* in four different clusters indicates their significant difference from cluster I according to the variability of analyzed fifteen characters. According to the results of the study conducted by Suriygoda *et al.* (2011) traditional rice varieties were clustered into two major groups showing higher variation in morphological characters. According to the dendogram most related two varieties were *Al wee* and *Godamanel* as they have

shortest minimum distance between them forming the first cluster.

According to the results of PCA, five principle components (PCs) were identified as significant in creating variation having Eigen values greater than one (Figure 2). First five PCs accounts for the 79% of total variation. PC1 accounts for 30% and PC1 and PC2 together account for 51% of variance. Leaf length, leaf width, ligule length, culm circumference, culm length, panicle length, grain width and grain weight are significant components of PC1 which contributed positively (Table 2).

Significant components of PC2 are auricle length, culm length, days for 90% emergence and number of days for maturity.



Figure 2: Scree plot showing Principle components Extracted through PCA Components in which Eigen value greater than one are significant

Tehrim *et al.* (2012) reported the helpfulness of agro morphological characters in preliminary characterization of Pakistani rice cultivars which is complementary to this study. Further they stated that first two principle components account for 50 % of total variability which is nearly similar to results of this study. Significant components of PC1 and PC2 of their study are similar to extracted significant components of this study. PC1 shows highest score for *Mawee, Rathal, Gonabaru* and lowest for *Pachchaperumal* (Figure 3). Out grouped traditional varieties from cluster I shows extremely high PC1 scores. PC1 scores for traditional varieties in cluster I are lower than the scores other varieties. PC2 score is highest for *Dahanala* and lowest for *Kahatawalu*, though there is no clear difference of PC2 score among clusters.

Component	PC1	PC2	PC3	PC4	PC5
Leaf length	0.595	-0.16	-0.124	-0.028	-0.594
Leaf width	0.529	0.039	0.521	0.204	-0.472
Ligule length	0.616	-0.054	-0.161	-0.456	-0.14
Auricle length	0.065	0.669	-0.287	0.218	-0.047
Culm circumference	0.805	-0.121	0.341	-0.012	-0.219
Culm length	0.614	0.54	0.161	-0.184	0.378
Tiller number	-0.68	0.408	0.297	0.318	-0.007
Productive tillers	-0.694	0.337	0.377	0.336	-0.056
Panicle length	0.549	-0.551	0.288	-0.102	0.287
Days for 90% emergence	0.38	0.855	0.059	-0.114	-0.088
Days for 90% maturity	0.331	0.88	0.123	-0.136	-0.106
Spikelet fertility	0.235	-0.513	0.442	0.13	0.296
Grain length	0.358	-0.094	-0.728	0.439	-0.005
Grain width	0.654	0.031	0.168	0.639	0.112
Grain thickness	0.384	0.43	0.006	-0.178	0.5
Grain weight	0.776	-0.005	-0.22	0.455	0.22

Table 2: Component matrix extracted from PCA Components higher than 0.5 have significant contribution to PC



Figure 3: Score plot of PC1 and PC2 based on the results of PCA

26

According to the results, there is a variability in analyzed characters for selected varieties, though most varieties clustered into one group. Specifically IR64 clustered into a separate group. Therefore, it is clear that the descriptors, used in this study are suitable for studying variability of the selected rice varieties with respect to morphology. Wijayawardhana et al. (2015) has confirmed the effective use of agro morphological characters to characterize Sri Lankan rice accessions. Results of single linkage analysis together with PCA provide the evidence for suitability of morphological descriptors used for studying diversity of selected Sri Lankan traditional rice varieties

4. Conclusions

Selected Sri Lankan traditional rice varieties show a significant variation according to the clustering pattern. Out of descriptors used in this study, significant descriptors of PC1 to PC5 can be used to differentiate the selected Sri Lankan traditional varieties.

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