

Technical Session (Oral) B3: Biology

Diversity Analysis of Selected Traditional Rice Accessions with the Same Name

V.V. Karunamuni, A.L. Ranawake*, and S.G.J.N. Senanayake
Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna

Abstract

Morphological characterization of 22 traditional rice accessions, based on 14 agronomic traits was done in a field experiment in Yala, 2013 at the field of Faculty of Agriculture, University of Ruhuna, Mapalana, using the seeds obtained from PGRC, Gannoruwa, Sri Lanka. The aim of the experiment was to study the variations among the accessions and to identify whether the selected traditional rice accessions those were given the same name are similar in their agronomic traits. Ten day old rice seedlings were transplanted in rows with 15 cm × 20 cm spacing according to the randomized complete block design, with 3 replications, having 3 rows per replicate and 20 plants per each row. Observations on the plant height, number of tillers/plant, number of fertile tillers/plant, panicle length, panicle weight, filled grains/panicle, total grains/panicle, filled grain percentage, 100 grain weight, total grain weight/plant, bio mass and harvest index were recorded according to the Standard Evaluation System for Rice, IRRI, in the middle row plants. The data were statistically analyzed using the SPSS version 20 software.

Principal component analysis (PCA), cluster analysis and a morphological dendrogram using Ward Linkage were used to assess the patterns of the morphological variation. PCA sorted the accessions in to 3 principal components that had within cluster similarities and inter-cluster morphological variations. Over 80% (83.830%) total variance was explained by the resulted principal components. Cluster analysis revealed seven groups at the rescaled cluster distance of 5. All the rice accessions were clustered in to two distinct groups at cluster distance 25 where Suduru Samaba (Acc. No. 2202) was in a distinct group from all other accessions. Two Suduru Samba accessions were grouped in to two clusters at cluster distance 25 while four Dahanala accessions were clustered in to two groups at cluster distance 20. Six Kalu Heenati accessions were clustered in to two distinct clusters at cluster distance 7. However both Kalubala Wee accessions were clustered together into the same group. The genetic diversity of these accessions must be assessed by molecular markers in future studies.

Keywords: *Agronomic characters, Field Experiment, Sri Lanka, IRRI Standard Evaluation System, Traditional rice cultivars*

* lankaranawake@agbio.ruh.ac.lk