

MOLECULAR VARIATION OF RICE ACCESSIONS DETECTED BY RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD)

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Rice (*Oryza sativa* L.) is one of the most important crops in the world. Genetic resources available for the cultivar improvement are abundant within the species, and there are more than three thousand accessions in Sri Lanka. This investigation was carried out with the objectives of assessing genetic variation and detection of duplicates within locally collected rice accessions using Randomly Amplified Polymorphic DNA (RAPD).

Thirty rice accessions comprising traditional varieties, some newly improved varieties and a few IRRI collections were used in the experiment. The DNAs from accessions were extracted using CTAB method with slight modifications. RAPD profiles of these accessions were generated with 11 decamer random primers (OPN1, N2, N3, N4, N8, N10, N11, and N14 and OPE1, E2 and OPF1), of which the data from the three primers (OP N3, N4 and F1), resulting in reproducible amplification products, were considered for analysis. Based on the presence or absence of bands, a similarity matrix was computed. A dendrogram was constructed by UPGMA method based on the pair wise similarities amongst the RAPD profiles using the SAS (version 8).

The thirty rice accessions analyzed formed one major cluster and a small cluster (c) at the average genetic distance 1.18 level. The major cluster was sub clustered into two groups, A and B at the average genetic distance of 1.15. Group A was mostly composed of newly improved rice accessions while one traditional variety Dahanala and two IRRI varieties namely IR 28 and IR 1721 were also included in the same cluster. Group B mainly had BG varieties. It was interesting to note that majority of traditional rice varieties were clustered in group C while one IRRI accession namely IR 50 also was included in this cluster.

The dendrogram showed that the DNA diversity among the accessions in groups A and B were somewhat heterogeneous whereas the accessions in group C showed more homogeneity. The accessions were finally clustered into 10 groups at the 0 average genetic distance level implying that there is high genetic similarity among the members with the respective groups. However, for confirmation of duplicates more primers should be investigated.