Thesis Abstract

Genetic Diversity Assessment of Myanmar Rice (*Oryza sativa* L.) Varieties using Morphological Characters and SSR Markers

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This study was conducted to assess the genetic diversity of Myanmar rice varieties using morphological characters and SSR markers.

Genetic diversity of the Myanmar rice varieties was analyzed using Shannon Weaver diversity index (H'). The mean (H') of quantitative traits, qualitative traits, and both of these traits were 0.71, 0.52, and 0.57, respectively. It indicated that a moderate level of diversity exists for morphological characters in Myanmar rice varieties. Cluster analysis for quantitative traits, qualitative traits and their combination generated two groups where most of the accessions belong to group I.

SSR analysis revealed high variation among the Myanmar rice varieties using 34 SSR primers. A total of 202 alleles were identified. The dendrogram generated two clusters where *japonica, javanica* and high quality aromatic rice varieties belong to cluster I and typical *indica* varieties belong to cluster II.

RM1 locus showed 12 alleles and had polymorphic information content (PIC) of 0.89. Average allele per locus for Myanmar rice varieties was 5.79 and average PIC was 0.70. Of the SSR markers tested, RM1 showed the highest gene diversity among the Myanmar rice varieties studied.

According to cluster analysis and principal coordinate analysis, SSR characterization had a more similar grouping to that of isozyme classification as compared to morphological characterization.