

Pham Thi Be Tu. 2007. Genetic diversity analysis of ninety traditional rice (*Oryza sativa* L.) varieties from Cuu Long Rice Research Institute genebank, Vietnam. **MSc. Thesis.** University of the Philippines los Banos. Philippines; 110p. ([clrri@hcm.vnn.vn](mailto:clrri@hcm.vnn.vn))

### **ABSTRACT**

Analysis of the level of diversity among the 90 traditional varieties is useful in breeding programs as this influences parental selection in varietal development. The diversity of the 90 traditional varieties was assessed using SSR and quantitative morphological characters. The study aims to evaluate the genetic diversity of traditional rice varieties in the gene bank of Cuu Long Delta Rice Research Institute (CLRRI), Vietnam, analyse correlation of characters for application in plant breeding and relate the results between morphological characters and molecular markers.

In agro-morphology based analysis, ANOVA showed highly significant differences among the 90 traditional rice varieties; correlation coefficients showed that all the traits were significantly correlated with each other except yield. The standardized Shannon-Weaver diversity indices for the quantitative morphological characters ranged from 0.68 to 0.95 with a mean of  $H' = 0.88$ . Clustering analysis using UPGMA grouped the 90 traditional varieties generated eight clusters at 0.61 similarity coefficient. Some with the same variety names were grouped into different clusters. Though they belong to the same cluster based on morphological markers, molecular analysis showed that they were actually different. Most of the varieties (84%) belong to the same cluster (cluster VII). This indicates that these varieties are closely related.

Rainfed and deep water rice varieties were grouped separately (cluster IV for deep water rice genotypes and cluster VI for rainfed rice). Both the morphological and SSR markers were able to classify the rice varieties into these agro-ecological groups.