Evaluation of Genetic Diversity in Defferent Rice Populations (*Oryza sativa L.*) using microsatellite markers

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Abstract
This study was carried out to evaluate the genetic diversity and relationship between different rice populations (Local, Import & Breeding rice populations) with 25 microsatellite loci. The results revealed that all the primers showed polymorphism among the rice populations. A total of 164 alleles were detected. The number of alleles per marker ranged from 3 to 14 with an average of 6.56 alleles per locus. Result from UPGMA analysis clustered the different rice populations into Local, and Import-Breeding rice groups. Import rice populations were found to have the highest genetic diversity (0.831±0.445) while, the lowest were in Local rice populations (0.616±0.319). Genetic distance was estimated 0.213 between Local and Breeding rice populations and 0.038 between Import and Breeding populations. The result indicates that SSR markers possess suitable potential for recognizing and classifying rice populations.

Key words: Genetic diversity, Microsatellit markers, Rice

1. Introduction
Rice (*Oryza sativa* L.), one of the most widely cultivated crops, provides food for the world population (Guimaraes, 2009). Global rice production is 494.4 million tons (FAO, 2015). Genetic diversity of plant genotypes is the main step of breeding programs to use the best strategies for logical utilization of genetic resources within and among varieties. Today's traditional agriculture is being rapidly transferred into molecular genetics. Developing genetic resources and new plant varieties through genome research has become increasingly prevalent and the advent of molecular marker technology offers new opportunities to develop new varieties. Molecular markers are widely used for plant genetic diversity. There are several types of molecular markers. Among the most convenient types of DNA markers (PCR-based markers), microsatellites which are known as simple sequence repeats (SSRs) are considered desirable markers because of their distributions throughout the genomes, abundance, reproducibility, Mendelian inheritance, co-dominant inheritance, analytical simple, readily transferable and highly polymorphic (Rakoczy-Trojanowska and Bolibok, 2004; Toro *et al*., 2009). Meanwhile, SSR loci tends to be both multiallelic and polymorphic for repeat number, which is easily scored and used for genotyping (Liu *et al*., 2000). It has been widely utilized in plant genomic studies (Akkaya *et al*., 1992). Microsatellites are 2 to 6 base pairs (bp) tandemly repeated DNA sequences which dinucleotides [(CA)n (AG)n and (AT)n] are generally abundant in genomes (Gupta and Varshney, 2000; Ramakishana *et al*., 1994). SSR markers are