

OA6. Genetic relationship and genetic variation in *Oryza* species using MITE-AFLP

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Objectives

MITEs (miniature inverted-repeat transposable elements) are class 2 transposable elements (TEs) identified relatively recently in a various eukaryotic species (Wessler et al. 2001). Among the many different transposable elements, MITEs are one of the major transposable elements in rice. We identified a MITE element, *Pangrangja*, in rice through homology analysis with an repetitive DNA from *Aegilops speltoides* (Park et al. 2002). In this study, we present here the application of the MITE-AFLP using a consensus sequence domain in *Pangrangja* for phylogenetic analysis in *Oryza* species.

Materials and Methods

The materials consisted of 53 accessions of 13 different *Oryza* species. The genomic DNA was isolated from young leaves with the protocol of Dellaporta et al. (1983). The MITE-AFLP analysis was performed according to Wessler et al. (2001) with some minor modifications. Genetic similarity between accessions was based on the algorithm of Nei and Li (1979); $S_{xy} = 2N_{xy}/(N_x + N_y)$. The phylogenetic dendrograms were constructed by UPGMA in the NTSYS-pc program (Rohlf, 1989). Genetic variations within species and genetic distances between species were calculated with Microsoft Excel PC-program from the NYSYS data set.

Results and Discussion

MITE-AFLP markers were successfully used to study the genetic variation and species relationship in *Oryza* species. Analysis of 53 accessions of *Oryza* species with seven MITE-AFLP primer combinations detected a total of 250 polymorphic fragments. High polymorphism was detected within and between *Oryza* species. Species relationships were analyzed by the pattern of presence or absence of homologous fragments, because nucleotide sequences of the detected MITE-AFLP fragments revealed that the same fragments in different species shared very high sequence homology. The genetic distances, GDs, between species were higher than those within species and the GDs in Sativa complex were higher than those in Officinalis complex. The phylogenetic tree recognized two major groups at 62% genetic similarity group I consists of all AA genome species of the Sativa complex, and group II consists of BB-, CC-, EE- and BBCC genome species of the Officinalis complex. Therefore, this study demonstrated that the MITE-AFLP technique provide a tool for studying the genetic variation and species relationship in *Oryza* species.

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