

**A801**                    **Comparison of the Nuclear Ribosomal DNA ITS 1 region between *Acanthopanax koreanum* Nakai and *A. chiisanensis* Nakai**

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Two species of Korean endemic plant, *Acanthopanax koreanum* and *A. chiisanensis* growing in Cheju island were investigated. Genetic analysis in nuclear ribosomal DNA internal transcribed spacer 1 region showed that species of these had evolved as monophylogenetic in Cheju island respectively. From the fragment migration patterns obtained by single stranded conformation polymorphism technique, we could estimate that two species has obviously different type of secondary structure in this region. Also it means that two plants would have different sequence to each other. Throughout the automated DNA sequencing, it was revealed that SSCP result caused to nucleotide substitution on five sites. It has no difference in partial sequences of two coding regions; 5.8S and 18S rDNA included in amplified products. Also comparison of restriction enzyme recognition site in this region, that supported above all. Specific enzymes were divided them as two patterns, and digested patterns of common recognizing enzymes viewed as same. But it is said that these two species are the closest through restriction recognition investigation of ITS1 region in generic level of Araliaceae growing in Korea. Finally, we arrived at a conclusion that these two Korean endemic plants, growing in Cheju island, has been walking on so close and so far way of evolution.

**A802**                    **Genetic Relationship and Development of RAPD Specific Marker among *Abies* spp. Distributed in Korea**

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DNA from 14 taxa of *Abies* species was analysed using the polymerase chain reaction (PCR) with 10 arbitrary primers of 10 nucleotide length (10 mers) to determine the genetic relationship and development of random amplified polymorphic DNA (RAPD) specific marker. The RAPD specific markers showed the 1, 1, 6, 6, 1, 1, 8, 8, 6, 6, 10 and 10 in the 4 taxa of *A. koreana* for. *koreana*, 2 taxa of *A. koreana* for. *chlorocarpa*, 2 taxa of *A. koreana* for. *nigrocarpa*, 2 taxa of *A. nephrolepis* and 2 taxa of *A. holophylla*, respectively. The 10 primers yielded 102 useful polymorphisms that were evaluated according to the presence of absence of fragment of equal size. The phylogenetic tree was constructed from the RAPD fragment patterns by the neighbor-joining method. The distance between *A. koreana* for. *chlorocarpa* and *A. koreana* for. *rubrocarpa* was 0.127 and was the closest among any other pairs. On the other hand, the distance between *A. koreana* for. *nigrocarpa* and *A. holophylla* was 0.489. These results showed that PCR-RAPD analysis was a powerful tool for elucidating genetic relationship and development of specific marker in *Abies* species.