

**A201**ITS Sequences and Their Phylogenetic Implications in *Acer* Species (Aceraceae)

Hye-Jeong Cho\*, Sangtae Kim, Youngbae Suh<sup>1</sup> and Chong-Wook Park  
Department of Biology, Seoul National University; and Natural Products  
Research Institute, Seoul National University<sup>1</sup>

As a part of comprehensive phylogenetic studies on the genus *Acer* (Aceraceae), sequences of internal transcribed spacers (ITS) of nuclear ribosomal DNA were determined to study phylogenetic relationships among selected sections of the genus. The size of ITS 1 ranged from 230 to 237 bp, and ITS 2 from 227 to 239 bp. The 5.8S was 164 bp. The G + C contents of ITS 1 and 2 were 60.4-64.0% and 60.3-64%, respectively, and 55.5% for 5.8S. The nucleotide divergences was 0-11.50% at intra-sectional levels and 3.27-16.51% at inter-sectional levels. The molecular phylogeny based on ITS sequences were considerably different from ones proposed by various authors on the basis of morphology. Section *Platanoidea* was separated from other sections at the base of the phylogenetic tree and then section *Macrantha* was placed at the base among the rest. Sections *Negundo* and *Caudata* constituted a clade, serving as the sister group of '*Ginnala-Oblonga-Palmata*' clade. Section *Ginnala* was placed as the sister group of '*Oblonga-Palmata*' clade. In the clade of '*Oblonga-Palmata*', two species of section *Oblonga* were not tied by a monophyly. *Acer burgerianum* was placed as a sister group to the clade of *A. oblongum* and three species of section *Palmata*.

**A202**Molecular Evidence for the Origin of a Hybrid Species of *Viola* from Ullung Island

Taejin Kim,\* Jung Hee Park, Youngbae Suh<sup>1</sup> and Byung Yun Sun  
Department of Biology, Chonbuk National University; and Natural Products  
Research Institute, Seoul National University<sup>1</sup>

A *Viola* species in Ullung Island, which have been erroneously recognized as *V. albida* var. *takahashii*, displays intermediate characteristics in major morphological features such as stigma type, sepal appendages, flower colors and leaf shape of *V. albida* var. *chaerophylloides* and *V. selkirkii*, suggesting that the species should be formed by the hybridization between these two species. The parts of nuclear ribosomal DNA (nuclear genome) and *ndhF* (chloroplast genome) were analyzed by PCR-mediated RFLP. The molecular data clearly demonstrated that the parents of the hybrid species are *V. albida* var. *chaerophylloides* and *V. selkirkii*. In addition, the analyses of two genome systems provided the solid proof that the paternal line of the hybrid species is *V. albida* var. *chaerophylloides* and the maternal line is *V. selkirkii*.