

A220

Phylogenetic relationships of the genus *Angelica* and related genera (Umbelliferae): Inference from internal transcribed spacer sequences

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Many different views on taxonomic treatments and phylogenetic relationships in the genus *Angelica s. l.* have been proposed because they show the complex morphological variation and the range of variation is often overlapped. The sequences of internal transcribed spacers (ITS) of nuclear ribosomal DNA were determined to examine taxonomic delimitations and phylogenetic relationships of the genus. The size of ITS1 was 213 - 219 bp and ITS2 217 - 220 bp. The variation of ITS sequences ranges from 3.2 to 26.4% for ITS1 and from 2.3 to 22.2% for ITS2. Phylogenetic analyses show that the genus *Ostericum* is distantly related with other species of *Angelica s. l.* by being separated at the base of the tree. *Dystaenia takesimana*, an endemic species of Ullung Island, is placed as a sister group to the clade of *Angelica s. str.* and *Peucedanum*.

A221

Molecular Phylogenetic Study of *Polygonum sect. Tovar* (Polygonaceae) with Disjunct Distribution in Eastern Asia and Eastern North America

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Sequences of internal transcribed spacer (ITS) regions of nuclear ribosomal DNA were determined in *Polygonum sect. Tovar* to examine phylogenetic relationships in the section and to measure the extent of differentiation between disjunct species in Asia and North America. The section includes three controversial species; *P. filiforme* and *P. neofiliforme* of eastern Asia, and *P. virginianum* of eastern North America. The ITS1 was 241 or 242 base pairs (bp) long and ITS2 244 bp. The ITS sequences clearly separate North American species, *P. virginianum* from eastern Asian species, *P. filiforme* and *P. neofiliforme*. The molecular data also provide strong support for the closely allied relationship between two Asian species. Nucleotide divergence between eastern Asian and eastern North American species ranges 3.3 - 3.7% for ITS1 and 8.3 - 9.8% for ITS2.