

AN ITS-BASED CLASSIFICATION OF APIACEAE SUBFAMILY APIOIDEAE

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At present, and likely in the foreseeable future, nrDNA ITS sequences comprise the most comprehensive database for Apiioideae phylogenetic study. These sequences are readily obtainable, even from old herbarium specimens, the phylogenies at low taxonomic levels are generally congruent with those inferred from chloroplast markers, and the few intra-individual polymorphisms revealed to date do not interfere with the phylogeny estimation. Phylogenetic analysis of 1240 ITS sequences of subfamily Apiioideae currently available in GenBank and numerous unpublished sequences was carried out to recognize monophyletic groups that can be tested using evidence from cpDNA. Approximately half of these sequences had data for the intervening 5.8S gene region. These 1240 accessions represent 292 genera and 959 species from throughout the geographic range of the subfamily and include all tribes and major clades defined on the basis of previous molecular systematic studies except its most early diverging branches (Heteromorphae, Annesorhiza clade, *Lichtensteinia* clade), basal genera of uncertain phylogenetic position (*Astydamia*, *Choritaenia*, *Ezosciadium*, *Molopospermum*), and a lineage characterized by rapid ITS sequence evolution relative to its sister group (“North American Endemics” clade of tribe Oenantheae). All taxa excluded from this investigation have ITS sequences that cannot be readily aligned with those of most members of the crown clades. Based on taxonomic congruence among the results of phylogenetic analyses of diverse molecular data sets (cpDNA gene and intron sequences, cpDNA restriction sites, ITS sequences), the following 10 tribes are erected or confirmed as monophyletic: Aciphyllae, Bupleureae, Careae, Coriandreae, Echinophoreae, Oenantheae, Pleurospermeae, Pyramidopterae, Scandiceae (incl. subtribes Daucinae, Ferulinae, Scandicinae, Torilidinae, and the *Glaucosciadium* clade), and Smyrnieae. In addition, the results of previous and present phylogenetic analyses of only ITS sequences support four monophyletic tribes (Apiaceae, Selineae [incl. *Arracacia*, *Johrenia*, and “Perennial Endemic North American Apioid” clades], Tordylieae [incl. *Cymbocarpum* and “African Peucedanoid” clades], Pimpinelleae) and the following 12 informally recognized, major clades of largely uncertain relationship (asterisks denote clades that are monogeneric): *Acronema*, *Arcuatopterus**, *Cachrys*, *Chamaesium**, *Conioselinum*, *Conium**, *Diplolophium**, *Erigenia**, *Komarovia*, *Opopanax*, *Physospermopsis* (“East Asia clade”), *Sinodielsia*. Several of these clades are not well supported and intergrade in some phylogenetic analyses; however, each of the 1240 accessions examined can be unambiguously assigned to a particular tribe or major clade. Numerous genera are not monophyletic within their respective groups. Furthermore, 26 genera are assigned to two or more of the aforementioned tribes or major clades. Five of these genera (*Angelica*, *Peucedanum*, *Physospermopsis*, *Seseli*, *Trachyspermum*) are each assigned to three or four major lineages, and three genera (*Ligusticum*, *Pimpinella*, *Pleurospermum*) occur in five or six. Like the “*Peucedanum* problem” of current worldwide interest, any one of these highly polyphyletic genera can therefore be considered for further collaborative study. Misidentifications of Apiioideae ITS sequences in NCBI’s taxonomic database are plentiful, as are the placements of many genera in incorrect tribes or clades. Moreover, nomenclatural changes proposed in recent studies are not usually reflected in GenBank, leading to taxonomic confusion. The limitations of ITS data in resolving the higher-level phylogenetic relationships among many of these tribes and major clades are severe, particularly those of the apioid superclade. Further resolution of these relationships, as well as the possible recognition of these 12 clades at tribal levels, must await supporting data from the conservatively evolving plastid genome. A standardized system of phylogenetic classification for the subfamily is required, with sampling in future systematic studies directed by the results obtained using these ITS sequence data.

