

TRIBES AND CLADES WITHIN *APIACEAE* SUBFAMILY *APIOIDEAE*: THE CONTRIBUTION OF MOLECULAR DATA

S. R. DOWNIE ^{a1} , **G. M. PLUNKETT** ^{a2} , **M. F. WATSON** ^{a3} , **K. SPALIK** ^{a4} ,
D. S. KATZ[hyphen]**DOWNIE** ^{a1} , **C. M. VALIEJO**[hyphen]**ROMAN** ^{a5} , **E. I. THERENTIEVA** ^{a6} , **A. V. TROITSKY** ^{a5} , **B.**[hyphen]**Y. LEE** ^{a1} , **J. LAHAM** ^{a7}
and A. EL[hyphen]**OQLAH** ^{a7}

^{a1} Department of Plant Biology, University of Illinois, Urbana, IL 61801, USA

^{a2} Department of Biology, Virginia Commonwealth University, PO Box 842012, Richmond, VA 23284, USA

^{a3} Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 9NL

^{a4} Department of Plant Systematics and Geography, Warsaw University, Aleje Ujazdowskie 4, 00[hyphen]478 Warsaw, Poland

^{a5} A. N. Belozersky Institute of Physico[hyphen]Chemical Biology, Moscow State University, Moscow 119899, Russia

^{a6} Botanical Garden, Moscow State University, Moscow 119899, Russia

^{a7} Department of Biological Sciences, Yarmouk University, Irbid, Jordan

Abstract

Phylogenetic analyses of chloroplast gene (*rbcl*, *matK*), intron (*rpl16*, *rps16*, *rpoC1*) and nuclear ribosomal DNA internal transcribed spacer (ITS) sequences and chloroplast DNA restriction sites, with supplementary data from variation in size of the chloroplast genome inverted repeat, have been used to elucidate major clades within *Apiaceae* (*Umbelliferae*) subfamily *Apioideae* Drude. This paper summarizes the results of previously published molecular cladistic analyses and presents a provisional classification of the subfamily based on taxonomic congruence among the data sets. Ten tribes (*Aciphylleae* M. F. Watson & S. R. Downie, *Bupleureae* Spreng., *Careae* Baill., *Echinophoreae* Benth., *Heteromorphae* M. F. Watson & S. R. Downie, *Oenantheae* Dumort., *Pleurospermeae* M. F. Watson & S. R. Downie, *Pyramidoptereae* Boiss., *Scandiceae* Spreng. and *Smyrnieae* Spreng.) are erected or confirmed as monophyletic, with *Scandiceae* comprising subtribes *Daucinae* Dumort., *Scandicinae* Tausch and *Torilidinae* Dumort. Seven additional clades are also recognized but have yet to be treated formally, and at least 23 genera examined to date are of dubious tribal or clade placement. The utility of these different molecular markers for phylogenetic inference in *Apioideae* is compared based on maximum parsimony analyses of subsets of previously published molecular data sets. Of the six loci sequenced, the ITS region is seen to be evolving most rapidly and *rbcl* is the most conservative. Intermediate in rate of evolution are *matK* and the three chloroplast introns; with *rpl16* and *rps16* evolving slightly faster than *matK* or *rpoC1*. The analysis of restriction sites, however, provided 2–4 times more parsimony informative characters than any single DNA locus sequenced, with estimates of divergence just slightly lower than that of the ITS region. The trees obtained from separate analyses of these reduced data sets are consistent with regard to the major clades inferred and the relationships among them. Similar phylogenies are obtained by combining data or combining trees, representing the supermatrix and supertree approaches to phylogenetic analysis, respectively. The inferred relationship among the tribes and informally recognized major clades within *Apioideae* is presented.