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Radiation and Speciation

Farewell to dichotomous models of phylogeny: Reconstructing patterns of low-level evolution in maples

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The evolutionary unfolding of *Acer* section *Acer* (17 species and subspecies from North America, East Asia, and western Eurasia) is evaluated using splits-based networks, ITS motif analysis, and morphology. Molecular analyses are based on 276 ITS clones obtained from 101 wild specimens that represent all species and most subspecies. Formerly recognized (sub)species are largely supported; in addition, the combination of molecular and morphological criteria leads to refined taxon circumscriptions and supraspecific groups. Partly incompatible phylogenetic signals captured in ITS sequences suggest that section *Acer* underwent three major radiations, and unhindered horizontal gene flow is indicated between ancestors of extant taxa that are isolated at present times. Analyses of chloroplast DNA (based on ~6600 nt from 6 regions) and nuclear DNA (600 ITS sequences) also point to cases of lineage sorting within *Acer* during the Tertiary. The level of ITS derivation in section *Acer* corresponds to levels of morphological differentiation and (palaeo) biogeographical patterns. Based on our results, we question the utility of cladistic approaches for inferring low-level evolution in section *Acer*, mainly because of reticulate evolution. Our findings in *Acer* are comparable to those in other Northern Hemisphere tree genera, such as *Fagus* and *Platanus*. The combination of methods used here allows to trace pathways of low-level evolution and to analyse multi-signal data sets with a less restricted (i.e. non-dichotomous) and dynamic phylogenetic concept.