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Clearing up the “thicket of life”: How to include fossils in phylogenetic reconstructions

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In contrast to extant data sets, the fossil record provides the only archive of evolution covering both space and time. Thus, the inclusion of fossils in phylogenetic reconstructions is essential to track the evolutionary unfolding of (modern) life. Unfortunately, the nature of fossil data is challenging for commonly applied phylogenetic methods, e.g. inference of a most parsimonious tree. The number of characters that can be scored (defined) for phylogenetic reconstructions is naturally limited due to preservation issues and the incompletely known fossil record. This affects the result of any phylogenetic inference, e.g. when the reconstruction relies on concatenated (combined) molecular and morphological data, and our interpretation of its result(s). Moreover, there is no reason to assume that fossils necessarily are extinct sister lineages. Rather, they may represent ancestral taxa, or taxa that are morphologically highly similar to the actual ancestor(s) of modern taxa. Including ancestors and their descendants in one matrix and analysis violates the basics of cladistics and, indeed, has unwanted effects on phylogenetic inference of trees. As a consequence, resolution and support of phylogenetic trees that include fossils are often low. One straightforward alternative is to simply use a molecular backbone tree and to place fossil taxa using a morphological character partition and parsimony or maximum likelihood as optimality criteria. On the other hand, molecular phylogenies of modern taxa are not necessarily fully resolved. At low taxonomic levels reticulation occurs and pathways of evolution become less and less tree-like. Another alternative is the application of less restricted methods of phylogenetic inference accounting for ambiguous (due missing data) and incompatible (due to ancestral or “primitive” taxa) phylogenetic signal. For instance, consensus networks based on trees (e.g., bootstrap replicates or most parsimonious trees) allow visualizing competing topologies. Furthermore, networks based on morphological distances directly allow inferring the degree of incompatibility and general patterns of similarity. In my talk, I will show the limitations, but also the potential of various tree-building methods to place fossil taxa in an evolutionary (non-cladistic) context. I will also outline how consensus and distance-based networks can be interpreted in the light of ancestor-descendant relationships and, hence, can help to clear the thicket of life.