

IS ACCURATE PHYLOGENY RECONSTRUCTION POSSIBLE IN PALEONTOLOGY?

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An unprecedented amount of evidence now illuminates the phylogeny of living mammals and birds on the Tree of Life. We use this tree to measure phylogenetic value of data typically used in paleontology (bones and teeth) from six datasets derived from five published studies. We ask three interrelated questions: 1) Can these data adequately reconstruct known parts of the Tree of Life? 2) Is accuracy generally similar for studies using morphology, or do some morphological datasets perform better than others? 3) Does the loss of non-fossilizable data cause taxa to occur in misleadingly basal positions? Adding morphology to DNA datasets usually increases congruence of resulting topologies to the well-corroborated tree, but this varies among morphological datasets. Extant taxa with a high proportion of missing morphological characters can greatly reduce phylogenetic resolution when analysed together with fossils. Attempts to ameliorate this by deleting extant taxa missing morphology are prone to decreased accuracy due to long-branch artefacts. We find no evidence that fossilization causes extinct taxa to incorrectly appear at or near topologically basal branches. Morphology comprises the evidence held in common by living taxa and fossils, and phylogenetic analysis of fossils greatly benefits from inclusion of molecular and morphological data sampled for living taxa, whatever methods are used for phylogeny estimation.