

Endopterygote Study

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Reconstructing the relationships among the >10 million species on our planet is one of the frontiers in biodiversity research (e.g., see NSF's [ATOL program](#)). But which kind of data should be used? This question is particularly important for the 4-5 million insect species with holometabolous development (egg, larva, adult). In this review A/P R. Meier and his postgraduate student G. S. Lim document how the data that is used for the reconstruction of the Tree-of-Life has changed over the past 20 years. We then explore the relative merits of using information from the immature and adult stages, quantify congruence and conflict between data sources, and make recommendations for future studies.

This study is part of the ongoing efforts of the Evolutionary Biology Laboratory to contribute to the Tree-of-Life, develop tools for species identification, and study the evolution of Diptera. These efforts included organizing an [international conference](#) dedicated to Tree-of-Life research in 2009 and publishing papers that are recommended readings by the *Faculty of 1000* (3 publications) and/or *highly cited* according to *ISI Thomson* (2 publications).



ENDOPTERYGOTE STUDY: (From left) sepsid egg, sepsid larva head and sepsid adult