

## **No DNA? No problem: How to phylogenetically place fossil Darwin wasps (Ichneumonidae)**

Alexandra Viertler

Ecology and Evolution, University of Bern; Life Sciences, Natural History Museum Basel

Alexandra Viertler, Karin Urfer, Georg Schulz, Seraina Klopffstein, Tamara Spasojevic

The parasitoid Darwin wasps are among the most poorly studied groups of organisms. Their fossil record is even more poorly understood than their extant diversity but is fundamental for reconstructing the evolutionary history of the group. One of the prerequisites to improve its quality, is a reliable taxonomic placement of newly described fossils.

Here, we perform a total-evidence phylogenetic analysis, which combines morphological and molecular data, extant and fossil taxa, to aid taxonomic placement of four new fossil Darwin wasp species in amber. We based our analysis on a published total-evidence dataset for Ichneumonidae, that contains 222 morphological characters and 10 molecular genes. However, we revised the morphological matrix and extended it with nine newly defined characters (225 in total) and 20 fossil and extant species (230 in total) relevant for the placement of the new fossils. To increase the number of scored characters for the fossils, we also performed micro-CT scans and 3D reconstructions. For the newly added extant taxa, we amplified three (28S, COI, CAD) out of the 10 genes.

A Bayesian total-evidence analysis was performed using RevBayes and the trees from posterior distribution were used to summarize the attachment probability of the fossils to branches in the phylogeny with RoguePlots.

We show that a total-evidence phylogenetic analysis, based on a careful assessment of morphological characters from fossils and their micro-CT scans, can significantly improve taxonomic placement of amber fossils. Increasing the precision of fossil placement is key to improving parameter estimates in dating and diversification analyses.