

Building a fossil insect phylogeny

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Introduction:

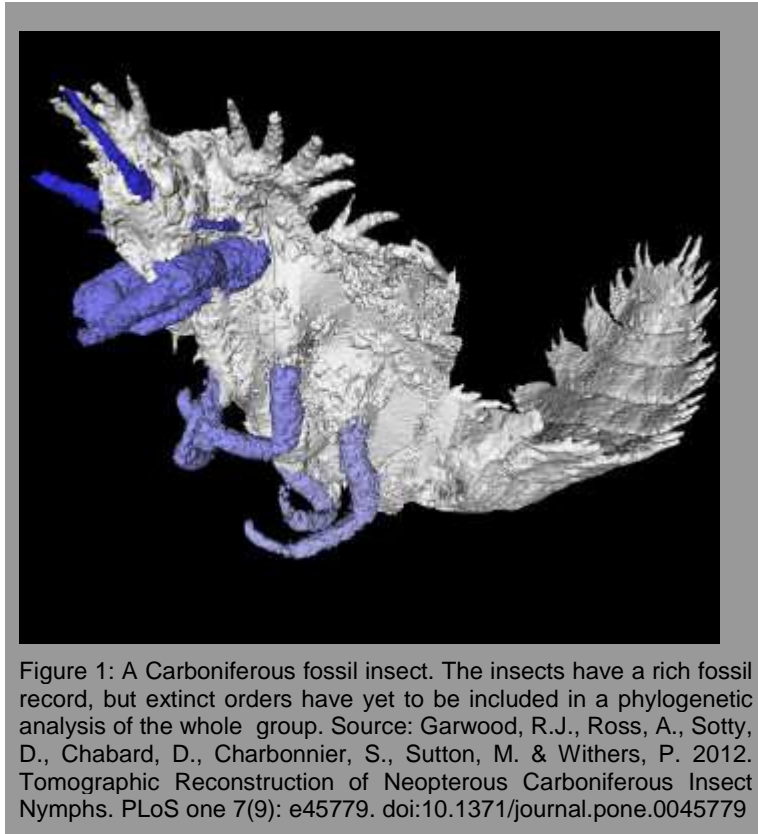
Insects alone constitute more than half of all described species. They are ubiquitous: present in, and integral to, all known terrestrial ecosystems. As pollinators, pests, and vectors of disease, they impact on myriad aspects of human culture and activities. In recent years phylogenomic work has provided a backbone tree for the majority of extant insect orders (Misof et al. 2014). The insects have a rich fossil record (e.g. Figure 1), and there are, numerous orders with no living representatives, which have yet to be placed within the evolutionary tree of the insects. The aim of this project is to create cladistic dataset that will allow these orders to be placed within the insect tree. This has the potential to answer key questions in insect evolution, and will be used as a tool to identify patterns in the evolution of this hyperdiverse group, and use them as a model group for studying broader evolutionary topics.

Project Summary:

The aim of the project is to construct the first insect-wide phylogeny to include extinct orders. The key objective will be to create a large morphological cladistic matrix: by doing so, fossil orders can be placed reproducibly on the insectan tree, and uncertainty regarding their affinities quantified. The matrix will then be combined with previously published phylogenomic data to create dataset that will allow this hyperdiverse group to be used as a means of studying evolution in deep time. Through the inclusion of extinct taxa in a phylogenomic insectan analysis, this project will achieve:

- The deepest nodes in the insect tree, which are at the moment subject to the greatest uncertainty (Figure 2), will be better resolved, because extinct species will break up long branches.
- An increased number of fossil calibrations, with reproducible placements of calibrations, will provide a more accurate timescale for insect evolution through molecular clock dating of the phylogenomic datasets. Newer techniques such as tip dating will also be possible.
- This dataset can be used to look for important patterns in the evolution of the insects: for example, a key aim will be to test for causal links between radiations in the group, and key physiological, developmental, and ecological innovations within and without the group.
- We will also identify potential biases and patterns in the fossil record of the insects, carefully assessing the utility of this unique resource for studying evolution.

Trees will be constructed using both parsimony, and bayesian phylogenomic inference. The data will be thoroughly interrogated for sensitivity to different approaches and coding strategies, and used as the basis for molecular clock analyses. Fit with the fossil record will be assessed using stratigraphic congruence indices, and links between innovations and radiations will be studied using approaches such as BAMM (Bayesian analysis of macroevolutionary mixtures), allowing uncertainty to be quantified.



Successful applicants will have the opportunity to learn a broad range of computational and phylogenetic tools, and build expertise in the morphology, evolutionary history, and fossil record of the insects. This project forms part of a thriving cross-disciplinary research area at the University of Manchester. A large group of academic staff and associated researchers are addressing evolutionary and palaeobiology questions through studying ancient life and living groups, supported by Manchester's Interdisciplinary Centre for Ancient Life (<http://www.ical.manchester.ac.uk/>) and the Evolution, Systems and Genomics Domain (<https://www.bmh.manchester.ac.uk/research/domains/evolution-systems-genomics/>).

References

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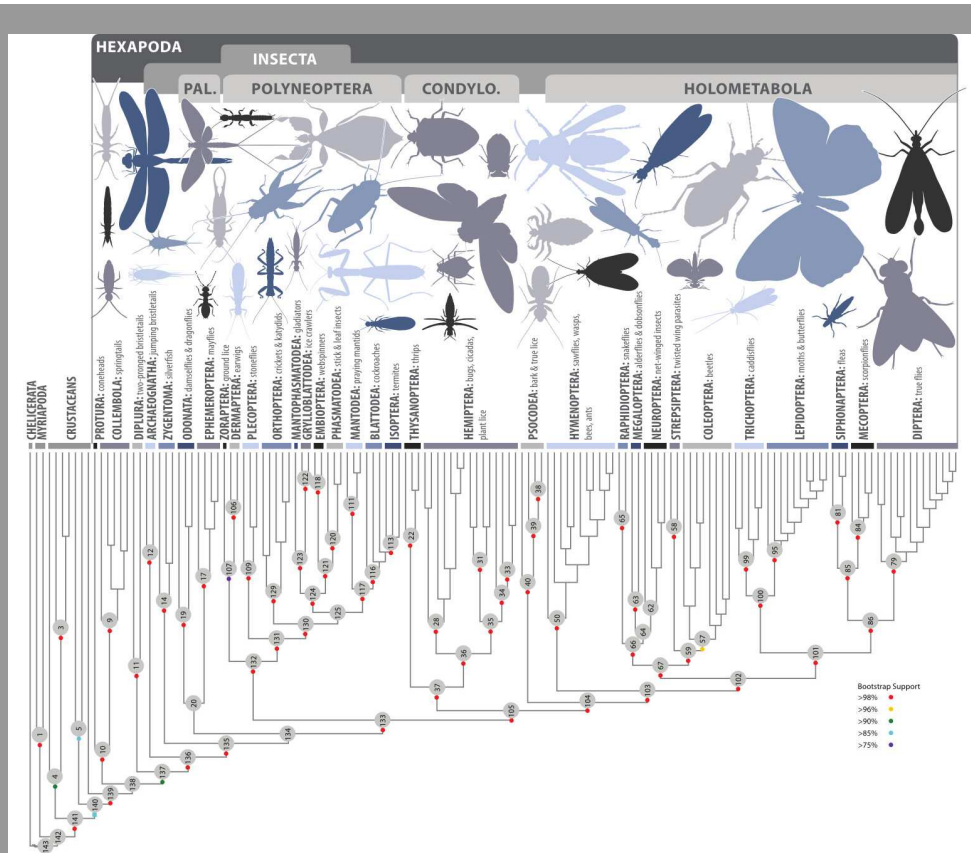


Figure 2: A recent insect phylogeny including all extant orders (Source: Misof et al 2014).