



Phylogeny of World Tachinidae Project

Continuing progress towards a phylogeny of Tachinidae

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Readers of this newsletter are likely familiar with our ongoing project to establish a framework phylogeny of world Tachinidae (see articles in *The Tachinid Times* 26 and 27). This collaborative project, involving myself, Jim O'Hara, Kevin Moulton, Pierfilippo Cerretti, Isaac Winkler and a long list of collaborating tachinidophiles was initiated in 2012 with funding from the U.S. National Science Foundation. Our goal is to produce a robust phylogenetic framework of Tachinidae that can be used to inform tachinid taxonomy, systematics research, and the patterns of tachinid evolution. In previous issues of *The Tachinid Times* we summarized our progress to date in terms of obtaining taxa (e.g., Cerretti *et al.* 2013, O'Hara *et al.* 2014) and some of our preliminary phylogenetic findings (Stireman *et al.* 2013, Winkler *et al.* 2014). Here, we provide a brief update on some of our recent progress and associated products.

Products and Progress

Since the last edition of this newsletter, we have continued to acquire specimens and data for our mission to reconstruct relationships of Tachinidae. In early 2014 we published the first major paper from the project, a morphology-based phylogenetic reconstruction led by Pierfilippo Cerretti (Cerretti *et al.* 2014). This analysis of 180 genera based on 135 characters produced a number of interesting results, some supporting previous hypotheses (e.g., a grouping of Phasiinae + Dexiinae, and Tachininae + Exoristinae) and some suggesting new ones (e.g., derived ovipary, and a non-monophyletic Dexiinae). Rather than elaborate on all of the findings here, we invite the reader to read the paper itself (available from any of the authors). Perhaps most importantly, this paper provides a morphological foundation with which to compare our emerging molecular-based inferences. It also illustrates the

difficulty of reconstructing phylogenetic relationships among tachinid clades, showing how small differences in character coding or weighting can result in substantial differences in inferred relationships.

Our preliminary molecular analysis using a “test-set” of 32 taxa, representing 22 tribes and nine genes provides a further backbone for tachinid phylogeny that strongly supports the usefulness of “new” nuclear loci developed by J.K. Moulton. This manuscript has experienced some delays in publication due to technical issues, but hopefully should be “in press” by the time you read this article.

As far as a detailed molecular phylogeny of the family goes, we have largely completed our sequencing of 28S rDNA and CAD genes (Fig. 4), although some holes remain to be filled. Preliminary trees are consistent with our multi-gene “test-set” analysis (above), yet reveal a number of finer scale relationships within and between tribes. We have also made great progress with the nuclear genes MAC and MCS (developed by Moulton), having acquired partial sequences for more than 100 taxa for each of these genes. Notably, we are sequencing large fragments of these genes (1700–2000 base pairs each), which takes more effort than smaller fragments, but promises to enable us to make more robust inferences about relationships. Sampling and sequencing of the Phasiinae, the focus of PhD student Jeremy Blaschke in the Moulton Lab, is largely completed with sequences from the genes CAD, MAC, MCS and LGL already acquired. We hope to be more or less finished with sequencing in the next six months, with perhaps some continuing efforts to acquire sequence data for key taxa, and it will probably take another six months to figure out what these data can tell us. Perhaps by this time next year, we will have a manuscript of a comprehensive molecular phylogenetic analysis nearing completion or in review.

PhD students Jeremy Blaschke and Kai Burington are making good progress with their respective subprojects. As stated earlier, Jeremy has nearly completed a molecular phylogenetic analysis of Phasiinae using four nuclear genes which will be used for tracing the evolution of taxonomically important characters throughout the Tachinidae. He is also conducting tachinid faunistic studies in Great Smoky Mountain National Park and creating preliminary species trees of selected Nearctic phasiine genera. Kai is currently preparing for a proposal defense of her research which involves taxonomic and systematic studies of the genus *Eucelatoria* Townsend, a focused phylogenetic study of ‘keel and piercer’ genera within the tribe Blondeliini, and examination of geographic patterns of tachinid diversity.



Figures 1–3. 1. *Imitomyia sugens* (Loew), male. 2. *Freraea montana* (Coquillett), male. 3. *Germaria angustata* (Zetterstedt), male.

Tachinid taxa

We have been able to obtain additional taxa for key groups from both our own collecting efforts and those of our collaborators. Notably, Jim O'Hara was able to obtain specimens of the small tribes *Imitomyiini* (*Imitomyia* Townsend, Fig. 1) and *Freraeini* (*Freraea* Robineau-Desvoidy, Fig. 2) on a successful collecting trip to the western United States. We were able to obtain a specimen of *Germaria angustata* (Zetterstedt) (Fig. 3) through Jim's colleague Syd Cannings from the so-called "Carcross Desert" in Canada's Yukon Territory, as well as *Germaria hispanica* Mesnil from Spain (collected by P. Alvarez and acquired by P. Cerretti). In addition, I (Stireman) recently collected material in Costa Rica and received the calyprate material in alcohol from Brown and Sharkey's former T.I.G.E.R. Malaise trapping project in Thailand (kindly forwarded by Thomas Pape), which will take a long time to properly sift through. Still, there remain a few small tribes for which we have yet to obtain representative taxa, including the *Iceliini*, *Doleschallini*, *Anacamptomyiini*, *Protohystriciini*, and *Trichodurini*. We also remain interested in obtaining additional genera of certain tribes such as *Ethillini*, *Macquartiini*, *Neaerini*, and *Blondeliini*. Jeremy is continuing to acquire a few remaining taxa of the Phasiinae including anything in *Parerigonini* or *Leucostomatini* (especially *Cinochira* Zetterstedt and relatives) and the Australasian genera *Pentatomophaga* de Meijere and *Saralba* Walker. We would be very grateful for any material from these groups or from any rarely collected genera that you (the community of those interested in Tachinidae) may come across. We would also like to acknowledge the many people who have generously sent us material or who have otherwise contributed to the project including Monty Wood, Hiroshi Shima, Diego Inclán, Steve Gaimari, Martin Hauser, Jaakko Pohjoismäki, Theo Zeegers, Thomas Pape, Rudi Schnitzler, Neal Evenhuis, Jeff Skevington, Greg Dahlem, Piluca Álvarez, Syd Cannings, Daniel Whitmore, Ashley Kirk-Spriggs, Brian Brown and Mike Sharkey (sorry if we missed anyone!).

In the process of collecting material for the tachinid phylogeny project, we have obtained preserved tissue from thousands of specimens, most of which we will not use for the current project. Generally, this consists of 1–3 legs preserved in 95% ethanol and stored at –20 or –80°C, as well as the mounted remainder of the specimen as a voucher. Much of this material is from North America, but all biogeographical regions are represented. We hope to take advantage of many of these preserved samples in future systematic projects involving Tachinidae, but we also realize that this tissue collection represents a potentially useful resource for other researchers working on various tachinid groups. Thus, if you (or one of your students) are planning to use DNA data in taxonomic or systematic studies of a particular tachinid taxon, please contact us, and we may be able to help you obtain samples of representative taxa.

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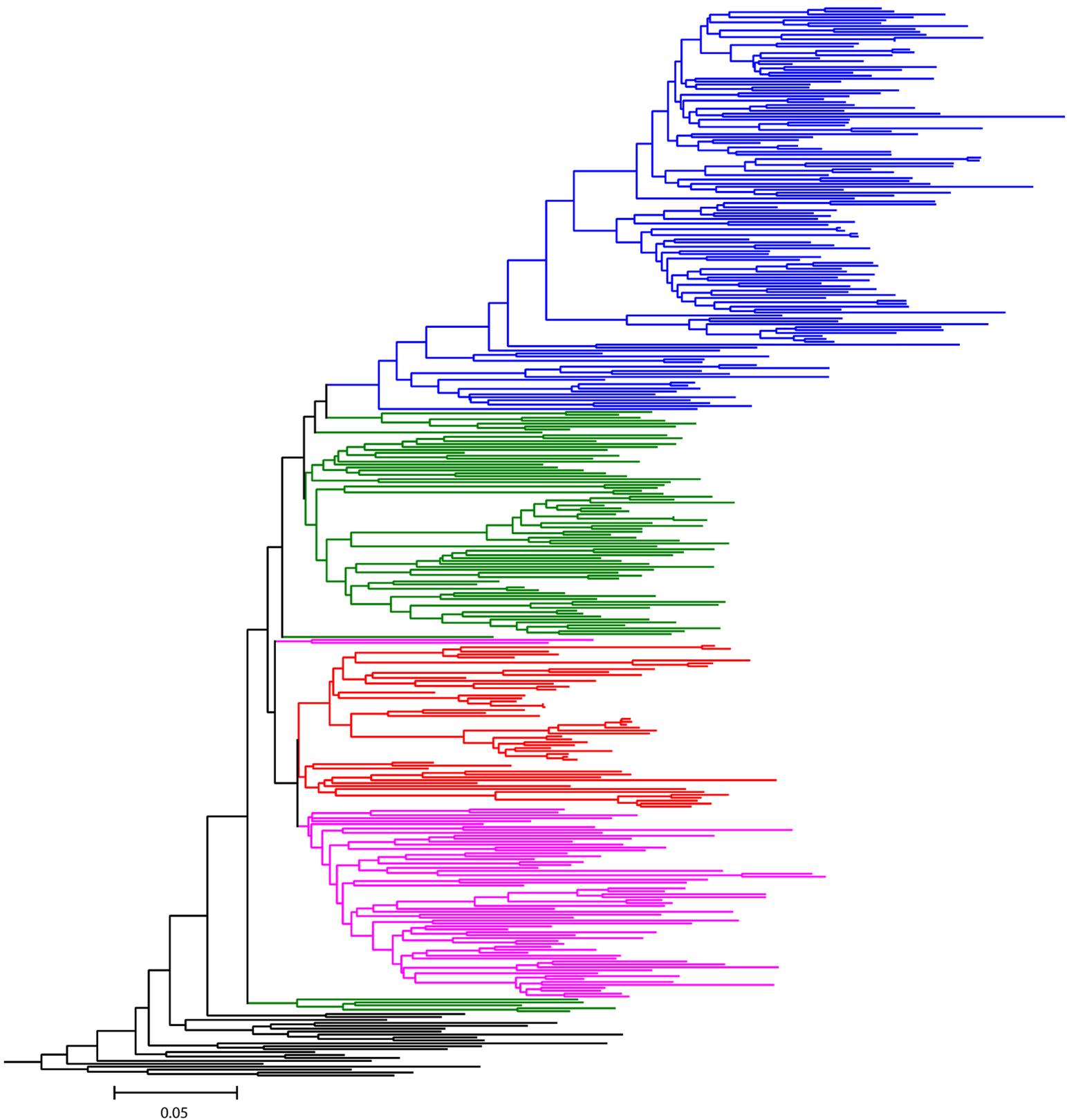


Figure 4. A preliminary phylogenetic reconstruction of 369 tachinid taxa based on 28S rDNA and the nuclear gene CAD, with taxa colored according to subfamily: blue=Exoristinae, green=Tachininae, magenta=Dexiinae, red=Phasiinae, black=outgroups. Taxon names are omitted as we would like to wait until all data is collected and analyzed before presenting our full results.