

Progress towards a molecular phylogeny of Tachinidae, year two

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We reported last year (Stireman *et al.* 2013) in *The Tachinid Times* on our collaborative project, funded by the U.S. National Science Foundation, to study the phylogeny of Tachinidae on a worldwide scale. Since that report, we have made some significant progress towards our goal of assembling a robust phylogenetic tree for Tachinidae. Notably, Cerretti *et al.* (in press) completed a phylogenetic study using 135 morphological characters from 180 tachinid genera. Results from this study largely reflect, with some interesting exceptions, what we are finding from preliminary analyses of our molecular data. Although sampling of taxa and genes for the molecular phylogeny is not yet complete, we will give here a brief update on progress and results so far.

The original goal for the project was to sample five genes from 200–300 tachinid genera representing all of the 59 (or so) recognized tribes. Because a great deal of material had already been accumulated at the time the project officially began, the major difficulty we faced was sampling the smaller, more restricted tribes (see Fig. 1). About half of the tachinid tribes include 30 or fewer described species and just a handful of genera, and ten of these are not found in North America. Some of these smaller tribes undoubtedly represent lineages that are of key importance in

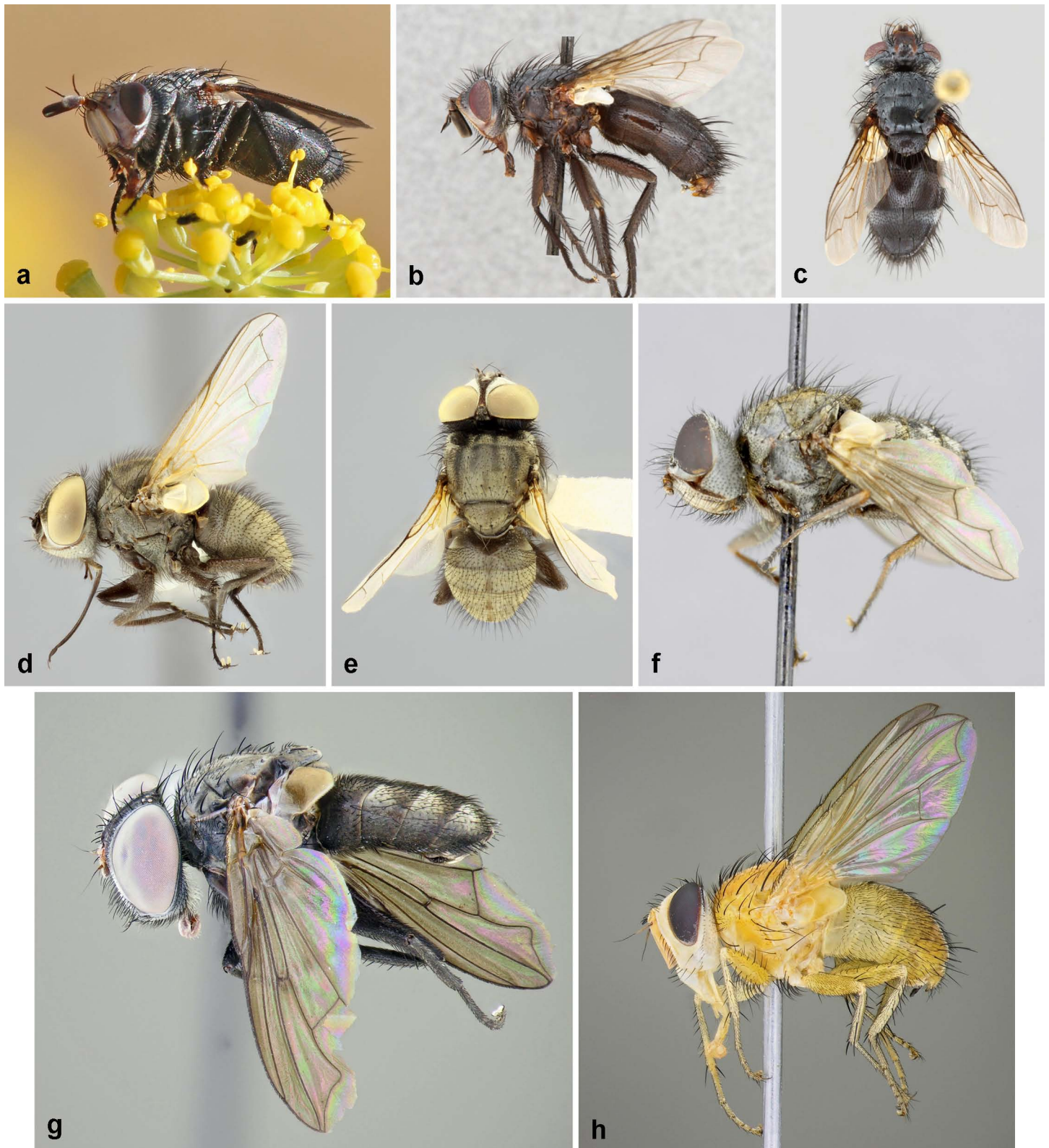


Figure 1. Haves and have-nots. Examples of tachinid genera from small, obscure tribes that we have recently sampled (f–h), or hope to obtain (a–e). **a.** *Germaria hispanica* Mesnil (Spain). **b, c.** *Germaria angustata* (Zetterstedt) (Carcross sand dunes, Yukon, Canada). **d, e.** *Imitomyia sugens* (Loew) (Morinville, Alberta, Canada). **f.** *Rondaniooestrus apivorus* Villeneuve (Swartberg Pass, Western Cape, South Africa). **g.** *Myiotrixia prosopina* Brauer & Bergenstamm (Mt. Allan, Conondale National Park, Queensland, Australia [26°38.39'S 152°38.07'E]; type locality of this species in Australia is unknown). **h.** A probable new genus of Glaurocarini (Mt. Moffatt, Carnarvon National Park, Queensland, Australia).

helping us understand tachinid phylogeny and its implications for the evolution of host use and other characters, while others are possibly nested within larger tribes. We have made some good progress during the last year in obtaining representatives of these smaller tribes. Jaako Pohjoismäki and Theo Zeegers recently sent Palaearctic representatives of Nearerini, Pelatachinini and Germariochaetini, as well as important genera in other tribes. During our recent trip to Australia (see report elsewhere in this newsletter) we were able to obtain specimens of Glaurocarini (Fig. 1h) and the endemic Myiotrixini (Fig. 1g). Last year's trip to South Africa (Cerretti *et al.* 2013) yielded Rondanioestrini (Fig. 1f), parasites of honeybees, and specimens of the isolated genus *Litophasia* Girschner, one of the only tachinids without a developed subscutellum. Rudi Schnitzler in New Zealand is generously sending material of the tribe Occisorini, an endemic radiation that makes up a significant part of the tachinid fauna of New Zealand.

We are still lacking material from seven tribes, some of these widespread across the Palaearctic and/or Nearctic regions but rare. We would especially be grateful for any material from these missing tribes: Imitomyiini (widespread; Fig. 1d,e), Iceliini (Nearctic/Neotropical), Doleschallini (Oriental/Australasian), Anacamptomyiini (Afrotropical/Oriental/Australasian), Protohystriciini (Australasian [New Zealand]), Freraeini (Nearctic/Palaearctic), and Germariini (Palaearctic/Nearctic [Yukon]; Fig. 1a–c).

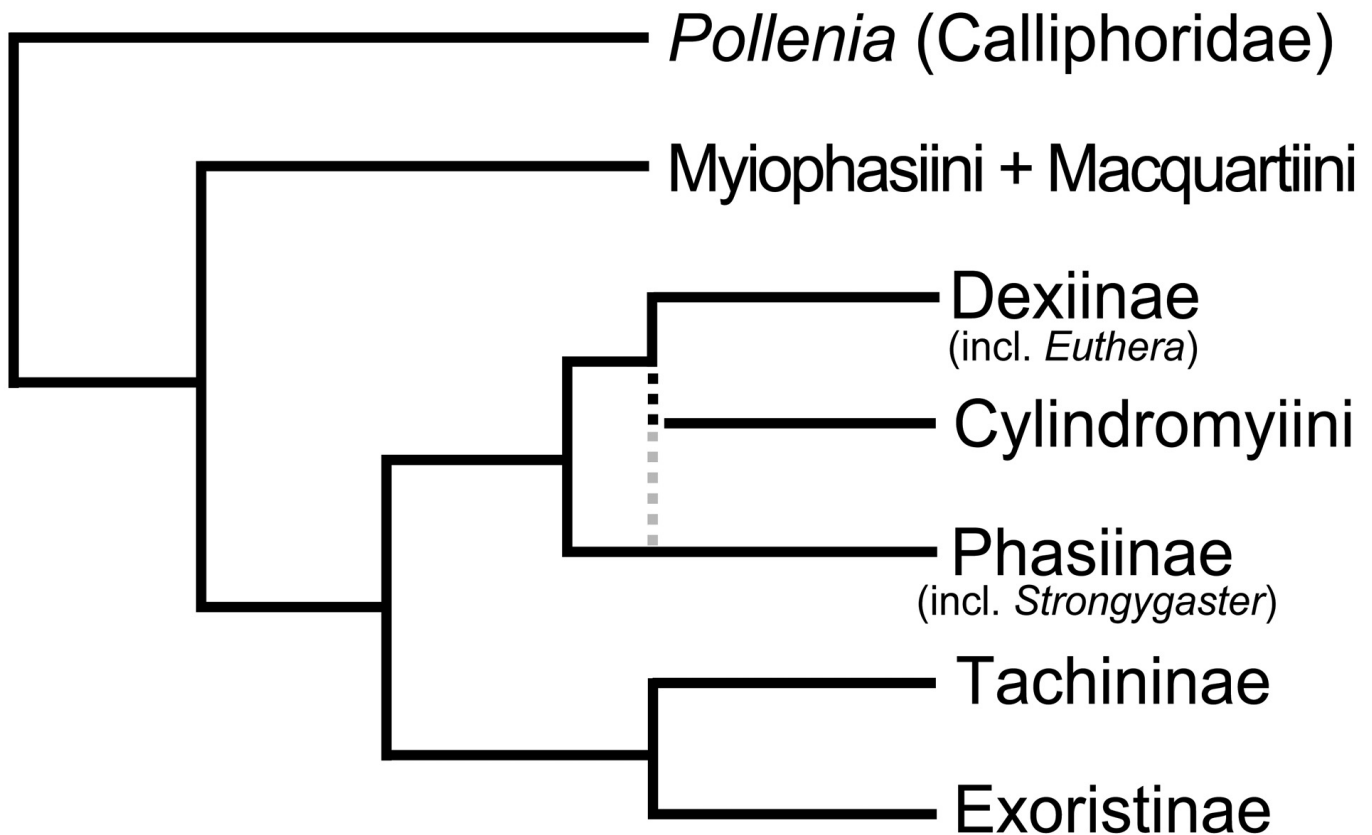


Figure 2. Summary of some major results from ongoing analyses of tachinid phylogeny using molecular data.

Progress on sequencing work in the Stireman Lab is moving along. We are focusing first on the 28S and CAD genes, and have these sequences nearly complete for about 300 genera. We anticipate adding 30–50 additional genera to this total, including specimens from our recent Australia trip. We will be focusing next on MAC and MCS, two genes that are being newly developed (along with a few others) for phylogenetic use by Moulton. In a smaller pilot study (22 tachinids, 9 genes) that will be submitted soon for publication, these last two genes showed very good potential for resolving tachinid relationships. In addition to sequencing the MAC, MCS and LGL genes for the pilot study, Blaschke has been using these genes to focus on the phylogeny of Phasiinae. His results so far are reported in his recently defended Master's thesis (http://trace.tennessee.edu/utk_gradthes/2393/).

Although we are still in the process of assembling and analyzing data, there are some interesting early results that we can share (Fig. 2). First, our results suggest that the calliphorid subfamily Polleniinae is the nearest relative of tachinids. *Pollenia* Robineau-Desvoidy is a genus of widespread (and widely introduced) common flies that are parasitoids of earthworms. We also have evidence for an early-branching lineage within Tachinidae consisting of beetle parasitoids in the tribes Myiophasiini and Macquartiini, which may be the sister to all remaining tachinid tribes. Both of these results are exciting for their implications for the early evolution of host use in Tachinidae. Our results regarding subfamily monophyly are not yet wholly clear. While Exoristinae are strongly supported as monophyletic, Tachininae are very weakly so. We find Dexiinae to be monophyletic, but Cylindromyiini sometimes groups with Dexiinae instead of the remaining Phasiinae. Some tribes are monophyletic, but many are not, including Voriini, Thelairini, Phasiini, Minthoini, Leskiini, Ernestiini, Eryciini, Goniini, and Ethillini. Blondeliini, a tribe of particular interest to our project, is largely composed of a single monophyletic lineage, but certain aberrant genera (e.g., *Phyllophilopsis* Townsend, *Trigonospila* Pokorny) appear to have a more basal position within Exoristinae (see also Stireman 2002, Tachi & Shima 2010). Our data are able to place certain tribes whose subfamily placement has been debated; for example, we find *Euthera* Loew near the base of the Dexiinae, and *Strongygaster* Macquart well-nested within Phasiinae (see also discussion in Cerretti *et al.* in press).

Our picture of tachinid phylogeny grows clearer each time we add new data to the analysis, and we should soon have a fairly complete outline of tribal relationships. As usual, a close look at the details will bring up numerous additional questions that will keep us busy for years to come.

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