

# DNA barcodes for north European Tachinidae: preliminary results and material request

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DNA barcodes based on the mitochondrial cytochrome c oxidase subunit I gene (COI) have proven to be practical and functional for Tachinidae in a number of studies (e.g., Stireman 2010 and references therein). To support the efforts to obtain a good coverage of tachinid sequences, we have initiated the DNA barcoding of north European Tachinidae as part of the Finnish Barcode Of Life (FinBOL, [http://www.finbol.org/eng/ENG\\_finbol.html](http://www.finbol.org/eng/ENG_finbol.html)) in 2011. So far the project has produced barcodes for 225 tachinid species, all of which are stored in the BOLD database (<http://www.boldsystems.org/>). We have recently secured more funding and are currently sequencing large numbers of additional specimens, consisting of a total of 380 species. About 75% of the specimens originally come from Jaakko Pohjoismäki's private collection, now stored in the Tampere Museum of Natural History, Tampere, Finland and the rest are located either in the Finnish Museum of Natural History in Helsinki, other museums or private collections.

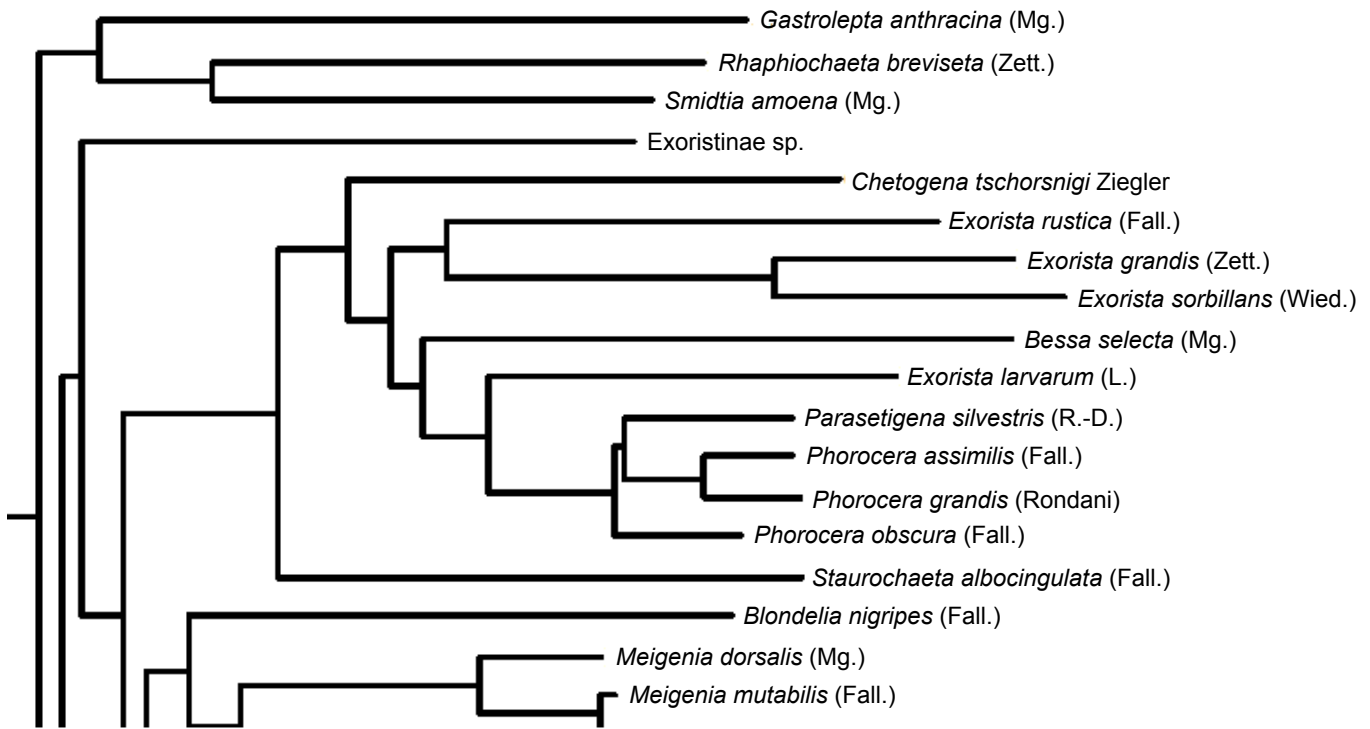
The majority of the material has been collected post-2000 and stored as pinned dry specimens. The specimens have worked well, with sequencing success rate of 90%. Most failures have been due to age of the sample but sometimes for unknown, likely trivial reasons. For example some specimens from the same alcohol-preserved trap material gave good quality sequences while others did not. The oldest sample that so far has worked successfully using the standard approach is a pinned *Xylotachina diluta* (Meigen) from 1994. This is important to note as recent material for

many of the rare species is difficult to find.

Although not being yet publicly available, the DNA barcodes stored in BOLD already serve as an identification tool for database searches against given sequences. Although COI is not in itself adequate for reconstructing phylogenies, it can provide important insight into species limits and genetic distances within closely related species. For example, *Parasetigena silvestris* (R.-D.) (formerly in *Phorocera* R.-D.) is clearly placed within the large *Phorocera*, whereas externally very similar *Exorista grandis* (Zetterstedt) and *E. sorbillans* (Wiedemann) are well separated (Fig. 1). Interestingly, *Microsoma exiguum* (Meigen) shows rather large genotypic variability from the Mediterranean to Finland, whereas COI sequences of *Triarthria setipennis* (Fallén) from these locations are identical (Fig. 2).

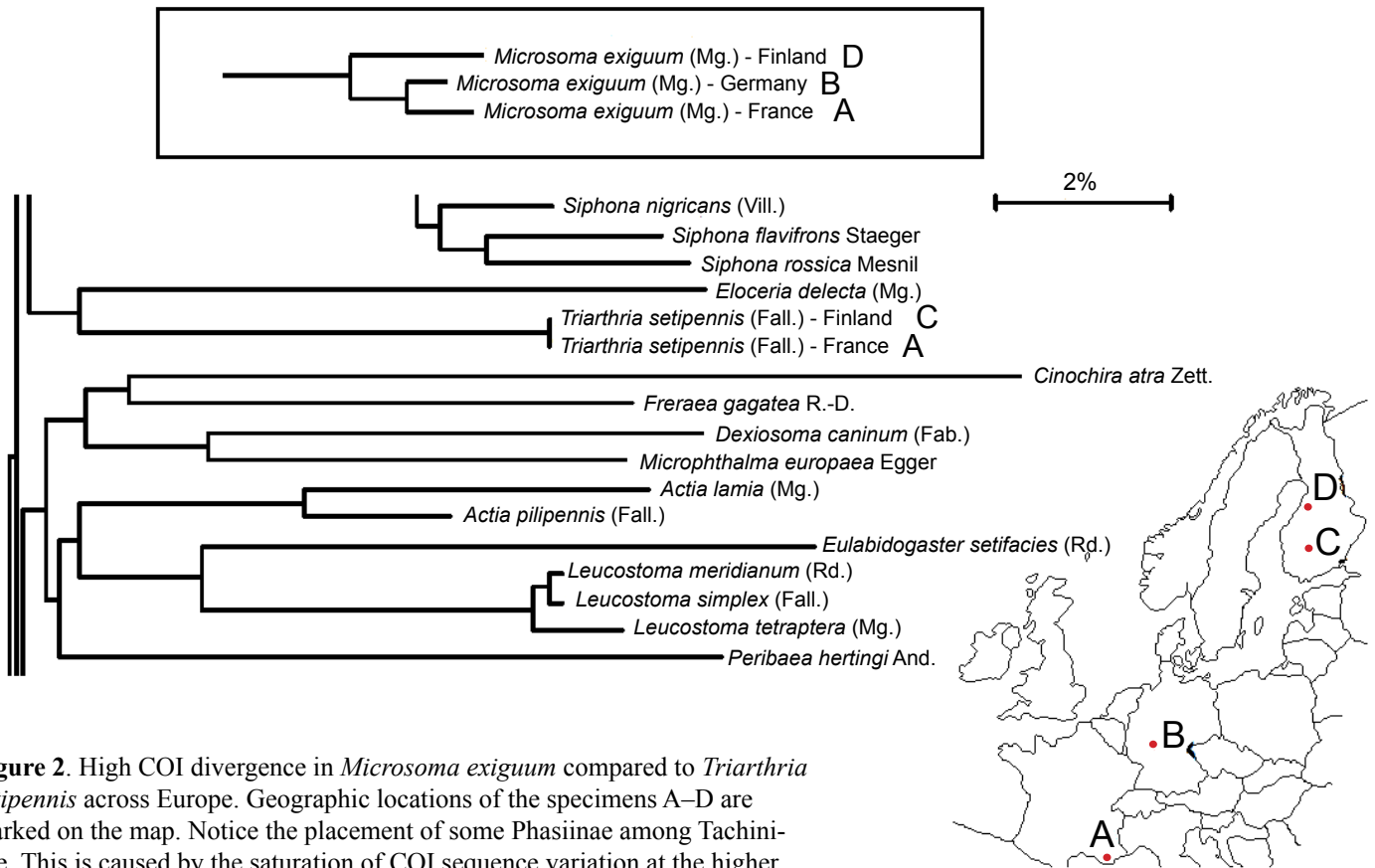
Similarly, COI data can also be used to identify Holarctic distribution patterns in cases where the Palaearctic and Nearctic populations have been described as distinct species. For example, the case of *Cyrtophloeoba vernalis* (Kramer) and *C. nitida* (Curran) is intriguing; the sequenced Finnish *C. vernalis* is within 99.6% similarity embedded among Canadian sequences of *C. nitida* (BOLD Barcode Index Number BOLD:AAP3780). The two species, if distinct at all, are clearly closely related.

However, it is clear that many more samples from various locations need to be sequenced in order to get an impression of the intra- versus interspecific variability within such groups.



**Figure 1.** Neighbor-joining tree of some example Exoristinae based on COI sequence similarities. Notice the position of *Parasetigena* within *Phorocera*.

2%



**Figure 2.** High COI divergence in *Microsoma exiguum* compared to *Triarthria setipennis* across Europe. Geographic locations of the specimens A–D are marked on the map. Notice the placement of some Phasiinae among Tachiniinae. This is caused by the saturation of COI sequence variation at the higher taxonomic divergences. For this reason DNA barcodes alone are often not used in a phylogenetic context. However, this problem might be overcome by using increased taxon sampling (Wilson 2011).

As mentioned earlier, many tachinid species are rarely collected, making it difficult to find specimens suitable for DNA sequencing. We are therefore very grateful for having received several rare specimens as donations from Dr. Hans-Peter Tschorsnig (Stuttgart, Germany), Dr. Joachim Ziegler (Berlin, Germany), Theo Zeegers (Soest, The Netherlands), Mr. Antti Haarto (Mietoinen, Finland), Mr. Kaj Winqvist (Turku, Finland), Mr. Kari Varpenius (Raahe, Finland) and Mr. Jussi Koistinen (Espoo, Finland). However, there is still a number of interesting species missing or needing additional specimens, for which we request assistance from other tachinid enthusiasts:

### Exoristinae

*Admontia seria* (Meigen)  
*Bessa parallela* (Meigen)  
*Carcelia puberula* Mesnil, *C. tibialis* (R.-D.)  
*Chetogena* apart from *C. tschorsnigi* Ziegler  
*Drino atropivora* (R.-D.), *D. bohémica* Mesnil, *D. gilva* (Hartig)  
*Erycia* apart from *E. fatua* (Meigen)  
All *Exorista* sg. *Adenia* apart from *E. rustica* (Fallén)  
*Exorista fasciata* (Fallén)  
All *Istocheta* spp.  
*Ligeriella aristata* (Villeneuve)  
*Medina luctuosa* (Meigen)  
*Myxexoristops arctica* (Zetterstedt), *M. bonsdorffi* (Zetterstedt)  
*Oswaldia eggeri* (B. & B.), *O. reducta* (Villeneuve)  
*Phebellia clavellariae* (B. & B.)  
*Policheta unicolor* (Fallén)  
*Senometopia confundens* (Rondani), *S. intermedia* (Herting), *S. lena* (Richter)  
*Thecocarcelia acutangulata* (Macquart)  
*Vibrissina turrata* (Meigen)  
*Winthemia erythrura* (Meigen), *W. venusta* (Meigen)

### Tachininae

*Actia infantula* (Zetterstedt), *A. maksymovi* Mesnil  
All *Anthomyiopsis* spp.  
All *Aphantorhaphopsis* spp.  
*Ceranthia pallida* Herting, *C. tristella* Herting, *C. vernerii* Andersen  
*Ceromya dorsigera* Herting, *C. flaviceps* (Ratzeburg), *C. flaviseta* (Villeneuve)  
*Cleonice keteli* Ziegler, *C. nitidiuscula* (Zetterstedt)  
All *Germaria* spp.  
All *Graphogaster* spp.  
*Linnaemya haemorrhoidalis* (Fallén), *L. olsuffjevi* Zimin, *L. rossica* Zimin

*Macroprosopa atrata* (Fallén)  
*Panzeria laevigata* (Meigen), *P. vagans* (Meigen)  
*Peleteria ferina* (Zetterstedt), *P. popelii* (Portshinsky)  
*Peribaea longirostris* Andersen, *P. setinervis* (Thomson)  
*Phytomyptera nigrina* (Meigen), *P. riedeli* (Villeneuve), *P. vaccinii* Sintenis  
*Siphona grandistylum* Pandellé, *S. hungarica* Andersen, *S. immaculata* Andersen, *S. variata* Andersen

### Dexiinae

*Billaea fortis* (Rondani)  
*Blepharomyia piliceps* (Zetterstedt)  
*Dexia vacua* (Fallén)  
All *Pandelleia* spp.  
All *Rondania* spp.  
*Stomina tachinoides* (Fallén)  
*Villanovia villicornis* (Zetterstedt)

### Phasiinae

*Besseria melanura* (Meigen)  
*Opesia cana* (Meigen)  
All *Strongygaster* spp.

The specimens should preferably be collected in the 2000s, but as noted earlier we welcome also older samples. Dry and ethanol-preserved material are both acceptable. Ideally, we would like to borrow the whole specimen for documentation purposes. If you do not wish to donate the specimen, then it will be returned after sampling (removing a leg) and documenting together with a label, which helps to connect the specimen with the barcode in the future. Please feel free to contact us with your thoughts and suggestions. We're hoping to hear from you!

### REFERENCES

- Stireman, J.O. III. (2010) A modest (?) proposal: the phylogeny and evolution of world Tachinidae (Diptera). *The Tachinid Times*, 23, 2–3.  
Wilson, J.J. (2011) Assessing the value of DNA barcodes for molecular phylogenetics: effect of increased taxon sampling in Lepidoptera. *PLoS ONE*, 6 (9), e24769. doi: 10.1371/journal.pone.0024769.