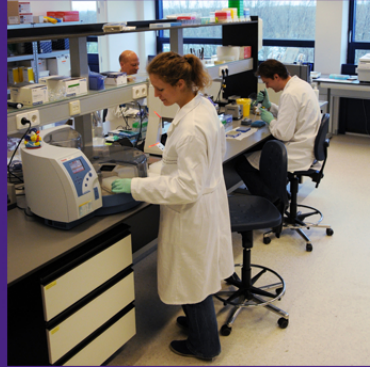
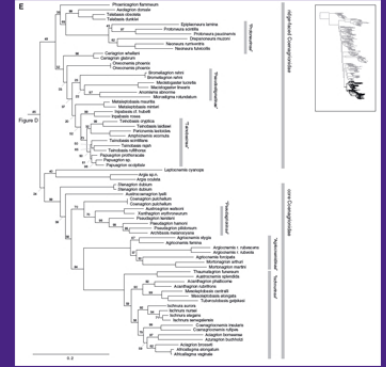
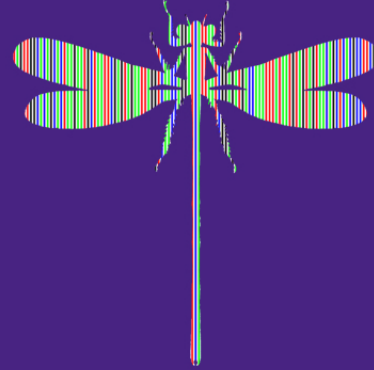


Frank Stokvis
senior research technician



All Odonate barcoding project
7816 COI sequences



(student) supervision
(stacking microscope) photography
graphic design, ion torrent

16S, 28S, ITS
±1100 sequences
MrBayes, RAxML, PAUP*

```
TITLE: METH024_PHYLOGENETIC_ANALYSES      Author: Frank Stokvis
Version: METH024.01                       Authorization Date:

5.2 BAYESIAN INFERENCE

5.2.1 Determining best fit nucleotide substitution model
The best-fit nucleotide substitution model can be assessed with MrModeltest 2.3
Make a copy of the MrModeltest 2.3 folder for each data partition to prevent the output from being
overwritten.
PAUP
- File/Open/nexus file
- File/Open/All Files/!MrModeltest/

MrModeltest 2.3
- Run 'run_mm_bar'
- Open 'PAUPBlock.br' with WordPad (if 'PAUPBlock.br' has not been generated, run 'mm_bar'
in a shorter path on disc e.g. C:\MrModeltest)
- Copy the MrBayes settings from the 'HIERARCHICAL LIKELIHOOD RATIO TESTS (hLRTs)
PAUP
Letet nst=6 rate=i gamma:
Reset statefreq=dirichlet(1,1,1,1);

- Open nexus file with WordPad. Turn off word wrap. View/Word wrap
- Paste the MrBayes settings at the bottom of the nexus file

5.2.2 Adjusting MrBayes settings
WordPad
Copy the following MrBayes settings
BEGIN MRBAYES:
log start filename=log_hcmp.cwk append;
Letet nst=6 rate=i gamma:
Reset statefreq=dirichlet(1,1,1,1);
```

