

Phylogenetic inference of calyptrates, with the first mitogenomes for Gasterophilinae (Diptera: Oestridae) and Paramacronychiinae (Diptera: Sarcophagidae)

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Abstract :

The complete mitogenome of the horse stomach bot fly *Gasterophilus pecorum* (Fabricius) and a near-complete mitogenome of Wohlfahrt's wound myiasis fly *Wohlfahrtia magnifica* (Schiner) were sequenced. The mitogenomes contain the typical 37 mitogenes found in metazoans, organized in the same order and orientation as in other cyclorrhaphan Diptera. Phylogenetic analyses of mitogenomes from 38 calytrate taxa with and without two non-calytrate outgroups were performed using Bayesian Inference and Maximum Likelihood. Three sub-analyses were performed on the concatenated data: (1) not partitioned; (2) partitioned by gene; (3) 3rd codon positions of protein-coding genes omitted. We estimated the contribution of each of the mitochondrial genes for phylogenetic analysis, as well as the effect of some popular methodologies on calytrate phylogeny reconstruction. In the favoured trees, the Oestroidea are nested within the muscoid grade. Relationships at the family level within Oestroidea are (remaining Calliphoridae (Sarcophagidae (Oestridae, Pollenia + Tachinidae))). Our mito-phylogenetic reconstruction of the Calyptratae presents the most extensive taxon coverage so far, and the risk of long-branch attraction is reduced by an appropriate selection of outgroups. We find that in the Calyptratae the ND2, ND5, ND1, COIII, and COI genes are more phylogenetically informative compared with other mitochondrial protein-coding genes. Our study provides evidence that data partitioning and the inclusion of conserved tRNA genes have little influence on calytrate phylogeny reconstruction, and that the 3rd codon positions of protein-coding genes are not saturated and therefore should be included.

Key Word :

mitogenome, gene contribution, taxon sampling, long-branch attraction, phylogeny, Oestroidea, Calyptratae.

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