



DNA Barcoding: Mixed results for big-headed flies (Diptera: Pipunculidae)

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Abstract

Sequence data from 658 base pairs of mitochondrial cytochrome c oxidase I (*cox1*) were analysed for 28 described species of Pipunculidae (Diptera) in an effort to test the concept of DNA Barcoding on this family. Two recently revised but distantly related pipunculid lineages with presumed different evolutionary histories were used for the test (*Clistoabdominalis* Skevington, 2001 and *Nephrocerus* Zetterstedt, 1838). An effort was made to test the concept using sister taxa and morphologically similar sibling species swarms in these two genera. Morphological species concepts for *Clistoabdominalis* taxa were either supported by *cox1* data or found to be too broad. Most of the discordance could be accounted for after reassessing morphological characters. In these cases, the molecular data were invaluable in assisting taxonomic decision-making. The radiation of Nearctic species of *Nephrocerus* could not be diagnosed using *cox1*. The ability of *cox1* to recover phylogenetic signal was also tested on *Clistoabdominalis*. Morphological data for *Clistoabdominalis* were combined with the molecular data set. The pipunculid phylogeny from molecular data closely resembles the published phylogeny based on morphology. Partitioned Bremer support is used to localize areas of conflict between the datasets.

Key words: Pipunculidae, Diptera, DNA Barcoding, phylogeny, mitochondrial rDNA, *cox1* gene, COI, molecular systematics, morphology, total evidence

Introduction

It has been proposed that the mitochondrial gene cytochrome c oxidase I (*cox1*—also referred to as COI) can be used as the core of a global identification system for animals (Hebert et al. 2003a). We decided to test this concept of ‘DNA barcoding’ on big-headed flies (Pipunculidae) using two recently revised genera. Six hundred and fifty-eight base pairs of *cox1* were sequenced for 17 of 29 species of Australian *Clistoabdominalis* and all six species of Nearctic *Nephrocerus*. Three Palaearctic species of *Nephrocerus* were included in the analysis to help interpret the results for this lineage.

Background and Philosophy of DNA Barcoding

Molecular data has long been used to help with species delimitation (Sperling 2003). In bacterial systematics, 16S rRNA has been the standardized dataset used for new species description for years (Lipscomb et al. 2003; Theron and Cloete 2000; Vandamme et al. 1996). In bacteriology, it has often also been used as the only dataset for phylogeny reconstruction and classification and as a result has many detractors (e.g. Gest 1999).

Only recently has there been a push to use a specific standardized molecular dataset across the animal kingdom (Hebert et al. 2003a). A call to focus on only four genes, including COI, across all insects was made