

## DNA barcodes: Evaluating the potential of COI to differentiate closely related species of *Elachista* (Lepidoptera: Gelechioidea: Elachistidae) from Australia

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### Abstract

We compared DNA barcoding to “traditional” taxonomic tools in clarifying relationships in complexes of closely related, putative “species” of Elachistinae moths (Gelechioidea: Elachistidae) occurring in Australia. A 705 bp fragment of the 3'-end of cytochrome c oxidase subunit I gene (COI) was used. This mtDNA fragment did not differentiate between all species-level taxa that could be defined by morphological and/or ecological differences. Different evolutionary rates of COI among closely related lineages were observed. Although our findings are based on the variability of the 3' end of the COI gene and not the 5' end barcode fragment, we are convinced that thorough exploration of traditional morphology and ecology is a prerequisite for exploring insufficiently known taxonomies by the barcode approach. The sole use of COI barcoding, whether considering COI-5' or COI-3' fragment, may fail to recognize closely related species. Our results discourage this approach for delimitation of closely related species, but its use is encouraged as an additional tool for exploring little known taxonomies or as an identification tool for previously thoroughly studied species complexes.

**Key words:** barcode, COI-3', taxonomy, *Elachista*, identification, delimitation of species, morphology

### Introduction

DNA barcoding proposes the use of DNA sequences to identify and classify an organism. The potential of a 650 bp fragment of the 5'-end of mitochondrial cytochrome c oxidase subunit I (COI)-based species identification system was proposed and partially demonstrated by Hebert *et al.* (2003b). Among the benefits of this particular gene is its ease of acquisition and alignment, in addition to the fundamental criterion, a high level of