

1 Testing the utility of mitochondrial COI sequences for the  
2 identification and phylogenetic analysis of New Zealand  
3 caddisflies (Trichoptera)

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22 Running head: mtDNA identification and phylogeny of New Zealand caddisflies

23 **Abstract** We tested the hypothesis that cytochrome *c* oxidase subunit 1 (COI) sequences  
24 would successfully discriminate recognised species of New Zealand caddisflies. We  
25 further examined whether phylogenetic analyses, based on the COI locus, could recover  
26 currently recognised superfamilies and suborders. COI sequences were obtained from 105  
27 individuals representing 61 species and all 16 families of Trichoptera known from New  
28 Zealand. No sequence sharing was seen between members of different species and  
29 congeneric species showed from 2.3 - 19.5% divergence. Sequence divergence among  
30 members of a species was typically low (mean = 0.7%; range 0-8.5%), but two species  
31 showed intraspecific divergences in excess of 2%. Phylogenetic reconstructions based on  
32 COI were largely congruent with prior conclusions based on morphology, although the  
33 sequence data did not support placement of the purse-cased caddisflies (Hydroptilidae)  
34 within the uncased caddisflies, and in particular, the Rhyacophiloidea. We conclude that  
35 sequence variation in the COI gene locus is not only a useful tool for the identification of  
36 New Zealand caddisfly species, but that it can provide preliminary phylogenetic  
37 inferences. Further work is needed to ascertain the significance of the few cases of high  
38 intra-specific divergence and to determine if any cases of sequence sharing will be  
39 detected with larger sample sizes.

40 **Keywords** Aotearoa, aquatic insects, Arthropoda, barcoding, mtDNA, phylogeny,  
41 systematics, taxonomy