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Using various lines of evidence to identify *Chironomus* species (Diptera: Chironomidae) in eastern Canadian lakes

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Abstract

Chironomus Meigen (Diptera, Chironomidae) larvae are usually the largest sediment-burrowing chironomids, and as such often constitute a major part of the freshwater infaunal biomass. However, use of this genus in ecological, environmental and paleoecological studies is hampered by the fact that *Chironomus* larvae are difficult to identify to species because the larvae of many species are morphologically similar. We used a combination of morphological, cytological and genetic techniques to distinguish *Chironomus* larvae collected from 31 water bodies located in eastern Canada, producing 17 distinguishable groupings. These groups of larvae were ultimately identified as belonging to 14 known species (*C. anthraci-*

mus, *C. bifurcatus*, *C. cucini*, *C. decorus*-group sp. 2, *C. dilutus*, *C. entis*, *C. frommeri*, *C. harpi*, *C. maturus*, *C. nr. atroviridis* (sp. 2i), *C. ochreatus*, *C. plumosus*, *C. staegeri* and *C. 'tigris'*) and three other species that remain unidentified (*C. sp.* NAI-III). No single approach served to delimit and identify larvae of all 17 *Chironomus* species that we collected. Although we expected that morphological criteria alone would be insufficient, our results suggest that DNA barcoding, using either the mitochondrial *cox1* or the nuclear *gb2 β* gene, was also inadequate for separating some *Chironomus* species. Thus we suggest that multiple approaches will often be needed to correctly identify *Chironomus* larvae to species.

Key words: *Chironomus*, morphology, cytology, DNA barcoding, *cox1*, *gb2 β* , Canada

Introduction

The insect genus *Chironomus* Meigen (Diptera, Chironomidae) is found in fresh waters on all continents except Antarctica. It includes several hundred species, now classified into three subgenera (*Chaetolabis*, *Chironomus*, *Lobochironomus*) (the subgenus *Camptochironomus* is no longer recognized—see Sæther (2012)), as well as other species that are yet to be described (Ryser *et al.* 1985; Ashe & Cranston 1990; Martin 2013). In lakes from the tropics (Hare & Carter 1986), to the temperate (Jónasson 1972), to the Arctic (Butler 1982), *Chironomus* larvae are usually the largest sediment-burrowing chironomid and often represent a major part of the infaunal biomass. Thus *Chironomus* larvae can be an important source of food for fish and are widely used in ecological (Jónasson 1972), environmental (Martin *et al.* 2008) and paleoecological (Brooks *et al.* 2007) studies of fresh waters. If we are to understand their roles in aquatic ecosystems, it is important to be able to correctly identify *Chironomus* species.

The identification of *Chironomus* larvae to species can be problematic because there are few conspicuous morphological differences among many *Chironomus* species (Lindeberg & Wiederholm 1979). As a result, larvae are often referred to simply as *Chironomus* spp. (Nyman *et al.* 2005) or at best are grouped into types according to the presence and form of their abdominal tubules (Shobanov *et al.* 1996) or the shape of their mouth parts (Brooks *et al.* 2007). Such groupings can limit the use of *Chironomus* larvae in ecological, environmental and paleoecological studies because behavioural and ecological differences among species are often important. For example, cadmium concentrations in sympatric *Chironomus* species can vary by an order of magnitude because of differences in their feeding habits and consequent contaminant exposure (Martin *et al.* 2008; Proulx & Hare 2008, 2013). Pooling such species would clearly limit their use as contaminant biomonitors. If we cannot correctly identify *Chironomus* larvae to species, then it is difficult to use them to infer environmental impacts.

In early studies, features of the head capsule and abdominal tubules were used to identify *Chironomus* larvae to species (Johannsen 1937). Subsequently, *Chironomus* species were also separated on the basis of the structure of polytene chromosomes located in their salivary glands (Keyl 1962; Martin 1979; Wülker *et al.* 1989). In the last decade or so, genetic techniques have been used to supplement these earlier taxonomic methods. For example, the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) approach has been used to produce species-specific DNA profiles that can differentiate among *Chironomus* species (Carew *et al.* 2003; Sharley *et al.* 2004). This technique involves first amplifying specific genes or regions with PCR, and then digesting the resulting PCR amplicons with restriction endonucleases. Restriction endonucleases cut PCR amplicons differentially based on nucleotide differences in their DNA sequence, thereby generating a species-specific RFLP or DNA profile. The DNA profiles are visualised by gel electrophoresis as DNA fragments of different lengths. Although this method is inexpensive and useful for screening large numbers of individuals, it only examines a subset of the variation present in PCR amplicons (Pfrender *et al.* 2010).

Another genetic technique used to separate and identify species is DNA sequencing (also known as Sanger sequencing) of PCR amplicons. This technique, referred to as DNA barcoding when used for identifying species, is more exact than PCR-RFLP as it detects all nucleotide differences. The standard gene used for DNA barcoding is the 3' end of the mitochondrial *cytochrome oxidase subunit I* (*cox1*; Hebert *et al.* 2003). Advantages of using the *cox1* gene are that universal primers are able to amplify this gene from many animal groups (Folmer *et al.* 1994) and sequence variations in *cox1* can be used to discriminate among many closely-related species (Hebert *et al.* 2004a). In insects, DNA barcoding using the *cox1* gene has been used to identify species from a range of groups including the Collembola (Hogg & Hebert 2004), the Ephemeroptera (Ball *et al.* 2005; Elderkin *et al.* 2012), the Coleoptera (Davis *et al.* 2011) and the Chironomidae (Carew *et al.* 2007; Ekrem *et al.* 2007; Pfenninger *et al.* 2007; Sinclair & Gresens 2008; Ekrem *et al.* 2010; Carew *et al.* 2011; Stur & Ekrem 2011). Although *cox1* sequences can

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