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Morphology and molecules say: *Tanytarsus latens*, sp. nov. from Finland (Diptera: Chironomidae)

WOJCIECH GIŁKA^{1,4}, LAURI PAASIVIRTA², PIOTR GADAWSKI³ & MICHAŁ GRABOWSKI³

¹University of Gdańsk, Faculty of Biology, Department of Invertebrate Zoology and Parasitology, Laboratory of Systematic Zoology; Wita Stwosza 59, 80–308 Gdańsk, Poland

²Ruuhikoskenkatu 17, 24240 Salo, Finland

³Department of Invertebrate Zoology and Hydrobiology, University of Łódź; Banacha 12/16, 90–237 Łódź, Poland

⁴Corresponding author. E-mail: wojciech.gilka@biol.ug.edu.pl

Abstract

Tanytarsus latens sp. nov. is described from Finland (Ostrobothnia borealis, Satakunta). Both morphological and molecular analyses indicate that *T. latens* belongs to the *mendax* species group. The adult male hypopygium of the new species resembles that of *Tanytarsus occultus* Brundin and of *T. desertor* Giłka et Paasivirta, while the molecular analysis based on the mitochondrial cytochrome oxidase (COI) gene fragment evidences that *T. latens* is a sister species to most of European *Tanytarsus* of the *mendax* group's core, for which the COI barcodes are known. Notes on biology of *T. latens* are also provided.

Key words: Diptera, Chironomidae, systematics, DNA barcoding, new species, Finland

Introduction

Chironomidae, with nearly 7,500 specific and 550 generic names, is one of the largest and most diverse dipteran families (Pape *et al.* 2011). The species richness in the 12 known chironomid subfamilies is, however, much unequal, and the majority of described species belongs to Orthoclaadiinae and Chironominae. Tanytarsini is one of three tribes in the subfamily Chironominae. It comprises approximately 10% of all known chironomid species, including those belonging to the largest genus *Tanytarsus* van der Wulp. Recent inventories indicate that *Tanytarsus* comprises 355 known valid species worldwide (Lin *et al.* 2018b). Most of them are clustered into species groups. Systematic relationships within and between several species-rich groups, in particular the *chinyensis*-, *eminulus*-, *gregarius*-, *lugens*- and *mendax* groups, have been comprehensively analysed on the basis of both morphology and DNA sequences, including the best-known species recorded from Europe (e.g. Ekrem 2001, 2002, 2003, 2004; Ekrem *et al.* 1999, 2003; Giłka & Paasivirta 2007; Giłka 2010, 2011a, b; Lin *et al.* 2017, 2018b). However, the above groups have recently been profoundly revised, and the previously proposed concepts were refuted (Lin *et al.* 2017, 2018b). As a result, both the *chinyensis*- and *eminulus* groups were split into several groups, the *gregarius*- and *lugens* groups were merged, while a core of the *mendax* group was redefined after exclusion of *Tanytarsus aculeatus* Brundin, *T. formosanus* Kieffer and *T. ovatus* Johannsen.

Major pros of molecular methods, such as DNA barcoding, in complementing the morphological studies are evident in the case of immature stages, damaged and neglected specimens, when phenotypic characters are difficult to define or if a researcher lacks experience to identify taxa on the basis of their morphology (Ball *et al.* 2005, Geraci *et al.* 2011, Hebert *et al.* 2003, Janzen *et al.* 2005, Savolainen *et al.* 2005, Montagna *et al.* 2016a). DNA-based diagnostic characters may also serve as the backbone for a taxonomic description of newly discovered cryptic species (e.g. Anderson *et al.* 2013).

The DNA barcoding or, more recently developed, metabarcoding have been proposed, and successfully adopted as an efficient method for species identification and habitat biodiversity assessment using standardized