



Conference Abstract

DNA barcoding reveals an unknown Chironomidae diversity from the freshwater biodiversity hot-spot: comparison between local and the European datasets

Piotr Gadawski[‡], Matteo Montagna[§], Bruno Rossaro^l, Wojciech Giłka[¶], Vladimir Pesic[#], Michal Grabowski[‡], Giulia Magoga[§]

[‡] Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland

[§] Department of Agricultural and Environmental Sciences – Production, Landscape, Agroenergy, University of Milan, Milan, Italy

^l Department of Food, Environmental and Nutritional Sciences, University of Milan, Milan, Italy

[¶] Department of Invertebrate Zoology and Parasitology, Laboratory of Systematic Zoology, University of Gdańsk, Gdańsk, Poland

[#] Department of Biology, University of Montenegro, Podgorica, Montenegro

Corresponding author: Piotr Gadawski (piotr.gadawski@biol.uni.lodz.pl)

Received: 04 Mar 2021 | Published: 04 Mar 2021

Citation: Gadawski P, Montagna M, Rossaro B, Giłka W, Pesic V, Grabowski M, Magoga G (2021) DNA barcoding reveals an unknown Chironomidae diversity from the freshwater biodiversity hot-spot: comparison between local and the European datasets. ARPHA Conference Abstracts 4: e65498.

<https://doi.org/10.3897/aca.4.e65498>

Abstract

In the present study, we developed and evaluated the first reference barcode library for non-biting midges (Diptera: Chironomidae) as flagship taxa of freshwater ecology from Skadar Lake system (Montenegro and Albania), a well-known hotspot of freshwater biodiversity composed by the young lake Skadar (originated 1200 before present) and by its old system of springs (originated during Pliocene). Using an expanded reference library and records deposited in Barcode of Life Database (BOLD), we estimated DNA barcoding efficiency for the European Chironomidae. Study provides COI barcodes for 770 Chironomidae individuals assigned, based on morphology, to 77 species collected in the Skadar Lake basin. Molecular analyses assigned sequences to 100 BINs and 104 OTUs (all records from this area are new for online repositories) and confirms the usefulness of

DNA barcoding for the identification of non-biting midges. Additionally, we explored chironomid species distribution patterns in Europe using universal Barcode Index Number (BIN) with a discussion of problematic species groups, both for traditional taxonomy and DNA barcoding. The results of our study provide the first insight into the factual chironomid species diversity of the Lake Skadar basin, in comparison with chironomid fauna at the European scale. The results fill a significant gap in knowledge of biodiversity in the Balkan region. Based on the results of Chironomidae fauna investigation, we conclude that the Skadar Lake basin is now well sampled and such a high representation of species from various sampling sites provides reliable estimation of the non-biting midges fauna.

Keywords

Chironomidae, DNA barcoding, distribution, Europe

Presenting author

Piotr Gadawski

Presented at

1st DNAQUA International Conference (March 9-11, 2021)

Funding program

Polish National Science Centre, Polish National Agency for International Exchange

Grant title

Species diversity and origin of Chironomidae fauna from geologically young Lake Skadar (Montenegro/Albania) and its old spring system based on morphological characters and Next Generation Sequencing Techniques.