

New molecular methods to assess biodiversity. Potentials and pitfalls of DNA metabarcoding: a workshop report

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Reviewable v1

Received: 08 Aug 2019 | Published: 08 Aug 2019

Citation: Kahlert M, Alfjorden A, Apunte-Ramos K, Bailet B, Pérez Burillo J, Carrera Gonzalez AG, Castro D, Di Bernardi C, Dully V, Fekete J, Frühe L, González R, Gratsia E, Hanjalić J, Kamberović J, Kelly A-M, Meriggi C, Nousiainen I, Ørberg SB, Orr J, Quintana CO, Papatheodoulou A, Sargac J, Shahbaz M, Tapolczai K, Tosic K, Wallin I, Zupančič M, Bohman P, Buttigieg PL, Häubner N, Leese F, Macher JN, Peura S, Roslin T, Strand M, Terenius O, Vasselon V, Weigand AM (2019) New molecular methods to assess biodiversity. Potentials and pitfalls of DNA metabarcoding: a workshop report. *Research Ideas and Outcomes* 5: e38915. <https://doi.org/10.3897/rio.5.e38915>

Abstract

This report presents the outcome of the joint work of PhD students and senior researchers working with DNA-based biodiversity assessment approaches with the goal to facilitate others the access to definitions and explanations about novel DNA-based methods. The work was performed during a PhD course (SLU PNS0169) at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden. The course was co-organized by the EU COST research network DNAqua-Net and the SLU Research Schools Focus on Soils and Water (FoSW) and Ecology - basics and applications. DNAqua-Net (COST Action CA15219, 2016-2020) is a network connecting researchers, water managers, politicians and other stakeholders with the aim to develop new genetic tools for bioassessment of aquatic ecosystems in Europe and beyond. The PhD course offered a comprehensive overview of the paradigm shift from traditional morphology-based species identification to novel identification approaches based on molecular markers. We covered the use of molecular tools in both basic research and applied use with a focus on aquatic ecosystem assessment, from species collection to the use of diversity in environmental legislation. The focus of the course was on DNA (meta)barcoding and aquatic organisms. The knowledge gained was shared with the general public by creating Wikipedia pages and through this collaborative Open Access publication, co-authored by all course participants.

Keywords

DNA barcoding, biodiversity, aquatic organisms, molecular identification, metabarcoding

Date and place

The intensive, week-long PhD course workshop was held from 25th to 29th of March 2019 at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden. The entire course period, including the individual and independent contributions before and after the workshop, lasted from March 8th to May 31st 2019 (Fig. 1).



Figure 1. [doi](#)

MVM house at SLU. Picture Mark Harris.

Introduction

This workshop report gives an overview of the outcomes of the SLU PhD course PNS0169 held in March 2019. As we assume that the course content, i.e. a basic introduction to DNA (meta)barcoding and its application in environmental monitoring and assessment, is of interest to a broader audience, we decided to share this information by editing and creating public Wikipedia pages, and a *Suppl. material 1* with common terms. To explain the background and to summarize the actual work within the course, we publish the course content and outcome as a workshop report.

The course was co-organized by the EU COST Action DNAqua-Net (CA15219), a transdisciplinary and international network that aims to develop new genetic tools for

bioassessment of aquatic ecosystems in Europe and beyond, and the SLU Research Schools Focus on Soils and Water (FoSW) and Ecology - basics and applications. The course attracted 27 participants from 14 countries, and teachers were researchers from SLU and other organisations, among them from DNAqua-Net (Fig. 2, Table 1). The schedule included drafting content for the Wikipedia page on DNA barcoding as well as on metabarcoding of different organism groups, and creating definitions for some common terms ([find the syllabus here](#)) used in organism identification (traditional and molecular). The resulting texts were further developed into full Wikipedia pages and into this workshop report, both during the intense course week at SLU in Uppsala and as joint homework after the course.

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Figure 2. [doi](#)

Participants of the PhD course PNS0169 at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden.

Aims

The main aim of the course was to give the students an insight into the paradigm shift from traditional morphology-based species identification to novel organism-identification approaches based on molecular markers. The course topics also included basic understanding of DNA (meta)barcoding and its potentials and pitfalls. In a broad sense, the course also aimed to educate the public, including interested stakeholders, by using the joint efforts of the students and teachers to create public information on the course topics. The aim of the course was to provide an overview of identification tools and methods currently used in environmental monitoring and research, including recent advances and challenges. The course touched on aquatic organisms, freshwater and marine, and provided additional sources for more information regarding certain organism groups as well as tools and methods. During the course, the students actively acquired information about the ongoing paradigm shift in identifying aquatic organisms for biodiversity and environmental assessment. With this information, the students should now be able to critically evaluate studies that utilized DNA-based taxonomy, and to judge in which contexts DNA-based results might differ from traditionally obtained ones. The students also got the opportunity to work on their own project as a supplementary, optional part of the course. While the course had an aquatic focus, the methodology is universal, and non-aquatic approaches were covered as well.

Key outcomes and discussions

The knowledge gained about the paradigm shift from traditional morphology-based species identification to the use of novel molecular methods was summarized by creating public Wikipedia pages, a Glossary, and this collaborative Open Access publication coauthored by all workshop participants.

Wikipedia pages

Instead of ordinary examinations, the course required an active participation in creating or editing Wikipedia pages about DNA barcoding. To ensure their content quality, the PhD students and senior researchers (the teachers) worked jointly on those pages during and after the course. In this way we aimed at high quality and relevant content to inform the public, stakeholders and other researchers about the ongoing paradigm shift in identifying aquatic organisms for biodiversity and environmental assessment, and to learn about advances and challenges. In combination with a Glossary, which was also created as a course outcome, we hope that our work can help not only the participants of the course, but also a broader public, to gain knowledge about DNA (meta)barcoding and its application potential. The edited or newly created Wikipedia pages are:

- [DNA barcoding](#)
- [Microbial DNA barcoding](#)

- [Algae DNA barcoding](#)
- [Fish DNA barcoding](#)
- [Aquatic macroinvertebrate DNA barcoding](#)
- [DNA barcoding in diet assessment](#)

Glossary: terms related to traditional and molecular identification

During the course participants discussed terms related to traditional and molecular identification and the PhD students defined these terms in discussions with the teachers in their own words, or based on existing definitions from other sources. We hope that this *Glossary* (Suppl. material 1) can provide a good introductory overview of both traditional and molecular terms often used in the context of taxonomic identification.

Funding program

1. COST Action CA15219, 2016-2020 ("DNAqua-Net").
2. Faculty funding for SLU Research Schools of the Swedish University of Agricultural Sciences.

Grant title

1. DNAqua-Net.
2. SLU NJ-faculty research schools.

Hosting institution

Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden

Author contributions

All authors contributed jointly to the content of this report.

Conflicts of interest

There are no conflicts of interest.

Supplementary material

Suppl. material 1: Glossary: terms related to traditional and molecular bioassessment [doi](#)

Authors: PhD students of the SLU course PNS0169, in 2019

Data type: Glossary with definitions in students' own words

Brief description: Given terms related to traditional and molecular identification, the PhD students were asked to define them in their own words using external sources. Terms were defined by the course participants under supervision of the senior researchers. Please use the glossary as a first help and overview, not as an authoritative source. Be assured, there are many definitions out there!

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