ARPHA Conference Abstracts 4: e65473
doi: 10.3897/aca.4.e65473

Conference Abstract

Mind the gap-analysis! – How complete are DNA barcode reference libraries for monitoring-relevant aquatic species in Europe?

Hannah Weigand

Corresponding author: Hannah Weigand (hannah.weigand@mnhn.lu)

Received: 03 Mar 2021 | Published: 04 Mar 2021

Citation: Weigand H (2021) Mind the gap-analysis! – How complete are DNA barcode reference libraries for monitoring-relevant aquatic species in Europe? ARPHA Conference Abstracts 4: e65473. https://doi.org/10.3897/aca.4.e65473

Abstract

Molecular species identification with DNA metabarcoding can potentially accelerate, streamline and standardise biomonitoring routines. Currently, it is tested how this new technique can be implemented for the European Water Framework Directive (WFD) and the European Marine Strategy Framework Directive (MSFD). To connect the results from DNA metabarcoding with the current monitoring routines, an extensive, high-quality DNA barcode reference database is required. Hence, a gap-analysis of the Barcode of Life Data Systems (BOLD) was performed as part of the EU-COST Action DNAqua-Net (Weigand et al. 2019), which was updated in 2021. It aimed to analyse the completeness of BOLD for species on the national WFD monitoring lists and for marine species on the ERMS (European Register of Marine Species) and AMBI (AZTI Marine Biotic Index) lists. The data were supplemented by MitoFish for freshwater fish and Diat.barcode for diatoms.

Several thousands of species were included in the gap-analysis, although not all countries currently apply species-level data for all WFD biological quality elements. The barcode coverage of the different taxonomic groups varied strongly, with high levels (> 80%) for fish and freshwater vascular plants, and low levels for diatoms and freshwater plathelminths (< 15%). As a general pattern, species monitored by several countries had a higher coverage compared to those monitored only by a single country.

The gap-analysis focused additionally on the availability of metadata (e.g., geographical origin of the specimen or determiner name) for the barcodes. Hence, we analysed if the data were stored public (with access to metadata) or private (without access to metadata) in BOLD or if the data were mined from GenBank (metadata are potentially available but not easy to access). Although public data were stored for many species (43% of freshwater macroinvertebrates and 21% of AMBI marine species), the proportion of species without public metadata was not neglectable (22% of freshwater macroinvertebrates and 22% of AMBI marine species).

Another issue that emerged from the gap-analysis was that several deposited barcodes were identified by reverse taxonomy (RT), i.e., specimens were molecularly identified via its DNA barcode and the barcode itself is stored in BOLD with the associated species name. This can be problematic as originally misidentified samples can lead to false RT-identifications, making the data appear more trustworthy than it actually is. For the analysed freshwater macroinvertebrates, 39% of all barcodes and 65% of all public data originated from RT, impacting 11% of all monitored species. As the information about RT is only available for publicly stored data, the real impact of RT might even be higher.

Keywords

gap-analysis, reference library, biological monitoring, DNAqua-Net

Presenting author

Hannah Weigand

Presented at

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

References

- Weigand H, Beermann AJ, Čiampor F, Costa FO, Csabai Z, Duarte S, Geiger MF, Grabowski M, Rimet F, Rulik B, Strand M, Szucsich N, Weigand AM, Willassen E, Wyler SA, Bouchez A, Borja A, Čiamporová-Zaťovičová Z, Ferreira S, Dijkstra KD, Eisendle U, Freyhof J, Gadawski P, Graf W, Haegerbaeumer A, van der Hoorn BB, Japoshvili B, Keresztes L, Keskin E, Leese F, Macher J, Mamos T, Paz G, Pešić V, Pfannkuchen DM, Pfannkuchen MA, Price BW, Rinkevich B, Teixeira MA, Várbíró G, Ekrem T (2019) DNA barcode reference libraries for the monitoring of aquatic biota in Europe: Gap-analysis and recommendations for future work. Science of the Total Environment 678: 499-524. https://doi.org/10.1016/j.scitotenv.2019.04.247