ARPHA Conference Abstracts 4: e65255
doi: 10.3897/aca.4.e65255

Conference Abstract

DNA barcodes for UK freshwater arthropod species: coverage, quality and implications

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Received: 28 Feb 2021 | Published: 04 Mar 2021

Citation: Davidson L (2021) DNA barcodes for UK freshwater arthropod species: coverage, quality and implications. ARPHA Conference Abstracts 4: e65255. https://doi.org/10.3897/aca.4.e65255

Abstract

DNA-based identification methods have been shown to have high detection capability and reduced costs compared to traditional methods and can also enable the detection of species that might be missed using traditional methods (e.g. rare species, cryptic species, larval stages). The success of DNA-based identification is dependent on the 'DNA barcodes' of target species being present in a barcode reference database. In order to use DNA-based identification methods to assess and monitor UK freshwater arthropods for biodiversity and ecological quality assessments, it is vital that comprehensive reference databases are available. Incomplete reference databases result in many sequences derived from metabarcoding not being assigned to species.

Two current projects aim to create collections of high-quality sequences from expertly identified specimens of UK species. The Darwin Tree of Life project aims to sequence the genomes of all the eukaryotic species in Britain and Ireland and FreshBase aims to create a genomic reference collection for UK freshwater invertebrates. The Barcode of Life Data System (BOLD) is one of the main reference databases for animal barcodes. Prioritising the sequencing of UK freshwater arthropod species that are not yet represented in BOLD, would enable more complete identification of UK freshwater biodiversity using metabarcoding and would enable the development of primers to target specific arthropod groups or species.

We analysed the coverage of UK freshwater arthropod species in BOLD. Our analyses show that coverage varies between taxonomic groups and large proportions of sequences

in some orders are only represented by privately stored sequences in BOLD. Analyses of intra- and inter-specific variation in sequences stored in BOLD show that misidentifications or errors can reduce the barcode gap in some species which could cause difficulties in accurately identifying sequences derived from metabarcoding. Representation in BOLD by specimens from the UK is extremely low and analyses show that high geographic variation in sequences in some species could be important for accurate DNA-based identification of UK species. Our results have implications for prioritising the sequencing of UK freshwater arthropods and for the quality control of stored sequences in order to reduce the occurrence of misidentifications and errors that could impact the accuracy of DNA-based identification.

Keywords

DNA barcoding, reference database, freshwater arthropods, CO1, identification

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Presented at

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