

# **FROM DNA BARCODES TO MONITORING OF AMPHIPOD COMMUNITIES: STATUS AND RELEVANCE OF CURATION AND ANNOTATION OF DNA SEQUENCE DATA**

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Amphipod assemblages are often dominant and ecologically relevant components of benthic communities, which in turn are key elements of monitoring programs imposed by the EU Water Framework Directive (WFD). Taxonomic expertise in multiple phyla is essential to assure the scientific rigor and detail of the data produced in monitoring campaigns, but often taxon-specific experts are not available. It is not uncommon to find amphipods identified only to family or genus level in monitoring reports, thus missing essential species-level information; on the other hand, there is no way to verify species-level assignments, and as a result misidentifications can be kept indefinitely in such publications.

With the application of the DNA barcode approach for amphipod species identification, we aim to help streamlining the monitoring of amphipod assemblages, while providing reliable species-level data that could be directly compared across time and space with similar sequence data obtained elsewhere. The success of such an approach depends on a comprehensive and certified reference library of DNA barcodes for all

European amphipods. The reference library must include voucher specimens stored in a public collection, which are clearly linked with its metadata and barcode-standard sequence data. Although several of these (and other) quality-control elements are already implemented in DNA barcoding projects, we propose additional operational steps, which involve revision, validation and annotation of databases. Here we merge public CO1-barcode data available for Amphipoda together with our own unpublished sequences to make a preliminary assessment of challenges and prospects in the creation of a validated reference library of DNA barcodes for Amphipoda. This publicly accessible library will be of utmost importance in a context of increasing implementation of WFD monitoring across Europe, and of the emergence of applications of second-generation sequencing in monitoring programmes.