

A curated SEQUENCE LIBRARY: the fundament of all DNA-based monitoring

WHY is a sequence library necessary for DNA-based monitoring?

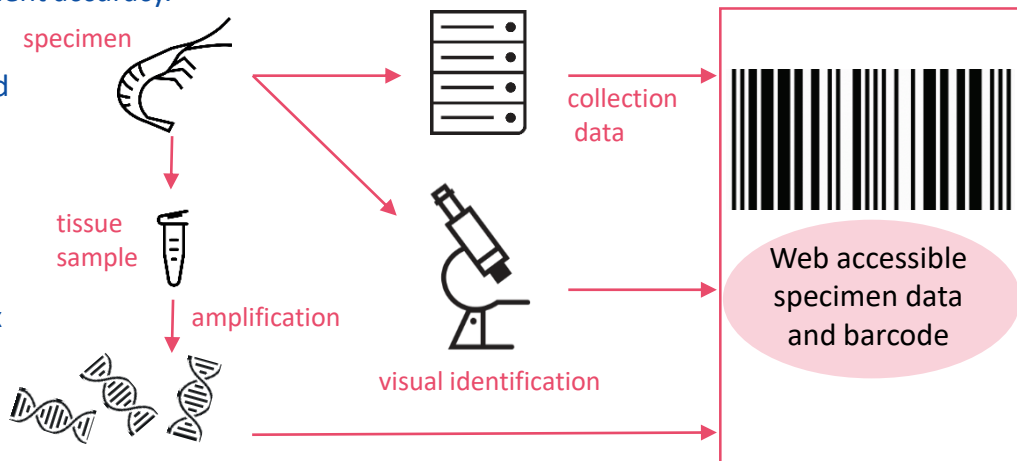


Comprehensive and taxa specific barcode libraries are integral to monitoring and conserving aquatic biodiversity. The reference library is what **allows the identification of the species** found in metabarcoding analyses.

A reference library contains **short DNA fragments** that can be used for the effective identification of species (DNA barcoding). Each DNA sequence corresponds to a known species, that has been reliably identified by a taxonomist. Both taxonomically comprehensive coverage and content quality are important for sufficient accuracy.

HOW is it built?

All the short DNA fragments are uploaded to a **data platform** where they are clustered based on their similarity, and get allocated a unique number (Barcode Index Number System, BIN).



HOW MUCH does it cost?



Each short DNA fragment costs between **6-9 euros** to be produced from the time it enters the lab. Additional costs should be estimated for the sampling as well as visual identification.

HOW is it is QUALITY controlled and protected?



Quality control is performed by a **taxonomic curator**, who

- 1/ stays updated on nomenclature (species names)
- 2/ makes sure the specimens are identified by experts
- 3/ quality controls the sequences that enter the reference library

4/ compares the sequences that belong to the same species and makes sure they are similar by performing various analyses

5/ controls the influx of information to prevent non-curated specimens to enter the library