Barcoding of marine invertebrates from Norway through NorBOL

Katrine Kongshavn1,*, Jon A. Kongsrud1, Tom Alvestad1, Endre Willassen1
1) University Museum of Bergen, Department of Natural History, PO. Box 7800, 5020 Bergen, Norway
Katrine.Kongshavn@uib.no

Abstract
The University Museum of Bergen coordinates the marine efforts of the NorBOL – Norwegian Barcode of Life – project. Through our own research, as well as collaboration with several Norwegian Taxonomy Initiative projects, we have submitted over 8000 samples of close to 3000 species, primarily of marine invertebrates. Sequencing success vary with taxonomic groups, but averages on 75 % of the submitted morpho-species. We find cases of apparently over-split species, indicated by identical sequences. Much more frequently we come across morphologically defined species with genetic divergence, sometimes as high as 30 %.

In both cases these issues will require integrated studies by taxonomic specialists.

Study area and material
Norwegian waters span a wide range of habitats with variable topography from fjords and coastal waters to deep shelf areas and abyssal waters. Obtaining material for DNA-sequencing of marine invertebrates is logistically challenging as old museum material is often unsuitable, and marine sampling is expensive and time consuming. We have done extensive sampling ourselves, and collaborate closely with ongoing mapping surveys (e.g. MAREANO) and environmental monitoring activity to get fresh ethanol fixed material from a wide range of localities (Fig. 1).

Sequencing results
Four years into a five-year project, we have made substantial headway on some groups from Norwegian waters (Figs. 2, 3), whilst other phyla remain unexplored.

The priority of groups is based on availability of taxonomic expertise to aid in selecting of specimens for barcoding and to linking barcodes with nominal species. Through the Norwegian Taxonomy Initiative (NTI) funding has been made available to support this activity, especially focusing on less well-known animal groups.

We are getting barcodes for an average of 62 % of the specimens, and 75 % of the (morpho-)species submitted.

At present, 2800 samples have not (yet) sequenced successfully. Thus we miss a considerable part of the species diversity with the standard Cox1 barcoding procedures. Working with the highly diverse marine fauna, additional DNA-markers may be necessary in order to genetically characterize the fauna (e.g. posters 474 and 485).

However, our DNA-barcoding results provide new insight into species diversity and distributions (e.g. Figs. 4 and 5).

One BIN, several names: Over-split species?

Within BIN (AA95S11)
Max distance 1.83%, average 0.68%
NN BIN: 9.94% different

One name, several BINs: Undescribed diversity
Ophelina cylindricaudata
(Polychaeta: Ophelidae)
1 species, 3 BINs
BINs correspond to biogeography

Library progress and future perspectives
We have invested special effort in collection building for the purpose of DNA-barcoding of marine animals, and are currently serving many research and species mapping projects with material.

DNA barcoding indicates a significantly higher diversity in Norwegian waters than presently recognized. Four years of barcoding activity on marine fauna has already provided validated molecular characterization of more than 1000 recognized marine species.

Additionally more than 1200 specimens with sequences are currently awaiting integration for which DNA barcoding indicates several genetically distinct clades in different biogeographical regions.

Acknowledgements
We are grateful for the contributions from the Norwegian Taxonomy Initiative projects, our collaborators in SweBOL material project (e.g. MAREANO), CGB, G.A.J footprint Centre, SpitzGES, BMBF, and other projects. Blog of the invertebrate collections: https://invertebrate.in.uib.no/