



Towards whole mitogenome sequencing as DNA based tool for North Sea biodiversity assessments

PhD total period

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Motivation

The North sea is intensively used for industry, such as fishing and energy production. This alters the habitat of marine animals, but also brings opportunity for new life to settle and expand. To optimally guide activities in the North Sea towards preserving and improving the marine ecosystem, its biodiversity needs to be closely monitored. Identification of animals based on their DNA is potentially a fast, cheap and accurate way to do this. We focus on developing and applying novel techniques based on mitochondrial genomics for improved monitoring of biodiversity in the North Sea.

Aims and Objectives

- 1) Evaluate reproducibility and robustness of current DNA based benthic biodiversity assessment approaches.
- 2) Develop whole mitogenomics methods to increase accuracy of North Sea biodiversity measurements.
- 3) Apply mitogenomics as approach to identify the diet composition for cod (*Gadus morhua*).
- 4) Apply mitogenomics as approach for eDNA based fish biodiversity monitoring.

Method

Based on long read Oxford nanopore DNA sequencing technologies, we aim to develop a PCR free method for sequencing whole mitochondrial genomes. This will be applied both for single species and also for simultaneous identification of mixed communities. By applying our novel methods to field samples and comparing it to current morphological and genetic methods, we will explore the possibility to apply mitogenomics as a genomic approach for biomonitoring of the North Sea.

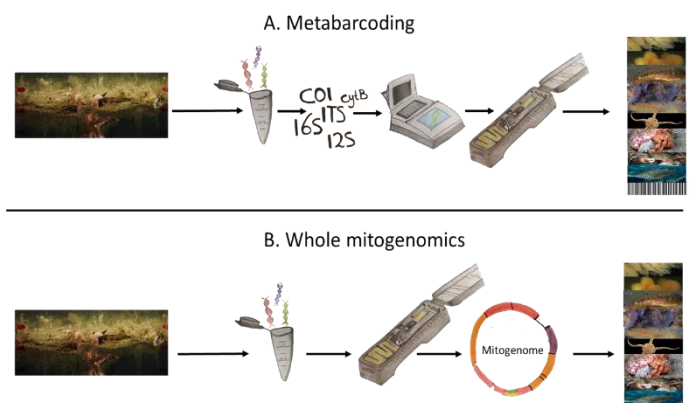


Fig 1. Visual represent of the workflow A.) currently used DNA based identifications approaches and B.) proposed for whole mitogenomics.

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