

Arctic ecosystems are increasingly exposed to dramatic environmental changes and multiple stressors arising both from climate warming and intensifying anthropogenic pressures. Scientists have reported increasing inflows of warm Atlantic waters to the Arctic, with profound effects on local climate. Moreover the intensifying Atlantic water advection hauls numerous boreal organism that impacts Arctic communities species composition and food webs. Glaciers retreat is progressing that also influences coastal ecosystems functioning. Many pollutants like black carbon, heavy metals or persistent organic pollutants are transported by air masses, even from very distant places, and deposited in the Arctic. According to recent predictions all these processes are supposed to increase and intensify in the nearest future.

Thanks to relatively low mobility, long life span, high species richness and specific vulnerability to several environmental stressors benthic invertebrates are regarded as an efficient indicator group. They are commonly used both in anthropogenic impact assessments and natural environmental variability monitoring, including monitoring of effects of stressors related to climate change in the Arctic. Traditionally these studies are performed using morphology based species composition assessments which are costly, time-consuming, demand taxonomic expertise and still are usually limited only to larger organisms (macrofauna).

In mid-2000s next-generation DNA sequencers were introduced allowing the so called metabarcoding assessments what revolutionized biodiversity studies of aquatic ecosystems. Metabarcoding analyses provide a faster, and often more objective tool, in many cases proved to be a more sensitive indicator of environmental pressures than data derived from traditional morphology based surveys. In metabarcoding approach DNA is extracted from a collection of organisms or extracellular DNA (i.e. environmental DNA [eDNA] in water or sediments). eDNA analyses can encompass the wider range of taxonomic groups and allows to include the diversity of microscopic biota that is difficult to obtain using traditional taxonomic tools. In this study we will apply sediment eDNA analyses (in comparison to morphology based species inventories) to understand environmental effects on the coastal benthic organisms diversity in the warming Arctic ecosystems.

The **project goals** are to: 1) compare the efficiency of morphology and metabarcoding based methods in discrimination of ecological assemblages along the environmental stressors gradients; 2) compare the effects of environmental stressors on different biota across benthic eucaryotes, especially by comparing patterns of biodiversity changes for microscopic unicellular organisms and larger macroscopic taxa; 3) identify the key indicator taxa (and/or 'indicators sequences' of DNA) that can be used as biological indicators of the disturbance regimes (anthropogenic and natural); 4) explore how taxonomic diversity scales with organism size in the Arctic coastal systems.

To complete our goals the study will be organized around **three scientific tasks**. First we will focus on the assessments of the benthic diversity along the glacial disturbance gradient in one of Svalbard fjords. Stations located along the fjords axis/glacial disturbance gradient will be surveyed for morphology based and whole benthic community metabarcoding diversity assessments accompanied by environmental variables measurements. Second task will analyze multiple stressors effects on the benthic eukaryotic composition and diversity in glacial (or glaciofluvial) bays, the land/ocean interface systems. Third task will focus on temporal variability in benthic eDNA diversity, explored by eDNA sampling in four consecutive years (2019-2022) at three monitoring stations in Hornsund, Svalbard (monitored using traditional macrofauna methods by Institute of Oceanology PAS for almost 20 years).

We **hypothesize** that (compared to morphology based assessments) the **metabarcoding** based approach will produce **stronger signals of benthic diversity response to environmental stressors** due to wider taxonomic spectrum. We will provide a novel tool to assess and monitor the Arctic ecosystem status and trends in the era of increasing pressures related to anthropogenic activity and climate change. We will also provide the first complete eDNA picture of eukaryotic benthic diversity in the Arctic coastal sediments.