# The Arctic microbiome during the winter-spring transition: nitrogen-cycle genes

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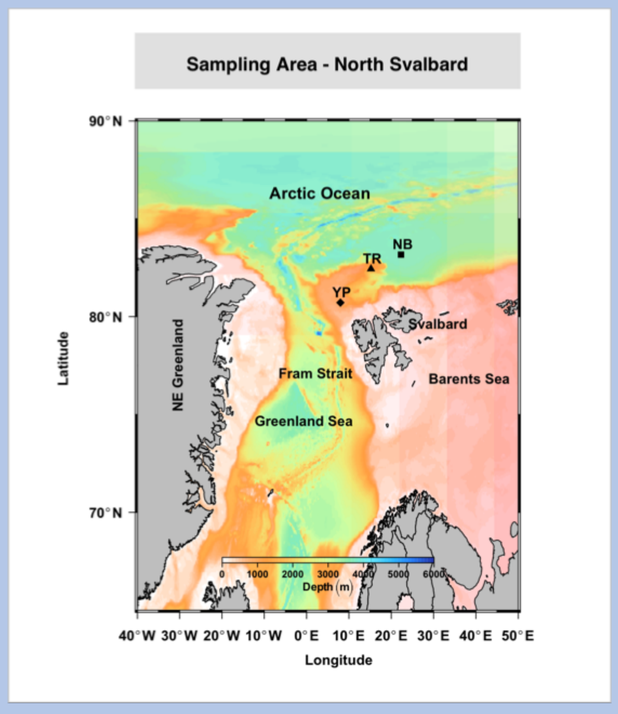
## Motivation

- **Pelagic microbial communities are a key component of the Arctic Ocean when evaluating the ecological impact of the thinner Arctic icescape, as they constitute the basis of the marine food web and biogeochemical cycles.**

## Objectives

- **This study made used of Illumina paired-end reads from SSU rRNA amplicon and metagenomes in order to focus on the study of composition, diversity and key nitrogen-cycling functions of the Arctic´s microbiome through the winter-summer transition.**

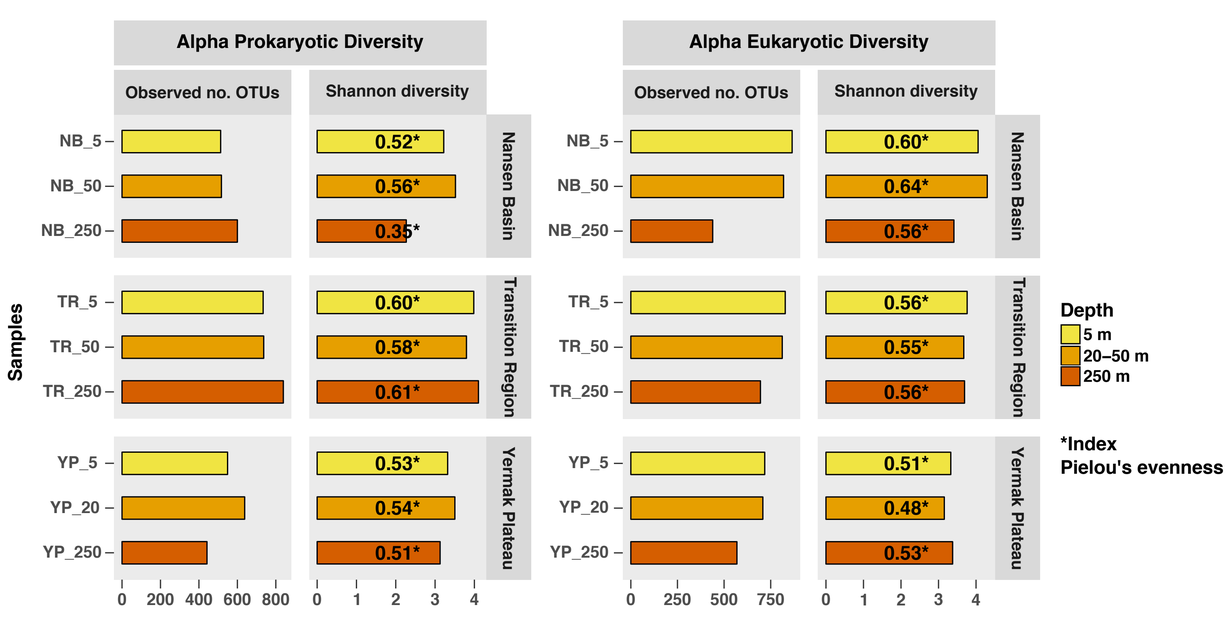
## Sampling Area & Procedures



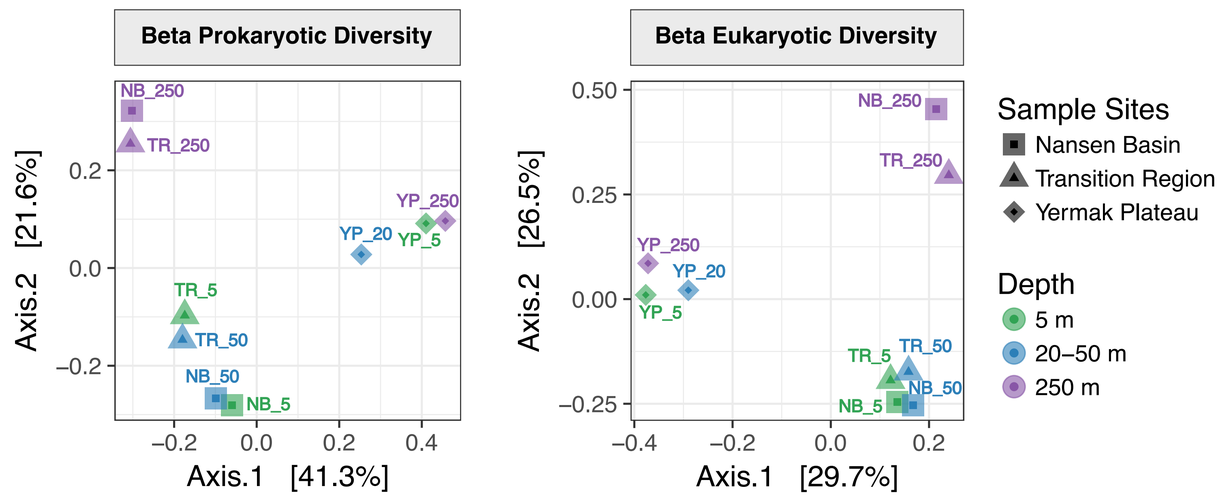

- **During the Norwegian young sea ICE expedition (N-ICE2015), seawater was collected underneath the winter-spring pack ice at 5, 20 or 50, and 250 m depth at:**
  - **Nansen Basin (square)**
    - **9th March**
  - **Transition Region (triangle)**
    - **27th April**
  - **Yermak Plateau (diamond)**
    - **16th June**

**Microbial Collection: Sterivex (0.22µm)** → **16S rRNA gene (V4-V5) + 18S rRNA gene (V4) + metagenomics** → **Illumina MiSeq (2x300 bp )**

## Alpha- & Beta-Diversity

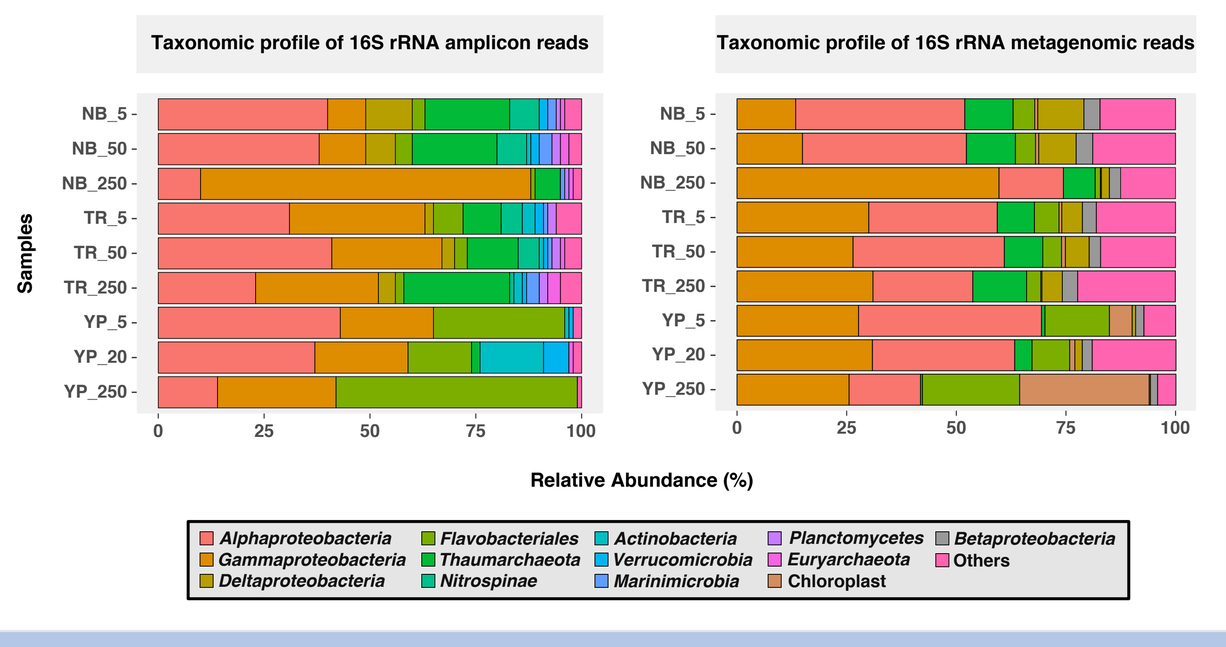



- **Opposite patterns of richness between prokaryotic-eukaryotic communities;**
- **Prok. and euk. observed no. OTUs does not agree with Shannon diversity index reflecting the evenness of these communities.**

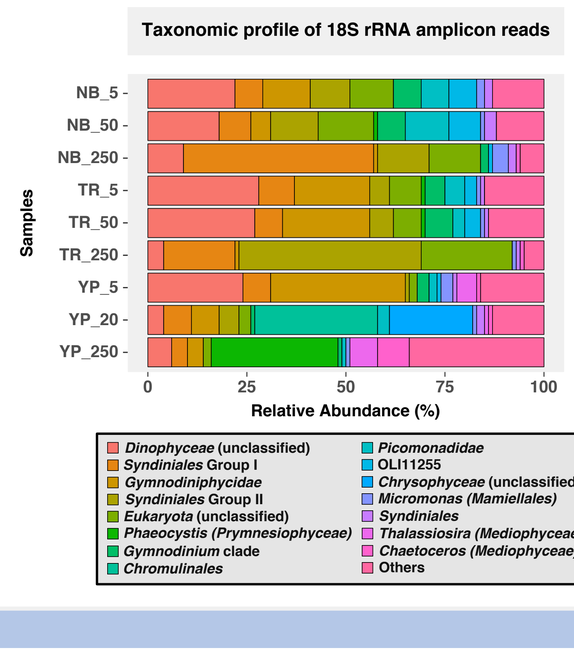



- **Microbial assemblages clustered as epipelagic or mesopelagic communities (exception YP).**

## Composition

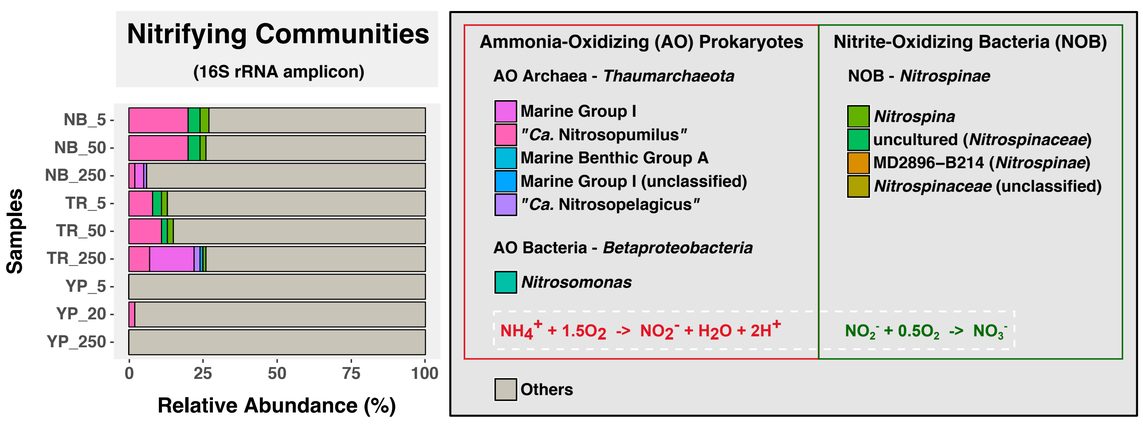



- ***Alpha-* and *Gammaproteobacteria* (30.6% and 28.6%) > *Flavobacteriales* (13.7%) > *Thaumarchaeota* (10.4%) - amplicon (left);**
- **16S rRNA amplicon (left) agrees well with the metagenomics 16S rRNA data (right).**




- **Phylotypes affiliated with *Dinophyceae* and *Syndiniales* dominate most of the samples;**
- **Exception made to YP_20 and YP_250 samples, which are instead predominated by *Chrysophyceae* (at YP_20), *Diatomea* and *Prymnesiophyceae* (at YP_250).**

## Nitrogen-Cycle Genes




- **MGI represents 1% across the epipelagic waters but it increases >2-fold than "*Ca.* Nitrosopumilus" at mesopelagic depths; AOA and NOB have a high frequency of occurrence in the subsurface waters underneath of winter-spring pack ice (<50m depth), but they are nearly absent close to summer;**
- ***Amo/PmoA*:*Urease* ≈ 1 suggest that deeper thaumarchaeal populations may have the ability to couple AO with ureolysis.**