

# ARCTIC MICROBIAL EUKARYOTES IN THE NORTHERN BAFFIN BAY

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## 1. NORTHERN BAFFIN BAY (NBB)

Pelagic microbial eukaryotes include phytoplankton and single-celled microzooplankton and are at the base of the food chain that supports higher trophic levels.

Recent changes in ice conditions mean historical patterns are not reliable indicators of present day seasonal and spatial patterns. In particular, remote sensing and *in situ* data has shown that the highly dynamic and productive Northern Baffin Bay (NBB) referred to as *Pikialasorsuaq* by the Inuit, has undergone marked changes in regional biomass and productivity patterns over the last 15 years. Given their fundamental role in food webs, knowing microbial eukaryote composition is essential if we are to understand ecosystem responses in the face of global change.

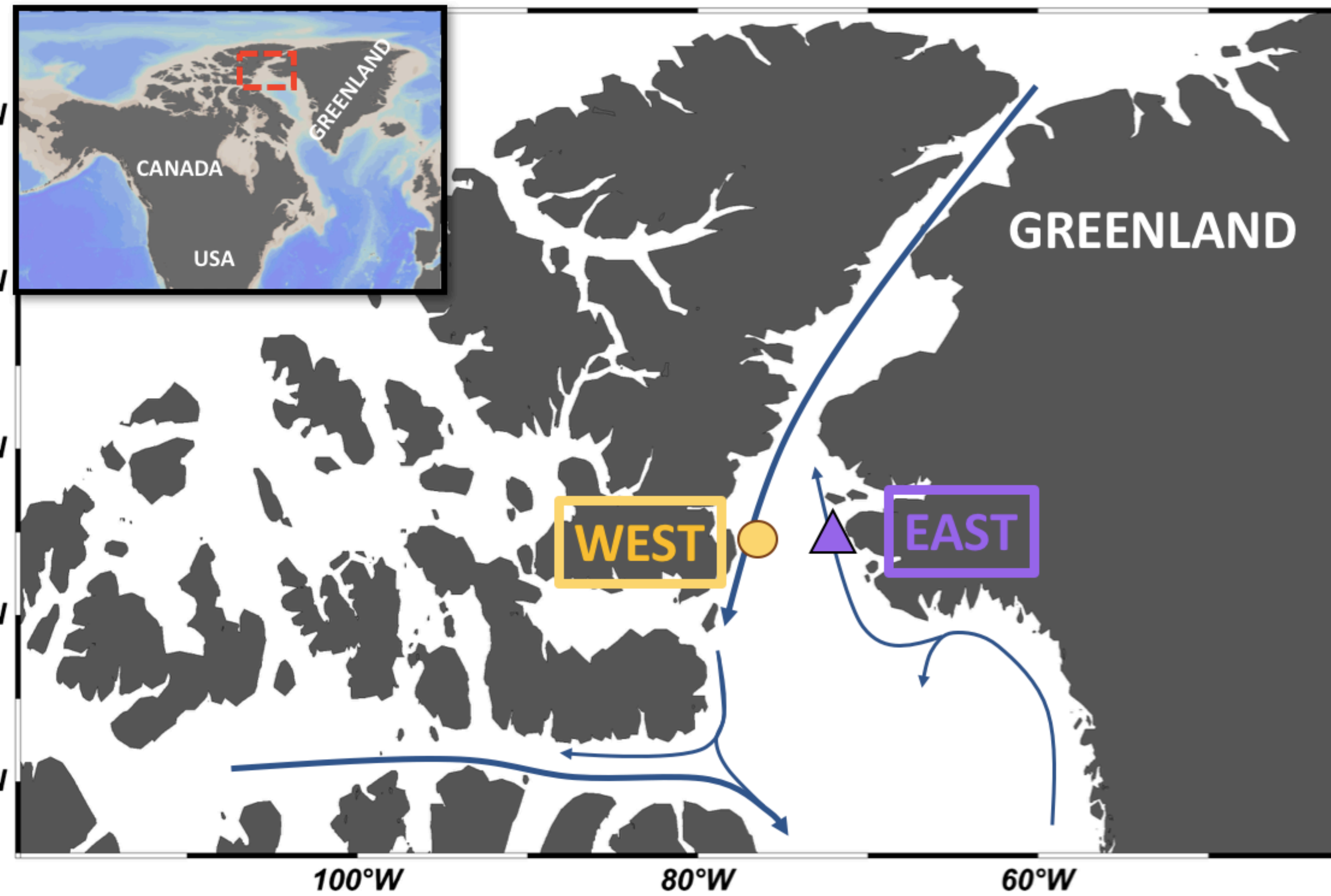


Fig.1: Sampling sites aboard Canadian research icebreaker CCGS Amundsen.

General circulation in Baffin Bay (blue arrows, Fig.1). The WEST side is influenced by a cold and fresher current from the Arctic Ocean. In contrast, the EAST side is marked by a saltier and warmer current from modified Atlantic waters [1 & 2].

## OBJECTIVES

Identify summer-fall temporal and spatial variability of microbial eukaryotic communities between two contrasting sides of NBB from 11 years of data

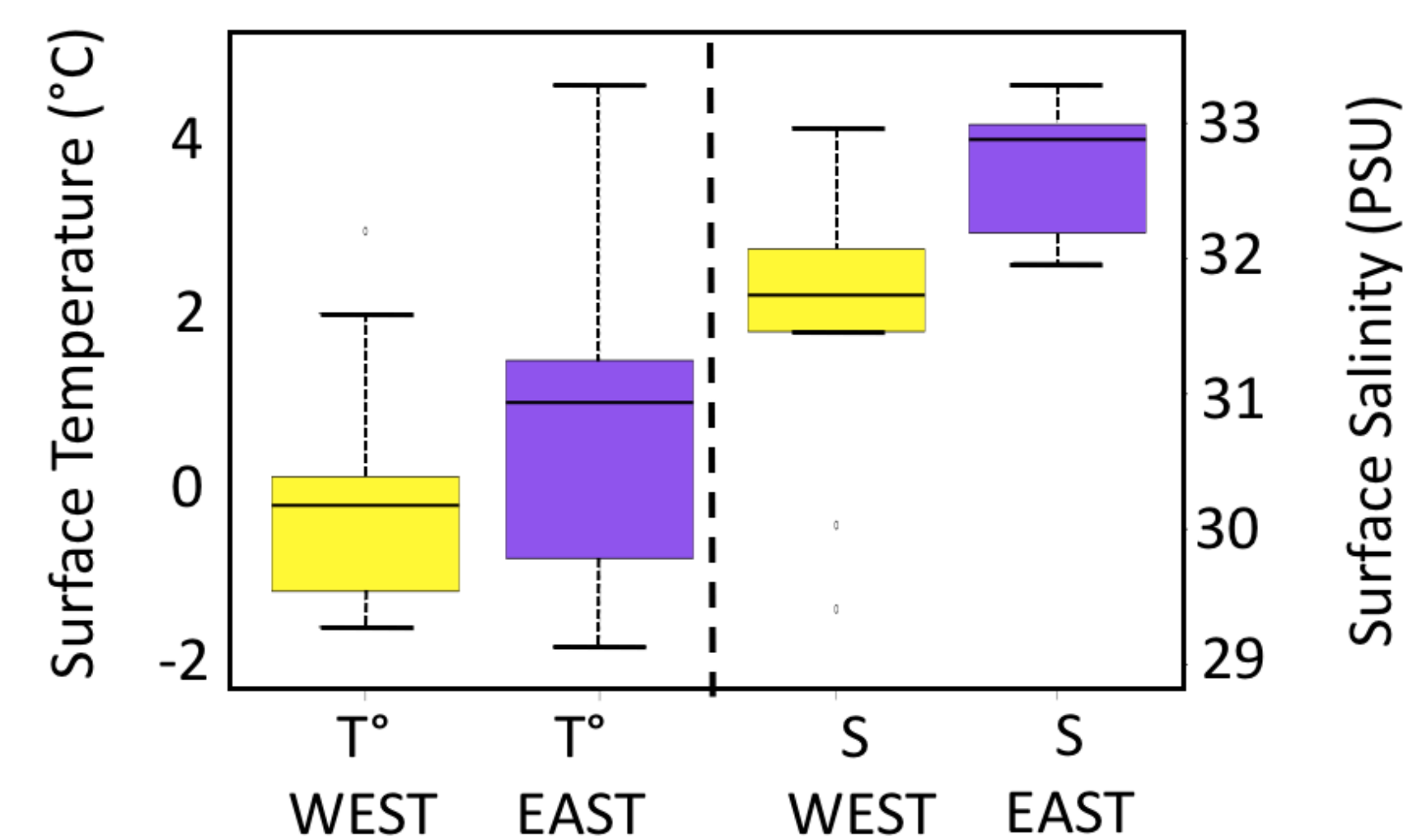


Fig.2: Boxplot of surface (5-30m) temperatures ( $T^\circ$ ) and salinities ( $S$ ) measured during ArcticNet missions to the two sides of NBB. The bottom and top of the box are the 25<sup>th</sup> and 75<sup>th</sup> percentile and the line near the middle of the box is the median. The upper and the lower whiskers represent the maximum and minimum values that do not exceed a certain distance from the middle 50% of the data.

We observed that generally the Greenland EAST (purple) side is saltier and warmer than the Canadian WEST (yellow) side. Temperature was more variable on the EAST side (Fig.2).

## 2. METHODOLOGY

1. Water sampling from Niskin bottles, temperature and salinity from CTD data
2. Successive filtrations: 3  $\mu\text{m}$  & 0.2  $\mu\text{m}$  filters
3. Extraction of DNA and RNA: only DNA surface samples are shown here
4. Sequencing: V4 region (300 bp) of the 18S rRNA gene, Illumina MiSeq
5. Bioinformatics analyses: QIIME, Rstudio

**Canada WEST side:**  
Stations 101 & 105  
2006 – 2017 (except 2007 & 2011-2012)

**Greenland EAST side:**  
Station 115  
2005 – 2017 (except 2007 & 2012)

## 3. RESULTS: a changing biodiversity?

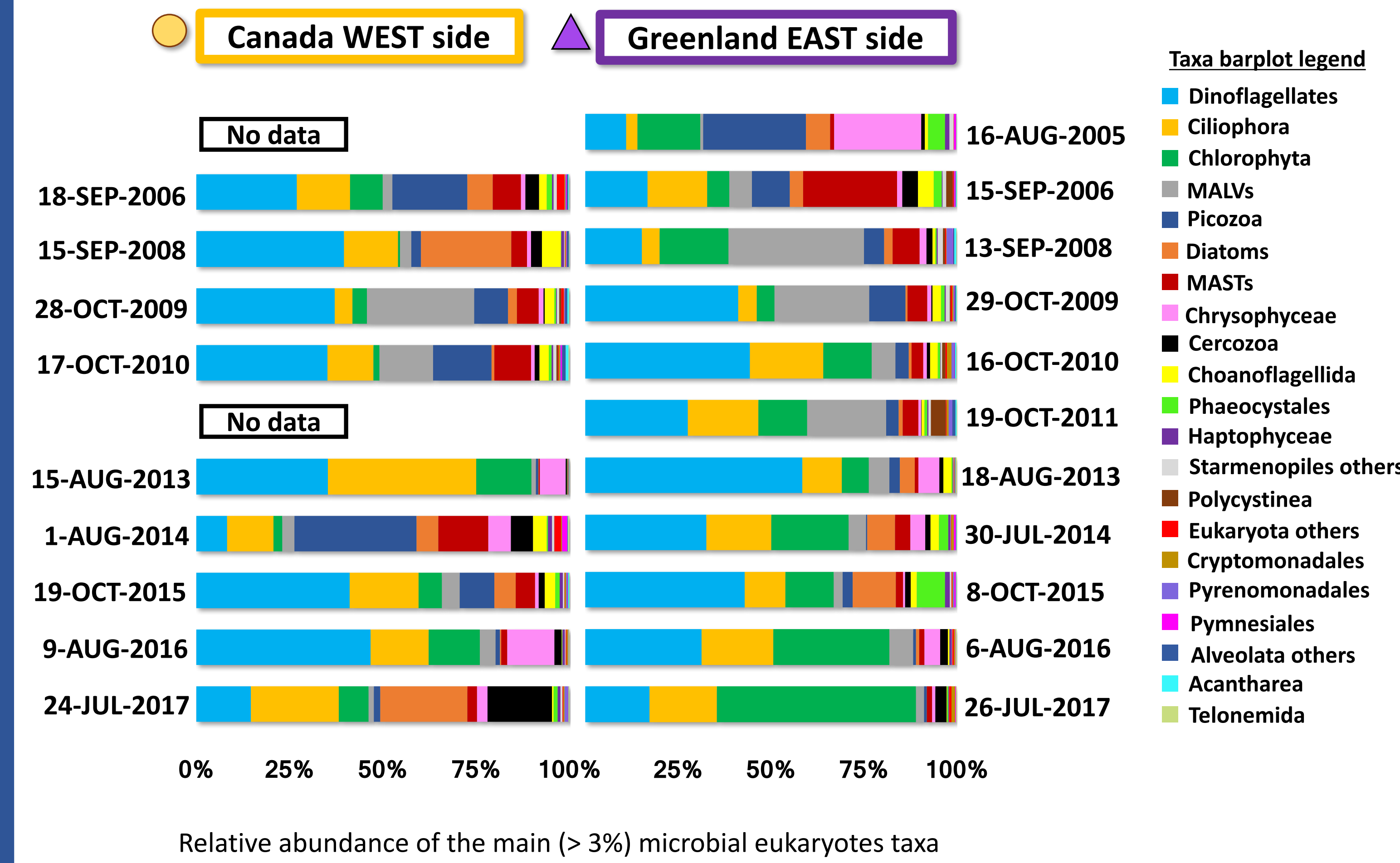


Fig.3: Microbial eukaryote community composition

The most abundant Operational Taxonomy Units (OTUs) were **dinoflagellates** (*Gyrodinium*) and **ciliates** (Oligotrichida) on **both** sides; except Picozoa in 2005 on the EAST side and in 2014 on the WEST side (Fig.3). Green algae (**Chlorophyta**) including *Micromonas* were more abundant on the **EAST** side especially in **August**. *Chaetoceros* was the most abundant **diatom** on both side.

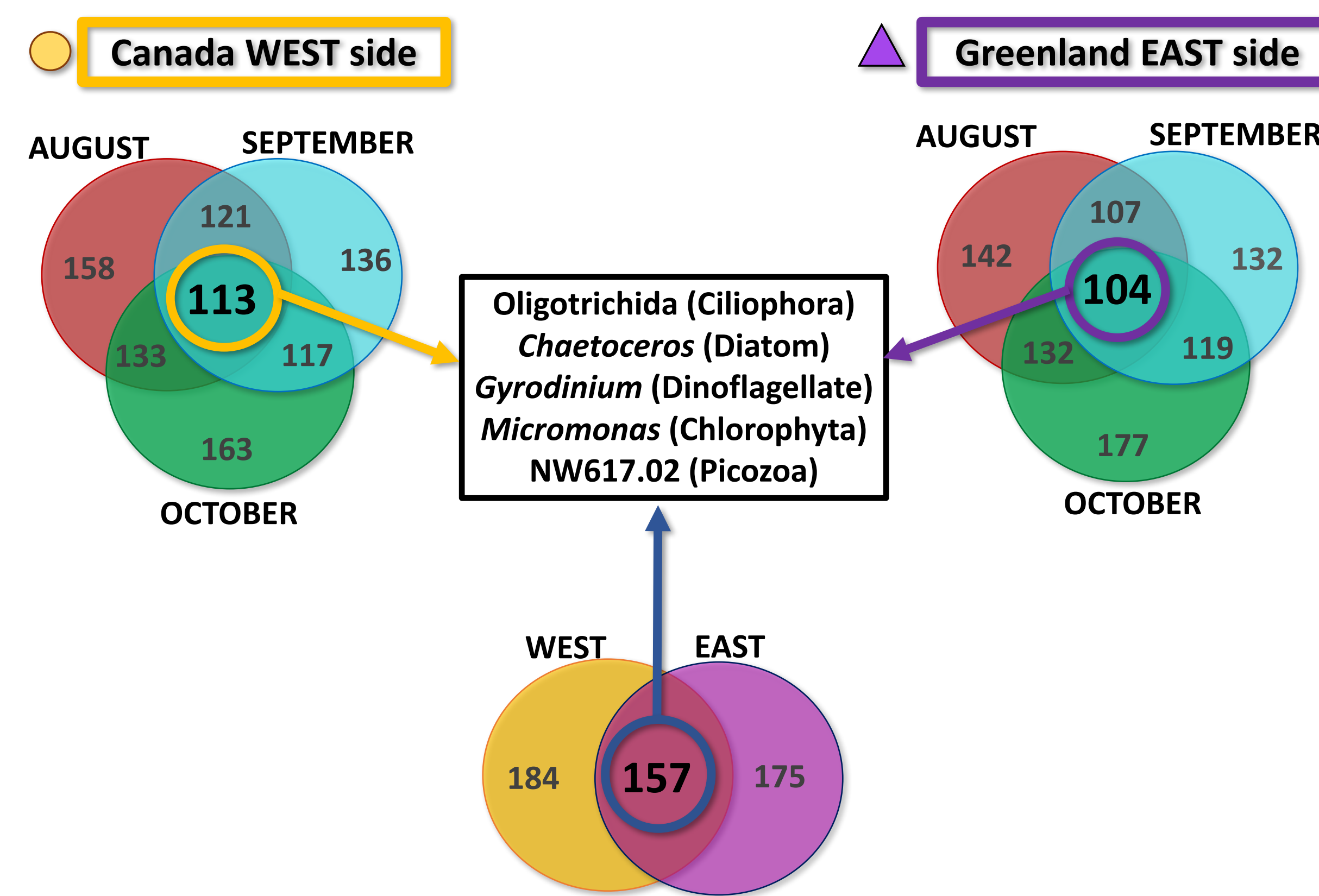


Fig.5: OTUs shared between months and sides

Venn diagrams of OTUs with highest abundance (> 3%). Over the different months of sampling within a side about 100 OTUs were shared (Fig.5). The bottom Venn diagram indicates that overall 157 OTUs were shared.

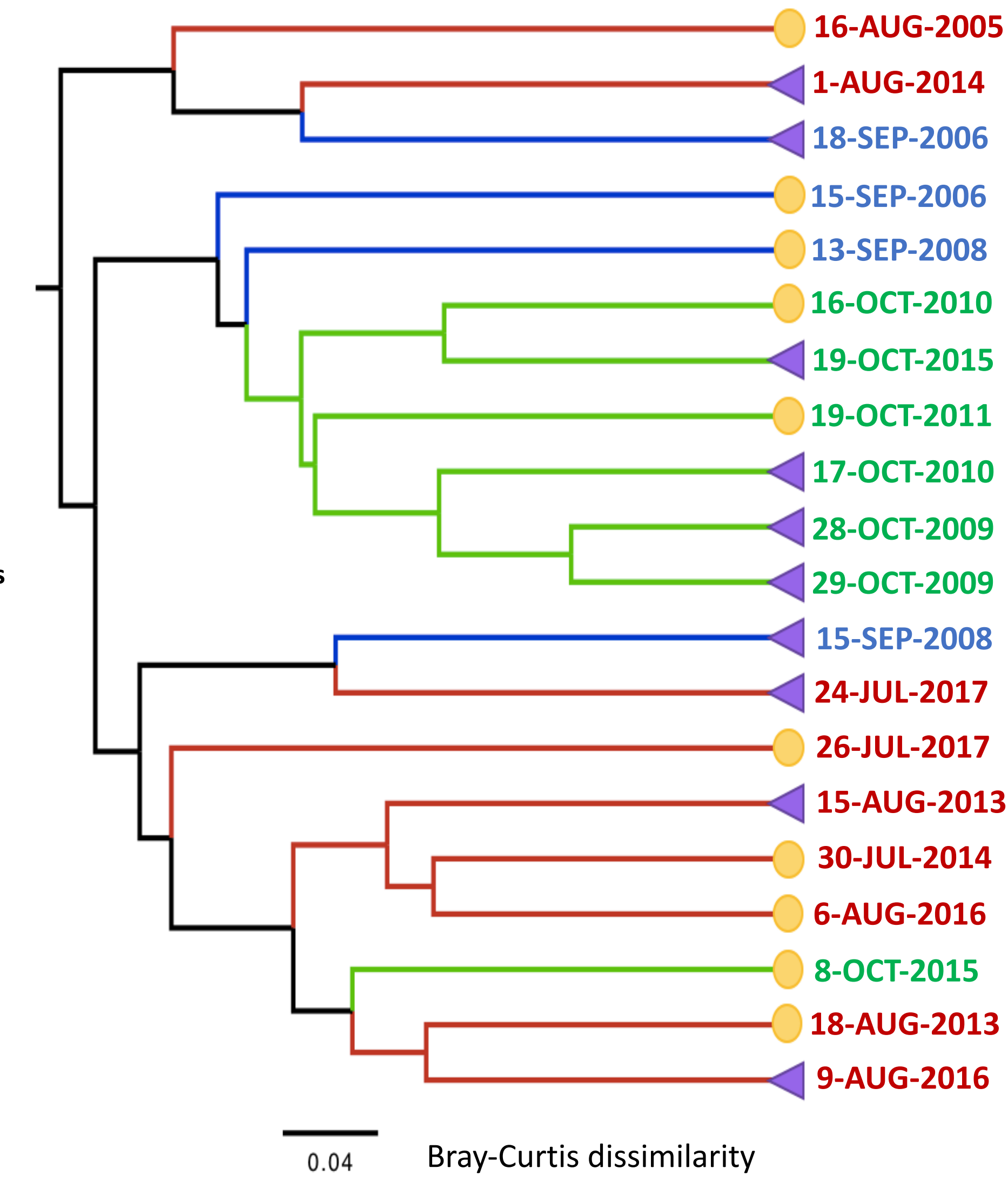


Fig.4: Community clustering

Surface microbial eukaryote communities clustered primarily by month (Fig.4).  
→ Communities on both sides were similar.

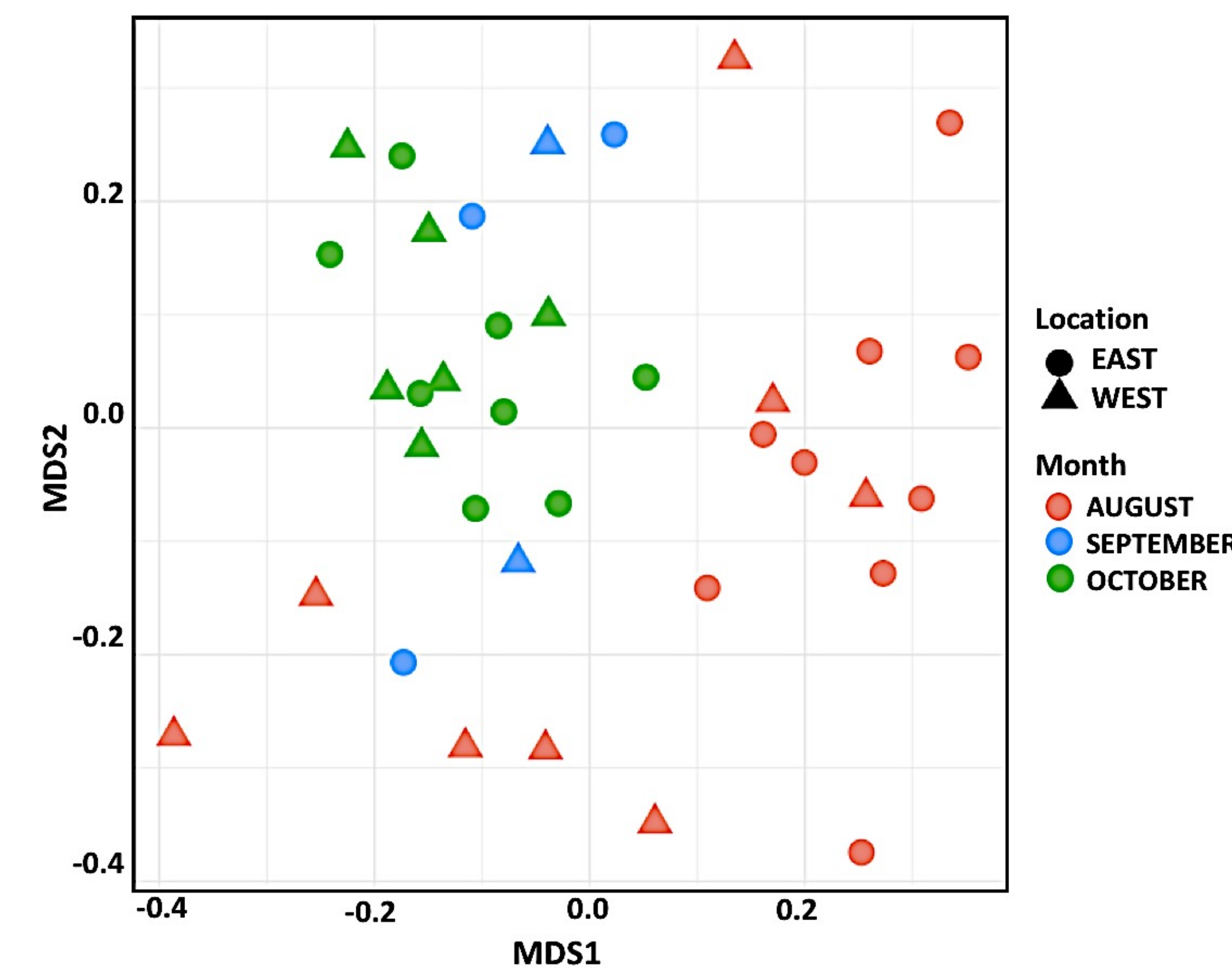


Fig.6: NMDS (non-metric multidimensional scaling)

Summer (July to August) and fall (September to October) samples tended to cluster separately (Fig.6). There was no clear separation between the EAST and the WEST sides.

## 4. CONCLUSION & PERSPECTIVES

Our preliminary results infer that the overall composition of **microbial eukaryotic communities is similar on both sides** of NBB and the successional stage of communities was a major structuring force.

Community changes seem to be related to environmental drivers. For example, we noted that several **ciliates** were more often found on the **WEST** side. In contrast, **dinoflagellates** and **chlorophytes** made up a larger portion of reads on the **EAST** side.

As the Arctic Ocean freshens, the NBB **microbial communities are being exposed to greater salinity fluctuations over shorter periods of time**. Our analyses are on-going and we plan to add results from **more depths** and from **RNA samples**, and investigate the influence of salinity on communities.

### ACKNOWLEDGMENTS

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REFERENCES: [1] Curry et al., *Journal of Physical Oceanography* 2011; [2] Preußner et al., *Remote Sensing* 2015