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Composition and Functional Diversity of Zooplankton-associated Prokaryote Communities in a Greenlandic Fjord

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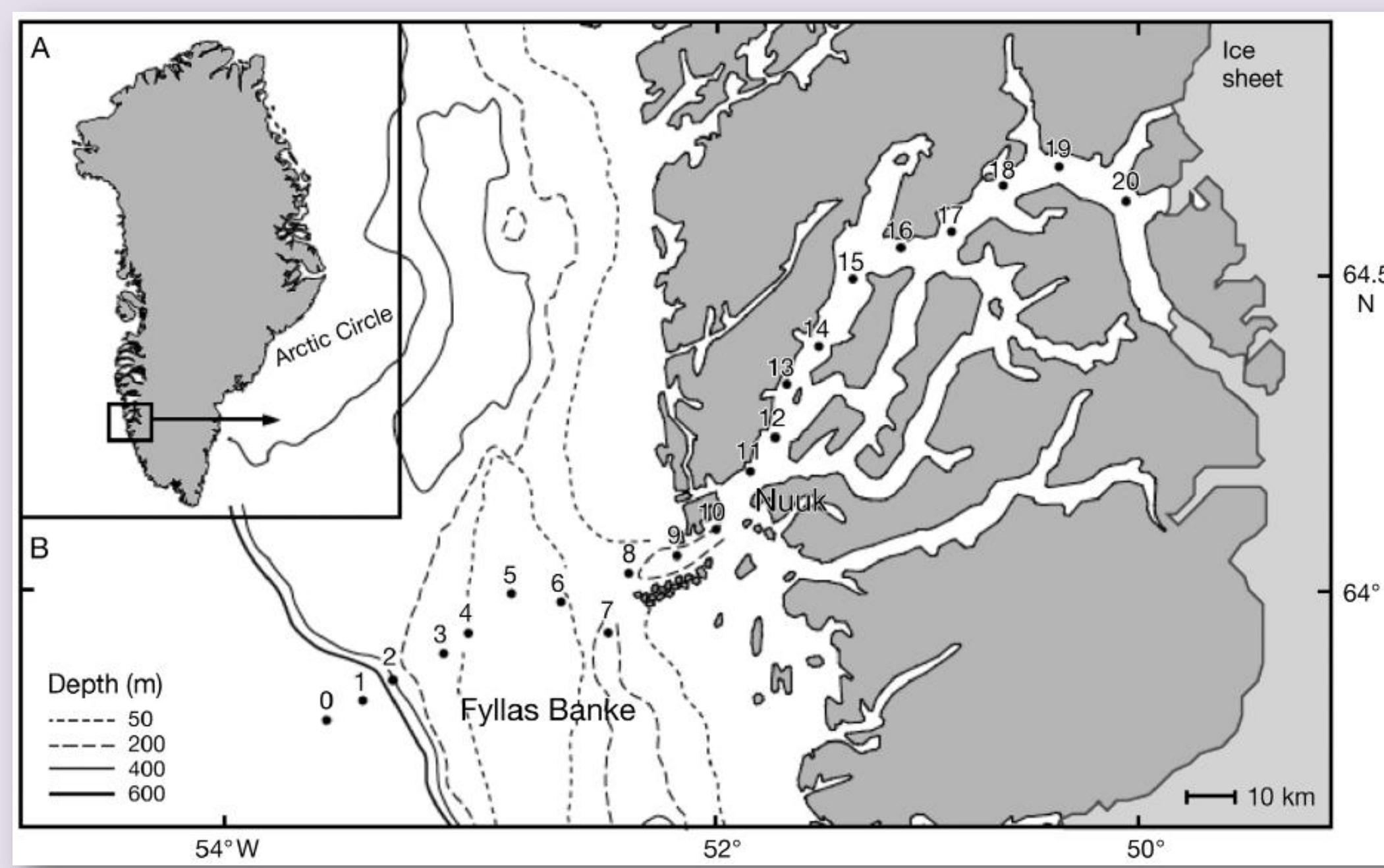
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Background

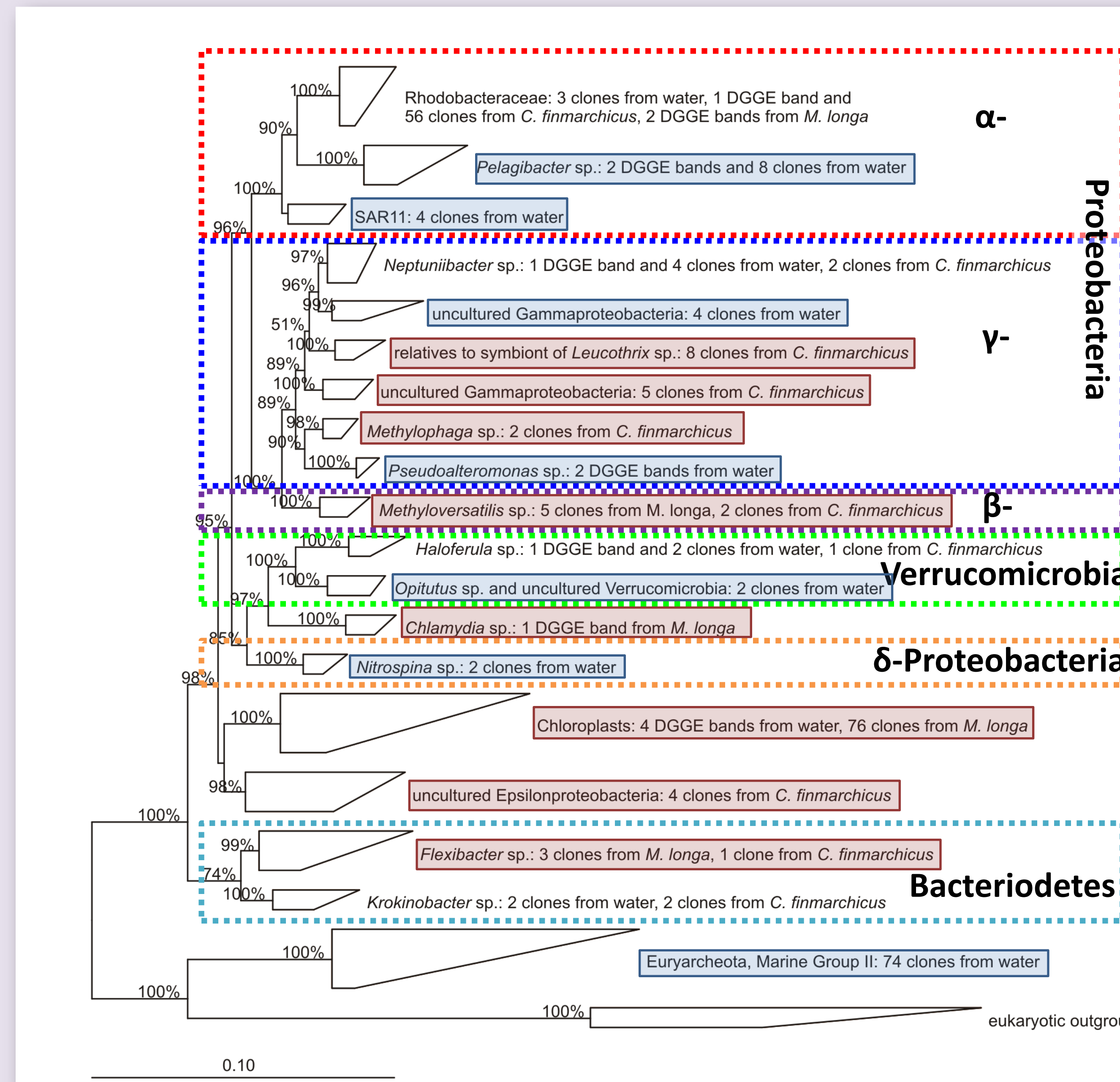
• Prokaryotes densely colonize zooplankton bodies (Tang 2005, Grossart et al. 2009), but they are often poorly sampled or characterized (Tang et al. 2010).

• Greenlandic fjords are very productive ecosystems, but information on free-living and zooplankton-associated prokaryotes there is very limited.

• We compared the prokaryote communities in pelagic water samples and those associated with zooplankton along a salinity gradient in Godthåbsfjord, Greenland (Tang et al. 2011a).



Phylogenetic tree of prokaryotes in zooplankton and water samples



Summary

• Zooplankton-associated prokaryotes increased the overall prokaryote diversity in the water column, consistent with studies in other aquatic systems (Grossart et al. 2009, Tang et al. 2009).

• Anoxic zooplankton guts may support anaerobic microbial activities within the oxygenated water column (Tang et al. 2011b), which was supported by our PCR functional gene analysis.

• Potential changes in plankton compositions in Greenland fjords in response to rapid climate change could lead to corresponding changes in prokaryote diversity and biogeochemical functions.

Outreach Efforts

• Plankton and bacteria are not familiar to Greenlanders, but they are important for sustaining Greenland fisheries.

• We worked with reporters to disseminate our research via internet blogs and local newspaper articles.

Methods

• Surface water and zooplankton samples were collected during the ECOGREEN (2008) and BOFYGO (2010) expeditions in the spring on board R/V Dana.

• Prokaryote community compositions were analyzed by DGGE and clone libraries.

• PCR screening was done to look for specific functional groups.

PCR screening for specific prokaryote functional groups

| Prokaryote group | Functional gene | Sample type | | | | |
|------------------------------------|-----------------|----------------------------|------------------------|-----------------------|-------------|-------|
| | | <i>Calanus hyperboreus</i> | <i>Pareuchaeta sp.</i> | <i>Metridia longa</i> | Chaetognath | Water |
| Methanogens | <i>mcrA</i> | ✓ | | (✓) | ✓ | |
| Sulfate reducers | <i>dsr</i> | ✓ | | | ✓ | |
| Nitrogen fixers | <i>nifH</i> | ✓ | | | ✓ | |
| Denitrifiers | <i>nirK</i> | | | | ✓ | |
| Denitrifiers | <i>nirS</i> | | | | ✓ | |
| NH ₃ -oxidizing archaea | <i>amoA</i> | ✓ | | | | ✓ |
| Planctomycetes | | ✓ | ✓ | | ✓ | |
| Archaea | | ✓ | ✓ | | | ✓ |

- Some prokaryote groups were found exclusively in zooplankton.
- Functional genes indicated occurrence of anaerobic microbial processes in zooplankton: methanogenesis, sulfate reduction, nitrogen fixation and denitrification.

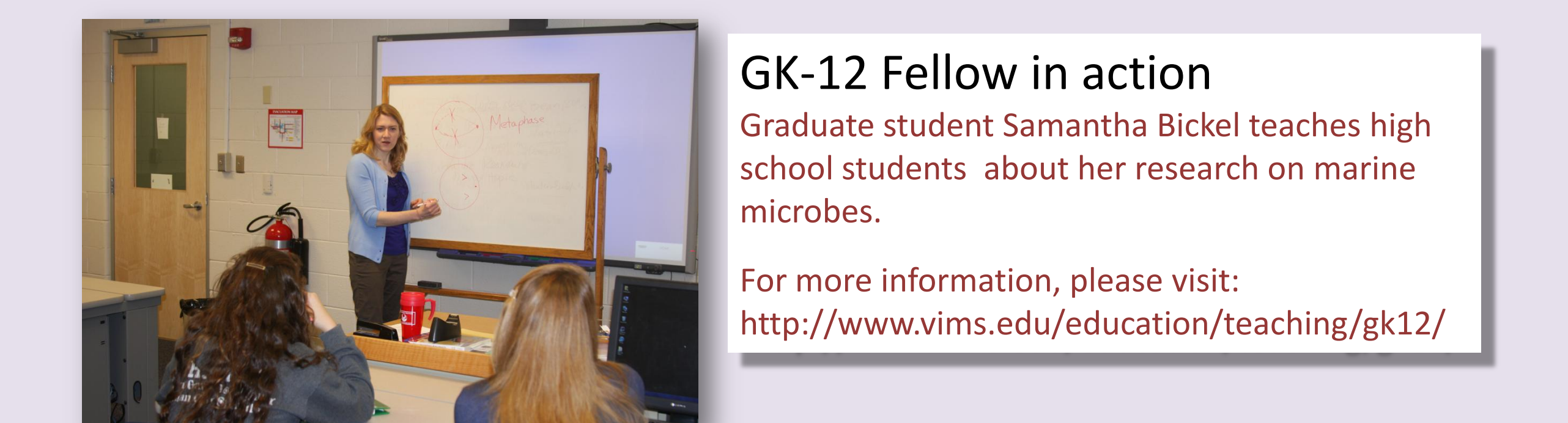
Statistical analysis of environmental factors structuring prokaryotic community composition in the water column

| | all | salinity | temperature | fluorescence | density | depth | station |
|------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|
| Bacteria | R=0.246 p<0.001 | R=0.12 p=0.014 | R=0.011 p=0.388 | R=0.134 p=0.008 | R=0.113 p=0.018 | R=0.116 p=0.011 | R=0.52 p<0.001 |
| Archaea | R=0.137 p=0.018 | R=0.143 p=0.020 | R=0.051 p=0.203 | R=-0.01 p=0.528 | R=0.13 p=0.022 | R=0.115 p=0.006 | R=0.116 p=0.025 |
| α-Proteobacteria | R=0.211 p<0.001 | R=0.282 p<0.001 | R=0.113 p=0.029 | R=0.087 p=0.056 | R=0.276 p<0.001 | R=0.175 p<0.001 | R=0.427 p<0.001 |
| Actinobacteria | R=0.073 p=0.088 | R=0.047 p=0.173 | R=0.028 p=0.284 | R=-0.018 p=0.616 | R=0.042 p=0.185 | R=0.043 p=0.139 | R=0.262 p<0.001 |

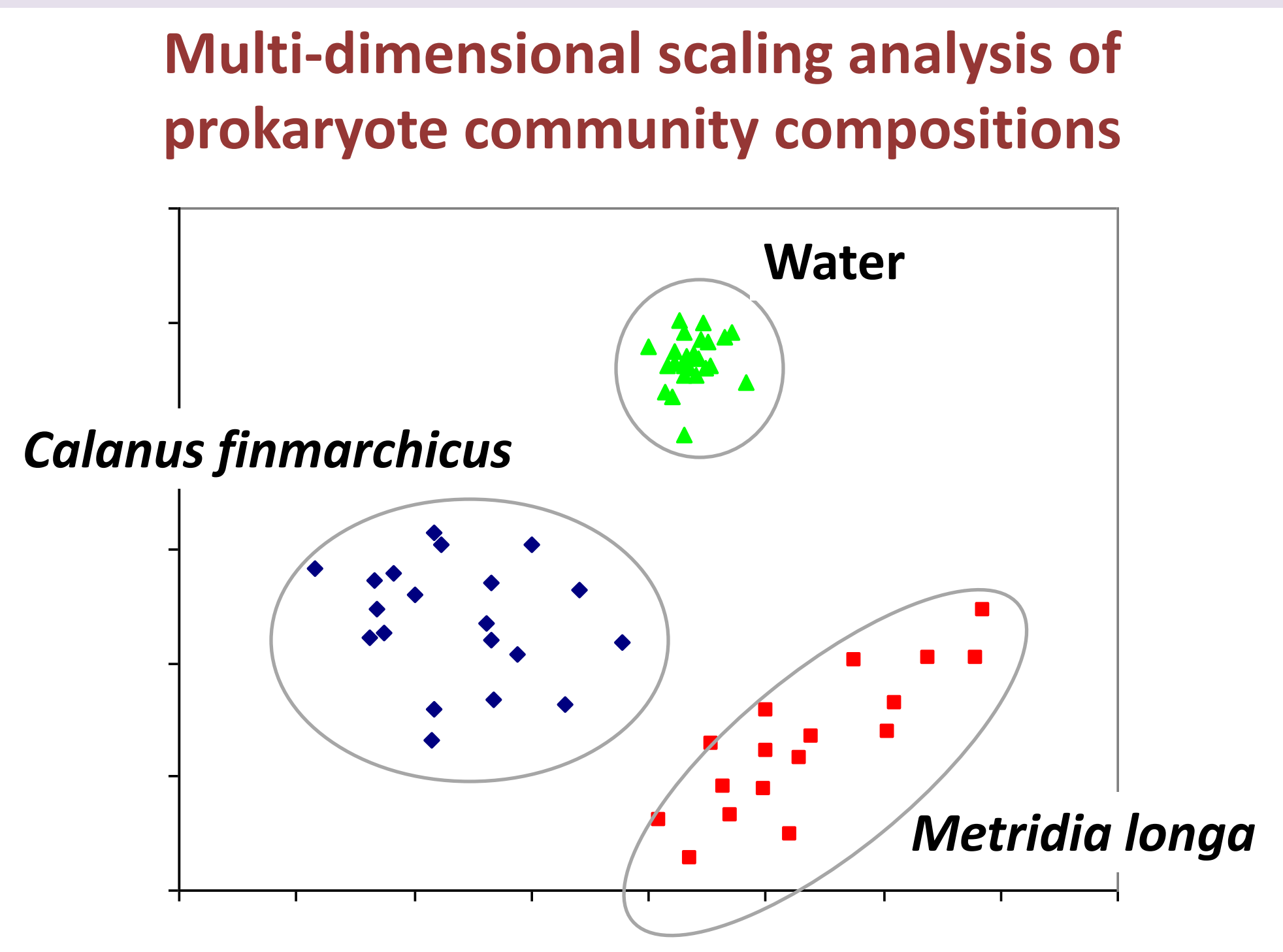
- Mantel-Test revealed spatial variation of community structure of Bacteria, α-Proteobacteria, and Archaea along the salinity gradient.
- Density, depth and station also influenced prokaryotic community structure.



- Microbes are not “charismatic megafauna” that K-12 students normally encounter in their curricula.
- Tang worked with his graduate student Samantha Bickel through the NSF-funded **GK-12 PERFECT** project at VIMS to bring microbial ecology into grade 10 classrooms.



GK-12 Fellow in action
Graduate student Samantha Bickel teaches high school students about her research on marine microbes.
For more information, please visit:
<http://www.vims.edu/education/teaching/gk12/>



- *Calanus*, *Metridia* (calanoid copepods) and water samples formed distinct clusters in terms of prokaryote compositions.
- *Calanus* feeds mainly on diatoms in the spring; *Metridia* feeds omnivorously throughout the year.
- Dietary differences could lead to delivery of different prokaryotes to the two copepod species (Tang 2005, Tang et al. 2009).

Related Oral Presentation
Zooplankton-associated bacterial abundance and community composition in the York River tributary of Chesapeake Bay
Samantha L. Bickel, Kam W. Tang, Hans-Peter Grossart [Abstract 11633; Tuesday 9:15 am, session 153 Ballroom D]

References and Acknowledgements
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