

DNA barcoding marine biodiversity in the Canadian Arctic: establishing a baseline for future biomonitoring



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ALGA

Algal Life Global Audit

international
BARCODE
OF LIFE



■ Initiated 2009

■ DNA barcodes for 30,000 red, brown & green algae!!!

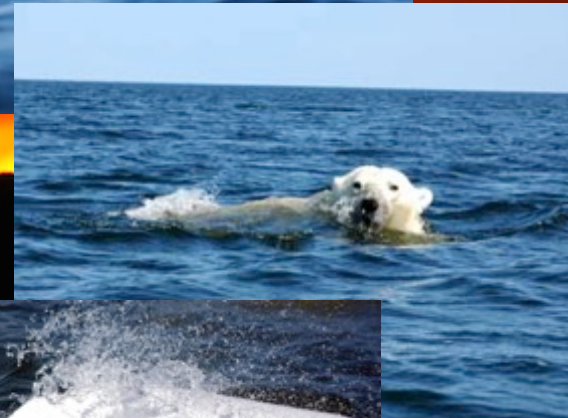
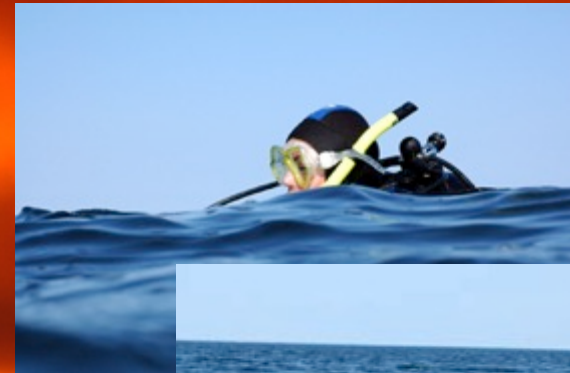
Barcode Survey of Churchill Seaweed

■ Canadian Arctic flora (Hooper et al. 2002):

- ca. 150 species
- Depauperate extension of the cold temperate North Atlantic flora

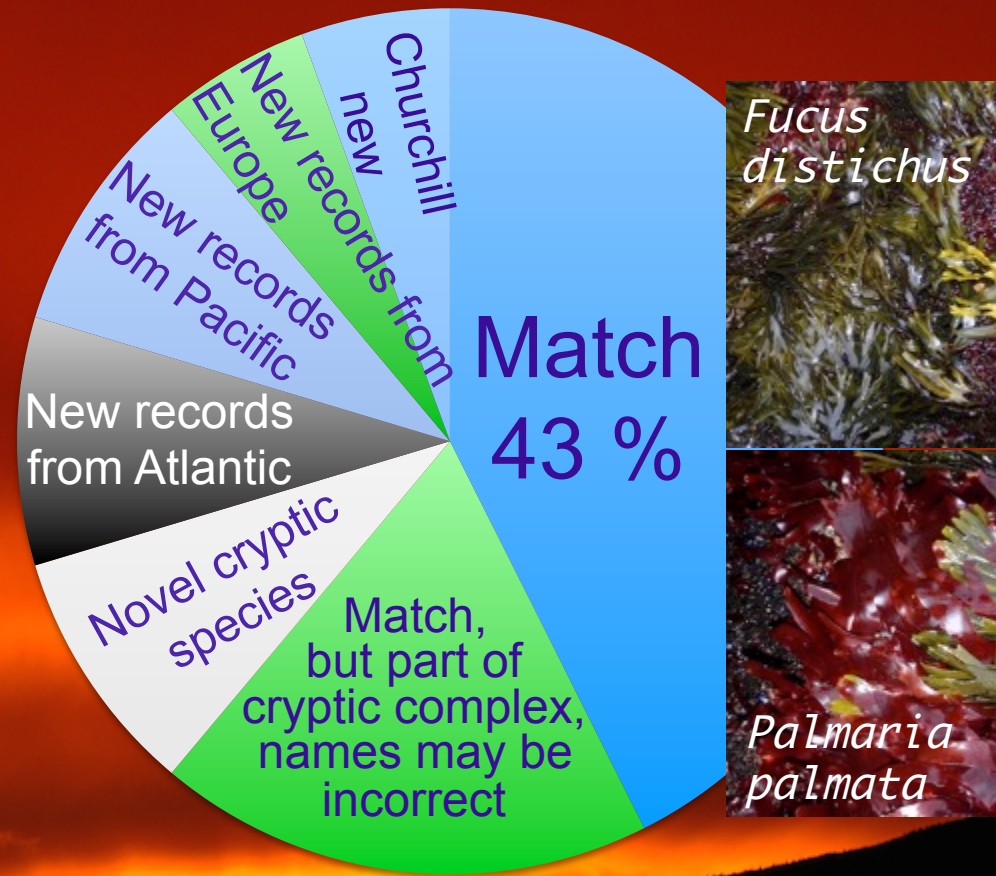
■ Churchill flora (Taylor 1957)

- ca. 50 species
- “Hudson Bay area is little known, but from the three or four papers which describe its flora we may judge that ... we have a relatively poor flora”
- We sampled this flora in 2006 & 2007 and acquired ~400 collections



Barcode Survey of Churchill Seaweed

- Uncovered ~ 50 morphospecies
- Resolved 57 genetic groups indicating cryptic diversity
- However, only 43% Match between lists
- Many Churchill species are range extensions of overlooked North Pacific species not the North Atlantic counterpart as believed, e.g., Churchill "*Halosiphon tomentosus*" is actually a newly discovered Alaskan *Halosiphon* sp.



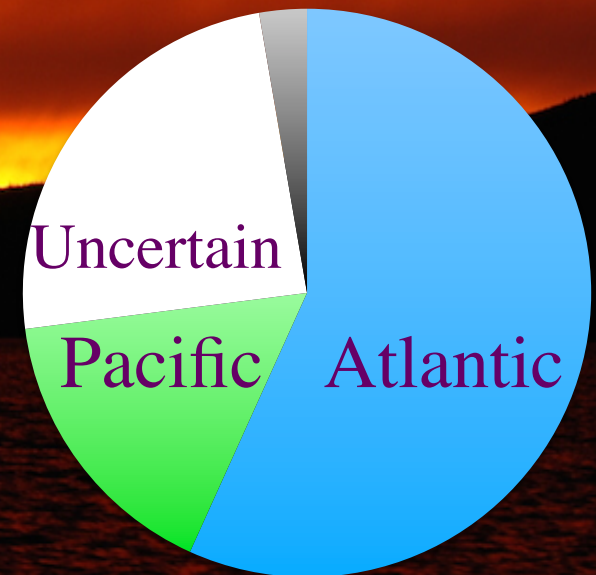
Halosiphon tomentosus – *Halosiphon* sp.

What we learned

- Pre-barcode consensus
 - Canadian arctic flora is a depauperate extension of North Atlantic flora with minimal Pacific influence
- Post-barcode consensus
 - Morphology is largely misleading
 - Discovered that minimally ~21% (possibly ~44%) of Churchill flora is Pacific in origin
 - Discrepancy – cryptic complexes, poor taxonomy and undetected population structure in data



Atlantic & Pacific



Trans-Arctic Invasion

- Global warming will radically alter benthic algal diversity in the Arctic & Atlantic as Pacific species join the 'Trans-Arctic Biotic Exchange'
- How advanced is the current invasion?
- More sampling is critical

The Coming Arctic Invasion

Geerat J. Vermeij¹ and Peter D. Roopnarine²

The current episode of climate warming is having drastic consequences for animal and plant life worldwide. Besides the expected poleward expansion of temperate and tropical species and the latitudinal contraction of cold-adapted ones, an even more dramatic interoceanic invasion will ensue in the Arctic: North Pacific lineages will resume spreading through the Bering Strait into a warmer Arctic Ocean and eventually into the temperate North Atlantic.

Trans-Arctic invasion began about 3.5 million years ago during the warm mid-Pliocene epoch (1). A combination of northward flow through the Bering Strait, high productivity in the Bering Sea (the geographic source of trans-Arctic invaders) (2), favorable conditions for rapid growth and dispersal in the Arctic Ocean, and the removal through extinction of many species during the mid-Pliocene in the North Atlantic (3) enabled hundreds of marine in-

In a future warmer climate, mollusks and other species are likely to migrate from the Pacific to the Atlantic via the Bering Strait.

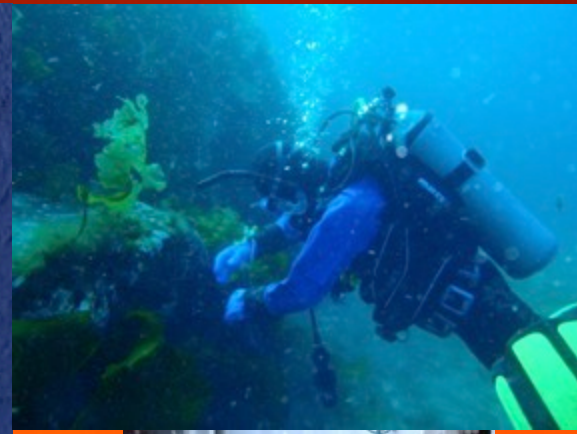


Source regions of potential trans-Arctic invaders. Fifty-six molluscan lineages present in the Bering and Chukchi seas (light-blue region) have not yet participated in trans-Arctic expansion but have the potential to do so; 28 of these species extend as far north as the Pribilof Islands and Anadyrski Gulf. Another 19 mollusk species are separated from related temperate Atlantic relatives by a genetic and geographic gap. These numbers exclude North Pacific lineages whose participation in the trans-Arctic interchange during the Pliocene led to the formation of species still living in the high Arctic.

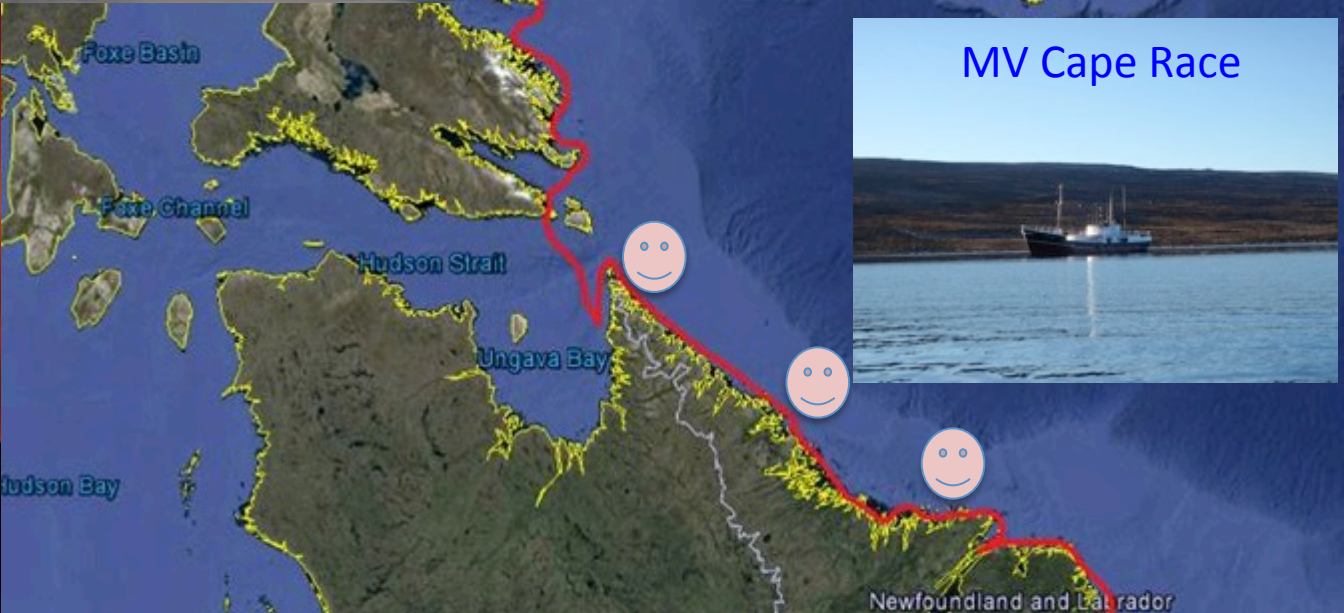


Arctic Biodiversity Survey (Sept 1-17, 2014)

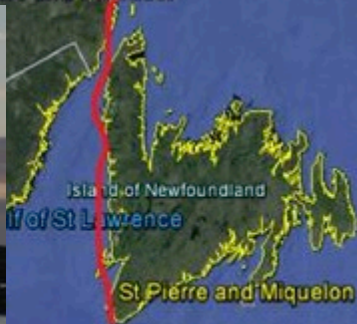
Qikiqtarjuaq



MV Cape Race



St. Pierre



Subtidal Collecting Followed by a Feeding Frenzy



Hebert Lab (Guelph)

Paul Hebert & Kara Layton
Biodiversity Institute of Ontario
University of Guelph

- Cataloguing marine invertebrate diversity in the Canadian Arctic through DNA barcoding
- Probing patterns of population structure in Holarctic species (i.e., *Macoma balthica*, *Hiatella arctica*)

Flabellina salmonacea



Psolus fabricii



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Lane Lab (URI)

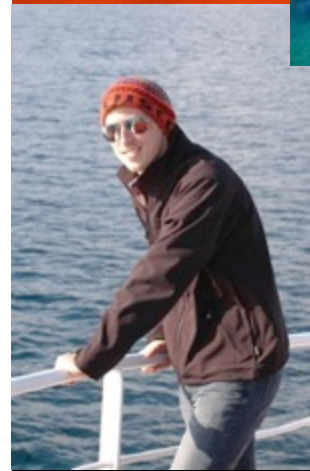
Arctic Red Algal Parasites



3 undescribed parasitic red algae
2 on the same host species

Saunders Lab

- Trevor Bringloe, Kyatt Dixon & G.W. Saunders
- Seaweed biodiversity including:
 - Species inventories
 - Northern/southern range limits
 - Biogeography
 - Phylogeography
- Total of ~550 specimens
- Also lab member (Meg Bruce) in the Beaufort; ~110 specimens
- Total Arctic: ~1100 seaweed specimens



Reyes Lab (UNB)

Survey of Microbial Eukaryote Diversity in Eastern Canadian Arctic (Freshwater)

- Samples sequentially filtered through 47 mm polycarbonate filters: 10.0, 3.0 & 0.2 μm
- Filters conserved in *RNA Later* (Sigma-Aldrich) and stored at 4°C
- Total DNA extracted from filters using *PowerWater DNA Isolation Kit* (MO BIO Laboratories)
- Dual-Indexed 16S rRNA and 18S rRNA libraries prepared using the Illumina *Nextera XT DNA Sample Preparation* kit
- Multiplexed libraries were sequenced using Illumina *MiSeq System*



Future Plans to Study Arctic Seaweeds

- Continue collaboration in Beaufort (Prudhoe Bay) ☉
- Submitted grant to NSF for targeted collecting ○



- Need collections from Barents and/or Greenland Seas – any assistance or advice welcome (Svalbard, Tromsø?)

Conclusions

- Most of what we know about coastal Arctic biodiversity in the Canadian Arctic is based on:
 - Morphological identifications, which can be significantly misleading in some groups
 - A very limited level of collecting effort
- Barcoding helps to resolve the previous two shortcomings by providing accurate identifications and allowing substantially more samples to be processed per site
- Changes are inevitable, indeed already taking place in the coastal communities of the Arctic
- The time to collect data is now!



Tip of the
Iceberg





GenomeCanada

Acknowledgments



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