Lateral gene transfer in Arctic sea ice?

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Guiding Hypothesis
Sea ice acts as a "hotspot" for lateral gene exchange and hastens microbial adaptation to changing conditions in the marine environment.

Lateral Gene Transfer (LGT)
The transfer of genetic material from one organism to another by non-reproductive means, including:

Transformation: the uptake of free (i.e. dissolved, extracellular) DNA from the environment;

Transduction: the infection by phage (viruses) that pick up and transmit foreign DNA; and

Conjugation: the plasmid-mediated transfer of DNA by direct contact between cells.

Importance in the marine environment
Lateral gene transfer is important in a number of marine processes and microorganisms including *Vibrio cholerae* pathogenesis, cyanobacterial phage defense mechanisms and perhaps proteorhodopsin phototrophy.

Spatial heterogeneity and temporal dynamics of particles, bacteria, and pEPS in Arctic winter sea ice

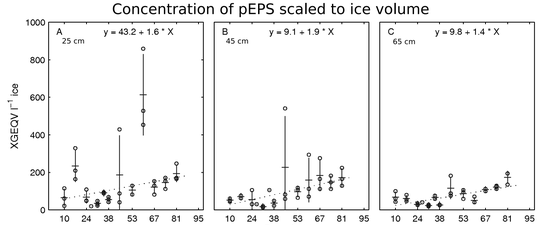
We recently participated in the Canadian Arctic Shelf Exchange Study (CASES) overwintering expedition in Franklin Bay, NWT, Canada. During the study we sampled sections of first year sea ice centered at depths of 25, 45, and 65 cm over the course of 12 weeks.

Concentrations of bacteria decreased as a function of ice volume over time (see figure in box H1) in the upper ice sections. However, when scaled to the volume of brine in which the majority of microorganisms are found, the concentrations did not change over time. This finding emphasizes the importance of measuring and understanding the physical microenvironments in which biology operates.

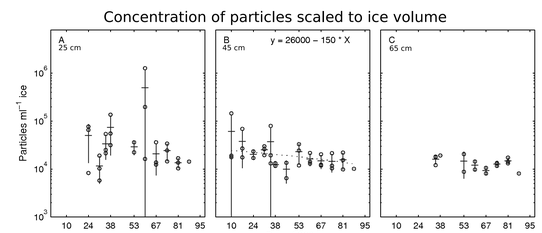
Extracellular polymeric substances (EPS) are thought to act as cryoprotectants for microbes in the ice. Consistent with this hypothesis we found that the concentration of particular EPS increased over time in all ice sections, at rates consistent with bacterial production.

Finally, we found greater variability in concentrations of particles, bacteria, and pEPS in the upper ice sections, which we attribute in part to spatial heterogeneity, and may hint at unexamined microhabitats for microbes in the ice. This variability was probably due to the dynamic nature of early frazil ice formation, in combination with decreasing concentrations of particles and bacteria in the underlying seawater following initial sea ice formation.

Concentration of pEPS scaled to ice volume

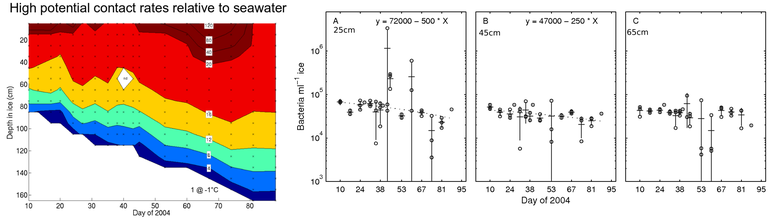


Concentration of particles scaled to ice volume



H1. The concentration of large numbers of cells, particles, and viruses in sea ice allows high potential contact rates among them, providing more frequent opportunities for lateral gene transfer (LGT) than in the underlying seawater.

High potential contact rates relative to seawater



Modeling by LE Wells has shown that potential contact rates between microbes and viruses in sea ice brines can be tens to hundreds of times greater than in the underlying seawater.

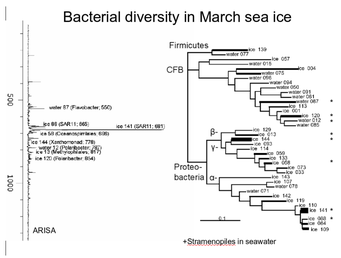
Microbial abundance in winter sea ice declines in the upper ice but bacteria and archaea persist throughout the ice.

H3. The release of extracellular DNA by cell lysis (e.g. from physical disruption or viral attack) of a diverse group of microorganisms provides the raw materials for transformation to occur. Additionally, concentration of extracellular DNA dissolved in seawater may occur during sea ice formation.

A diverse group of microbes is found in Arctic winter sea ice including MGI and MGII archaea, alpha-, beta-, gamma-proteobacteria, Gram-positive Firmicutes and a variety of CFB.

Preliminary measurements of extracellular DNA in stored sea ice cores are relatively high compared to other aquatic environments.

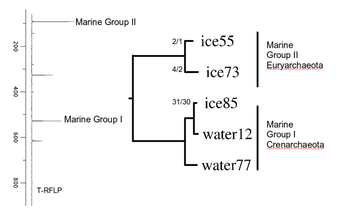
Bacterial diversity in March sea ice



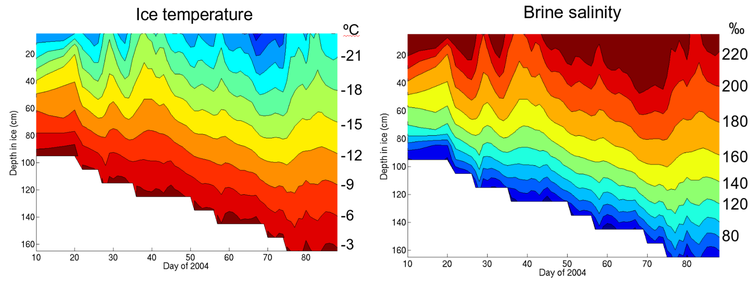
Environmental Extracellular DNA (ng ml⁻¹)

Location	Environment	min	max	Technique	Reference
Hawaii	Freshwater	1	88	CTAB->DABA fluorescence	Karl and Bailiff 1989
NOW'99 B	**Sea ice**	**70**		**PicoGreen fluorescence**	**this experiment**
Florida	Freshwater	2	44	Hoescht 33258 fluorescence	Paul et al. 1988
Mediterranean Sea	Marine offshore	2	31	Hoescht 33258 fluorescence	DellAnno et al. 1998
Hawaii	Marine coastal/estuarine	12	28	CTAB->DABA fluorescence	Karl and Bailiff 1989
NOW'99 A	**Sea ice**	**28**		**PicoGreen fluorescence**	**this experiment**
Florida	Marine coastal/estuarine	10	19	Hoescht 33258 fluorescence	DeFlaun et al. 1987
Antarctica	Marine coastal/estuarine	6	15	CTAB->DABA fluorescence	Bailiff and Karl 1987
Lake Washington	Freshwater	4	9	DABA fluorescence	Minear 1972
Adriatic Sea	Marine coastal/estuarine	2	7	Hoescht 33258 fluorescence	Turk et al. 1992
Gulf of Mexico	Marine offshore	2	5	Hoescht 33258 fluorescence	DeFlaun et al. 1987
Hawaii	Freshwater		4	CTAB->DABA fluorescence	Karl and Bailiff 1989
Portage Bay	**Freshwater**		**3**	**PicoGreen fluorescence**	**this experiment**
Hawaii	Marine coastal/estuarine	2	3	CTAB->DABA fluorescence	Karl and Bailiff 1989
Hawaii	Marine coastal/estuarine		3	PicoGreen fluorescence	Brum et al. 2004
Bahamas	Marine coastal/estuarine		2	Hoescht 33258 fluorescence	Paul et al. 1991
Station ALOHA	Marine offshore		1	PicoGreen fluorescence	Brum et al. 2004

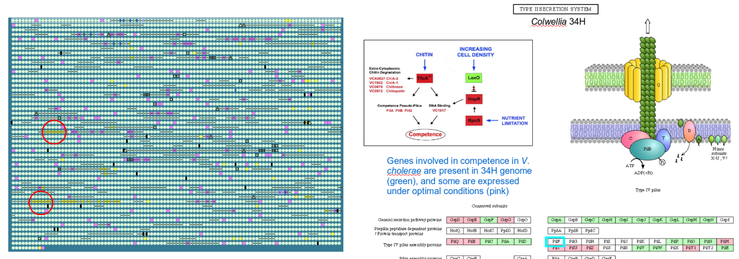
Archaeal diversity in March sea ice



H2. The mechanisms of LGT are triggered by environmental stressors prevalent in sea ice, including low temperature, salinity changes, high cell density, and exposure to radiation.



A model psychrophilic bacterium with a completed genome sequence, *Colwellia psychrerythraea* 34H, is being investigated for its potential to undergo LGT in conditions approximating those found in sea ice (where close relatives have been identified). The 34H genome contains putative evidence for the LGT of a compatible solute-degrading sarcosine-oxidase pathway, and preliminary proteomics work suggests that some cellular machinery necessary for transformation is expressed by 34H under optimal growth conditions.



H4. Sea ice is an efficient vector for the generation, transportation, distribution, and release of recombinants in the world's oceans.

Ice and ocean modeling experiments could estimate and compare the rate at which recombinant genomes are exported from their place of origin in sea ice and seawater to predict the relative importance of LGT in sea ice as a mechanism of microbial evolution. Models constructed to track chemical contaminants in the Arctic might be useful starting points.