Community Characterization of Microbial Populations Found in Supraglacial Icings at Borup Fiord Pass

Christopher B. Trivedi[1], Graham E. Lau[2], Alexis S. Templeton[2], Stephen E. Grasby[3], John R. Spear[1]

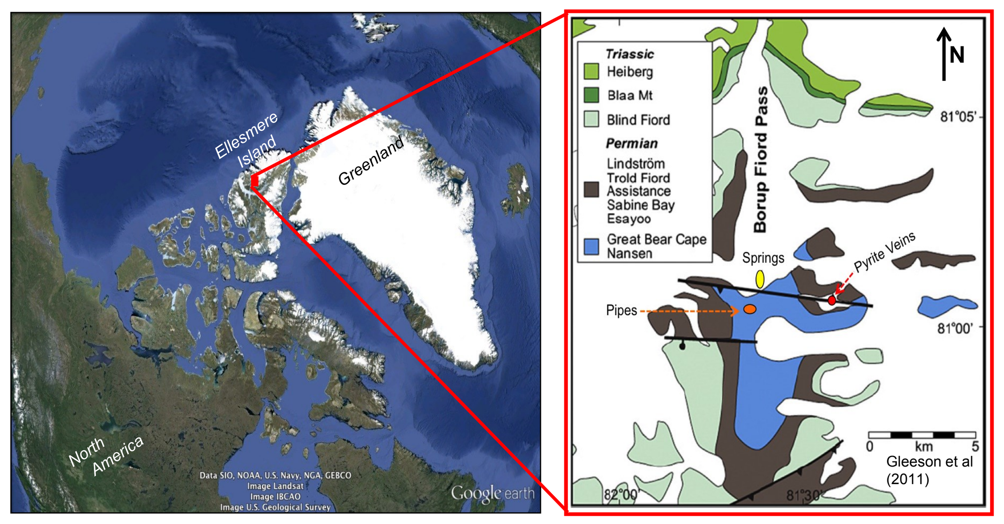
[1]Colorado School of Mines, [2]University of Colorado Boulder, [3]Geological Survey of Canada - Calgary

Borup Fiord Pass

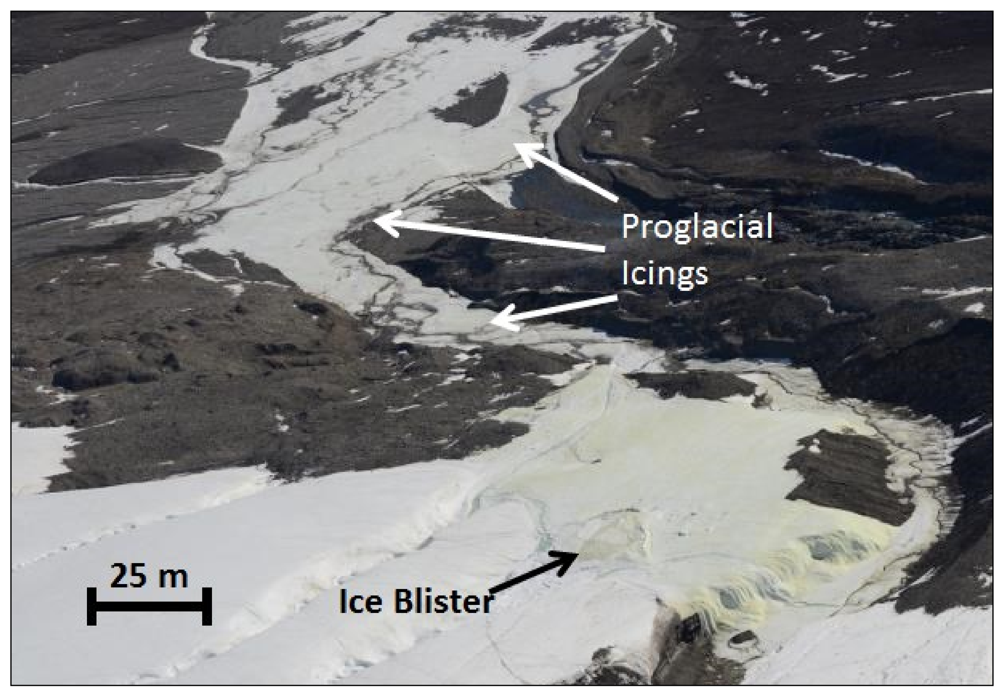
Borup Fiord Pass, on Ellesmere Island in the Canadian High Arctic, presents a system where subsurface fluids express as sulfidic springs at the toe of a glacier where large sulfur mineral icings are formed. This system provides a potential analogue to the Galilean moon Europa.

Past research at the site has shown that sulfate reduction and sulfide oxidation is likely microbially-mediated [1]. The energy released from these reactions can support numerous microbial metabolisms even in this low temperature environment and may be a valuable representation of the subsurface and surface processes occurring on Europa.

Although no spring was observed in 2014, icing samples representative of the interface between the subsurface and surface were sampled. We hypothesize that the icing samples serve as a preserved form of spring flow. Analysis of the geochemistry and microbial communities found within will allow for characterization of the sulfur-cycling dynamics and mineralization processes occurring at this site.



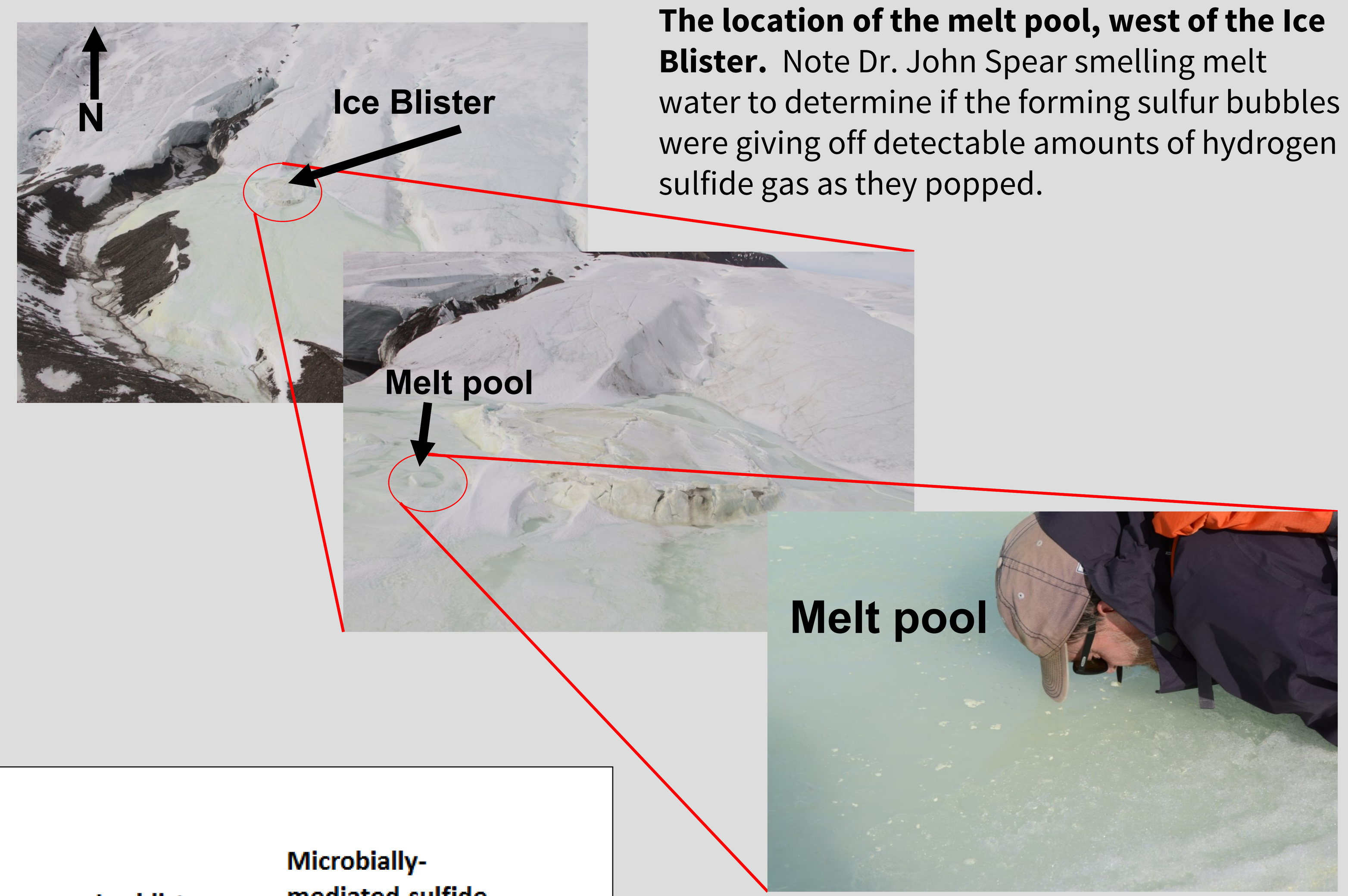
Site Location and Geology. Borup Fiord Pass glacier is situated within a North-South trending valley within the Kreiger Mountains of Ellesmere Island.



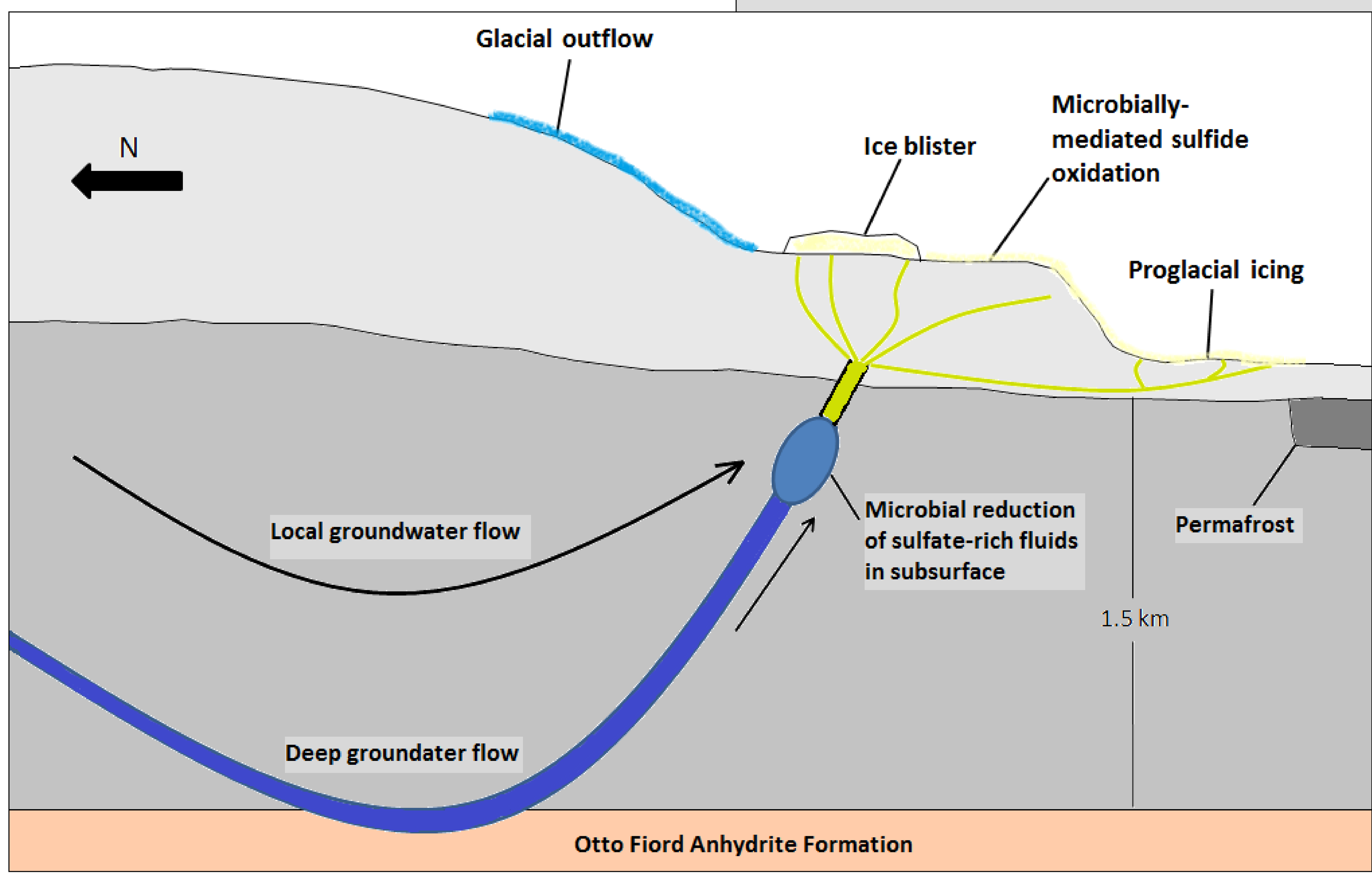
Sulfur staining on icings and location of Ice Blister at Borup Fiord Pass. The deposition of elemental sulfur at the toe of the Borup Fiord Pass glacier. Also note the 'ice blister' which was a main focus of our sampling efforts during the 2014 expedition.

Borup Fiord Pass – Melt Pool

- **Contained large amounts of sedimented sulfur compounds as well as bubbles of sulfur that formed as a sheen on top of melted ice. Each day this small pool would freeze and melt, continually changing.**
- **Geochemical analysis of the melt pool revealed high amounts of aqueous sulfide (1.8 mM). Bubble stripping of melted water also showed very high levels of hydrogen (29 nM).**

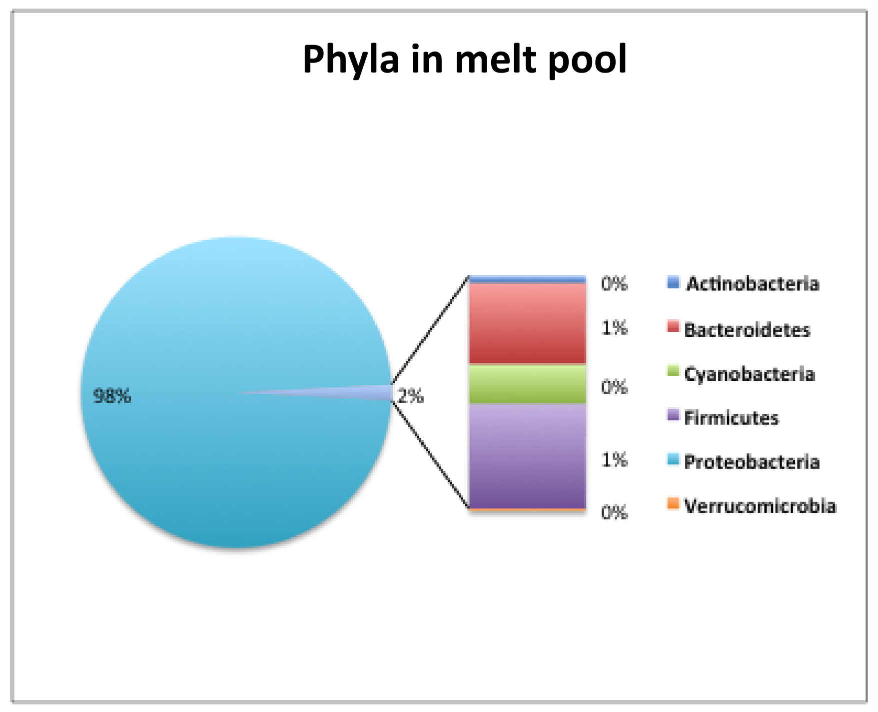


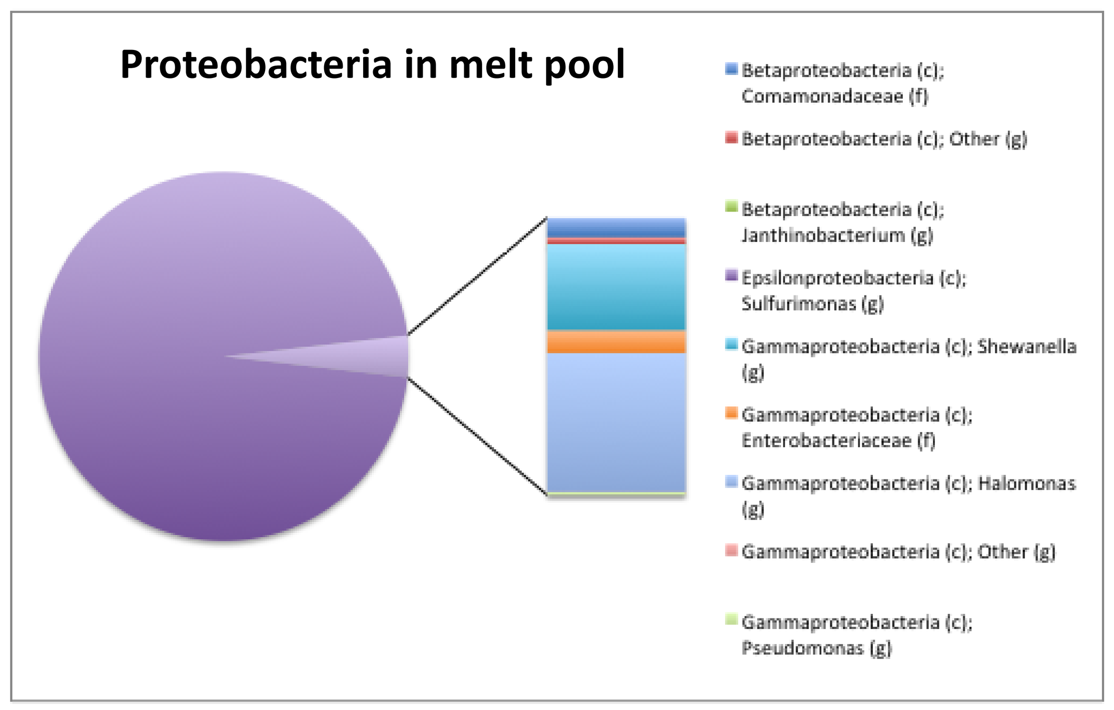
The location of the melt pool, west of the Ice Blister. Note Dr. John Spear smelling melt water to determine if the forming sulfur bubbles were giving off detectable amounts of hydrogen sulfide gas as they popped.



Proposed conceptual model of sulfur cycling at Borup Fiord Pass. The model makes use of glacial meltwater as the main source feeding the ice blister and proglacial icings. Note zones of potential microbially-mediated subsurface sulfate reduction, and subsequent surface sulfide oxidation. We hypothesize that permafrost intrusion and retreat plays a role in spring formation on a yearly basis.

16S rRNA Analysis of Melt pool

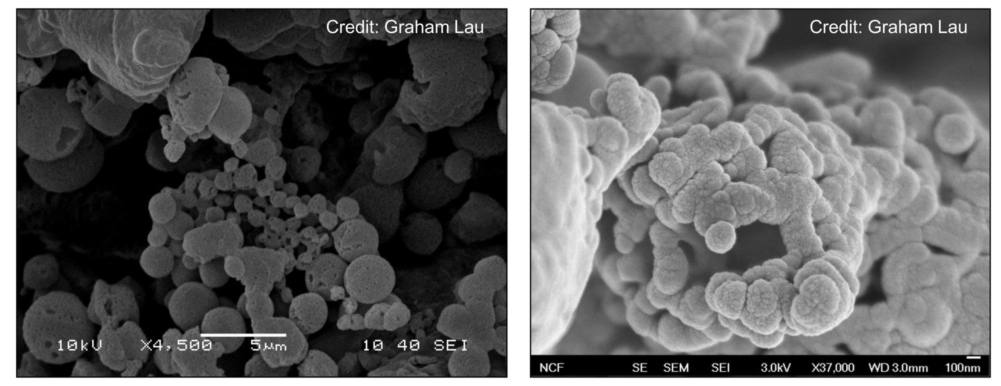




Initial taxonomic analysis of 16S rRNA data from the melt pool. Left: taxonomy at the Phylum level. Note the melt pool is ~98% Proteobacteria.

Right: Proteobacteria scaled to genus level. ~97% of Proteobacteria are Epsilonproteobacteria of the *Sulfuromonas* genus. OTUs below 1% abundance were filtered out as "not significant" at this level.

- **Previous analysis of Borup Fiord Pass samples (sediment) revealed a large abundance of *Sulfurovum* and *Sulfuricurvum* [2] both of which are found in the same family of Helicobacteraceae as *Sulfuromonas* (melt pool).**
- ***Sulfuromonas* is a known chemolithoautotroph and has the ability to oxidize zero valent sulfur as well as other reduced sulfur compounds during cellular metabolism.**



FE-SEM imaging and EDXS of the sediments and sulfur bubbles from the melt pool confirm the presence of sulfur compounds in the form of sulfur globules.

Future work

The Spear lab at the Colorado School of Mines will further characterize the microbial communities in samples collected in 2014. Our efforts will focus on drawing meaningful linkages between geochemistry, microbiology, and potential reaction pathways. Metagenomic and RNA-seq techniques will be used to explore sulfur metabolisms, while genes of interest including *sox*, *sor*, *sqr*, *apr*, *psr*, *ttr*, and *dsr* will be examined in order to elucidate the gene expression of S-metabolizing organisms.

We are currently employing microscopic and spectroscopic techniques in the Templeton Lab to assist in the characterization of the sulfur rich materials. These tools will help to better illuminate the mechanisms of sulfur cycling as well as inform us of the geochemical and biosignature inventory of sulfur-rich icy ecosystems.

Conclusions

- **Arctic subsurface/surface interfaces provide a unique geochemical environment that play host to microbes utilizing S-cycling metabolisms. Areas where surface icings represent subsurface fluids present likely targets for astrobiological research.**
- **Detectable microbial communities in the melt pool suggest key biological roles in sulfur reduction and oxidation pathways at Borup Fiord Pass.**
- **Together these analyses will provide guidance into potential astrobiological targets, predominantly in regions where subsurface fluids interact with the surface.**

References

[1] Grasby S. E. et al. (2003) *Astrobiology, 3(3)*, 583-596.

[2] Wright K. E. et al. (2013) Frontiers in Microbiology, 4(63), 1-20.

Acknowledgements

Our current work at Borup Fiord Pass is funded through Exobiology grant #NNX13AJ32G from the NASA Astrobiology Institute (NAI).

Contact Information for Chris Trivedi:

ctrivedi@mines.edu

christrivedi.com