BIOLOGICAL CHARACTERIZATION OF MICROENVIRONMENTS IN A HYPERSALINE COLD SPRING MARS ANALOGUE. H. M. Sapers[1,2,3], J. Ronholm[3,4], R. Comrey[3], I. Raymond[3], L.G. Whyte[3]. [1]Centre for Planetary Science and Exploration (*Centre for Planetary Science & Exploration C/O Faculty of Science Room 191, Western Science Centre Western University 1151 Richmond Street London, Ontario, Canada N6A 5B7)*, [2]University of Western Ontario, [3]McGill University, [4]Health Canada, Bureau of Microbial Hazards

Introduction: The polar desert environment of Axel Heiberg Island is an important Mars analogue and the perennial, hypersaline cold springs on the Island serve as proxies for putative Martian subsurface brines [1]. The Gypsum Hill spring system is a well studied [2] perennial cold springs located on in the Expedition Fjord area of Axel Heiberg Island.

Gypsum Hill Spring: Gypsum Hill (GH) is a microaerophilic (0.05 – 0.2 ppm dissolved O_2), hypersaline (8-9 % salinity), cold spring (3.9 – 6.6 ^oC) e.g. [3] located in the Canadian high Arctic. Previous studies have determined diverse active microbial communities in the spring [4]. These studies isolated predominantly psychrotolerant, facultative anaerobes that grow at salt concentrations at least as high as the *in situ* salinity from the GH springs. Sequencing studies indicate that the microbial community of GH is primarily sustained by chemolithoautotrophic primary production performed by sulfur-oxidizing bacteria [5]. Recent field-work (summer 2013) identified local patchy color variation over a centimeter scale in outflow channels. Areas dominated with green filamentous streamers (GC) were observed to be spatially associated with areas of red-brown sediment mats (RC).

Microbiology: 16S rRNA sequencing revealed distinct bacterial communities between the visually distinct microenvironments with only 29.4% similarity. Sulphur metabolizing phylotypes including several strict anaerobes dominate GC. A more diverse set of ecological niches are identified in RC indicative of more aerophilic conditions. *Marinobacter,* one of only 20 shared phylotypes, is a dominant component of both communities (27% of GC OTU reads, 41% of RC OTU reads) and is capable of both aerobic and anaerobic metabolism and may therefore play a critical role at the oxic/anoxic interface.

Microbe-substrate interaction: Scanning electron microscopy of GC samples revealed a massive biofilm (Fig. 1A, B). Specific cell-substrate associations were not observed. SEM of RC samples revealed intimate associations between cocci and rod-shaped bacteria and the mineral substrate through filament-like extensions of extrapolymeric substance (Fig. 1C). These results suggest that substrate-cell interaction and possible chemoautolithotrophy play and important roll in the RC communities compared to the GC communities.

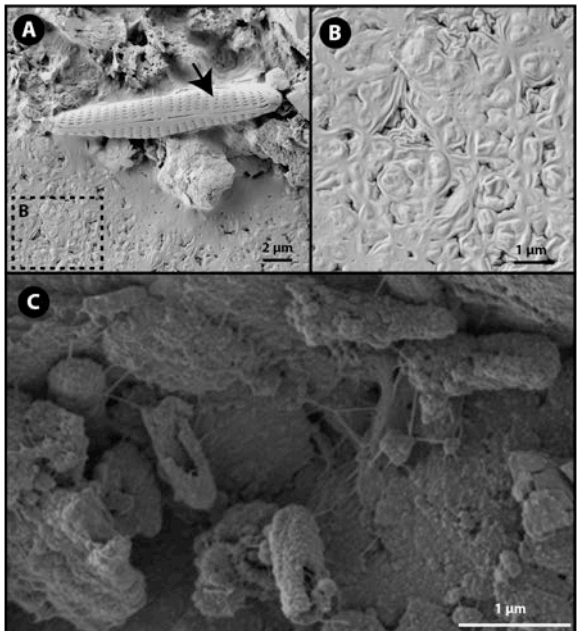

Figure 1: substrate-cell interfaces in visually differentiated microenvironments. A) Diatom (black arrow) on top of sediment matter. A massive biofilm (B) forms a matrix supporting sediment material and lacks specific cell-substrate associations. C) Rod-shaped bacteria adhered to sediment material through EPS-like extensions. Massive biofilms were not observed.

Conclusions: We have been able to link macroscale visual differences to distinct microbial communities that show very different micro-scale cell-substrate associations. The microbial communities of RC and GC differ also from the reported microbial communities of the Gypsum Hill outlet. Our data suggests that minor variations in chemistry, even between propinquitous sites, can have significant implications for community structure. Further work is required to define and resolve the physio-chemical parameters for RC and GC. This work has implications for assessing potentially habitable environments on Mars within spatially restricted areas.

References: [1] Andersen, D.T. et al. (2002) *J. Geophys. Res. 107*, 1–7. [2] Pollard, W.H. et. al. (1999) *Can J. Earth Sci. 36, 105–120*. [3] Omelon, C.R. et. al (2006) *Appl. Geochem. 21, 1–15*. [4] Perreault, N.N. et. al (2007) *Appl. Environ. Microbiol. 73, 1532–1543*. [5] Perreault, N.N. et. al. (2008) *Appl. Environ. Microbiol 74, 6898–6907.*