Abstract
Northern ecosystems are subject to atmospheric mercury (Hg) deposits from distant industrial activity. Precipitation events lead to an accumulation of mercury in northern environments. Once delivered, Hg is subject to transformations depending on its transport and fate. It can bind with sediments and be carried with snow and rain runoff to aquatic systems. In lake bottom sediments, Hg is converted to toxic methylmercury (MeHg) by a group of microbes known as sulfur-reducing bacteria (SRB). The alteration of inorganic Hg to MeHg enables bioaccumulation through the food chain, causing potential harm to humans, terrestrial and aquatic organisms. Investigations to identify bacterial production of MeHg in a northern ecosystem will help assess the potential impact on higher organisms. Currently, the role of SRB in mercury methylation has only been assessed in temperate and marine environments.

In this study, the relation of Hg and MeHg with total bacteria and SRB will be determined for a sub-arctic lake. A sediment core will be extracted from Kusawa Lake, Yukon, located approximately 120km southwest of Whitehorse. Core slices will be analyzed for total Hg and MeHg, trace metals, total organic carbon, diatoms, total bacteria and SRB and will be dated using $^{210}$Pb and $^{137}$Cs isotopes.

Summary of work
Over the past two years I have been working on the challenging field of molecular genetics work. The samples from Kusawa Lake were found to consist primarily of clay, which tightly binds DNA in soils. After several months of troubleshooting to determine a method to free DNA from the core samples, I found a MOBio DNA extraction kit that specialized in difficult samples. While some DNA was obtained, it was still typically very low but I did my best to move forward.

The next step was polymerase chain reaction (PCR) in preparation for cloning. This also required extensive troubleshooting as the primers were degenerative, meaning they select for numerous different DNA sequences and need to be optimized for your target gene. This again took a couple months and was finally achieved during spring 2012. After all samples were successfully amplified using PCR I moved onto the ligation and cloning reactions. Again, this was not straightforward. After a few experimental investigations, it was found that the E.coli cells I was using to transform were either no longer viable or no longer competent. A different strain of E.coli cells were tested and proved functional. Currently, I have 50% of my samples to this step.
Future work

As cloning is finally going well, I am hoping to send my samples out for sequencing within the next two weeks. At that time I will begin qPCR, which is notorious for being difficult but I am optimistic the process will go well. I cannot predict the timing for this project until I begin it.

I anticipate beginning analyzing and writing my thesis between now and December with a defense date sometime in Winter 2013.

Other considerations

Along with my Master’s obligations, I was also selected as one of the inaugural Jane Glassco Arctic Fellows with the Walter and Duncan Gordon Foundation. This two-year award from June 2010-2012 was very educational as well as time consuming in terms of completion of my project. I researched and made recommendations for the Yukon’s developing Water Strategy, which was based on interviews, hard science and social science periodicals and a legislative review. I concentrated on this work as opposed to my Masters during summer and fall 2011. I also took a leave during the latter half of summer and fall 2010 due to a family illness and death. Overall, my time spent strictly on my Masters’ has been limited, though it is now my sole task and is finally moving in an optimistic direction.