

Environmental DNA Sampling Along the Upper Half of Yukon River and Major Tributaries to Determine Present Fish Species



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Top Left to Right
Figure 1. Hil and Lil sampling at sample site 5, Lac Laberge
Figure 2. confluence of Teslin (silty) and Yukon Rivers
Figure 3. Signs along river of seemingly conflicting interest groups, Newmont gold mine and the Tr'ondek Hwech'in people.
Figure 4. Canoeing across Lac Laberge



Materials and Methods

I paddled the upper half of the Yukon River from June first to the middle of July. During this expedition, I collected eDNA data at the confluences of major tributaries and other points of interest along the Yukon River. During the expedition, samples were taken with an eDNA citizen science sampler. The filters were then transported in a waterproof container to the takeout at the Yukon River Bridge where the river crosses under the Dalton Highway. I sampled twelve sites of interest and used two to four filter samples per sample site with a goal of filtering one thousand milliliters (mL) per sample. Some sample sites had a very high sediment load making it hard to filter all one thousand mL but the filtered amount was recorded. Qualitative data in the form of written descriptions of habitat characteristics from all sample sites will be recorded using the ADF&G format. Since the expedition was completed around mid July samples have been processed in the Ichthyology lab at UAF. DNA was isolated from the filters. Briefly, a continuation of this project is to use templates for preparation of DNA sequencing libraries targeting a short segment of mitochondrial genomes. Mitochondrial DNA sequences obtained from river samples will be compared against reference databases to determine which species were present near each site. Another use for these samples would be to use quantitative PCR as an estimator of species abundance.

Discussion

While out taking samples, the main struggle I encountered was the amount of sediment in the Yukon and some tributaries. To try and collect as much DNA as was possible, I took extra samples. It is possible that a filter with slightly larger pore size would help this problem. One of the challenges we have encountered in this process is that eDNA is a relatively new method. The universal fish primers that are typically used to distinguish fish species do not do the best differentiating Alaskan fish species (in particular distinguishing salmonid species). I look forward to continuing work with this data to determine the species present. Below is a QR code to the website where I will eventually share my results.

sites.google.com/Alaska.edu/upper-yukon-river-expedition-2/home

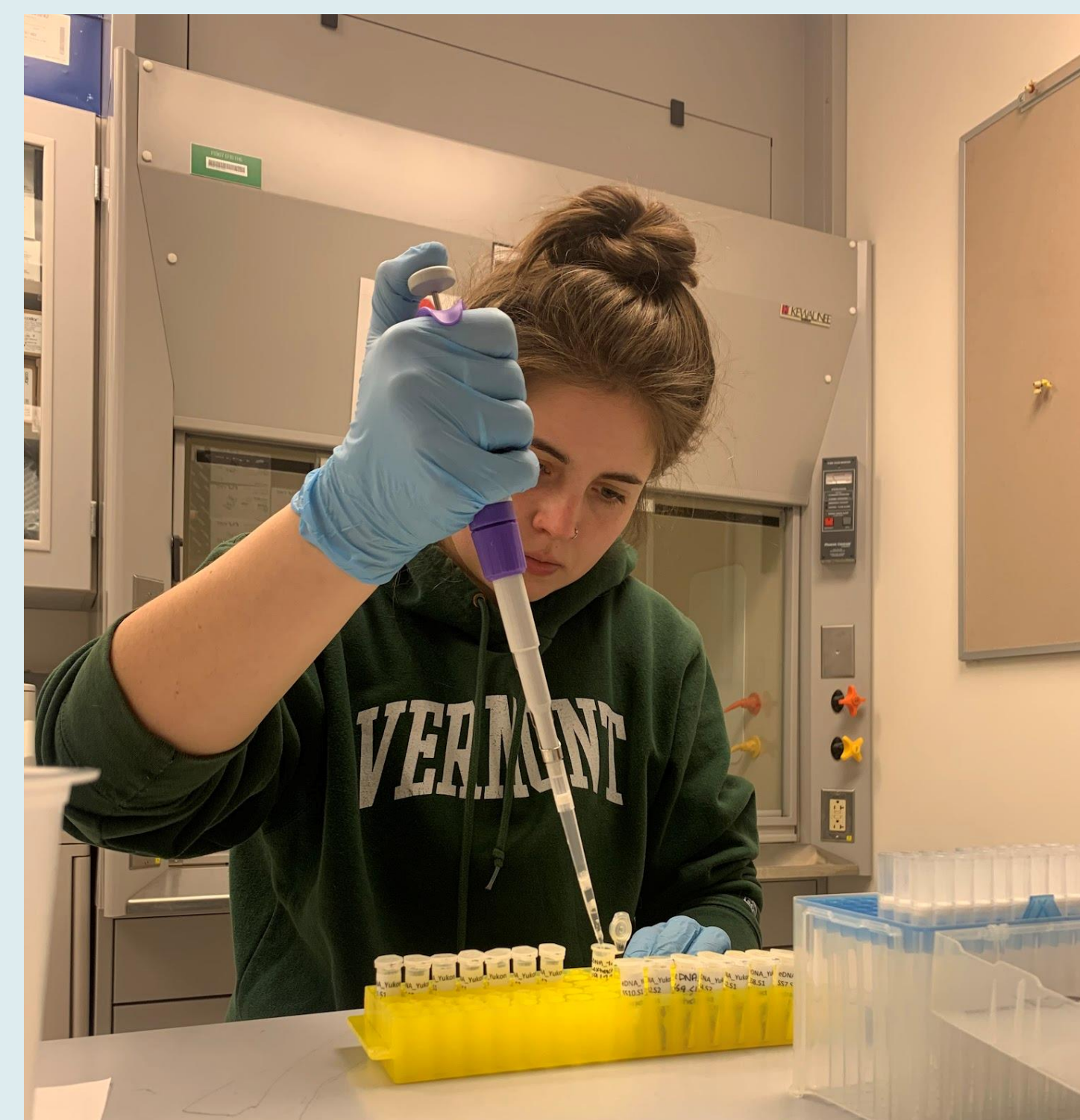


Figure 9. Above, Lillian being cautious not to contaminate the DNA, transferring extracted DNA into aliquots.

Significance

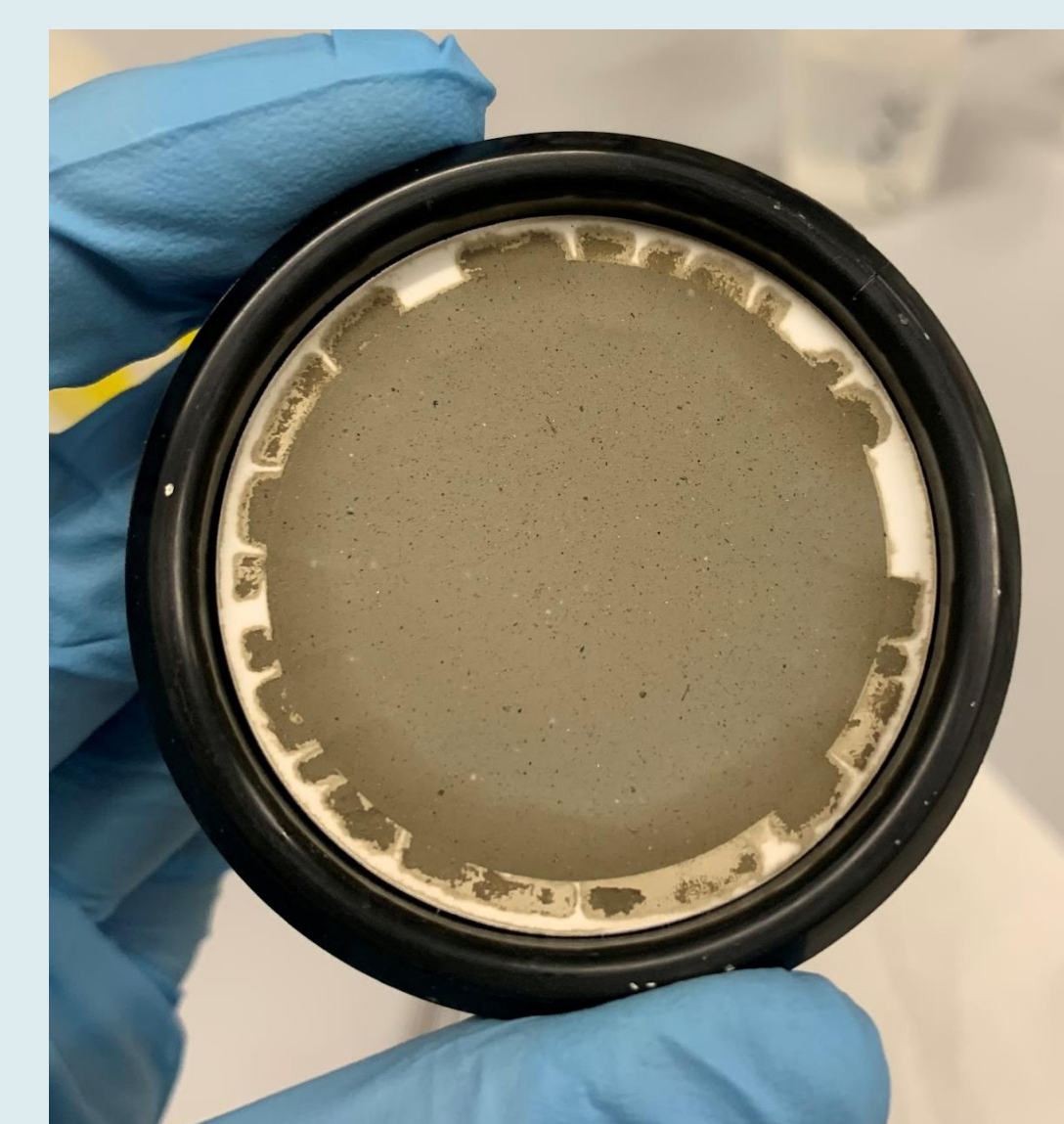
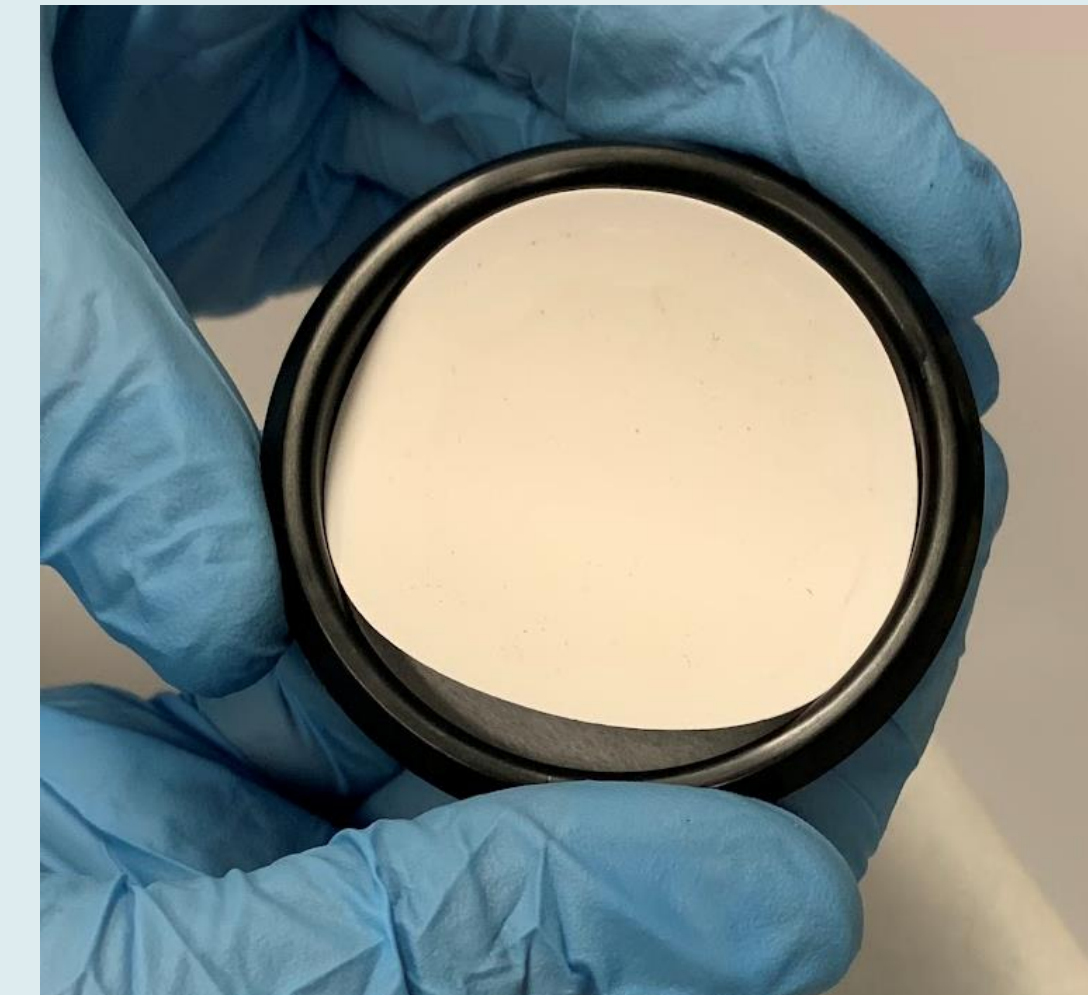
The impending impacts of climate change combined with other human pressures (i.e. fishing, pollution, damming, etc) on the river system are likely to continue changing the Yukon River. This research ought to relate to the effects of trawling at the Yukon River delta particularly in regard to anadromous species. With the likelihood of continued major changes to this river ecosystem, it is important to have baseline data for what fish are present along the river. By spending time at each sample site and recording the environment that samples are taken, the data found can be extrapolated to more generally represent the fish that ought to be present in the surrounding areas and tributaries. Additionally, as eDNA is still a relatively new research method, this experiment will serve as a test case and continued "proof of concept" for the use of eDNA metabarcoding as a tool in fish and fisheries research on the Yukon River and remote areas of Alaska.

Abstract

As the third longest river in North America, the Yukon river is a vital indicator of the health of arctic and subarctic aquatic health. With many interest groups, including indigenous communities and commercial fisheries, reliant on the fish that are present in this river, it is vital to know and monitor species distributions. Last summer I embarked on a canoe expedition with five of my peers on the upper half of the Yukon river (from Whitehorse to the Yukon River Bridge at the Dalton Highway) in canoes. As I was already planning this expedition, it was possible to conduct this expedition while collecting Environmental DNA samples at places of interest such as confluences with tributaries. I collected eDNA samples by filtering river water at twelve sites. DNA has been extracted from the samples and is still awaiting PCR and metabarcoding to determine species of fish present. This is important information to know for the Yukon River as climate change and the decreasing fish populations continue to affect this system.



Figure 5. Above, map of Yukon River with sample sites (SS) marked. Inset map highlights major tributaries of the Yukon watershed with SS marked
Figure 6. Top right, filter from Lac Laberge. **Figure 7.** Middle right, filter from White River. **Figure 8.** Bottom right, difference in sediment coloration prior to cleaning the extractions.



Acknowledgements

I would like to thank the expedition members, Zoe, Grace, Haley, Anna, Mo, and Puff, because without their support and patience for when I was taking samples, this project would not have happened. I would also like to thank Andrés Lopéz for mentoring throughout this project, as well as Maggie Harings for being there with me for many days in the lab. This expedition was also special because of the river community that gifted us hospitality, food, advice, stories, and kindness. Of course many thanks to URSA for facilitating this super cool opportunity! Major thanks to Blender and Goodr for many sponsored sunglasses, go check them out! Thanks always to the mighty Yukon River and all of the unceded indigenous land we were privileged to travel through.