From: Langara | Applied Research Center
To: Kyra Janot
Cc: Applied Research
Subject: Thank you for submitting your ARC Final Report
Date: Wednesday, August 28, 2024 3:25:29 PM

Thank you for submitting

ARC Final Report

Our team may reach out to you with follow-up requests for clarification regarding your submission.

Review your submission responses below:

Researcher First Name: Kyra

Researcher Last Name: Janot

Department: Biology

Other Department:

Project Title: Seasonal seaweed diversity in the intertidal zones of Greater Vancouver

Start semester: 9/1/2023

End Semester: 8/31/2024

Introduction - Please introduce yourself and include pertinent background information as it relates to your project's research area. I am both an instructor in the

Biology department and a marine biologist with a background in seaweed evolution and ecology. Having worked extensively in the past with seaweeds in more remote locations of British Columbia, I wanted to gain a better understanding of what seaweed diversity looks like in Vancouver, a city centre that is population dense yet notably close to nature.

Please discuss your educational background and your work experience as it relates to this project. If possible, include a quote that helps define your interest in the project. I hold a BSc in Marine Biology and a PhD in Botany. Prior to this research my graduate work was focused on understanding how certain seaweed species have evolved to withstand wave-swept intertidal zones, using a combination of molecular, chemical, and mechanical analyses. This work was done in British Columbia, and involved a significant number of field collections that helped me to build up a knowledge base on many of the common seaweed species of the Pacific Northwest. As my graduate research required extensive molecular work to genetically distinguish between similar-looking species, I was also able to leverage this experience to identify several cryptic species for this project. I have also been involved in several annual seaweed surveys on Calvert Island coordinated by the Hakai Research Institute, which allowed me to modify pre-existing survey protocols to get data that would be comparable with other datasets. My interest in this project stems from conversations with other local phycologists (seaweed scientists), wherein we mutually recognized that there is a surprising lack of recent and systematically collected data on local intertidal biodiversity. What does exist tends to focus more on animals, yet these same animals are reliant on seaweed as both food source and habitat. My aim, therefore, was to not only start documenting this diversity, but to develop methods that would make monitoring easier to maintain in the future.

Please summarize your project in plain language that others not in your field could understand. Seaweeds are a critical component of marine ecosystems off the coast of British Columbia, providing both food and habitat for a huge diversity of vertebrate and invertebrate animals. Yet despite their ecological importance we do not have a comprehensive description of the health of seaweed communities in the Greater Vancouver area, and factors such as pollution, vessel traffic, and climate warming may be putting them at risk. This project aims to document the ecological diversity of local seaweed communities using a combination of ecological surveys and environmental DNA sampling, establishing a baseline for comparison that can be used to understand how these communities may be impacted by human activity in the future.

Identify the project goals and objectives. Explain how the results may be used to solve a problem or inform further research in the field. The major goal of this project was to contribute to both academic and practical knowledge of local seaweed communities in several key ways: 1) establishing a baseline for seaweed species diversity at multiple sites in the Greater Vancouver area; 2) documenting seasonality of common seaweed species with respect to when they “bloom” and die off each year, and 3) developing environmental DNA sampling techniques to make future monitoring more comprehensive and efficient. Data from field surveys has already been made publicly available via the St. Lawrence Global Observatory Database, and may be downloaded and used to make comparisons with other locations or with future local work. This data includes information on which seaweeds were visually observed at four different locations in August 2022, November 2022, and February 2023, including corresponding tidal heights

and abundances. As seaweeds are at the base of the food chain for marine ecosystems, understanding their abundance and seasonality is a critical component of understanding fluctuations in abundance/seasonality of other species – if the timing of seaweed blooms or die-offs shift with ongoing climate change, documenting that shift may allow us to understand what is going on at higher levels up the food chain as well. Environmental DNA sampling is a technique where DNA is extracted from samples of water or substrate. Organisms are constantly shedding tissues/cells into the environment, and so DNA extracted in this way should allow for a snapshot of all the organisms that are present in the area (or that were present recently). Samples were collected monthly between August 2022 and March 2023. The data is still being analysed, but preliminary results suggest that the range of several “introduced” seaweed species may have to be expanded to include Vancouver. The data is also currently being used to build a taxonomic classification tool which, if successful, will allow for classification of “unknown” species to higher taxonomic levels (e.g., genus, family, and so on). While similar tools exist for microbial communities, there is not currently one available for seaweeds.

Briefly explain the steps taken (methods used) to conduct the research, and describe the key findings. The large dataset generated from the environmental DNA samples still needs to be fully analysed, particularly sequences that do not match any known species in publicly accessible databases. In collaboration with Ido Hatam and a bioinformatics student, we are working on building a tool that will hopefully allow for identification of these sequences to higher taxonomic levels such as genus, family, etc. Once this is done, the dataset will be used to look for patterns in seasonality/location. If the results look comparable to what was shown in the transect surveys, I intend to work on a proposal for ongoing eDNA monitoring at a more limited number of sites.

Who was involved in this project (eg. faculty, students, community partners)? How did their involvement contribute to the project’s success? Were there any challenges to overcome? All challenges faced during this project (funding, troubleshooting protocols, safety and logistics, training in new techniques, concerns over respectful sampling of specimens) were ultimately surmounted with the help of Langara’s faculty and students, patient individuals from various municipalities and First Nations, a network of collaborative scientists, and a handful of community volunteers. The Department of Fisheries and Oceans was a huge financial contributor to this project, providing just over $50,000 towards equipment, consumables, and student salaries. Several DFO scientists (Janet Mossman, Paul Covert, and Natasha Salter) were also instrumental in helping me develop the ideas and scope of the project, as was Bridgette Clarkston from UBC. Sue Velaquez from Hakai Research Institute trained me on how to collect and process environmental samples and provided me with a sampling pole for water collections, ensuring that my results would be comparable with other marine datasets collected in BC. Both Natasha Salter from DFO and Travis George from the Tsleil-Waututh Nation attended and assisted on several field surveys. Beau Gravlin (spouse) volunteered his time for all field surveys and eDNA collections, which was critical for both logistics and safety. A total of eight students from Langara worked on this project in some capacity, whether funded through the DFO grant, the ARC fund, or WOC/SWAP hours. Steven Guo and Adrian Ruiz assisted me in the field as well as during initial protocol development and troubleshooting for DNA extractions, providing insights that ultimately helped streamline processes for both. Carmen Fong did the vast majority of the molecular work for both survey

and eDNA samples, with the assistance of Marielle Mauro later on in the project. Jen Shannon helped clean up specimens for submission to the UBC Herbarium, and took numerous photos of tissue samples under the microscope that proved necessary for later species identification. Gavin Ieong, Rae Parsons, and Mendel Kwan all contributed their bioinformatics skills to cleaning up and analysing the massive dataset generated from eDNA sampling. Biology faculty members Ji Yong Yang and Ido Hatam provided critical advice and guidance for different parts of the project, particularly molecular protocols and data analysis. Ji's students Avneet Kaur and Yukiko Inokuchi helped to train my students in molecular work. Finally, both Ji and Brendan Morris-Reade (ARC Research Assistant) provided back-up student supervision on several occasions. The city of West Vancouver and the Vancouver Parks Board provided me with written permission to perform collections in the relevant municipalities, while the cities of Surrey and North Vancouver verbally expressed that they had no concerns. I also communicated with representatives of the Musqueam, Tsleil-Waututh, Squamish, Tsawwassen, and Katzie Nations regarding any potential concerns about this work, and all took the time to respond and let me know that they had no concerns with the proposed work as described. Several also expressed support and a request to receive the data at the end of the project, which was motivational in seeing the project through to the end.

Please share any personal stories that made this research experience memorable/valuable.

The experience of taking students out into nature to engage in real ecological research was incredibly rewarding. Despite frustrations with getting new protocols to work, problem-solving how to deal with tricky landscapes, and the stress of needing to get everything done within a narrow window of time due to rising tides, their enthusiasm and resilience was impressive. There were several instances in which they picked out unique species that I would have otherwise passed over. It was an important reminder that being a good scientist is not just about academic performance and training – creativity, flexibility, and a natural curiosity are equally as important, if not more so. With students working in the lab, watching them develop their skills and become more and more independent was also very rewarding. Seeing the value of hands-on-learning in such a direct way really drove home the importance of giving students as many opportunities to apply their skills, make mistakes, and adjust accordingly. Their work ethic and determination to figure out issues (which were almost always because of protocols rather than human error) were additional reminders of the importance of "soft" skills in science.

What are the next steps for this project and for you as a researcher?

This project involved performing three sets of transect surveys in the intertidal zone at four sites (Brockton Point in Stanley Park, Cates Park, Crescent Beach, and Lighthouse Park) and collecting monthly substrate and water samples from each site. Surveys were performed during low tide by laying out four vertical transect lines from the high intertidal to the tideline, with a 1x1 m grid laid down along each transect line every 5 m. Percent cover of each visually distinct species was estimated within the grid, and recorded along with tidal height. Representative specimens of hard-to-identify species were collected as vouchers, and samples were taken for DNA extraction and sequencing. Environmental DNA ("eDNA") was also extracted from water and substrate samples and subsequently sequenced. Sequences were compared to a public database of sequences from "known" seaweed species, to get information on which species were present at or near the time of sampling.

Species that were seen directly during surveys were compared with those identified via environmental samples, to investigate whether eDNA sampling is useful as an estimate of species diversity when standard surveys are not possible (due to time/safety constraints associated with late night low tides in the winter). In total 150 seaweed specimens collected during surveys were identified using DNA sequencing, with 141 vouchers send to the UBC Herbarium to become part of their long-term collection. While most of this was done using funds from the Department of Fisheries and Oceans, the ARC funds I received allowed me to perform additional sequencing on a second gene for specimens that were hard to identify in my initial attempts. Survey data was used to generate seasonal species lists for each of the four locations, and the full dataset was uploaded to the St. Lawrence Global Observatory Database (https://doi.org/10.26071/ogsl-a45b745e-a265). In addition to the general diversity baseline that this dataset provides, there were two particularly notable findings: 1) one specimen that was collected and sequenced is of a species that has not been previously documented in BC, and 2) two known introduced species were much more abundant than expected (unclear if this is due to a rapid increase in abundance, or insufficient historical data). DNA was extracted from a total of 48 water samples and 48 substrate samples, and preliminary monthly species lists have been generated. Due to limitations of the sequence database used for comparison there are large portions of the dataset that have yet to be identified to species, however preliminary results indicate presence of several species that have not been previously documented in the area. It is not clear whether they represent an established introduced population or residual organic matter from elsewhere (e.g., ballast water), but further investigation is warranted. Analyses of the remaining unidentified sequences is ongoing.

Please upload any images that will help to showcase your project.

By submitting, I consent to uploading my ARC Fund final report to the Langara Institutional Repository (The LaIR). True

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