

Dear Newnham US Bursary Selection Committee

I would like you to consider my application to the Newnham US Bursary 2019. I am a second year PhD student working on marine mammal metagenomics. Metagenomics is the study of genetic material recovered directly from environmental samples, in my case, marine mammal faecal samples. With the resources generously offered by the Newnham US Committee, I would be able to assist to the “Genomics of Disease in Wildlife Workshop” taking place in June 2019 at Colorado State University, Colorado, USA. This workshop is a unique opportunity for intensive hands-on training on genomic data analysis of both host and pathogens. In the rapidly evolving field of genomics, training resources are still rare in a wildlife context. This training is vital for my PhD but unavailable to me in this country. This workshop would also be a perfect opportunity to network with people working on similar topics and facing related issues as me, and help me to use my PhD to provide real policy recommendations around marine conservation and the fishing industry.

From food to oxygen, from transportation to CO2 regulation, oceans provide us with many essentials and extra benefits. Unfortunately, humans have not thoughtfully managed these precious resources. Various human activities are negatively affecting the health of marine environments, and the situation is now critical. Authorities from all over the world, including the United Nations, are urging and pushing for scientists to generate and provide as much information as possible. This information is critical to assess and understand the current situation accurately and to develop measures to mitigate, monitor and hopefully improve this marine environmental crisis.

Sentinel species or bioindicators are considered to be species that provide relevant information on various environmental stressors. Sentinels can be used to identify warning signals about harmful impacts on the health of the environment, including those with potential effects on human health. An excellent example of



sentinel species is the domestic canary, used in the past for detecting carbon monoxide in mines. In marine environments, marine mammals have multiple characteristics that make them

proficient native bioindicators. They are on top of the food chain, have long lifespans, are susceptible to various terrestrial pathogens and have large fat storage, which means they accumulate significant amounts of fat-soluble toxins including

heavy metals. For these reasons, I decided to work with the Juan Fernandez fur seal, a little-studied sentinel species that was once, considered extinct. This species only mate in an isolated archipelago



Illustration 1: Screenshot taken from the UNESCO website referring to ocean sciences. <https://en.unesco.org/ocean-decade>



600 km off the Chilean continental coast, named Juan Fernandez archipelago. This unique ecological region is a UNESCO Biosphere Reserve, one of the ten priority sites for the conservation of biodiversity in the Region of Valparaiso, and one of the 11 irreplaceable priority sites for marine conservation worldwide. In 2017 the waters surrounding the archipelago became the new Marine Protected Area called “Mar de Juan Fernandez”. Investigating the Juan Fernandez fur seal could be crucial for both, monitoring and managing this 11000 square kilometres protected area.



As a second year PhD student, I am interested in exploiting faeces as a non-invasive information source. Faeces can provide information about different aspects of an individual including hormones, diet and pathogen exposure. In my research, I am focusing on the faecal microbial community specifically, bacteria and viruses. The common perception is often to associate bacteria, viruses and other microorganisms directly with health deterioration. But the study on the microbiome, which is the entire bacterial community that inhabits an environment such as the gut, has shown the opposite



completely. Health instead, relies to a large degree on the interaction with these microbes as they undertake vital functions including metabolism and training the immune system while also, actively participating as an “immune soldiers” themselves. During my research, I am characterising for the first time, the faecal microbiome of the Juan Fernandez fur seal regarding viruses and bacteria. I am focusing in identifying differences in the composition of bacterial and viral communities across geographical location (proximity to human settlements), the presence of contaminants such as microplastics and heavy metals,

genetic background and diet. At the end of my research, I expect characterise the normal fur seal faecal microbiome, and understand how these communities shift in relation to different factors. With this information, I am interested in discovering microbial patterns that could later support monitoring efforts. By analysing the microbiome, I will also have the opportunity to identify potentially harmful viruses and bacteria. These findings would be crucial for disease surveillance concerning the fur seals, humans, and their domestic animals.

To identify the different components of the microbiome, I am using next-generation sequencing (NGS), which is a type of DNA sequencing technology. The field of genomics through next-

generation sequencing (NGS) is developing at a rapid rate, and with it, several training courses and other resources are now available with regards to human and domestic animals. But regarding wildlife, this is not the case, and scientist in this field often must adapt to what is available. On this matter, I have the chance to attend to one of the very few workshops oriented only to wildlife. This workshop is a unique opportunity to get intensive training at a critical stage of my PhD. I am currently in Robinson Crusoe island for about starting a third fieldwork season. By the end of this collection, I will have three years of faecal samples to process and analyse. Before starting this project, I did not have experience with bioinformatics, a knowledge that is critical for analysing raw DNA Sequences. I have undertaken some basic informatics training sessions provided by the University. However, this was not specific to the type of work I am doing, although I have applied it to bacterial analysis. Therefore, I have been predominantly using online resources that I tend to follow step by step. I would like to feel more confident in the appropriate bioinformatics approaches and would also want to be more critical about which type of analysis suits best my data so that confounding effects can be considered. Therefore, this training will allow me to become confident and independent, as well as academically rigorous.



Throughout my PhD, I have worked hard on identifying a variety of collaborators and sponsors, including Newnham, who have helped me to pursue my research goals. My robust network includes Cambridge Communications, who already published a short article in their magazine horizons and now, are willing to follow the evolution of my work. For my current fieldwork, they provided me with recording materials to capture my activities during the third and possibly last fieldwork. Through this and other social media channels, I would intend to acknowledge Newnham funding raising the profile of the college and graduate body. I would be thrilled to once more obtained Newnham's support to get the training I need. Newnham would contribute to developing skills that I can pass on once back in my home country. Finally, I would like to thank the U.S Newnham committee for opening this exceptional funding opportunity.

Sincerely,

Constanza Toro Valdivieso

**Costs and Funding**

Travel: USD 500

Tuition: USD 2500  
in tuition

Accommodation and maintenance: Included

Other: USD 500

**Total cost: USD 3500**

Will you be paid for this project? NO

If so, please give details:

Please attach a carefully worked out credible budget for the visit showing how you will be able to cover the balance of the cost (if any).