

Microbial Genomics Research Opportunity

Research Challenge:

The Wildlife Toxicology Research Section at Environment and Climate Change Canada (ECCC) is seeking a M.Sc. student to conduct research on microbial consortia using next generation sequencing technologies within the Soil Microbiology Assessment and Genomics Laboratory. This research will be conducted in collaboration with Dr. Daniel Gregoire at Carleton University and is funded under the Chemicals Management Plan to develop methods to support program goals under the Canadian Environmental Protection Act (Domestic Substances List (DSL) and New Substances Notification Regulations (Organisms) (NSNR(O)). Consortia are groups of microorganisms that can be adapted towards specific purposes such as biodegradation and environmental remediation. Canada requires products imported or marketed for these purposes to submit to regulatory review with a notification, unless they only contain organisms already on the DSL. Consortia propose a unique problem in that identifying and/or culturing constituents may not be trivial, unlike defined mixtures or single organisms on the DSL. The challenge is to adapt metagenomic and metatranscriptomic sequencing techniques to analyze the composition of microbial consortia and to help develop standards for quantification, classification, and limits of detection of constituents. The student's work would have direct applications in addressing existing challenges and may be used to facilitate guidance to Notifiers submitting applications under the NSNR(O). The project will also work towards developing methods to track the fates and interactions of constituents in environmental matrices, such as soil, as part of exploring new approach methodologies for risk assessments of complex mixtures and consortia. This research opportunity will help develop valuable skills using cutting-edge sequencing strategies and technologies as well as the opportunity to learn, use, and adapt bioinformatics workflows.

The project will commence in Fall 2022 with funding available for up to two years for research and student support.

Interested candidates are encouraged to contact Dr. Daniel Grégoire (DanielGregoire@cunet.carleton.ca) and Dr. Derek Smith (derek.smith2@ec.gc.ca) with a



PDF of their Academic CV, transcripts (unofficial is fine), and a description of their research and career interests (Statement of Intent).

Research Environment:

Research activities will take place at 335 River Road, Ottawa, ON in the Science and Technology Laboratories at ECCC and in the laboratory of Dr. Daniel Gregoire in the Carleton University Department of Chemistry. The ECCC facilities are well equipped with state-of-the-art sequencing technology and quality control equipment including an Illumina NextSeq 1000, Oxford Nanopore Technologies Minion MK1C/MK1B sequencers, Agilent TapeStation 4150, Nanodrop, and Qubit fluorometer. The laboratory at Carleton University will be equipped for aerobic and anaerobic experimentation with cultures, nucleic acid extractions, and extensive core facilities for microbial characterization. The student will also have access to high performance computing environments.

Research Activities:

Culturing and handling microorganisms and products containing microorganisms (including Risk Group 2 pathogenic organisms).

Completing DNA/RNA extractions from soils/environmental matrices, isolates, and consortia/mixtures.

Quantifying and performing quality control analysis of DNA/RNA using the Agilent TapeStation, Nanodrop, and Qubit fluorometry.

Preparing libraries for Illumina and Oxford Nanopore Technologies sequencing and performing PCR/qPCR.

Conducting bioinformatic analyses on Linux-based systems.

Optimizing analytical chemistry techniques to monitor microbial metabolic activity and contaminant concentrations.

Sourcing and ordering laboratory equipment and supplies.

Writing reports on research activities and carefully documenting work completed.

Designing presentations and/or posters and communicating scientific results to varied audiences.

Requirements:

Successful enrollment within a relevant graduate program at Carleton University ([Admissions - Department of Chemistry \(carleton.ca\)](#)). Research activities will require the use of facilities at 335 River Road, Ottawa, ON and within the Department of Chemistry at Carleton University.



Free parking and bike storage are available at ECCC. Public transportation access is available but currently has limited service hours to the facility.

Compliance with ongoing COVID-19 and general safety protocols including KN95/N95/medical mask usage and COVID-19 vaccination requirements (ECCC is operating with COVID safety measures in place).

Students must be willing and able to work safely with Risk Group 2 human pathogens and hazardous chemicals in a Containment Level 2 laboratory following standard operating procedures using appropriate personal protective equipment, engineering controls, and aseptic technique. Mandatory safety training will be required, and the student must be able to demonstrate proficiency with safe work practices after training to work in the laboratory. Local risk assessments may also require up to date vaccinations for relevant pathogens due to the nature of the laboratory work.

Eligible for Reliability security status.

The student should have completed course work (or related course work) and/or have research experience in at least one of the following subject areas or related disciplines: Microbiology, Biochemistry, Molecular Biology, Genomics, or Bioinformatics.

English essential.

Assets:

Preference will be given to interested students that are Canadian Citizens or Permanent Residents.

Previous experience working in a microbiological laboratory or laboratory setting.

Experience with programming (Python, R, Perl, Java, etc.), statistics, Linux command-line (shell scripting, UNIX tools (grep, awk, sed, etc.)), or next generation sequencing analysis.

Selected Relevant Publications:

*Prior related work

Xu, G., Zhang, L., Liu, X., Guan, F., Xu, Y., Yue, H., Huang, J.Q., Chen, J., Wu, N., Tian, J. (2022) Combined assembly of long and short sequencing reads improve the efficiency of exploring the soil metagenome. *BMC Genomics* 23:37.

Van Goethem, M.W., Osborn, A.R., Bowen, B.P., Andeer, P.F., Swenson, T.L., Clum, A., Riley, R., He, G., Koriabine, M., Sandor, L., Yan, M., Daum, C.G., Yoshinaga, Y., Makhalanyane, T.P., Garcia-Pichel, F., Visel, A., Pennacchio, L.A., O'Malley, R.C., Northen, T.R. (2021) Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. *Commun Biol* 4:1–10.

Jamy, M., Foster, R., Barbera, P., Czech, L., Kozlov, A., Stamatakis, A., Bending, G., Hilton, S., Bass, D., Burki, F. (2020) Long-read metabarcoding of the eukaryotic rDNA operon to



phylogenetically and taxonomically resolve environmental diversity. *Mol Ecol Resour* 20:429–443.

*Meier, M.J., Dodge, A.E., Samarajeewa, A.D., Beaudette, L.A. (2020) Soil exposed to silver nanoparticles reveals significant changes in community structure and altered microbial transcriptional profiles. *Environ Pollut.* 258:113816

*Subasinghe R.M., Samarajeewa A.D., Scroggins R., Beaudette L.A. (2019) Evaluation of denaturing gradient gel electrophoresis (DGGE) and next generation sequencing (NGS) in combination with enrichment culture techniques to identify bacteria in commercial microbial-based products. *J Microbiol Methods* Jun;161:118-130

Martijn, J., Lind, A.E., Schön, M.E., Spiertz, I., Juzokaite, L., Bunikis, I., Pettersson, O.V., Ettema, T.J.G. (2019) Confident phylogenetic identification of uncultured prokaryotes through long read amplicon sequencing of the 16S-ITS-23S rRNA operon. *Environ Microbiol* 21:2485–2498.

Tedersoo, L., Anslan, S. (2019) Towards PacBio-based pan-eukaryote metabarcoding using full-length ITS sequences. *Environ Microbiol Rep* 11:659–668.

Johnson, J.S., Spakowicz, D.J., Hong, B.Y., Petersen, L.M., Demkowicz, P., Chen, L., Leopold, S.R., Hanson, B.M., Agresta, H.O., Gerstein, M., Sodergren, E., Weinstock, G.M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. *Nat Commun* 10:5029

*Subasinghe, R.M., Samarajeewa, A.D., Meier, M.J., Coleman, G., Clouthier, H., Crosthwait, J., Tayabali, A.F., Scroggins, R., Shwed, P.S., Beaudette, L.A. (2018). Bacterial and fungal composition profiling of microbial based cleaning products. *Journal of Food and Chemical Toxicology* 116:25-31.

*Tayabali, A.F, Coleman, G., Crosthwait, K.C., Zhang, Y., Shwed, P. (2017). Composition and pathogenic potential of a microbial bioremediation product used for crude oil degradation. *PLoS One.* 2017 Feb 8;12(2):e0171911.

*Samarajeewa, A.D., Hammad, A., Masson, L., Khan, I.U.H., Scroggins R., Beaudette, L.A. (2015). Comparative assessment of Next-generation Sequencing, denaturing gradient gel electrophoresis, clonal restriction fragment length polymorphism and cloning and sequencing as methods for characterizing commercially available microbial consortia. *Journal of Microbial Methods* 108:103-111.

