Abstract:

Traditional methods to study fungi rely heavily on morphological characters to first identify field collections and cultures. Unfortunately, life history traits among the fungi vary widely making it difficult to observe, collect, and identify many specimens. ‘Omic’ studies are enabling us to study fungal phylogenetics and ecology in more comprehensive ways than ever before. In this seminar I would like to broadly address the use of molecular DNA-based methods to study fungal phylogenetics and ecology. First, I will talk about high throughput sequencing of fungal transcriptomes as a source for new markers in phylgenomics studies. The objective of this study was to elucidate relationships among the early diverging fungal lineages. Second, I will talk about PCR-based amplicon sequencing from soil to increase the diversity of fungi detected from environmental surveys. I will present the results from several studies to illustrate how the field of ‘metabarcoding’ in fungi has developed over the past decade. I will conclude by summarizing some of the most recent fungal sequencing projects and tools that will help further the study of fungal phylogeny and ecology.

Brief Bio:

Terri Porter is a mycologist and bioinformatician. She is a Research Scientist at Natural Resources Canada and is currently working as a Visiting Researcher in the Hajibabaei Lab. She did postdoctoral work with Dr. Brian Golding in the computational biology lab at McMaster University for the Biomonitoring 2.0 project focusing on species assignment methods. She also did postdoctoral work with Dr. Rytas Vilaglys in the mycology lab at Duke University for the Assembling the Fungal Tree of Life 2 project focusing on phylogenomics of the early diverging fungal lineages. She obtained her PhD in Ecology and Evolutionary Biology from the University of Toronto under the supervision of Dr. Jean-Marc Moncalvo in the field of mycology.