OCGC Seminar

Environmental DNA approaches to understand past, present and future ecosystems functioning

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Microbial eukaryotes play key roles in ecosystem functioning. The recent development of methods and technology to analyze microeukaryote gene sequences potentially permits for the cost effective exploration of extant and paleo-ecosystems. Moreover, the application of molecular techniques to enhance classical microbial ecological research has greatly increased our general knowledge of the ongoing processes, and to track the impact on lake ecosystems of stressors (e.g. road salt degradation; heavy metal contamination). In this presentation I will first present how we can use single cells and high throughput sequencing to answer complex ecological and biogeographical questions. In a case study using the *Nebela collaris* complex of species I will demonstrate that a careful determination based on genetic markers permitted a clear ecological delineation of these species. I will explore the biogeography of the iconic testate amoeba species *Hyalosphenia papilio*, and outline how with mathematical support it was for the first time possible to define a geographical origin of a microbe species! Finally, I will present a few examples of the use of these technics in studying freshwater and marine environment. I will also discuss how these methods are being developed as a promising tool to study paleo-lake sediments. In summary, molecular technics are a powerful approach to explore the diversity, ecology and biogeography of microeukaryotes.

Biography: David Singer studies the diversity, ecology and biogeography of microeukaryotes. He completed his PhD in the laboratory of Soil Biodiversity in the University of Neuchâtel (Switzerland). He now holds a joint Postdoc position at the Univesity of São Paulo in Brazil, and Carleton University. His research for this position will be to learn more about the transcriptomics and eDNA of microorganisms preserved in lakes sediments, and how it may be used in paleolimnological research.

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