**Lichen mycobiota: evolutionary and ecological factors driving endolichenic fungal communities**

François Lutzoni1\*; Jana M. U'Ren2; Jolanta Miadlikowska1; Ian D. Medeiros1; Carlos J. Pardo-De la Hoz1; Pierre-Luc Chagnon3; Shuzo Oita2, Reinaldo Vargas Castillo4, Adam Flakus5, Nicolas Magain6, A. Elizabeth Arnold2

1Duke University, USA; 2University of Arizona, USA; 3Université de Montréal, Canada; 4Universidad Metropolitana de Ciencias de la Educación, Chile; 5Polish Academy of Sciences, Poland; 6 Université de Liège, Belgium

\*E-mail: flutzoni@duke.edu

Lichen thalli host a wide array of microbes. In addition to the microorganisms colonizing the surface of lichens, diverse Bacteria, Archaea, and Fungi live inside their thalli. Fungi colonizing lichen thalli have been referred to as lichenicolous fungi if they are visible at the surface of lichen thalli or cause visible symptoms. Fungi that are not eliminated by a thorough surface sterilization of asymptomatic thalli have been referred to as endolichenic fungi, which form diverse mycobiota, comparable to fungal endophytic communities living in healthy leaves of plants. Endolichenic fungi are hyperdiverse and account for a large fraction of the unknown and undescribed species of Fungi, especially within the Pezizomycotina. We will report the results of culture-based and culture-free (i.e., next generation amplicon sequencing) sampling from sites across the United States, the circumboreal belt, Panama, and Chile. At each site, we sampled a wide spectrum of co-occurring lichen thalli, representing diverse lineages of lichen-forming fungi with different substrate preferences, to determine the role of lichens as hosts in shaping endolichenic fungal communities and biodiversity. Moreover, *Cladonia rangiferina* was sampled systematically along a transboreal latitudinal transect of ca. 1300 kilometers to determine the specific role of abiotic factors in shaping endolichenic fungal communities. With this broad sampling, we studied host specificity and phylogenetic structure of endolichenic communities using a new approach that takes into consideration availability and phylogenetic affiliations of OTUs. Funding: National Science Foundation (NSF, USA) GoLife grant DEB-1541548, https://mycophygolife.org.