

**Elucidating fungal endosymbiont interaction mechanisms between *Mortierella elongata* and *Mycoavidus cysteinexigens*.**J Uehling<sup>1</sup>, F Dietrich<sup>1</sup>, P Misztal<sup>2</sup>, G Bonito<sup>3</sup>, T Tschaplinski<sup>4</sup>, A Goldstein<sup>2</sup>, C Schadt<sup>4</sup>, J Labbé<sup>4</sup>, R Vilgalys<sup>1</sup><sup>1</sup>Duke University, Durham NC 27708, USA, [jku@duke.edu](mailto:jku@duke.edu), [fred.dietrich@duke.edu](mailto:fred.dietrich@duke.edu), [fungi@duke.edu](mailto:fungi@duke.edu)<sup>2</sup>University of California at Berkeley, Berkeley, CA 94720 USA, [pkm@berkeley.edu](mailto:pkm@berkeley.edu), [ahg@berkeley.edu](mailto:ahg@berkeley.edu)<sup>3</sup>Michigan State University, East Lansing, MI 48823 USA, [gregory.bonito@duke.edu](mailto:gregory.bonito@duke.edu)<sup>4</sup>Biosciences Division, Oak Ridge National Laboratory, PO Box 2008 MS 6445, Oak Ridge, TN 37831-6445, USA, [labbejj@ornl.gov](mailto:labbejj@ornl.gov), [tschaplinstj@ornl.gov](mailto:tschaplinstj@ornl.gov), [schadtc@yahoo.com](mailto:schadtc@yahoo.com)

Recently efforts to catalog beneficial microbes associated with *Populus* have yielded cultures of diverse fungi including several *Mortierella elongata* (*Mortierellomycotina*) isolates. Some of these fungi including *M. elongata* strain AG77 harbor bacterial endosymbionts belonging to the Burkholderiales. We have sequenced the genome of *M. elongata* and its bacterial endosymbiont *Mycoavidus cysteinexigens*, and used comparative phylogenomics to infer this symbiosis is ancient and grounded in shared metabolites. We have used and developed methods to assemble single genomes from meta-genomic data and inferred several gene losses that make culturing endosymbiont *M. cysteinexigens* (AG77) challenging. To circumvent this research obstacle, we used an antibiotic treatment to create fungal strains with and without their long-term endosymbi-

onts for comparative multi-omic studies. The ability to contrast cleared *M. elongata* strains and their wild type, endosymbiont-housing relatives in the same genetic background allows us to ask the following questions: 1. *How does the presence or absence of long-term, co-evolved endosymbionts impact health and physiology of host fungi?* 2. *Which currently available methods can be used and modified to study interaction dynamics for systems involving multiple intractable microbes?* Our research goals through this work were to develop -omics and imaging pipelines that allow the study of bacterial fungal interaction mechanisms. To this end we have used genome sequencing, transcriptomics, metabolomics, and volatomics for studying fungal endosymbiont interaction dynamics. The results of these experiments will be further discussed.