Evolution and functioning of bacterial endosymbionts in fungi that are part of the core *Populus* microbiome



Contact: Gregory Bonito (bonito@msu.edu); (517)884-6958; Chongle Pan (pan@ornl.gov); 574-1281; Jessy Labbé(<u>labbejj@ornl.gov</u>); (865) 576-3478 Funding Source: DOE Office of Biological and Environmental Research, Genomic Sciences Program

Background

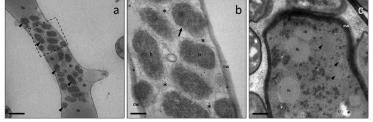
- *Mortierella elongata*, a root-associated fungus isolated from *P. deltoides*, harbors an endophytic symbiotic bacterium.
- Endobacteria can boost fungal energy production, promote plant growth and enhance plant resistance to pathogenic fungi.
- The genomes of *M. elongata* and its endobacterium, *Mycoavidus cysteinexigens,* were sequenced. Metabolomics and proteomics studies characterized the metabolic response of the symbiosis, particularly during nitrogen (N) limitation.

Science

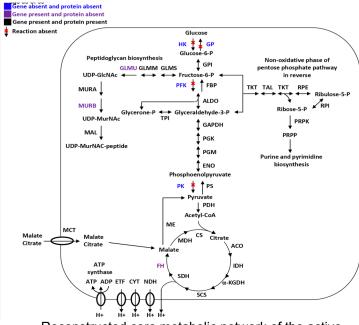
- The *M. elongata* genome features a core set of primary metabolic pathways for degradation of simple carbohydrates and lipid biosynthesis.
- Phylogenomic analysis revealed the *Mycoavidus*, and *Ca*. Glomeribacter species, comprise a monophyletic lineage of fungal endosymbionts that are sister clade to *Burkholderia*.
- Endobacterium suppression, using antibiotics, significantly changed the abundances of many proteins and metabolites.
- Metabolomic and proteomics analyses during N limitation suggested that the endobacterium maintained independent ATP production through an active TCA cycle and electron transport chain and that *M. elongata* re-wired its carbon and N flows.

Significance

- This is the first integrated application of proteomics and metabolomics to a fungal/endobacterial system.
- This work contributes new knowledge about fungal endosymbiont evolution.



TEM microscopy of wild type (a,b) and cured (c) strains of *M. elongata*. The endosymbiont is shown in Fig. a and b (arrow). *Mycoavidus* cells are surrounded by a tangled complex of membranes (panel b, *). The cured strain shows a cytoplasm rich in mitochondria (arrowhead, panel c).



Reconstructed core metabolic network of the active endobacterium



Li Z., *et al.* (2016). Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungalendobacterial system, Env. Micro, 19(3): 1041-1053; Uehling *et al.* (2017). Comparative genomics of *Mortierella elongata* and its bacterial endosymbiont *Mycoavidus cysteinexigens*, Env. Micro, 19(8): 2964-2983.