Environmental genomics of uncultured microbial lineages

For a long time, scientists have discovered and characterized microorganisms by culturing and maintaining them in laboratory settings. However, it has long been established that a large fraction of microorganisms in nature are not amenable to current isolation processes. This significant fraction of microbial diversity has been dubbed the “microbial dark matter”, and many of them belong to phylogenetically novel bacterial and archaeal lineages. Understanding the metabolic capabilities, physiological preferences, and ecological roles of the microbial dark matter represents one of the current “grand challenges” of microbial ecology.

Fortunately, The convergence of multiple experimental and computational advances has provided great impetus to our efforts towards characterization of microbial dark matter. Our laboratory has been active in analyzing genomes of novel microbial lineages since its establishment at in 2007. Our work has yielded multiple insights into the biology of novel microorganisms and has resulted in multiple high impact publications in leading scientific journals. We have a wide network of collaborators and coauthors from leading national and international scientific institutions and strive to be always in the forefront of this exciting research area.
Possible Figures

A typical metabolic reconstruction map of the metabolic capabilities of a yet-uncultured archaeal phylum (Diapherotrites), data from Youssef et al. *The ISME Journal* (2015) 9, 447–460
Fluorescent In-situ hybridization image depicting the filamentous nature of a yet uncultured bacterial phylum (Absconditabacteria, previously candidate phylum SR1), from Davis et al. *Appl. Environ. Microbiol.* **75**:4139-4148.
An In-Silico Analysis demonstrating the occurrence of a cellulosome within members of an uncultured bacterial phylum (Latescibacteria, previously candidate phylum WS3), from Farag et al. *Appl. Environ. Microbiol.* 83:e00521.