**Title**

Creatures from the black lagoon: highlighting dark matter fungi in marine environments

**Abstract**

Fungi are among the most diverse groups of eukaryotes and occupy critical roles as degraders, parasites, and symbionts. However, the vast majority of fungal species still await discovery, and those that have been described belong overwhelmingly to just two phyla. These gaps in our understanding of fungal diversity, which complicate efforts to answer important questions of fungal evolution and ecology, are unlikely to be addressed by traditional isolation and culturing methods. High-throughput sequencing (HTS) has ushered in a new age of mycological exploration, revealing uncharacterized fungal diversity across disparate habitats. However, efforts to infer the true phylogenetic affinities of many novel fungal phylotypes are hampered by the maximum read lengths of most sequencing platforms (< 500 bp), which often provide little phylogenetic signal. Moreover, the increasing adoption of next-generation sequencing methods to characterize fungal communities supplants traditional culturing surveys, decreasing the generation and availability of high-quality reference sequences. Taxonomic identification of OTUs observed in environmental surveys hinges on well-curated databases of complete or nearly-complete reference sequences. Consequently, despite the detection of wholly unknown groups among the fungi, we are unable to put these taxa into a robust phylogenetic framework, nor can we add them to existing databases to inform future HTS studies. In this seminar, I will discuss my research which focuses on elucidating the breadth of fungal diversity from historically under-sampled marine habitats using high-throughput sequencing methods. In addition to identifying habitats harboring high levels of novel diversity, I will also demonstrate how existing fungal reference databases are taxonomically biased and fail to assign provisional identities to many putatively novel marine lineages. I will also discuss using emerging long-read sequencing to generate high-quality reference sequences for uncultured fungi and demonstrate that longreads provide improved taxonomic resolution, even overcoming the deficiencies of extant reference databases.