**Applying genome-resolved metagenomics to de-convolute the halophilic microbiome**

Overview:

1. How did MAG analysis improve our understanding of halophilic communities?
2. What are the current best practices for halophilic WMG experiment design and sequence analysis?
3. What are novel technologies and methods in other fields that can further our ability to de-convolute halophile WMG data?

The rapidly expanding field of whole-genome metagenomics (WMG) now allows for genome-resolved analysis of microbiomes through extraction of metagenome-assembled genomes (MAGs). In this review, we will explore how WMGs impacts the analysis of halophilic communities, and the types of information that can be gleaned from the high resolution that it offers. We describe the breakthrough research that MAG extraction from WMG data permitted, including analysis of CRISPR array evolution, virus-host interactions, functional potential and salt adaptations of individual strains, and strain dispersal and selection across time and space. Deconvolution of halophilic communities at the WMG level has been difficult due to the high GC content and high intra-sample strain heterogeneity, which made both metagenomic assembly assembly and binning a challenge. Additionally, the lack of reference environmental halophilic genomes in public databases made commonly used software ineffective at functionally annotating halophilic metagenomes and MAGs. However, the WMG field has rapidly expanded in the past decade, and the available tools have improved to a point where they are applicable to even the most complex microbiomes. With this in mind, many common WMG analysis methods that are already being applied to simpler communities can now be used to expand our understanding of halophilic communities. We will address the potential pitfalls and limitations of conventional WMG analysis being applied to halophilic communities, and propose experimental and analytical strategies to overcome them. Finally, we will speculate the potential applications of other next-generation sequencing technologies to halophilic communities. In particular, metatranscriptomics coupled with WMG show promise to uncover the metabolic activity of halophilic communities as well as individual strains, long read technologies such as Nanopore and PacBio technologies can aid in the assembly of highly similar microbial strains, and Hi-C can assist in the binning of highly heterogeneous closely-related strains.