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Genome-resolved metagenomics in globally distributed bacterial and archaeal lineages

The development of genome-resolved metagenomics has provided a robust method to recover complete or near-complete genome information for entire communities of bacteria, archaea, and viruses from the environment. In this seminar, Alexander Jaffe will demonstrate how this technique can be applied to illuminate the biology of Candidate Phyla Radiation (CPR) bacteria and DPANN archaea—novel microbial lineages recently resolved in the tree of life. Organisms from these lineages encode various RuBisCO-related proteins, which broaden our understanding of the diversity, function, and evolutionary history of this globally important enzyme family. Using publicly available metagenome data, he shows that CPR organisms have undergone multiple habitat transitions and display variable abundance patterns across global microbiomes, including those from marine and animal-associated environments. Patterns of co-occurrence and CRISPR-Cas targeting suggest that CPR may interact with diverse host cells from the Actinobacteria and bacteriophage with the potential to infect both symbiotic partners. Alex will also discuss how genome-resolved techniques show that the metabolic potential of both CPR bacteria and their surrounding microbial communities varies along an oxygen gradient from a stratified freshwater lake. Overall, his research concludes that ultra-small cells from phylogenetically diverse lineages may make important contributions to both the functioning of microbial communities and their impact on Earth's ecosystems.

Registration for this webinar is required and space is limited. [Please RSVP here.](#)