DEPARTMENT OF CHEMISTRY AND ENVIRONMENTAL SCIENCE
VIRTUAL SEMINAR SERIES
FALL 2020

DATE: WEDNESDAY, SEPTEMBER 16

TIME: 1:00-2:20pm

GUEST SPEAKER

Professor Lee Kerkhoff
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New Brunswick

TOPIC

Using the Oxford Nanopore MinION
(A portable DNA sequencer)
For Microbial Ecology

ABSTRACT

Nucleic acid-based methods investigating ribosomal RNA genes have become the most widely accepted way to characterize microbial communities in the last 35-40 years. Most recent approaches utilize short reads (<500 bp) with high sequence accuracy (~99%), but limited phylogenetic resolution. This presentation will describe a relatively new system for direct sequencing of individual strands of DNA, the Oxford Nanopore MinION system. Our laboratory has pioneered the profiling of microbial communities using ribosomal operons [16S-ITS-23S rRNA genes] and the MinION.

The approach yields an amplicon containing both small and large ribosomal subunits for detailed phylogenetic assignment (~4000+ bp of sequence), plus the internal spacer region (~500+ bp) containing species/strain information to resolve various members within the microbial community.

This presentation will describe our efforts to ensure the MinION provides: 1) a quantitative signal from the original sample; 2) an accurate microbial community assessment despite the higher error rate compared to short read approaches; and 3) strain level resolution using a simplified data analysis pipeline for rRNA operons. Examples of community profiles from the terrestrial soils, marine environments, and mammalian systems will be presented. Finally, since the MinION is small, portable, and can run on a laptop, the possibility of microbiome characterization in the field or on robotic platforms becomes realistic. Additionally, the long-read capability,

low cost, and ease-of-use makes the MinION the first widely affordable sequencing system for virtually any laboratory.

BIO

Dr. Lee Kerkhof has been a Professor at Rutgers for over 25 years. His research has focused on elucidating the active microbial "players" in a variety of complex environments to understand the mechanisms driving diversity and biogeochemical processes. He uses a variety of nucleic acid-based analyses to identify those microorganisms that are making ribosomes or incorporating C and N into their genomes. Recent efforts have focused on active bacteria in aeolian systems, in aquatic systems, in association with eukaryotic hosts, and in sediments/soils spanning a continuum from pure cultures, to engineered systems, to field measurements.

Committee members:
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