

Innovations and Metagenomic Workflows for Studying Extreme and Novel Environments

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ABSTRACT

The ability to perform metagenomic techniques on samples collected from novel sample types demands high performance reagents and techniques not commonly used in most labs today. The Extreme Microbiome Project was established in 2015 to develop novel sampling and DNA sequencing protocols for both routine samples as well as the most difficult. Samples have been collected and sequenced from around the world including, soil, sea and fresh water, air, deep ocean, thermophilic, halophilic, acidic, and alkaline ecosystems from locations such as Greenland, Antarctica, the Red Sea, Romanian sulfur caves, and the International Space Station. Techniques including novel concentrating devices, high performance lysis enzymes, ultra-low biomass handling, biofilm disrupting, and working with high host background from eukaryotic organisms have all been applied. In all cases, DNA, RNA, and PCR amplicon sequencing are performed using a combination of short and long-read technologies including Illumina, Singular G4, and Oxford Nanopore Technologies for characterizing functional and taxonomic features as well as MAG assembly of dark matter.

Keywords: Extreme microbiome project, Metagenomic technique, Taxonomic characterization

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