

A soil microbial workflow from DNA extraction to amplicon sequencing

Marie Dinh (marie.t.dinh@nasa.gov), NASA Ames Research Center, **Marie Dinh**, NASA Ames Research Center, **Valery Boyko**, GeneLab, **Charles Houseman**, SeqMatic LLC, **Yi Chun Chen**, NASA GeneLab, **Samrawit Gebre**, NASA Ames Research Center, **Michael Lee**, NASA Ames Research Center, **Courtney Creamer**, US Geological Survey, **Sylvain Costes**, NASA Ames Research Center, **Jonathan Galazka**, NASA Ames Research Center

GeneLab an open-access omics database created specifically for spaceflight studies. GeneLab also offers a leading-edge Sample Processing Laboratory (SPL) that is responsible for generating data from biological experiments conducted in space. While the GeneLab SPL typically uses its capabilities to process unused samples returned to Earth from space, it aims to serve a broader scientific community. One example effort involves analysis of soil microbial communities. The GeneLab soil workflow consists of DNA extraction, bacterial 16S (rRNA) and fungal ITS library generation, sequencing, and data processing. Here we show that this workflow can extract enough high-quality DNA from soil samples taken from burned and unburned plots, and that the 16S/ITS sequencing accurately captures the composition of mock community controls. In addition, we show a preliminary analysis of samples collected from the LNU Lightning Complex fires.