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THE MICROBIOME AND THE METABOLOME OF THE INTERNATIONAL SPACE STATION: THE 3DMM PROJECT

Abstract

The purpose of the 3-dimensional microbiome/metabolome (3 D MM)-based microbial detection project is to provide sequencing and bioinformatic analyses of metagenomes, and metabolomics data, on samples collected from 800 sites of various ISS environmental locations. Next-generation sequencers and high-throughput mass spectrometers have transformed microbiome and metabolome research, yet the generation and analysis of this data remain difficult for many investigators. The 3 D MM project uses start-of-the-art equipment and world-leading algorithms developed in-house to provide the essential DNA sequencing, mass spectrometry, and data analysis to render this data accessible and interpretable to the members of a wide range of scientific community. Alpha diversity analysis of the 16S sequencing profiles shows that some modules harbor richer microbiomes than others. Beta diversity analysis of 16S sequencing profiles shows that modules have unique microbial signatures, likely related to the predominant use of each specific module. A taxonomic classification of the organisms found on the ISS was generated, and a comparison with microbiomes from other terrestrial and host-associated environments reiterated that the ISS surface microbiome is dominated by human skin-associated microbes. Untargeted metabolomics data generation through High-Resolution Mass Spectrometry (HRMS) was also performed. Characterization of mass spectra was achieved through feature-based molecular networking with the Global Natural Product Social molecular networking (GNPS). The proportion of spectral matches (annotations) to GNPS was only 5