Microorganisms Found on Spacecraft and Associated Surfaces: Preservation, Identification, Characterization
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Project Objective: To archive incoming isolates from planetary protection bioassays and to identify those isolates using MALDI-TOF mass spectrometry and 16S rRNA identification

Background on Planetary Protection
• Aims to prevent the forward contamination of microorganisms between Earth and extraterrestrial bodies
• NASA Standard Spore Assay is used as a proxy to measure the microbial bioburden present on spacecraft hardware and associated surfaces.
• Microbes isolated as a result of this assay, are archived for long term preservation, documented, and identified.

Methods for Identification of Organisms
• Isolates were run on the MALDI-TOF (matrix assisted laser desorption/ionization time-of-flight) mass spectrometer
• Organism was initially run using RTC (real time classification), which compared organism spectra against the JPL in-house database
• If organism did not match to the database, an MSP (mass spectral profile) was added to the database for the organism and the MSP was named according to 16S rRNA identification
• Quality control measures in place ensured that adequate spectra were used to create an MSP (at least 10 good spectra needed)

Results
• 135 new M2020 isolates archived and identified this summer
• 40 MSP’s created for those M2020 isolates that did not match to the database
• 55 MSP’s renamed in the database: spectra re-evaluated and MSP named correctly according to 16S ID
• 24 MSP’s from the database were remade because they were created with poor spectra in the past

Future Directions
• Continually maintain and update an in-house database that encompasses the microbial diversity on spacecraft and associated surfaces
• Continue archiving, identifying, and characterizing samples collected from spacecraft and associated surfaces

Figure 1: A flowchart showing how an isolate is identified using the MALDI-TOF mass spectrometer.

Figure 2: A chart showing the results of all M2020 isolates when compared against the database. 88% matched to a spectra already in the database, 6% could not be run because of poor morphology, and 6% required MSP creation.

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