## SPACE LIFE SCIENCES SYMPOSIUM (A1) Astrobiology and Exploration (5)

Author: Mrs. Kelly Kwan United States, kelly.m.kwan@jpl.nasa.gov

Dr. Kasthuri Venkatweswaran

Jet Propulsion Laboratory - California Institute of Technology, United States, kjvenkat@jpl.nasa.gov Dr. James Benardini Jet Propulsion Laboratory - California Institute of Technology, United States, nickb@jpl.nasa.gov Dr. Christina Stam Jet Propulsion Laboratory - California Institute of Technology, United States, Christina.Stam@jpl.nasa.gov Dr. Moogega Cooper Jet Propulsion Laboratory - California Institute of Technology, United States, moogega@caltech.edu Mr. Myron La Duc Jet Propulsion Laboratory - California Institute of Technology, United States, Myron.T.Laduc@jpl.nasa.gov Dr. Parag Vaishampayan Jet Propulsion Laboratory - California Institute of Technology, United States, Parag.A.Vaishampayan@jpl.nasa.gov Mr. Giuliano Scalzi Jet Propulsion Laboratory - California Institute of Technology, United States, scalzig@unitus.it Dr. James A Spry National Aeronautics and Space Administration (NASA), Jet Propulsion Laboratory, United States, James.A.Spry@jpl.nasa.gov Dr. Gary Andersen United States, GLAndersen@lbl.gov Dr. Christine Moissl-Eichinger Germany, Christine.moissl-eichinger@biologie.uni-regensberg.de

## SAMPLING AND SAMPLE PROCESSING STANDARDIZATION FOR SPACECRAFT AND ASSOCIATED CLEAN ROOM SURFACES

## Abstract

Due to stringent cleaning procedures, the microbial burden of a typical spacecraft assembly clean room is lower in comparison to other indoor environments. This presents a challenge in the recovery of microorganisms and biomolecules from spacecraft surfaces. In order to obtain samples that are representative of both the diversity and richness of microbial species on spacecraft and associated clean room surfaces, current sampling and sample processing techniques needed to be evaluated for their efficiency in recovering microorganisms and targeted biomolecules. The effectiveness of several sampling devices and processing techniques were analyzed by doping a known concentration of microbial cells onto a surrogate spacecraft surface. The model microbial community used in this study consists of 11 species of extremophiles present in spacecraft assembly clean rooms and represents fungal, archaeal, and bacterial strains. Additionally, the community organisms possess multiple survival characteristics, such as resistance to gamma and UV radiation, hydrogen peroxide, and desiccation. The model community was analyzed at 0 hours and subsequent time points for cultivability, viability, cell concentration, DNA concentration, and species richness. Stainless steel coupons were spiked with equal aliquots of the model community, dried, and then sampled at different time points using a variety of sampling devices (swabs, wipes, and macrofoam sponges) for comparison. Extractions from each sampling device underwent the same downstream analysis as performed on the model community, specifically including colony/microscopic counts, ATP assay, a novel live-dead DNA intercalating dye analysis, rrn gene (16S and 18S) Q-PCR, and species-specific PCR. Results from this study will optimize current sampling and sample processing techniques while enabling planetary protection to obtain samples which are representative of spacecraft and associated surfaces. In addition to NASA astrobiology/planetary protection programs, the outcome of this research will be useful for the control of microbial contamination in the pharmaceutical, medical, food processing, and other industries in which clean rooms are essential.