APOLLO ENVIRONMENT SAMPLING: A 50 YEAR EXPERIMENT. M. Lupisella[1], J.P. Dworkin[1], D. Glavin[1], N. Petro[1], D. Williams[1], J. Bleacher[1], B. Cohen[1], R. Lewis[1], M. Wright[1], T. Stubbs[1], A. Burton[2], K. Rubins[2], A. Regberg[2], S. Wallace[2], S. Stahl[2], K. John[2], D. Archer[2], P. Niles[2], E. Rampe[2], M. Rucker[2], D. Smith[3], J. Russell[4], C. Chiu[5], M. Race[6], K. Bywaters[6], A Schuerger[7], P. Metzger[8] [1]NASA Goddard Space Flight Center, 8800 Greenbelt Rd, Greenbelt, MD, 20771 Mark.L.Lupisella@nasa.gov, [2]NASA Johnson Space Center, [3]NASA Ames Research Center, [4]MRIGlobal Microbial Genomics, [5]University of California San Francisco, Clinical Microbiology Laboratory, [6]SETI Institute, [7]Univ. of Florida, Exploration Park, [8]Florida Space Institute, Univ. of Central Florida

Introduction: Sampling Apollo landing sites offers opportunities to address a number of questions related to space biology, astrobiology, planetary protection, contamination, engineering and other human-environment interaction questions that can help inform future human missions to the Moon, Mars, and beyond. Apollo waste material, including human waste and food garbage, contains microbiological biomass that has been exposed continuously to deep space radiation and thermal cycling for over 50 years on the lunar surface. Obtaining samples of that material would offer an unprecedented opportunity to determine the resilience of terrestrial life and organic material on the lunar surface and assess the distribution of contaminants associated with human exploration. The mission could be performed with a rover retrieving samples and performing analysis, including via low-latency telerobotic operations by crew members in a lunar orbiting facility [1].

DNA was successfully sequenced in space for the first time on the International Space Station in 2016 using a miniature low-power biomolecular sequencer [2], and additional ISS end-to-end sequencing activities have been conducted since then, proving the feasibility of biomolecular sequencing by crew members in a space environment.

Previously, the Human Spaceflight Architecture Team (HAT) explored strategies and mission concepts for how a lunar orbiting facility could be utilized for science [3, 4], including the use of low-latency teleoperations (LLT) and crew-assisted sample return that could return significant sample mass to Earth.

An Apollo Environment Sampling mission would revisit an Apollo landing site, acquire samples, conduct preliminary analysis, and return samples (including possibly engineering samples) to a lunar orbiting facility and/or to Earth for subsequent investigations. Such data could contribute to a better understanding of the nature and size of contamination "footprints" of the Apollo missions, including sequencing of microbial and human DNA that could shed light on the effects of space radiation, temperature extremes, and UV irradiation on biological materials that have been on the lunar surface for almost 50 years. Sampling the Apollo landing sites would thus help inform future contamination dynamics and containment strategies, suggesting the need to baseline the Apollo contamination environment before new contamination is introduced [5, 6]. Such a mission could also act as a "dry run" for detecting biological signatures of life on Mars. An Apollo environment sample return mission can also help address Strategic Knowledge Gap II-B-4 on radiation shielding effects of lunar material, and could also inform the development of NASA protocols on how to protect the historic and scientific value of Apollo landing sites [7].

Significant communication delays to Mars, strict planetary protection requirements, and the potential need to perform challenging sample analysis at Mars suggest the utility of first performing LLT and robust analyses of Apollo site samples in cislunar space to help prepare for similar activities at Mars [8, 9].

References:

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