Deep Biosphere to Deep Space: Microbiome Insights for Life on Rocky Planets and Human Health during Long-Duration Spaceflight

Duane Moser (DRI), Natasha Sushenko (DRI/UNLV), Molly Devlin (DRI/UNLV), Alireza Saidi-Mehrabad (DRI), Diana Northup (UNM), Brian Hedlund (UNLV), Nitin Singh (JPL), Jennifer Blank (NASA Ames), and Kasthuri Venkateswaran (JPL)

Here we provide an overview of new and continuing NASA EPSCOR- and NVSGC-supported work in our lab in the fields of Astrobiology and Space Biology. Recent Astrobiology progress has been made on several projects focused on planetary analog environments, especially in the continental subsurface. This included a NVSGC-supported assessment of the possibility for microbial life and abiotic production of an inferred oxidant of Mars regolith, perchlorate, in hypersaline lithium brines at Bristol Dry Lake, CA. NVSGC student fellowships have also expanded the impact of our NASA PSTAR-funded research with NASA Ames in Lava Caves (NASA BRAILLE) and work focused on deep fractured-rock ecosystems, most recently, funded by the NSF Genomes to Phenomes program. These projects have illuminated one potential limit for life (i.e. molar concentrations of calcium), patterns of biodiversity across a gradient of biological-to-mineral-dominated surfaces in lava caves, and what may be the ultimate living fossil from the Death Valley Regional Flow System, a microbe that appears to have exhibited evolutionary stasis for at least 200 million years. Our Space Biology research, funded by NASA EPSCOR Rapid Response Research and augmented by a NVSGC student fellowship, seeks to gain a better understanding of the human health hazard posed by pathogens during long-duration spaceflight. This ongoing project, in collaboration with JPL, seeks to identify genomic responses of the Biosafety Level-2 pathogen, *Klebsiella pneumoniae* and *K. quasipneumoniae* from the International Space Station (ISS) to disinfectants (quaternary ammonium compounds (QACs)) used aboard the ISS. ISS-derived and terrestrial-origin reference *Klebsiella* strains will be subjected to multigenerational directed evolution under combined selective pressure from QACs at slightly below the minimum inhibitory concentration (MIC) and simulated microgravity. Towards this end, we have performed a mechanistic analysis of QAC killing in *Klebsiella* and conducted genomic assessments of the virulence-associated gene complement in *K. quasipneumoniae.*