Challenges of Spaceflight

HAZARD ONE
Space Radiation

HAZARD TWO
Isolation

HAZARD THREE
Distance from Earth

HAZARD FOUR
Gravity Fields

HAZARD FIVE
Hostile/ Closed Environments

Image credits: NASA
Risk of Adverse Health Effects Due to Host-Microorganism Interactions

Short Title: Microhost
Element: Human Health Countermeasures (HHC)
Evidence: Report
Risk Master Logic Diagram: Diagram
Point of Contact: Cherlie Oubre

### Risk Ratings and Dispositions per Design Reference Mission (DRM) Category

<table>
<thead>
<tr>
<th>DRM Categories</th>
<th>Mission Duration</th>
<th>Operations</th>
<th>Long-Term Health</th>
<th>Risk Disposition *</th>
<th>LxC</th>
<th>Risk Disposition *</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low Earth Orbit</td>
<td>6 months</td>
<td>1x3</td>
<td>Accepted with Monitoring</td>
<td>3x1</td>
<td>Accepted</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1 year</td>
<td>1x3</td>
<td>Accepted with Monitoring</td>
<td>3x1</td>
<td>Accepted</td>
<td></td>
</tr>
<tr>
<td>Deep Space Sortie</td>
<td>1 month</td>
<td>1x3</td>
<td>Accepted with Monitoring</td>
<td>3x1</td>
<td>Accepted</td>
<td></td>
</tr>
<tr>
<td>Lunar Visit/Habitation</td>
<td>1 year</td>
<td>1x3</td>
<td>Accepted with Monitoring</td>
<td>3x1</td>
<td>Accepted</td>
<td></td>
</tr>
<tr>
<td>Deep Space Journey/Habitation</td>
<td>1 year</td>
<td>1x3</td>
<td>Accepted with Monitoring</td>
<td>3x1</td>
<td>Accepted</td>
<td></td>
</tr>
<tr>
<td>Planetary</td>
<td>3 years</td>
<td>3x3</td>
<td>Requires Mitigation</td>
<td>3x3</td>
<td>Requires Mitigation</td>
<td></td>
</tr>
</tbody>
</table>

Note: LxC is the likelihood and consequence rating.

### Gaps (5)

- MICRO-01: We need to determine the efficacy of current countermeasures and the need for countermeasure development based on changes in microbial populations and characteristics. (Previous title: AEH 10)
- MICRO-02: We need to determine if spaceflight induces changes in diversity, concentration, and/or characteristics of medically significant microorganisms associated with the crew and environment aboard the International Space Station that could affect crew health. (Previous title: AEH 12)
- MICRO-03: We need to determine which medically significant microorganisms display changes in the dose-response profiles in response to the spaceflight environment that could affect crew health. (Previous title: AEH 13)
- MICRO-04: We need to determine how physical stimuli specific to the spaceflight environment, such as microgravity, induce unique changes in the dose-response profiles of expected medically significant microorganisms. (Previous title: AEH 14)
- MICRO-05: Current microbial standards identifying microbial risk limits need to be updated and microbial requirements need to be developed to include new technologies and future mission scenarios. (Previous title: AEH 15)

### Risk Statement

Given that evidence collected during space flight indicates alterations in microbial virulence and astronaut immune function, there is a possibility that infectious disease will be enhanced during spaceflight missions.
“Species that are uncommon, or that have significantly increased or decreased in number, can be studied in a “microbial observatory” on the ISS, in ground-based facilities, or both.”

“If these studies suggest that permanent changes have occurred within the species, approaches such as microarray analysis and whole-genome sequencing can be used to determine what modifications or mutations may have occurred to shift the microbial population dynamics.”

“The continuing decline in the cost and increase in speed of genomic analysis should facilitate the comprehensive study of any changes in these microbial populations in space. Wide dissemination of this rich collection of raw data within the scientific community will allow a variety of scientific investigations.”
Microbial Tracking 1

Microbial Tracking-1A (launched January 10, 2015)
Microbial Tracking-1B (launched April 14, 2015)
Microbial Tracking-1C (launched April 8, 2016)

One sampling location for the Microbial Observatory investigation. Credit NASA.

A petri dish contains colonies of fungi grown from a sample collected aboard the International Space Station during the first of the three Microbial Tracking-1 flights. Credit NASA.


Saaymanestani A, Singh NK, Vaisinhampan PK, Venkateswaran KJ. A novel strategy to sequence the S. kamarisil from the ISS air filter sample. International Space Station. Genome Announcements. 2017 August 31; 5(23): 2 pp. DOI: 10.1128/genomeA.00696-17 PMID: 28860236. DOI: 10.1128/genomeA.00696-17

Urbanik C, Checinskii Siefert A, Frey KG, Allen JE, Singh NK, Jaising C, Wheeler K, Venkateswaran KJ. Detection of antimicrobial resistance genes associated with the International Space Station environmental surfaces. Scientific Reports. 2018 January 16; 8(1): 814. DOI: 10.1038/s41598-017-18056-4 PMID: 29339831. DOI: 10.1038/s41598-017-18056-4


Using adhesive tape as a sampling device, Venkateswaran and Kaurouia demonstrate one of the methods that station crew used to collect microorganisms from surfaces for the Microbial Tracking-1 investigation. Credit NASA.
NASA GeneLab data system

- Mission: To enable scientific discovery and space exploration through multi-omics data-driven research.
- Currently funded by SLPSRA Space Biology program. Previously received funding from the ISS program.
GeneLab overview: Database content

GeneLab contains decades of Space Biology omics data

**STUDY TYPE**
- Spaceflight: 49%
- Ground: 50%
- Parabolic: 1%

**ORGANISM**
- Rodents: 34%
- Microbes: 18%
- Plants: 11%
- Human: 22%
- Fruit flies: 5%
- Invertebrates: 7%
- Fish: 3%

**ASSAY TYPE**
- Transcription profiling: 72%
- DNA methylation profiling: 7%
- Environmental gene survey: 2%
- Genome sequencing: 5%
- Metabolite profiling: 2%
- Protein expression profiling: 9%
- Deletion pool profiling: 1%

**TRANSCRIPTION PROFILING**
- Microarray: 73%
- RNA-seq: 27%

Total number of studies: 211 (09-03-2019)
Microbe datasets on GeneLab

- Understanding how microbes respond to spaceflight is critical to: Astronaut health and safety, Space biotechnology, Planetary protection, Astrobiology
- 31 studies: 17 transcription profiling, 7 genome sequencing, 2 proteomic, 6 microbiome profiling

Cross-kingdom datasets!

Phylogenetic Tree of Life

Wild space samples!

EXPOSE-R payload outside in Real Space!

Samples exposed to Real Space!

Credits: NASA

Credits: Wikipedia (Image is Public Domain)
## Microbiome profiling datasets on GeneLab

<table>
<thead>
<tr>
<th>GLDS</th>
<th>Title</th>
<th>Data type</th>
<th>Study type</th>
</tr>
</thead>
<tbody>
<tr>
<td>GLDS-26</td>
<td>Microbiomes of the Dust Particles Collected from the International Space Station and Spacecraft Assembly Facilities</td>
<td>Amplicon</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-65</td>
<td>Microbial Observatory (ISS-MO): Microbial diversity</td>
<td>Amplicon</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-66</td>
<td>Microbial Observatory (ISS-MO): Antimicrobial resistance genes</td>
<td>Antibiotic resistance</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-69</td>
<td>Microbial Observatory (ISS-MO): Microbial metagenomics</td>
<td>Whole Genome</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-72</td>
<td>Space environmental factor impacts upon murine colon microbiota and mucosal homeostasis</td>
<td>Amplicon</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-82</td>
<td>Microbial monitoring in the ISS-Kibo</td>
<td>Amplicon</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-126</td>
<td>Analysis of dust samples from the Russian part of the ISS</td>
<td>Amplicon</td>
<td>Spaceflight (ISS dust)</td>
</tr>
<tr>
<td>GLDS-146</td>
<td>Mouse fecal microbiome after exposure to high LET radiation</td>
<td>Amplicon</td>
<td>Ground analog (Irradiated mice)</td>
</tr>
<tr>
<td>GLDS-191</td>
<td>Temporal dynamics of the gut microbiota in people sharing a confined environment, a 520-day ground-based space simulation.</td>
<td>Amplicon</td>
<td>Ground analog (Humans on space mission)</td>
</tr>
<tr>
<td>GLDS-170</td>
<td>NASA Aircraft Bioaerosol Collector (ABC)</td>
<td>Amplicon</td>
<td>Ground analog (stratosphere)</td>
</tr>
<tr>
<td>GLDS-200</td>
<td>Quantitative evaluation of bioaerosols in different particle size fractions collected on the International Space Station (ISS)</td>
<td>Amplicon</td>
<td>Spaceflight (ISS)</td>
</tr>
<tr>
<td>GLDS-212</td>
<td>Reproducible changes in gut microbiome reveal a shift in microbial and host metabolism during spaceflight (Peng Jiang)</td>
<td>Amplicon</td>
<td>Spaceflight (Mouse)</td>
</tr>
</tbody>
</table>
Getting the data

**Microbial Observatory (ISS-MO): Study of BSL-2 bacterial isolates from the International Space Station**

In an on-going Microbial Observatory experimental investigation on the International Space Station (ISS) multiple bacterial isolates of BSL-2 (BSL-2) were isolated and identified. The antibiotic susceptibility pattern was tested in these BSL-2 isolates for the following antibiotics: cefazolin, cephalaxin, penicillin, rifampin, tetracycline and many of the BSL-2 isolates showed multiple drug resistance. Among these isolates 21 strains were characterized.

**Microbial Observatory (ISS-MO): Draft Genome Sequence of two Aspergillus fumigatus Strains Isolated from the International Space Station**

Aspergillus fumigatus is a saprophytic filamentous fungus that is ubiquitous outdoors (self-decaying vegetation) and indoors (hospitalised or closed habitats etc.). A. fumigatus can adapt to various environmental conditions and form airborne conidia that are inhaled for a variety of diseases (e.g., non-invasive pulmonary infections allergic bronchopulmonary aspergillosis etc.) in immunocompromised hosts. In an on-going Microbial Observatory Experiments on the International Space Station, A. fumigatus was isolated from the International Space Station (ISS).

**Microbial Observatory (ISS-MO): Antimicrobial resistance genes**

The environmental samples were collected with the polyester wipes from eight different locations in the International Space Station (ISS) during two consecutive sampling sessions (three months apart) within the ISS Microbial Observatory Experiment DNA extraction of each samples was used to create ampiclon libraries based on customized panel of 503 antimicrobial resistance genes followed by next generation sequencing. This is the first study of that shows the reservoir of antimicrobial resistance genes.

**Microbial Observatory (ISS-MO): Microbial diversity**

The environmental microbiome study was designed to decipher microbial diversity of the International Space Station surfaces in terms of spatial and temporal distributions using 16s and ITS 1.8S illumina sequencing. We hypothesized that the microbial population of environmental surfaces changes in time due to antiseptic event will change activity and might be location specific. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecutive sampling sessions.

**Microbial Observatory (ISS-MO): Molecular characterization of Bacillus licheniformis sp. nov. isolated from various quarters of the International Space Station**

As part of an ongoing effort to catalogue microbial communities inhabiting the International Space Station (ISS) crew-associated environmental samples were collected from the Japanese Kibo Japanese Experiment Module (JEM) (four from US Segment Harmony Node 2 and five from Russian Segment Zvezda module sites) of belonging to the Bacillus anthracis, B. cereus, B. thuringiensis.

**Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces**

Presented here is the environmental microbiome study of the International Space Station surfaces. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecutive sampling sessions (three months apart). The specific objective was to unveil the pool of genes for each location during two separate sessions to learn of functional and metabolic diversity of microorganisms in the ISS. The International Space Station (ISS) as a closed bio.

**GLDS-68: Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces**

This is the environmental microbiome study of the International Space Station surfaces. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecutive sampling sessions (three months apart). The specific objective was to unveil the pool of genes for each location during two separate sessions to learn of functional and metabolic diversity of microorganisms in the ISS.
How can YOU download and analyze this data?

Anyone:
1. Go to genelab.nasa.gov!
2. Download and begin analyzing!

Those with technical skills and an interest in collaborating with likeminded scientists:
1. Go to genelab.nasa.gov!
Thank you for listening!
Go to: genelab.nasa.gov