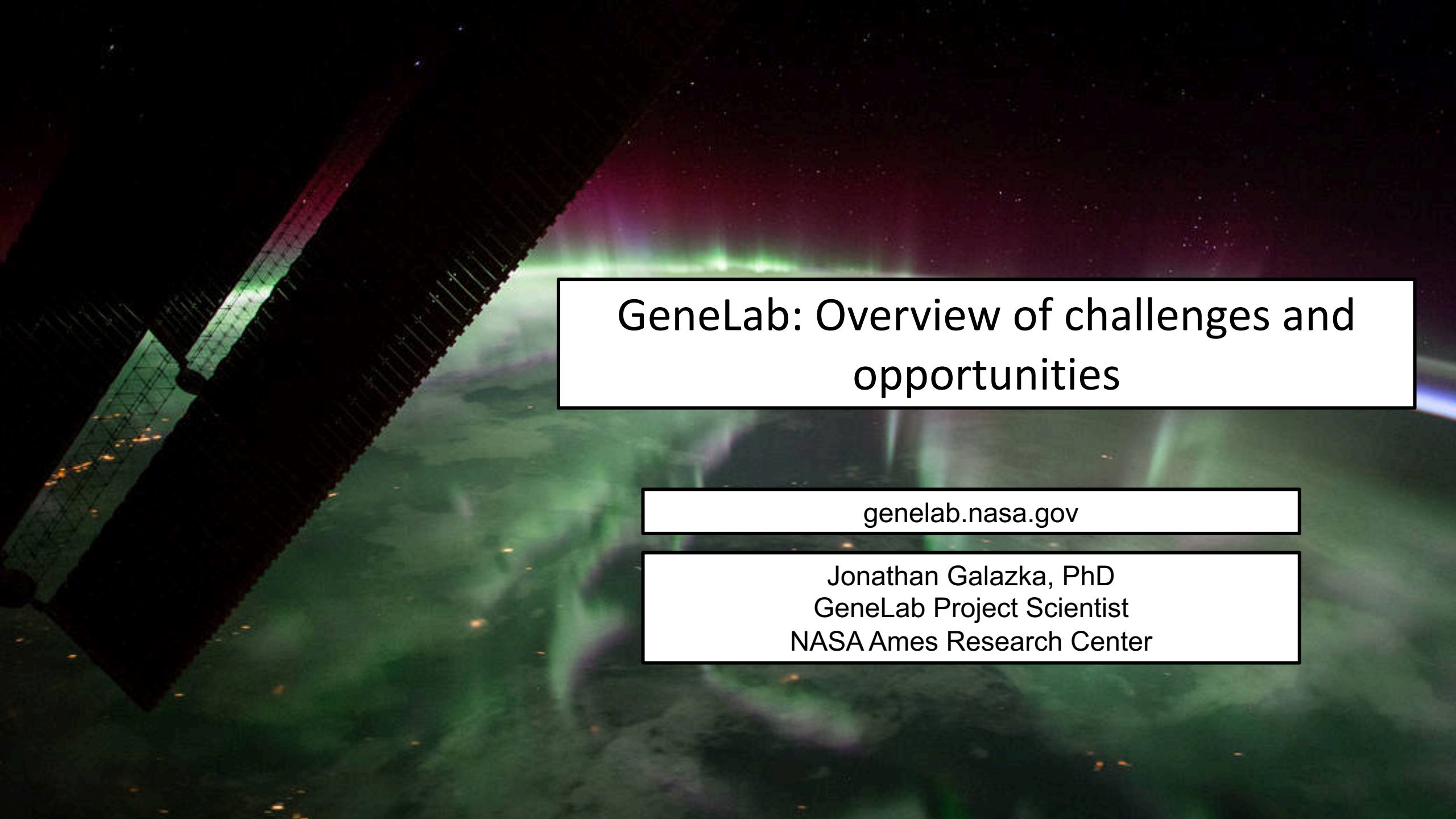
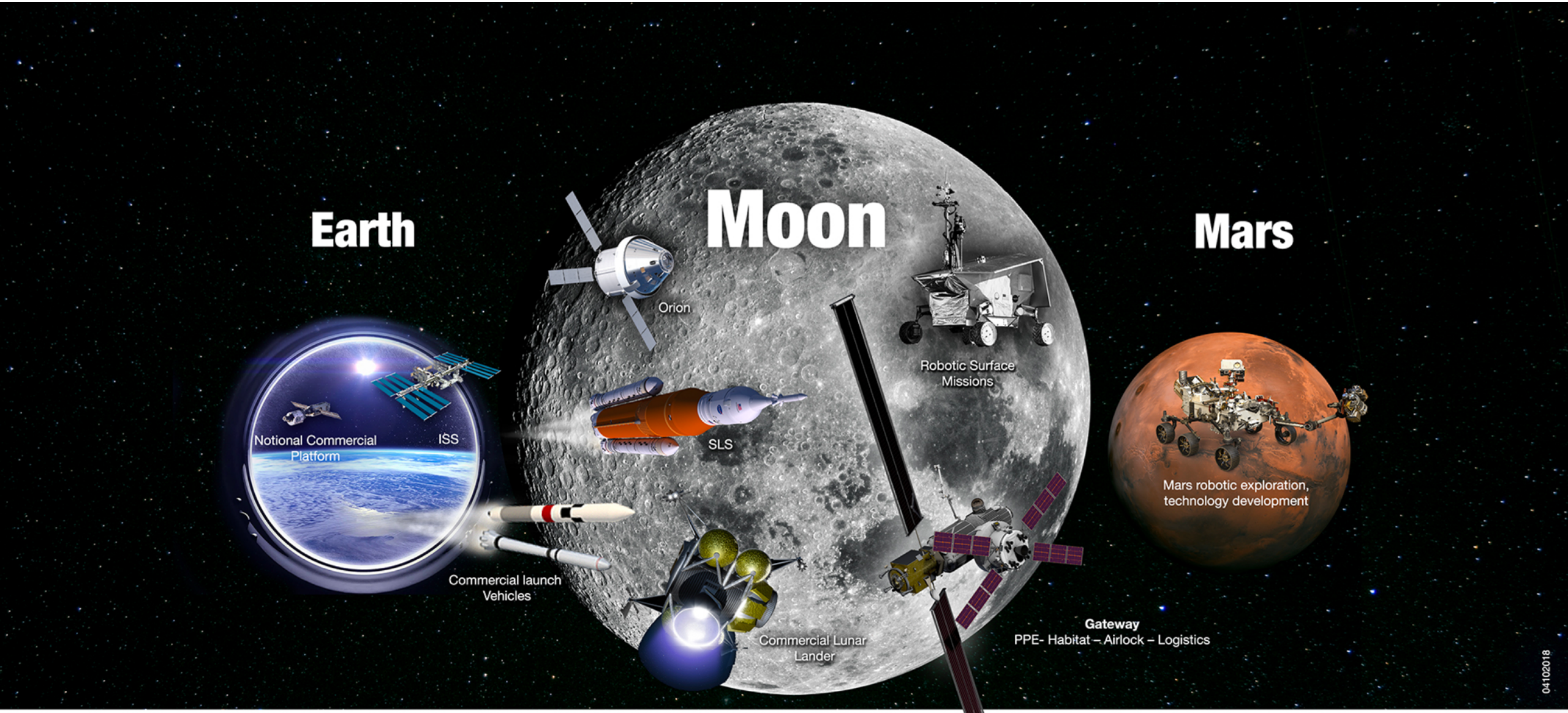


GeneLab: Overview of challenges and opportunities

genelab.nasa.gov

Jonathan Galazka, PhD
GeneLab Project Scientist
NASA Ames Research Center



In LEO
Commercial & International partnerships

In Cislunar Space
A return to the moon for long-term exploration

On Mars
Research to inform future crewed missions

Image credits: NASA

Image credits: NASA

Challenges of Spaceflight

Image credits: NASA

Risk of Adverse Health Effects Due to Host-Microorganism Interactions

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: Cherie Oubre

Last Published: 07/31/19 10:05:29 AM (Central)

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

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

Note: LxC is the likelihood and consequence rating.

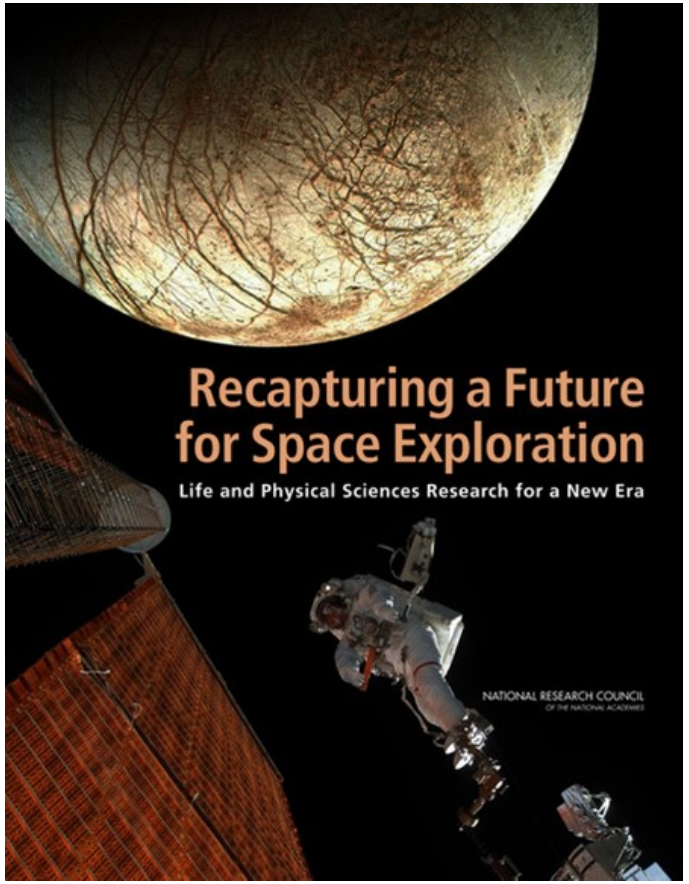
Risk Statement

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.

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)

2011 NRC Decadal Survey: “Microbial observatory” in space



National Research Council. 2011. *Recapturing a Future for Space Exploration: Life and Physical Sciences Research for a New Era*. Washington, DC: The National Academies Press. https://doi.org/10.17226/13048.

“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**.”

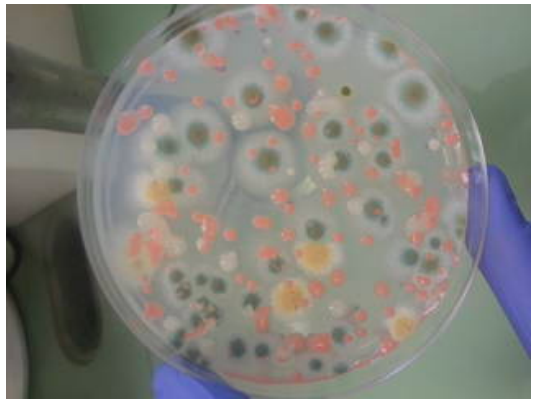
“The continuing **decline in the cost and increase in speed of genomic analysis** should facilitate the comprehensive study of any changes in these microbial populations in space. **Wide dissemination of this rich collection of raw data within the scientific community** will allow a variety of scientific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

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

One sampling location for the Microbial Observatory-1 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.

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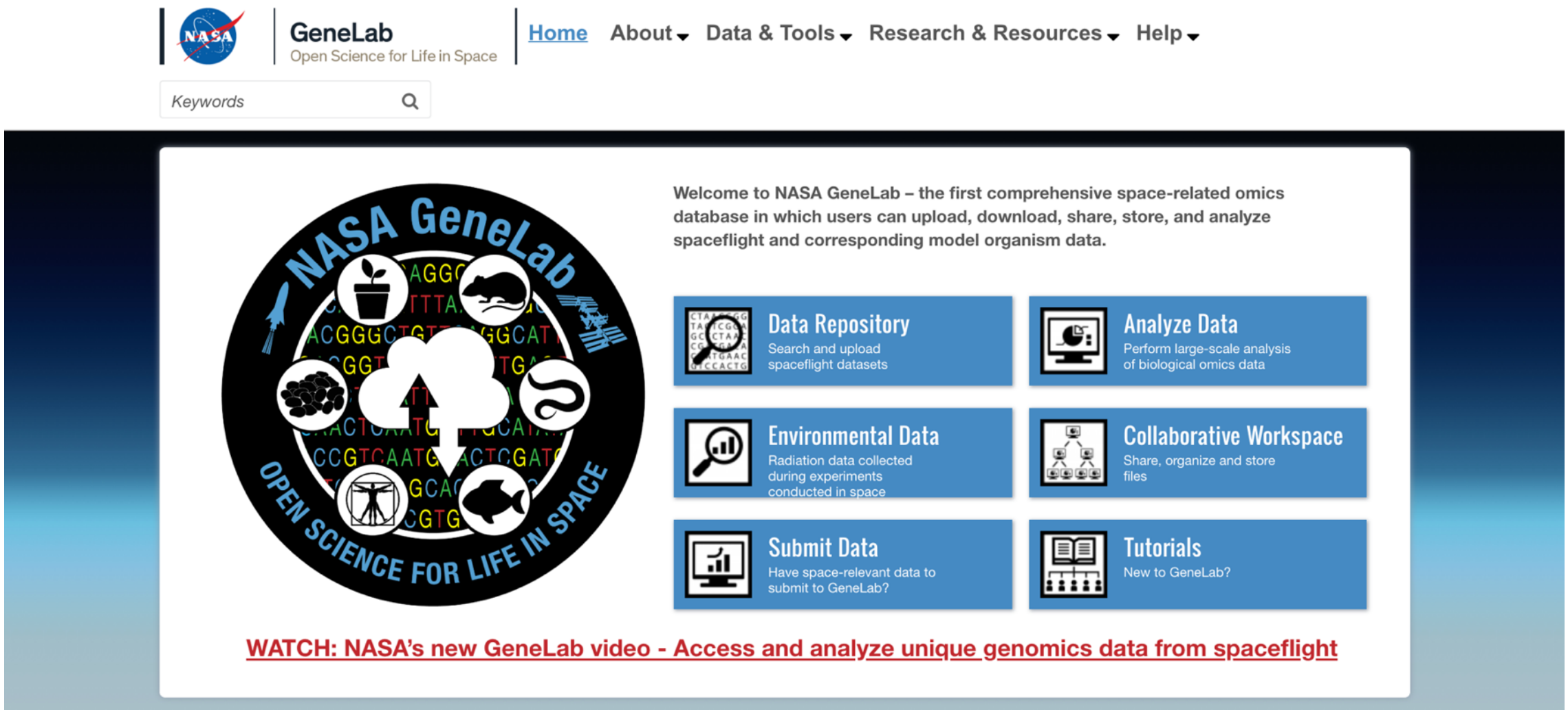
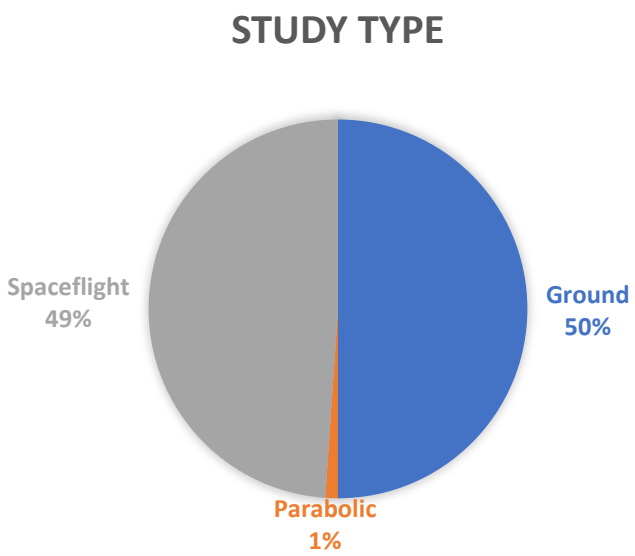
NASA GeneLab data system

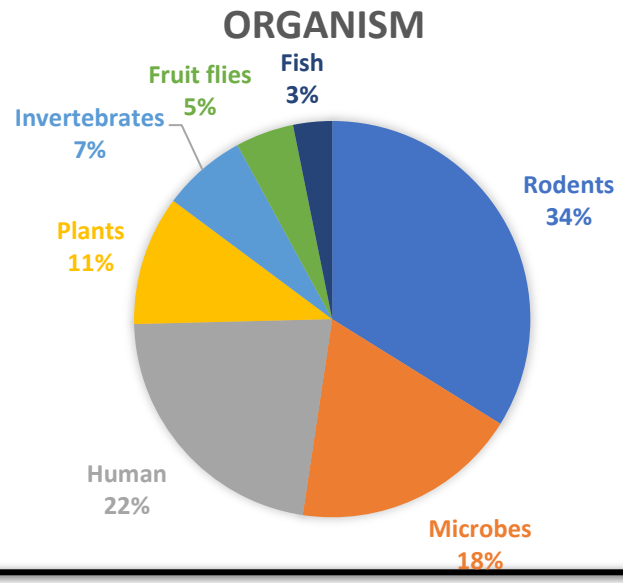
- Mission: To enable scientific discovery and space exploration through multi-omics data-driven research.
- Currently funded by SLPSRA Space Biology program. Previously received funding from the ISS program.

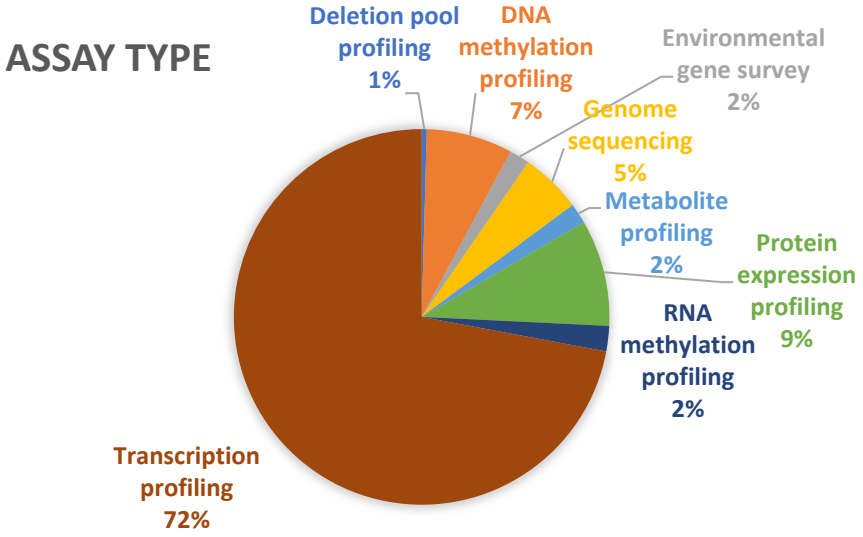


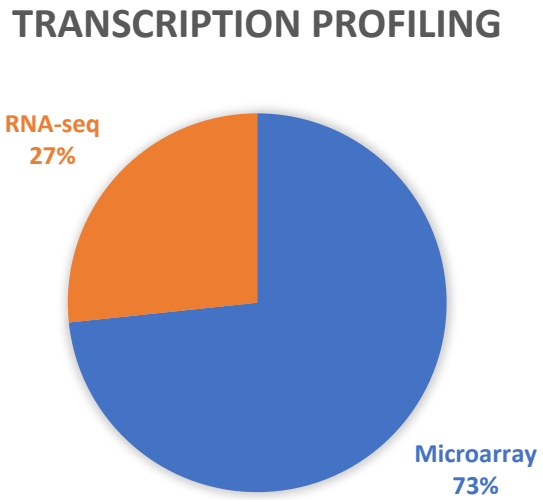
GeneLab overview: Database content

GeneLab contains decades of Space Biology omics data







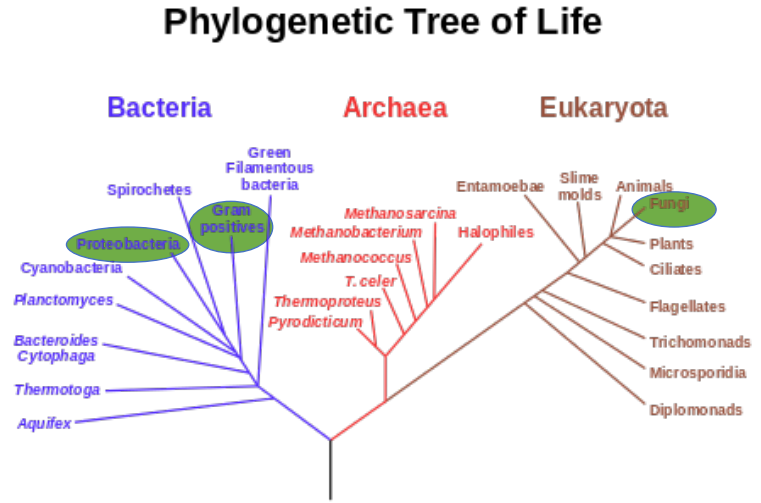


Total number of studies: 211 (09-03-2019)

Microbe datasets on GeneLab

- Understanding how microbes respond the 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!



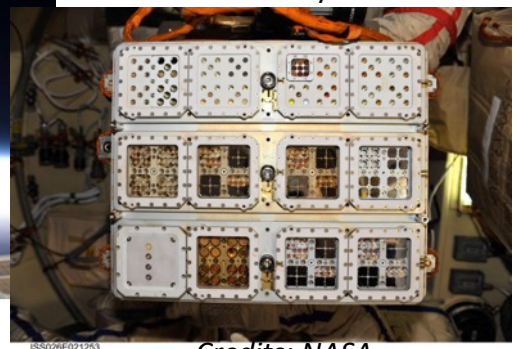
Credits: Wikipedia (Image is Public Domain)

Samples exposed to Real Space!

EXPOSE-R payload outside in Real Space!

Credits: NASA

EXPOSE-R Payload

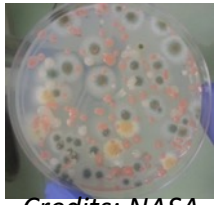


Credits: NASA

Wild space samples!

Mold on ISS

Credits: NASA



Credits: NASA

Microbiome profiling datasets on GeneLab

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

Getting the data

microbial observatory

All | GeneLab | NIH GEO | EBI PRIDE | ANL MG-RAST

Search Filters (GeneLab Only)

Project Type | Factors | Organisms | Assay Type | Clear

Search results for: **microbial observatory** using filter(s):

Total Search Results Found: **7**

Sort by Relevance | 25

1

Microbial Observatory (ISS-MO): Study of BSL-2 bacterial isolates from the International Space Station
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-67

In an on-going Microbial Observatory experimental investigation on the International Space Station (ISS) multiple bacterial isolates of Biosafety Level 2 (BSL-2) were isolated and identified. The antibiotic susceptibility pattern was tested in these BSL-2 isolates for the following antibiotics: cefazolin ciprofloxacin cefoxitin erythromycin gentamycin oxacillin penicillin rifampin tobramycin and many of the BSL-2 isolates showed multiple drug resistance. Among these isolates 21 strains were chos...

Organism: Klebsiella, Staphylococc... Factor: Microgravity Assay Type: genome sequencing Accession: GLDS-67 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 07-Jul-2016

Microbial Observatory (ISS-MO): Draft Genome Sequence of two Aspergillus fumigatus Strains Isolated from the International Space Station
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-68

Aspergillus fumigatus is a saprophytic filamentous fungus that is ubiquitous outdoors (soil decaying vegetation) and indoors (hospitals simulated closed habitats etc.). A. fumigatus can adapt to various environmental conditions and form airborne conidia that are the inoculum for a variety of diseases (e.g. non- and invasive pulmonary infections allergic bronchopulmonary aspergillosis etc.) in immunocompromised hosts. In an on-going Microbial Observatory Experiments on the International Space Sta...

Organism: Aspergillus fumigatus Factor: spaceflight Assay Type: genome sequencing Accession: GLDS-68 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 08-Jul-2016

Microbial Observatory (ISS-MO): Antimicrobial resistance genes
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-66

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 extracted from each of the samples was used to create amplicon libraries based on customized panel of 500 antimicrobial resistance genes followed by next-generation sequencing. This is the first study of that shows the reservoir of antimicrobial g...

Organism: cellular organisms Factor: spaceflight Assay Type: environmental gene survey Accession: GLDS-66 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 07-Jul-2016

Microbial Observatory (ISS-MO): Microbial diversity
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-65

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 iTag Illumina sequencing. We hypothesized that the microbial population of environmental surfaces changes in time due to astronauts xe2 x80 x99 activity and might be location specific. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecu...

Organism: cellular organisms Factor: spaceflight Assay Type: environmental gene survey Accession: GLDS-65 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 07-Jul-2016

Microbial Observatory (ISS-MO): Molecular characterization of Bacillus isensis sp. nov. isolated from various quarters of the International Space Station
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-64

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 Russian and US research modules. Initial analysis based on 16S rRNA gene sequencing identified 11 Bacillus isolates (two from Kibo Japanese Experiment Module (JEM) four from US Segment Harmony Node 2 and five from Russian Segment Zvezda module sites) all belonging to the Bacillus anthracis-B. cereus-B. thuring...

Organism: , Bacillus Factor: Spaceflight Assay Type: genome sequencing Accession: GLDS-64 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 08-Jul-2016

Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces
https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-69

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 bu...

Organism: cellular organisms Factor: Spaceflight Assay Type: metagenome profiling Accession: GLDS-69 PI/Contact: Kasthuri Venkateswaran
Release/Publication Date: 06-Jul-2016

GLDS-69: Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces Version 1

Select a Version: 1

Source Accession Number
Total Data Volume: 78.9 GB

Submitted Date: 03-May-2016
Release Date: 07-Jul-2016

DESCRIPTION | PROTOCOLS | SAMPLES | ASSAYS/MEASUREMENTS | PUBLICATIONS | STUDY FILES

DESCRIPTION

Study Description

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 built environment has its own environmental microbiome which is shaped by microgravity, radiation, and limited human presence. The microbial diversity associated with ISS environmental surfaces was investigated during this study. Polyester wipes and contact slides were used for sampling of eight various surface locations on the ISS at different time periods. The samples were retrieved and analyzed immediately upon the return to the Earth (via Soyuz TMA-14M or Dragon capsule from SpaceX). After surface sample collection, contact slides containing nutrient media for the growth of bacteria and fungi were incubated at 25C. The polyester wipes were processed to measure microbial burden (R2A, Blood Agar, and Potato Dextrose Agar) and recover cultivable bacteria as well as fungi. Subsequently, viable microbial burden was assessed using Adenosine Triphosphate (ATP) assay, and quantitative polymerase chain reaction (PCR) methods after propidium monoazide (PMA) treatment. The 16S-tag and metagenome analyses were used to elucidate viable microbial diversity. The cultivable bacterial population yield from the polyester wipes was very high (5 to 7-logs) when compared with the contact slides (102 to 103 CFU/m2). The PMA-qPCR analysis showed considerable variation of viable bacterial population (105 to 109 16S rDNA gene copies/m2) among locations sampled. Unlike contact slides, polyester wipes cover much larger sample surface (~1 m2) and produce much more reliable results of the microbial diversity of the ISS covering both cultivable and non-cultivable species. The cultivable, total, and viable microbial diversity was determined utilizing state-of-the art molecular techniques. The implementation of the PMA assay before DNA extraction allowed distinguishing viable microorganisms, which is crucial for determining their role to the crew health, the ISS maintenance and the general knowledge of the closed environmentally controlled built systems.

Contacts

NAME	ROLE	ORGANIZATION	E-MAIL
Kasthuri Venkateswaran	Principal Investigator	NASA	kjvenkat@jpl.nasa.gov

Study Design Factor(s)

FACTOR	ONTOLOGY: CONCEPT
Spaceflight	Space Flight

Organisms

cellular organisms

Assay(s)

ASSAY TYPE	DEVICE TYPE	DEVICE PLATFORM
metagenome profiling	nucleotide sequencing	Illumina

GLDS-69: Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces Version 1

Select a Version: 1

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Total Data Volume: 78.9 GB

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DESCRIPTION | PROTOCOLS | SAMPLES | ASSAYS/MEASUREMENTS | PUBLICATIONS | STUDY FILES

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  - Study Metadata Files
  - Whole Genome Sequencing Data

FILES	FILE SIZE	RESOURCE CATEGORY	RESOURCE DESCRIPTION
GLDS-69_wgs_5816_IIF1SW-P-M_F2_L1_PMA_FLT_R2-clean.fastq.gz	979.56 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.
GLDS-69_wgs_5816_IIF1SW-P-M_F2_L1_PMA_FLT_R1-clean.fastq.gz	976.56 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.
GLDS-69_wgs_SRX3808529_IIIF7SW-P-M_F3_L7_PMA_FLT_R2-clean.fastq.gz	951.87 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.
GLDS-69_wgs_5647_IF8SW-P-M_F1_L8_PMA_FLT_R1-clean.fastq.gz	939.76 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.
GLDS-69_wgs_SRX3808529_IIIF7SW-P-M_F3_L7_PMA_FLT_R1-clean.fastq.gz	933.78 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.
GLDS-69_wgs_5629_IF1SW-M_F1_L1_NORM_FLT_R2-clean.fastq.gz	915.39 MB	Whole Genome Sequencing Data	Raw sequencing data and sequencing assembly files and reports associated with this study.

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2. Download and begin analyzing!

Those with technical skills and an interest in collaborating with likeminded scientists:
1. Go to genelab.nasa.gov!
3. Join a NASA GeneLab Analysis Working Group (https://genelab.nasa.gov/awg/join)!

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