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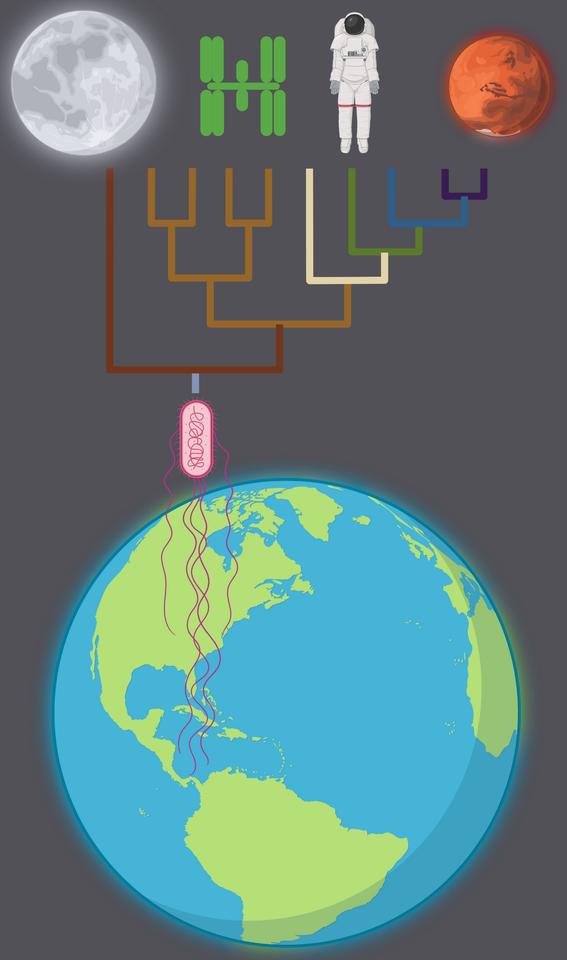
*M*icrobial *A*daptation to *S*pace *T*ravel



Responses of Microbes to Modeled Space Radiation

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Summary

Question: How do microbes adapt to the spaceflight environment?

Approach:

- We are studying how *Escherichia coli* responds upon exposure to modeled space radiation for thousands of cell divisions.
- Using DNA-sequencing, we will measure both the rate of mutation accumulation, and genetic adaptation by the inclusion or exclusion of population bottlenecks in our culturing.

Impact: These studies will enable the design of safer and more effective missions.

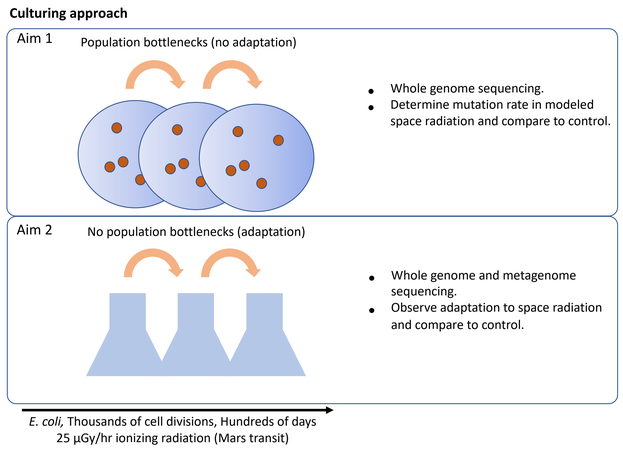
Background

Spaceships are host to a microbial community that affects crew and craft alike. The static composition of this community has been characterized and its temporal dynamics examined, but ***the mechanisms controlling its make-up and evolutionary trajectory are not understood.*** Systematic analyses of microbial diversity show consistent patterns in community composition and function. While understanding these patterns' ecological origins remains a significant challenge, it is known that ***the state and trajectories of microbial communities are in-part determined by their physical environment.***

The spaceflight environment includes interacting factors that differentiate it from Earth, including an altered atmospheric composition, altered gravity (and thus altered fluid dynamics), and increased ionizing radiation. These factors impart pressures on microbial communities that affect their evolutionary trajectories and thus the risks and benefits these communities represent.

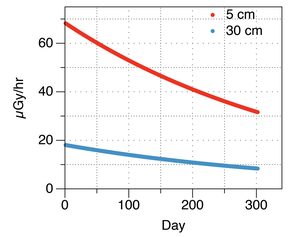
The radiation environment of space leads to ***chronic exposure to low doses*** and is difficult to mimic on Earth. Thus, little is known about how microbial communities in spacecraft will respond and evolve. Therefore, given the limitations of existing studies, we aim to ***empirically determine how exposure to low doses of ionizing radiation for thousands of cell divisions affects rates of mutation accumulation in bacteria and the trajectory of their evolution.*** In this way, we will provide a critical set of data for designing safe and robust space missions.

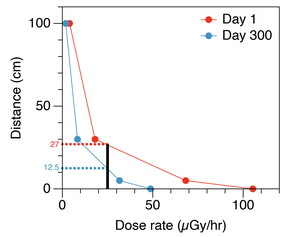
Approach & Results



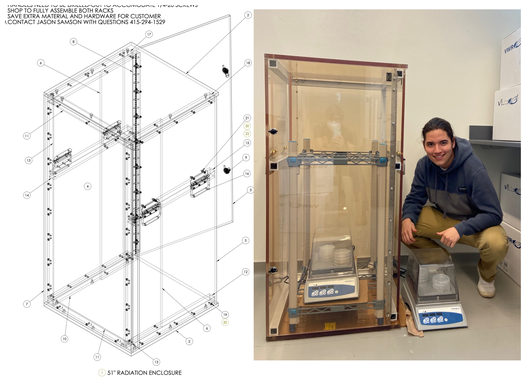
	Dose rate (µGy/hr)	Source
Earth background	0.03 – 0.05	Ruiz-Gonzalez et al.[1], Ruhm et al.[2]
Threshold for microbial response	0.45 - 20	Lampe et al.[3]; Ruiz-Gonzalez et al.[1]
ISS	10.6	Mean dose rate from ISS datasets in GeneLab
Mars cruise	18.8	Guo et al.[4]
Lunar mission	25	Nelson[5]
Mars mission	25	Nelson[5]

Relevant dose-rates





Low Dose Exposure: 300 days exposure. We will utilize a 25 mCi ^{57}Co plate (Sirona Complete Care #BM05-25) from Sept. 2019 to achieve the target low-dose-rate of 25 µGy/hr. Panel A shows the dose rate at 5 cm and 30 cm starting at day 1 until day 300 assuming an Oct. 2021 start date. Panel B shows the distance necessary to achieve dose rates between 2 µGy/hr and 105 µGy/hr on Day 1 (red) and Day 300 (blue). The target dose rate of 25 µGy/hr can be achieved at ~27 cm on Day 1 and ~12.5 cm on Day 2.



Low Dose Exposure: *E. coli* will be exposed to low-dose-rate radiation using ^{57}Co plates contained within a leaded acrylic box purpose built for this project. Adjustable shelf allows ^{57}Co to be moved to allow constant dose-rate. Control cultures will be cultured in parallel. NASA intern Emiliano Lopez-Ruiz included for scale.

	Clonal whole genome sequencing (>40x coverage)	Metagenomic (>100x coverage)
Aim 1. Mutation Accumulation (25 µGy/hr)	24 lineages x 4 time points = 96	None
Aim 1. Mutation Accumulation (background)	24 lineages x 4 time points = 96	None
Aim 2. LTEE (25 µGy/hr)	12 cultures x 4 clones = 48	Each of the 12 cultures every 30 days (10 timepoints) = 120
Aim2. LTEE (background)	12 cultures x 4 clones = 48	None

Datasets to be generated in this study.

Acknowledgements:

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References:

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3. Lampe, N. *et al.* Simulating the Impact of the Natural Radiation Background on Bacterial Systems: Implications for Very Low Radiation Biological Experiments. *PLoS ONE* **11**, e0166364 (2016).
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