Differential Gene Expression of Mice Pellet Microbial Communities Exposed to Simulated Microgravity

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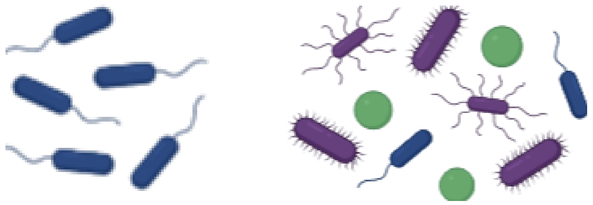
Background and Previous Research

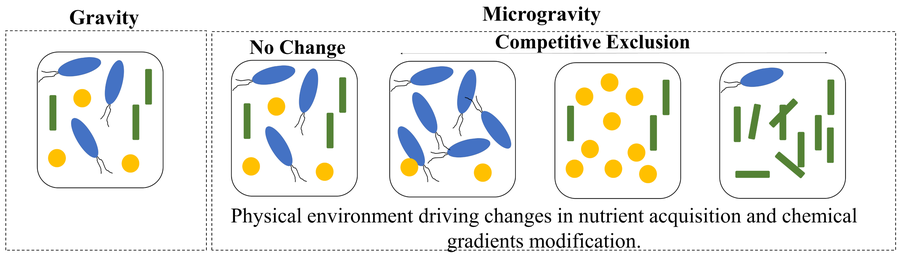
- Previous research has consisted of population studies to provide a baseline for how microgravity affects bacteria
- In nature, bacteria exist in communities made up of various bacterial species



Population Community

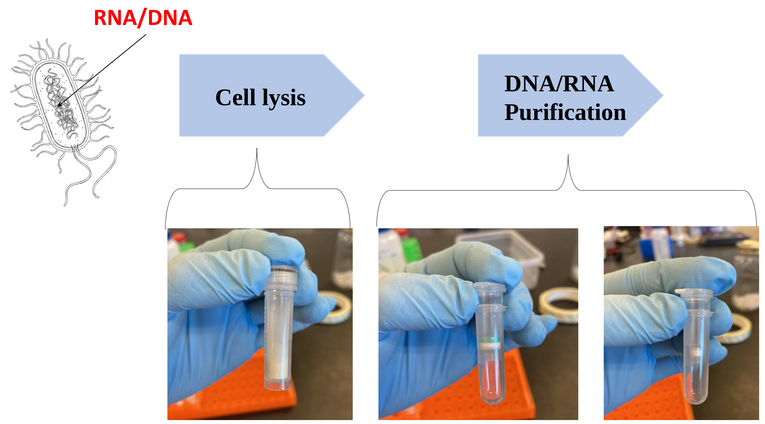
- Studies of microbial communities allow for more accurate interpretations of the effect of microgravity on the human gut microbiome

Microbial Communities



- The introduction of a stress changes the physical environment the bacterial live in
- Changes to the physical environment can favor one bacterium over others
- This shift from complex to simple microbial communities can greatly impact the health of astronauts

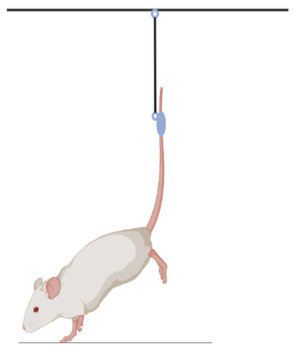
Metatranscriptomic Results



- A process of lysing and washes allows us to isolate and purify genetic material for sequencing and gene expression analysis

Sample Collection

- Mouse pellets were collected by Dr. Amber Paul and her team at Bookhaven National Laboratory

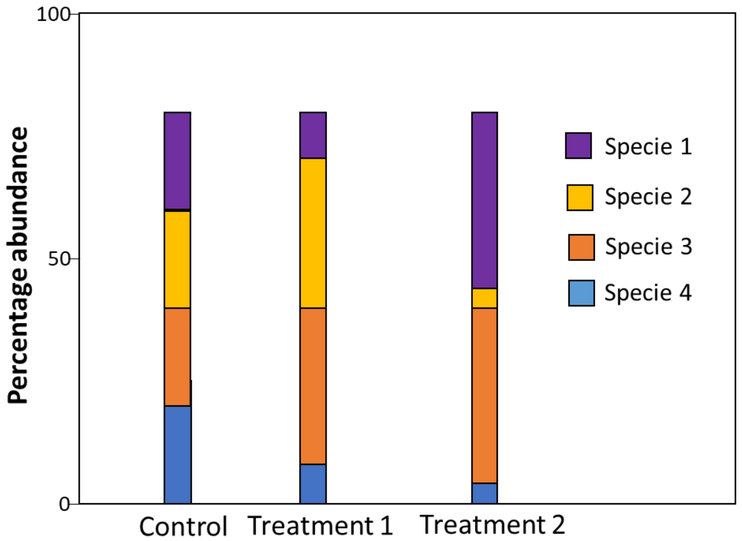


Mouse in hindlimb unloading

Mouse exposed to ionizing radiation

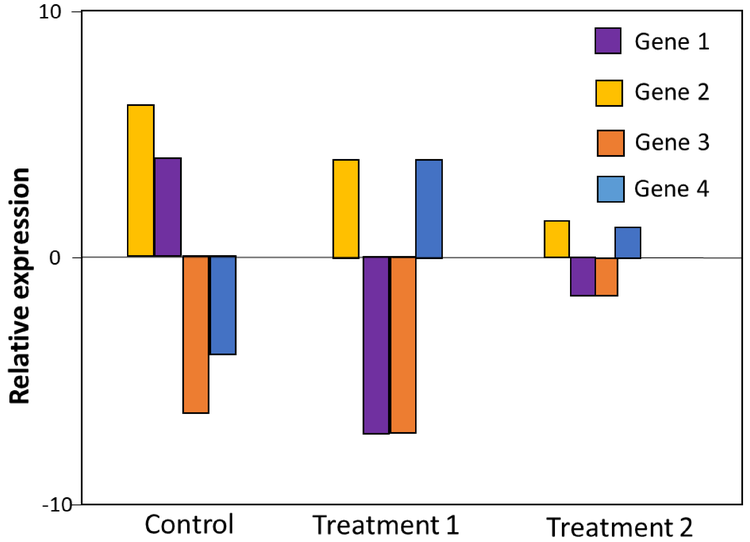
- Pellet samples were collected from mice exposed to microgravity (HU), ionizing radiation (IR), and both (HU+IR)
- Control samples were also taken from mice not exposed to any of the above conditions
- The use of HU and IR simulate spaceflight conditions that astronauts experience on the ISS
- DNA and RNA was extracted from the mice pellets for sequencing and genomic analysis

Metagenomic Results



- This graph shows how bacteria populations within a community may change depending on the type of treatment
- Metagenomics use DNA to analyze genomic content and identify which species are present within a community sample
- Metagenomic data highlights how different bacteria within a community respond to microgravity

Metatranscriptomic Results



- This graph illustrates how various genes may be expressed within a community depending on the type of treatment
- Metatranscriptomics uses RNA to measure the expression of genes within a community sample
- This data provides insight on the active functions of microbial communities and how that's impacted by microgravity