Evaluating the Spaceflight Infectious Disease Risk Potential of Pathogenic and Commensal microorganisms using *Caenorhabditis elegans* as a Human Surrogate Model for Infection

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Understanding the impact of the spaceflight environment on the disease-causing potential of a wide variety of pathogenic and commensal microbes is critical for ensuring crew health, safety and performance. Changes that occur to both the immune system of astronauts and pathogenesis of microbes during spaceflight could represent a formidable challenge to the successful transition from short-to-long duration missions. This is a critical issue to address since **a)** the crew's immune system is dysfunctional during flight, and **b)** results from our collaborative team and others have demonstrated that spaceflight and/or spaceflight-analogue culture globally alters the virulence, gene expression and/or pathogenesis-related phenotypes of several microbial pathogens. This study aims to further to improve infectious disease risk assessment for astronauts by investigating the likelihood that a variety of microorganisms may exhibit alterations in virulence in response to the microgravity environment. For this work we are profiling changes in virulence, persistence in the host, and targeted changes in gene expression of a **select panel of pathogenic and commensal microorganisms** exposed to spaceflight-analogue culture using the Rotating Wall Vessel (RWV) bioreactor. Microbes included in this study include 1) *Salmonella* Typhimurium, 2) *Staphylococcus aureus*, 3) a Space Shuttle environmental isolate of *Burkholderia cepacia*, and 4) *Lactobacillus acidophilus*, a commensal microorganism. The nematode *Caenorhabditis elegans* (*C. elegans*) is being used as a human surrogate model of infection to evaluate changes in microbial virulence in response to RWV culture and will also be profiled for targeted changes in the expression of genes important for host immunity. Moreover, as astronauts have dysfunctional immune systems during spaceflight, the susceptibility of an immunocomprised *C. elegans* mutant to infection with these same microbes will also be evaluated. Results from this work hold potential to provide deeper insight into the likelihood, consequence and respective uncertainties of this HRP risk.