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Radiation Fields, Effects and Risks in Human Space Missions (4)

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IMPACT OF WHOLE BODY IRRADIATION ON THE INTESTINAL MICROBIOME-CONSIDERATIONS FOR SPACE FLIGHT

Abstract

Human space travelers experience a unique environment that affects homeostasis and physiologic adaptation. Spaceflight-related changes have been reported in the musculo-skeletal, cardiovascular, neurovestibular, endocrine, and immune systems to just name a few. However, to date, radiation exposure is one of the main limiting factors for long duration space exploration missions and especially a mission to Mars.

Over the past few years through advances in technology, the characterization of the microbiome has revealed a large and complex community of microorganisms living in symbiosis with the human host. However, heterogeneity of the intestinal microbial spectrum in humans has been associated with a variety of diseases and susceptibility to infectious and toxic agents. Limited information is known about the influence of space environment in general and radiation in particular on the microbiome. Furthermore, multiple spaceflight and simulated microgravity experiments have shown changes in phenotypic microbial characteristics such as microbial growth, morphology, metabolism, genetic transfer, antibiotic and stress susceptibility, and an increase in virulence factors.

We now report a study of the bacterial composition of the intestine in C57BL/6NTAC mice and the types of microbes entering the body at two time points after the LD 50/30 dose of total body irradiation using microarray-based assay, G3 PhyloChip 16S rRNA, and bioinformatics methods. Bacteria and archaea taxon richness was determined at the genus level and ranged from 2 to 107 and 0 to 3 respectively. As expected, pre-exposure blood samples exhibited less bacterial and archaeal genus richness compared to all other samples. However, the study shows a significant shift in the mouse gut microbial speciation in several bacterial families, with increases in the Turicibacteraceae (Bacilli) and Enterobacteriaceae (Gammaproteobacteria) and decreases in the Lachnospiraceae (Clostridia), Ruminococcaceae (Clostridia), and Spingomonadaceae (Alphaproteobacteria) families. The findings most relevant to occupational human exposure, would likely relate to the increase in populations of Enterobacteriaceae, as multiple species within this family are known to produce disease in humans, including abscess formation, bacteremia, sepsis, disseminated toxins and even death. Therefore studies on the impact of the space environment and space radiation in particular on the astronaut's microbiome composition and pathogeneicity in addition

to the development of countermeasures are important steps in order to decrease risks associated with astronaut's health and mission integrity.