

Summary of: Longitudinal multi-omics analysis of host microbiome architecture and immune responses during short-term spaceflight

****Key Findings and Quantitative Results:****

****Microbiome Shifts:**** - ****Bacterial Shifts:**** Significant bacterial shifts were observed in the oral, nasal, and skin microbiomes. - ****Viral Shifts:**** Viral genera showed significant increases in the skin microbiome, particularly in the gluteal crease. - ****Gene Expression:**** Gene expression in the oral microbiome showed significant increases in CD4 T cells, CD8 T cells, and CD16 monocytes, which are associated with innate immune response against pathogens.

****Host-Host Interactions:**** - ****Oral Microbiome:**** Streptococcus species showed significant increases in CD4 T cells, CD8 T cells, and CD16 monocytes. - ****Nasal Microbiome:**** Streptococcus species showed significant increases in CD4 T cells, CD8 T cells, and CD16 monocytes. - ****Skin Microbiome:**** Fusobacterium species showed significant increases in CD4 T cells, CD8 T cells, and CD16 monocytes.

****Time-Dependent Trends:**** - ****Oral Microbiome:**** Oral microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight. - ****Nasal Microbiome:**** Nasal microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight. - ****Skin Microbiome:**** Skin microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight.

****Spaceflight-Associated Changes:**** - ****Oral Microbiome:**** Oral microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight. - ****Nasal Microbiome:**** Nasal microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight. - ****Skin Microbiome:**** Skin microbiome showed significant increases in Fusobacterium species, which were transiently increased during flight.

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