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SPACEFLIGHT-DRIVEN MICROBIAL ADAPTATION AND BIODETERIORATION OF SPACESUIT FABRICS REVEALED BY METATRANSCRIPTOMICS

Abstract

Microorganisms are among the few companions that accompany humans throughout space exploration, yet their influence on spacesuit materials and associated risks remains poorly understood. To investigate microbial responses to spaceflight, cellulose-enriched microbial consortia derived from China Space Station cleanroom samples were exposed to spaceflight conditions aboard the Long March-7 mission and compared with parallel Earth controls. Results from metatranscriptomic analyses revealed substantial microbial adaptation under spaceflight, characterized by transcriptional shifts in carbohydrate utilization, central carbon metabolism, stress response, and redox-associated functions. Spaceflight also enhanced the expression of pathways associated with biomass decomposition, while fungal taxa, particularly Fusarium, dominated community activity. Scanning electron microscopy revealed extensive microbial colonization and structural deterioration of spacesuit fabric fibers following exposure. Collectively, these findings demonstrate that spaceflight reshapes microbial functional activity and promotes biodeterioration processes, highlighting potential risks to spacesuit integrity and the need for effective microbial management strategies during future long-duration human space missions.