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Space Biofilms - Phenotypic and transcriptomic behaviour of *Pseudomonas aeruginosa* biofilms on board the International Space Station

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**Abstract**

Bacterial biofilms in space can have a positive or negative impact on the success of a mission. For example, in some instances, biofilms can improve plant growth, facilitate synthesis/recovery of metals from regolith, or bioremediate wastewater. On the other hand, biofilms can deteriorate or cause malfunctions of spaceflight hardware. Biofilms have been found on the wastewater tank of the Environmental Control and Life Support System (ECLSS), which poses a risk to the system. Even more alarming, some biofilms cause infections that may threaten astronauts’ health, like urinary tract infections that if left unclear could cause permanent damage to the kidneys. Given that biofilms can contribute to or hinder the efforts of space exploration, it is necessary to understand the effects of microgravity on biofilm behaviour. The Space Biofilms experiment intends to contribute to such understanding by analysing the morphology and transcriptomic profiles of *Pseudomonas aeruginosa* PA14 biofilms grown in spaceflight compared to matched ground controls. *P. aeruginosa* biofilms were grown onboard the International Space Station for 1, 2, or 3 days at 37°C over six surface materials: Stainless Steel 316 (SS316), passivated SS316, and a novel Lubricant Impregnated Surface (LIS) were grown in rich media supplemented with potassium nitrate (LBK) to simulate wastewater. While cellulose membrane, catheter grade silicone, and silicone with special nanotopography (DLIP) were grown in modified Artificial Urine Media supplemented with glucose and high phosphate (mAUMg-hi Pi) to simulate urine. Asynchronous ground controls replicated spaceflight procedures. Morphology analysis revealed that flight samples had a significant decrease in mass, thickness and surface area coverage in LBK. Additionally, biofilm surface coverage on LIS was only 11% of the equivalent samples on SS316 (p<0.001). Associated preliminary transcriptomic data will also be addressed.

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