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COMPARISON OF STAPHYLOCOCCUS DRAFT GENOMES ISOLATED FROM ASTRONAUTS
DURING SPACEFLIGHT WITH TERRESTRIAL- ISOLATED GROUND AND CLINICAL STRAINS.

Abstract

Staphylococcus is a common constituent of the human microbiome and is typically found on the skin and nasal cavity. Many space biology experiments to date have shown that bacterial properties change as a result of spaceflight, with some of those changes detrimental to astronaut health, such as increased virulence and increased antimicrobial resistance. *Staphylococcus* is one such organism affected by spaceflight, with a recent study showing that greater than 80% of *Staphylococcus* strains isolated from ISS surfaces to be resistant to more than one antibiotic. Of concern, is the fact that *Staphylococcus* increases in relative abundance in astronauts during spaceflight compared to pre-flight levels. Since *Staphylococcus* is a common constituent in the human microbiome, simple screening would not be enough to protect astronauts. Rather, in-depth knowledge about their genetic properties and changes upon exposure to the space environment is needed, in order to develop better screening measures. We hypothesize that *Staphylococcus* strains isolated from astronauts during spaceflight will have genetic differences compared to those isolated pre-flight, as well as from terrestrially isolated clinical strains. In order to examine this, draft genomes of *Staphylococcus epidermidis*, *Staphylococcus aureus* and *Staphylococcus haemolyticus*, isolated from four astronauts during spaceflight, will be compared with the same species isolated from each astronaut prior to launch. The whole genomes from the astronauts will also be compared with *Staphylococcus* draft genomes sequenced from clinical patients. A total of 270 astronaut isolates have been whole genome sequenced. Draft genomes of the same species, but from clinical isolates, have been downloaded from NCBI. Using computational methods, the genomes from pre-flight, in-flight, post-flight and clinical samples will be compared. Comparisons will include average nucleotide identity, digital hybridization, single nucleotide polymorphisms, metabolic capabilities (such as those involved in virulence), presence of antimicrobial resistance and virulence genes, and evidence and degree of horizontal gene transfer activity. This study will examine how a common opportunistic pathogen, present in the astronaut microbiome, may be affected by spaceflight and the consequence of these changes on astronaut health. Insight into changes in virulence, antimicrobial resistance, metabolism and horizontal gene transfer activity will help inform protocols for more applicable screening and counter measures.