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COMPARATIVE GENOMICS OF ANTIBIOTIC RESISTANT STAPHYLOCOCCUS SPECIES
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Abstract

As part of the Microbial Tracking-1 investigation a variety of bacterial and fungal species were identified including novel microbial genera and species. A total of 113 *Staphylococcus* strains comprising 9 known species and one potentially novel species were isolated from the International Space Station (ISS) and Commercial Resupply Vehicles (CRV). The whole-genome sequences (WGS) of these strains were generated and revealed the presence of multiple *Staphylococcus* species. The Average Nucleotide Index of the staphylococcal genomes allowed to unambiguously identify them as *S. aureus*, *S. caprae*, *S. capitis*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. saccharolyticus*, *S. saprophyticus*, and *S. warneri*. Disc diffusion assay tested for several antimicrobial resistance (AMR) revealed that some strains of *S. aureus*, *S. epidermidis*, *S. hominis*, and *S. saprophyticus* were resistant to rifampicin. However, *S. hominis*, a known BSL-2 microorganism was found to be differentially resistant to ceftazidime, oxacillin, penicillin, rifampicin, and tobramycin. The differential AMR profiles exhibited in staphylococcal strain might be potentially due to their acquired resistance when co-lived with other microorganisms. In addition to their potential pathogenicity, bacteria isolated from the ISS might adapt to the space conditions (such as, radiation and microgravity), and as a result pose a risk to immunocompromised astronauts. The comparative genome and pangenome analyses performed on the strains isolated from the ISS as compared to Earth analogs could reveal their respective AMR profiles and virulence properties. These types of studies are critical and would enable the development of suitable countermeasures to reduce their presence in the closed built environment of the ISS and ultimately preserve crew health and mission integrity.