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COMPARATIVE GENOMICS OF ANTIBIOTIC RESISTANT STAPHYLOCOCCUS SPECIES  
ASSOCIATED WITH THE INTERNATIONAL SPACE STATION**Abstract**

As part of the Microbial Tracking-1 investigation, various bacterial and fungal species were identified, including novel microbial genera and species. A total of 115 *Staphylococcus* strains comprising 9 known 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 us 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 differentially resistant to cefoxitin, 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 pose a risk to immunocompromised astronauts. The comparative genome and pangenome analyses performed on the strains isolated from the ISS 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.