Complete Genome Sequence of *Klebsiella quasipneumoniae* subsp. *similipneumoniae* Strain IF3SW-P1, Isolated from the International Space Station

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**ABSTRACT**  The 5.2-Mb circular genome of *Klebsiella quasipneumoniae* subsp. *similipneumoniae* strain IF3SW-P1, isolated from the International Space Station, was sequenced using Oxford Nanopore Technologies. The genome lacks a megaplasmid typical of hypervirulent and multidrug-resistant *Klebsiella* strains but does contain a chromosomally encoded OqxAB efflux pump associated with carbapenem resistance.

In 2014, two phylogroups of the opportunistic pathogen *Klebsiella pneumoniae* were described as the novel species *Klebsiella quasipneumoniae* (1). Since its definition as a species, *K. quasipneumoniae* has emerged as an understudied human pathogen with hypervirulent, multidrug-resistant (MDR), carbapenem-resistant, and hypermucoviscous strains isolated from both hospital-borne and community-acquired infections (2–5). Considering its prevalence on the International Space Station (ISS) (6), the newly recognized pathogenicity of *K. quasipneumoniae* increases concerns about the consequences of this species being exposed to the stresses of spaceflight, which are known to trigger bacterial virulence and antimicrobial resistance (7–10).

Strain IF3SW-P1 was isolated from the surface of the foot panel of the Advanced Resistive Exercise Device (ARED) on the ISS on 4 March 2015 (11) using a standard spread plate method on Reasoner’s 2A (R2A) agar and archived in glycerol cryostocks (6). For this study, strain IF3SW-P1 was subcultured from cryostock and grown to late exponential phase in Trypticase soy broth (TSB) at 37°C; genomic DNA was then extracted using the DOE Joint Genome Institute bacterial genomic DNA isolation protocol (12).

Oxford Nanopore Technologies sequencing was performed using a GridION MK1 sequencer on a R10.4 flow cell (FLO-MIN112) with a library synthesized from Q20+ EA (early access) ligation reagents (SQK-LSK112-XL). The raw reads were base called using MinKNOW v29.10.8, with a mean quality score of 16.3 and a mode of 18.03. The genome was assembled, circularized, and polished using Flye v2.9 with the parameters --nano-hq and --read-error 0.03 for the Q20+ data (13). The Flye-generated assembly contains two contigs, one 5.2-Mb circular chromosome and one 3-kb linear fragment confirmed via BLASTN v2.12.0 to be 99.8% identical to *Escherichia coli* strain Q4552 plasmid pECQ4552_IHU08 (GenBank accession number CP077071.1) (14). Notably, the genome does not encode any virulence- or drug resistance-associated plasmids, such as *bla*KPC and Inc(FII), which are known to occur in *Klebsiella* species (15).

The genome was identified as *K. quasipneumoniae* subsp. *similipneumoniae* by calculating the average nucleotide identity (ANI) using the EzBioCloud calculator compared to the two subspecies’ type strains, *K. quasipneumoniae* subsp. *quasipneumoniae* 01A030T (ANI, 96.63%) and *K. quasipneumoniae* subsp. *similipneumoniae* 07A044T (ANI, 99.03%) (16). Strain IF3SW-P1

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is also related to but distinct from eight previously published draft genomes of *K. quasipneumoniae* strains isolated from the ISS, with >99% ANI for all (6).

The assembly was annotated using RASTtk v1.3.0 (17) as part of the Pathosystems Resource Integration Center (PATRIC) v3.6.12 (18). Predicted virulence genes on the chromosome include *iutA*, which encodes a ferric aerobactin receptor, although the gene encoding the associated siderophore aerobactin (*iucA*) is not present (19). The IF3SW-P1 genome also contains genes for the multidrug resistance efflux pump OqxAB, associated with carbapenem resistance in *K. pneumoniae* (20, 21). OqxAB is reported to be associated with resistance to benzalkonium chloride, a quaternary ammonium compound used as a disinfectant on the ISS (11). Default parameters were used for all software unless otherwise specified. Additional assembly and annotation information is listed in Table 1.

**Data availability.** The genomic assembly and raw reads have been deposited at GenBank (accession number CP092121) and the Sequence Read Archive (SRR17974437). These data are also available at NASA GeneLab (GLDS-470).

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