




Draft Genome Sequences of Various Bacterial Phyla Isolated from the International Space Station

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ABSTRACT Whole-genome sequences were generated from 96 bacterial strains of 14 species that were isolated from International Space Station surfaces during the Microbial Tracking 2 study. Continued characterization of this closed habitat's microbiome enables tracking of the spread and evolution of secondary pathogens, which is vital for astronaut health.

The International Space Station (ISS) is currently the only long-term human habitat in space. Microgravity disrupts human immune function (1), and close monitoring of the ISS microbiome for increased pathogenicity is thus an ongoing critical task. Here, we report the draft genomes of 96 bacterial strains that were isolated from the ISS (Table 1). Eleven of the 14 species found are common members of the human microbiome, and most can act as opportunistic human pathogens.

Four species from the phylum *Actinobacteria* were isolated, from the genera *Pseudoclavibacter*, *Kocuria*, and *Micrococcus*, all of which are common in both environmental and human microbiomes (2–5). *Kocuria palustris* and *Micrococcus luteus* are opportunistic pathogens (5, 6). *M. luteus* can survive in a dormant state under extreme oligotrophic conditions (7) and has increased growth and increased biomass yield in microgravity (8).

Multiple coagulase-negative staphylococci (CoNS) were also isolated. CoNS are normal components of human skin flora (9) and are often resistant to antibiotics because of their ability to form biofilms (10); all CoNS in this report are documented opportunistic pathogens (11–15).

Three species from the phylum *Proteobacteria* were identified. *Acinetobacter pittii* is a less common nosocomial pathogen that causes pneumonia and meningitis in intensive care patients (16), *Pseudomonas fulva* is a commensal plant endophyte (17) that can also infect immunocompromised patients (18, 19), and *Pseudomonas granadensis* is a recently discovered soil bacterium (20).

Two other species in this report that are not associated with the human microbiome are *Cytobacillus horneckiae*, a Gram-positive UV-resistant endospore-former that was isolated from a clean room at the Kennedy Space Center (21), and *Methylobacterium organophilum*, a facultative methylotroph (22).

All strains reported here were collected aboard the ISS over the course of five flight missions between June 2017 and December 2018 (Table 1). Premoistened polyester wipes were used to collect samples from eight predetermined surfaces during each flight (see Table 1 for locations). After transport to Earth, the wipes were agitated in sterile phosphate-buffered saline, and the buffer was concentrated with an InnoPrep CP-150 concentrator. Concentrates were plated onto Reasoner's 2A (R2A) agar (25°C

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TABLE 1 Accession numbers, sampling locations, and assembly details for bacterial strains isolated from the ISS

Sample name	Bacterial species	WGS accession no.	SRA accession no.	Flight no.	Location ^a	Medium, temp (°C) ^b	No. of contigs	Genome size (bp)	N_{50} (bp)	Depth of coverage (×)	G+C content (%)	No. of filtered reads
F8_75_12B	<i>Acinetobacter pittii</i>	JAFDRK0000000000	SRR13530731	F8	Lab 3 overhead	R2A, 25	66	3,996,855	150,281	922.13	38.75	23,547,006
F8_75_13B	<i>Acinetobacter pittii</i>	JAFDRL0000000000	SRR13530730	F8	Lab 3 overhead	R2A, 25	71	3,995,968	150,376	735.67	38.75	18,785,602
F8_75_14B	<i>Acinetobacter pittii</i>	JAFDRM0000000000	SRR13530729	F8	Lab 3 overhead	R2A, 25	68	3,996,346	150,379	908.88	38.75	23,208,680
F8_75_15B	<i>Acinetobacter pittii</i>	JAFDRN0000000000	SRR13530728	F8	Lab 3 overhead	R2A, 25	70	3,995,502	132,238	679.63	38.74	17,354,664
F8_75_16B	<i>Acinetobacter pittii</i>	JAFDRO0000000000	SRR13530727	F8	Lab 3 overhead	R2A, 25	67	3,996,494	150,378	768.58	38.75	19,625,886
F8_75_17B	<i>Acinetobacter pittii</i>	JAFDRP0000000000	SRR13530725	F8	Lab 3 overhead	R2A, 25	69	3,996,521	150,203	717.48	38.75	18,321,172
F8_75_18B	<i>Acinetobacter pittii</i>	JAFDRQ0000000000	SRR13530724	F8	Lab 3 overhead	R2A, 25	69	3,995,985	150,209	813.82	38.75	20,781,150
F8_75_4B	<i>Acinetobacter pittii</i>	JAFDRX0000000000	SRR13530717	F8	Lab 3 overhead	R2A, 25	69	3,995,609	150,378	704.76	38.74	17,996,396
F8_75_5B	<i>Acinetobacter pittii</i>	JAFDRY0000000000	SRR13530716	F8	Lab 3 overhead	R2A, 25	66	3,995,688	150,370	583.20	38.74	14,892,212
F8_75_6P	<i>Acinetobacter pittii</i>	JAFDSA0000000000	SRR13530713	F8	Lab 3 overhead	BA, 37	67	3,996,523	150,212	1,115.49	38.75	28,484,452
F8_75_7B	<i>Acinetobacter pittii</i>	JAFDSB0000000000	SRR13530712	F8	Lab 3 overhead	R2A, 25	70	3,996,147	132,238	828.46	38.75	21,155,182
F8_85_11B	<i>Acinetobacter pittii</i>	JAFDSE0000000000	SRR13530709	F8	Crew quarters	R2A, 25	70	3,997,471	150,204	735.21	38.75	18,773,974
F8_85_12B	<i>Acinetobacter pittii</i>	JAFDSF0000000000	SRR13530708	F8	Crew quarters	R2A, 25	71	3,996,218	150,204	903.60	38.75	23,073,890
F8_85_2P	<i>Acinetobacter pittii</i>	JAFDSJ0000000000	SRR13530703	F8	Crew quarters	BA, 37	70	3,994,221	150,204	1,039.96	38.74	26,555,916
F8_85_6P	<i>Acinetobacter pittii</i>	JAFDSL0000000000	SRR13530701	F8	Crew quarters	BA, 37	71	3,997,028	150,211	939.87	38.75	24,000,022
F8_25_1P	<i>Cyrobacillus horneckiae</i>	JAFDQP0000000000	SRR13530754	F8	WHC	BA, 37	44	5,324,298	329,620	397.27	37.7	14,551,974
F5_75_P6	<i>Kocuria indica</i>	JAFDPQ0000000000	SRR13530782	F5	Lab 3 overhead	BA, 37	28	2,803,228	245,667	825.53	68.78	15,829,868
F6_35_P_1B	<i>Kocuria indica</i>	JAFDPV0000000000	SRR13530776	F6	ARED	BA, 37	27	2,803,211	245,667	1,412.10	68.78	27,077,776
F5_75_P11C	<i>Kocuria palustris</i>	JAFDPC0000000000	SRR13530748	F5	Lab 3 overhead	BA, 37	36	2,843,288	191,163	862.77	70.54	16,418,232
F5_75_P2A	<i>Kocuria palustris</i>	JAFDPI0000000000	SRR13530790	F5	Lab 3 overhead	BA, 37	33	2,844,036	191,163	873.89	70.54	16,629,878
F5_75_P2B	<i>Kocuria palustris</i>	JAFDPJ0000000000	SRR13530789	F5	Lab 3 overhead	BA, 37	32	2,843,686	262,144	1,100.95	70.54	20,950,750
F5_75_P7	<i>Kocuria palustris</i>	JAFDPR0000000000	SRR13530780	F5	Lab 3 overhead	BA, 37	32	2,844,494	271,586	897.37	70.54	17,076,656
F5_75_P8	<i>Kocuria palustris</i>	JAFDPS0000000000	SRR13530779	F5	Lab 3 overhead	BA, 37	49	2,843,644	130,397	648.47	70.54	12,340,212
F6_15_P_2	<i>Kocuria palustris</i>	JAFDPT0000000000	SRR13530778	F6	Cupola	BA, 37	31	2,844,162	271,218	1,262.76	70.54	24,029,822
F6_75_B_1	<i>Kocuria palustris</i>	JAFDQD0000000000	SRR13530767	F6	Lab 3 overhead	R2A, 25	34	2,843,704	191,187	595.66	70.54	11,335,110
F4_55_F1_F	<i>Methylobacterium organophilum</i>	JAFDOX0000000000	SRR13530793	F4	Overhead 4	PDA, 25	219	7,153,721	73,806	525.12	71	23,633,880
F5_75_P10B	<i>Micrococcus luteus</i>	JAFDOZ0000000000	SRR13530781	F5	Lab 3 overhead	BA, 37	309	2,634,797	18,596	695.07	72.51	11,589,510
F5_75_P11A	<i>Micrococcus luteus</i>	JAFDPA0000000000	SRR13530770	F5	Lab 3 overhead	BA, 37	249	2,437,588	21,893	526.53	72.95	8,779,392
F5_75_P1A	<i>Micrococcus luteus</i>	JAFDPG0000000000	SRR13530704	F5	Lab 3 overhead	BA, 37	289	2,643,054	17,191	831.59	72.54	13,865,910
F5_75_P1B	<i>Micrococcus luteus</i>	JAFDPH0000000000	SRR13530791	F5	Lab 3 overhead	BA, 37	163	2,662,630	32,991	717.06	72.61	11,956,220
F5_75_P2C	<i>Micrococcus luteus</i>	JAFDPK0000000000	SRR13530788	F5	Lab 3 overhead	BA, 37	274	2,435,899	17,792	894.45	72.84	14,913,960
F5_75_P3	<i>Micrococcus luteus</i>	JAFDPL0000000000	SRR13530787	F5	Lab 3 overhead	BA, 37	534	2,325,956	7,231	679.00	72.6	11,321,680
F6_35_P_1A	<i>Micrococcus luteus</i>	JAFDPU0000000000	SRR13530777	F6	ARED	BA, 37	68	2,461,417	58,867	1,075.33	73.05	17,930,076
F6_75_P_2	<i>Micrococcus luteus</i>	JAFDPQ0000000000	SRR13530765	F6	Lab 3 overhead	BA, 37	103	2,458,603	49,739	1,387.39	73.03	23,133,344
F6_35_P_6	<i>Pseudoclavibacter alba</i>	JAFDPW0000000000	SRR13530775	F6	ARED	BA, 37	8	2,211,951	1,246,034	2,314.39	64.46	33,024,422
F8_15_1P	<i>Pseudomonas fulva</i>	JAFDQJ0000000000	SRR13530762	F8	Cupola	BA, 37	52	5,220,099	212,004	747.60	61.24	23,764,838
F8_15_2P	<i>Pseudomonas fulva</i>	JAFDQK0000000000	SRR13530761	F8	Cupola	BA, 37	49	5,219,879	271,973	527.41	61.24	16,765,304
F8_15_3P	<i>Pseudomonas fulva</i>	JAFDQL0000000000	SRR13530760	F8	Cupola	BA, 37	45	5,222,637	279,059	640.19	61.24	20,350,344
F8_15_4B	<i>Pseudomonas fulva</i>	JAFDQM0000000000	SRR13530758	F8	Cupola	R2A, 25	50	5,219,467	212,004	595.41	61.24	18,927,008
F8_15_5B	<i>Pseudomonas fulva</i>	JAFDQN0000000000	SRR13530757	F8	Cupola	R2A, 25	50	5,220,771	212,004	522.35	61.24	16,604,570
F8_15_6B	<i>Pseudomonas fulva</i>	JAFDQO0000000000	SRR13530756	F8	Cupola	R2A, 25	51	5,220,269	228,990	581.78	61.24	18,493,586

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TABLE 1 (Continued)

Sample name	Bacterial species	WGS accession no.	SRA accession no.	Flight no.	Location ^a	Medium, temp (°C) ^b	No. of contigs	Genome size (bp)	<i>M</i> ₅₀ (bp)	Depth of coverage (X)	G+C content (%)	No. of filtered reads
F8_25_1B	<i>Pseudomonas fulva</i>	JAFDQ000000000	SRR13530755	F8	WHC	R2A, 25	51	5,220,561	212,004	672.65	61.24	21,382,176
F8_25_2P	<i>Pseudomonas fulva</i>	JAFDQ000000000	SRR13530753	F8	WHC	BA, 37	51	5,220,953	212,004	504.33	61.24	16,031,608
F8_25_3P	<i>Pseudomonas fulva</i>	JAFDQR000000000	SRR13530752	F8	WHC	BA, 37	51	5,219,857	266,892	746.18	61.24	23,719,826
F8_45_1B	<i>Pseudomonas fulva</i>	JAFDQS000000000	SRR13530751	F8	Dining table	R2A, 25	47	5,221,731	212,004	679.90	61.24	21,612,934
F8_45_16B	<i>Pseudomonas fulva</i>	JAFDQT000000000	SRR13530750	F8	Overhead 4	R2A, 25	46	5,221,547	266,892	690.69	61.24	21,955,880
F8_65_10B	<i>Pseudomonas fulva</i>	JAFDQU000000000	SRR13530749	F8	PMM port 1	R2A, 25	43	5,222,049	276,378	692.43	61.24	22,011,252
F8_65_11B	<i>Pseudomonas fulva</i>	JAFDQV000000000	SRR13530747	F8	PMM port 1	R2A, 25	45	5,221,141	272,009	763.66	61.24	24,275,474
F8_65_12B	<i>Pseudomonas fulva</i>	JAFDQW000000000	SRR13530746	F8	PMM port 1	R2A, 25	47	5,220,530	212,004	553.11	61.24	17,582,460
F8_65_13B	<i>Pseudomonas fulva</i>	JAFDQX000000000	SRR13530745	F8	PMM port 1	R2A, 25	46	5,222,282	228,990	767.70	61.24	24,403,836
F8_65_14B	<i>Pseudomonas fulva</i>	JAFDQY000000000	SRR13530744	F8	PMM port 1	R2A, 25	165	5,214,942	53,221	58.63	61.25	1,863,658
F8_65_15B	<i>Pseudomonas fulva</i>	JAFDQZ000000000	SRR13530743	F8	PMM port 1	R2A, 25	45	5,221,469	212,004	644.90	61.24	20,500,186
F8_65_15B	<i>Pseudomonas fulva</i>	JAFDRA000000000	SRR13530742	F8	PMM port 1	BA, 37	47	5,219,969	212,004	1,065.14	61.24	33,859,008
F8_65_3B	<i>Pseudomonas fulva</i>	JAFDRB000000000	SRR13530741	F8	PMM port 1	R2A, 25	45	5,222,269	271,999	911.16	61.24	28,964,010
F8_65_3P	<i>Pseudomonas fulva</i>	JAFDRC000000000	SRR13530740	F8	PMM port 1	BA, 37	45	5,221,425	212,004	1,002.77	61.24	31,876,344
F8_65_4B	<i>Pseudomonas fulva</i>	JAFDRD000000000	SRR13530739	F8	PMM port 1	R2A, 25	47	5,220,883	212,004	587.52	61.24	18,676,250
F8_65_5B	<i>Pseudomonas fulva</i>	JAFDRE000000000	SRR13530738	F8	PMM port 1	R2A, 25	44	5,222,120	276,382	507.87	61.24	16,144,410
F8_65_7B	<i>Pseudomonas fulva</i>	JAFDRF000000000	SRR13530736	F8	PMM port 1	R2A, 25	48	5,221,613	266,937	817.23	61.24	25,978,110
F8_65_8B	<i>Pseudomonas fulva</i>	JAFDRG000000000	SRR13530735	F8	PMM port 1	R2A, 25	48	5,220,807	266,892	666.04	61.24	21,172,172
F8_65_9B	<i>Pseudomonas fulva</i>	JAFDRH000000000	SRR13530734	F8	PMM port 1	R2A, 25	47	5,221,098	266,892	857.16	61.24	27,247,530
F8_75_10B	<i>Pseudomonas fulva</i>	JAFDRI000000000	SRR13530733	F8	Lab 3 overhead	R2A, 25	45	5,221,475	248,885	615.92	61.24	19,579,074
F8_75_11B	<i>Pseudomonas fulva</i>	JAFDRJ000000000	SRR13530732	F8	Lab 3 overhead	R2A, 25	44	5,223,496	276,366	714.44	61.24	22,710,854
F8_75_1P	<i>Pseudomonas fulva</i>	JAFDRK000000000	SRR13530723	F8	Lab 3 overhead	R2A, 25	46	5,221,397	248,885	734.17	61.24	33,338,010
F8_75_2P	<i>Pseudomonas fulva</i>	JAFDRS000000000	SRR13530722	F8	Lab 3 overhead	BA, 37	43	5,221,447	266,892	995.57	61.24	31,647,224
F8_75_3P	<i>Pseudomonas fulva</i>	JAFDRT000000000	SRR13530721	F8	Lab 3 overhead	R2A, 25	46	5,221,320	248,885	792.01	61.24	25,176,512
F8_75_2P	<i>Pseudomonas fulva</i>	JAFDRU000000000	SRR13530720	F8	Lab 3 overhead	BA, 37	48	5,221,068	211,998	726.98	61.24	23,109,428
F8_75_3B	<i>Pseudomonas fulva</i>	JAFDRV000000000	SRR13530719	F8	Lab 3 overhead	R2A, 25	43	5,222,387	279,059	657.54	61.24	20,901,852
F8_75_3P	<i>Pseudomonas fulva</i>	JAFDRW000000000	SRR13530718	F8	Lab 3 overhead	BA, 37	47	5,220,873	211,998	916.50	61.24	29,133,940
F8_75_6B	<i>Pseudomonas fulva</i>	JAFDRZ000000000	SRR13530714	F8	Lab 3 overhead	R2A, 25	48	5,222,006	211,998	610.88	61.24	19,418,924
F8_75_8B	<i>Pseudomonas fulva</i>	JAFDSC000000000	SRR13530711	F8	Lab 3 overhead	R2A, 25	45	5,221,151	211,998	675.48	61.24	21,472,302
F8_75_8B	<i>Pseudomonas fulva</i>	JAFDSD000000000	SRR13530710	F8	Lab 3 overhead	R2A, 25	43	5,221,838	248,885	817.24	61.24	25,978,556
F8_85_13B	<i>Pseudomonas fulva</i>	JAFDSG000000000	SRR13530707	F8	Crew quarters	R2A, 25	48	5,220,177	276,366	396.21	61.24	12,594,644
F8_85_1B	<i>Pseudomonas fulva</i>	JAFDSH000000000	SRR13530706	F8	Crew quarters	R2A, 25	45	5,222,394	326,740	612.35	61.24	19,465,438
F8_85_2B	<i>Pseudomonas fulva</i>	JAFDSI000000000	SRR13530705	F8	Crew quarters	R2A, 25	47	5,220,003	211,998	950.52	61.24	30,215,290
F8_85_3B	<i>Pseudomonas fulva</i>	JAFDSK000000000	SRR13530702	F8	Crew quarters	R2A, 25	49	5,220,696	228,990	740.00	61.24	23,523,202
F8_85_7P	<i>Pseudomonas fulva</i>	JAFDSM000000000	SRR13530700	F8	Crew quarters	BA, 37	48	5,221,111	212,004	877.89	61.24	27,906,690
F8_85_8P	<i>Pseudomonas fulva</i>	JAFDSN000000000	SRR13530699	F8	Crew quarters	BA, 37	50	5,221,099	212,004	1,153.25	61.24	36,659,886
F8_85_9P	<i>Pseudomonas fulva</i>	JAFDSO00000000	SRR13530698	F8	Crew quarters	BA, 37	44	5,216,552	212,004	725.04	61.25	23,047,660
F6_45_P_1A	<i>Pseudomonas granadensis</i>	JAFDPY000000000	SRR13530773	F6	Dining table	BA, 37	32	6,075,880	499,949	543.50	60.13	21,534,088
F6_45_P_1B	<i>Pseudomonas granadensis</i>	JAFDPZ000000000	SRR13530772	F6	Dining table	BA, 37	40	6,075,550	404,503	681.05	60.13	26,983,966
F6_45_P_1C	<i>Pseudomonas granadensis</i>	JAFDQA000000000	SRR13530771	F6	Dining table	BA, 37	36	6,074,831	411,755	526.75	60.13	20,870,328
F6_45_P_2	<i>Pseudomonas granadensis</i>	JAFDQB000000000	SRR13530769	F6	Dining table	BA, 37	36	6,075,345	409,624	849.89	60.13	33,673,758

(Continued on next page)

TABLE 1 (Continued)

Sample name	Bacterial species	WGS accession no.	SRA accession no.	Flight no.	Location ^a	Medium, temp (°C) ^b	No. of contigs	Genome size (bp)	<i>N</i> ₅₀ (bp)	Depth of coverage (X)	G+C content (%)	No. of filtered reads
F6_4S_P_5C	<i>Pseudomonas granadensis</i>	JAFDQC000000000	SRR13530768	F6	Dining table	BA, 37	35	6,076,644	529,557	356.66	60.13	14,131,340
F6_7S_P_1	<i>Staphylococcus capitis</i>	JAFDQE000000000	SRR13530766	F6	Lab 3 overhead	BA, 37	23	2,502,093	1,289,580	716.11	32.83	11,624,446
F6_7S_P_4	<i>Staphylococcus capitis</i>	JAFDQG000000000	SRR13530764	F6	Lab 3 overhead	BA, 37	16	2,451,586	1,282,189	1,422.62	32.78	23,092,982
F5_7S_P12B	<i>Staphylococcus caprae</i>	JAFDPE000000000	SRR13530726	F5	Lab 3 overhead	BA, 37	12	2,636,914	684,748	848.08	33.49	14,738,340
F6_3S_P_7	<i>Staphylococcus epidermidis</i>	JAFDPX000000000	SRR13530774	F6	ARED	BA, 37	32	2,474,746	167,947	1,420.95	32.03	22,991,394
F5_7S_P10A	<i>Staphylococcus saprophyticus</i>	JAFDOY000000000	SRR13530792	F5	Lab 3 overhead	BA, 37	27	2,660,926	711,481	814.84	32.99	14,003,764
F5_7S_P11B	<i>Staphylococcus saprophyticus</i>	JAFDPB000000000	SRR13530759	F5	Lab 3 overhead	BA, 37	26	2,617,222	1,361,305	964.97	32.98	16,583,928
F5_7S_P12A	<i>Staphylococcus saprophyticus</i>	JAFDPD000000000	SRR13530737	F5	Lab 3 overhead	BA, 37	27	2,663,655	707,529	1,202.62	32.99	20,668,282
F5_7S_P13	<i>Staphylococcus saprophyticus</i>	JAFDPF000000000	SRR13530715	F5	Lab 3 overhead	BA, 37	24	2,662,145	711,479	1,165.31	32.99	20,027,056
F5_7S_P5A	<i>Staphylococcus saprophyticus</i>	JAFDPN000000000	SRR13530785	F5	Lab 3 overhead	BA, 37	27	2,661,845	711,479	1,391.99	32.99	23,922,656
F5_7S_P5B	<i>Staphylococcus saprophyticus</i>	JAFDPO000000000	SRR13530784	F5	Lab 3 overhead	BA, 37	27	2,661,424	711,481	989.97	32.99	17,013,600
F5_7S_P5C	<i>Staphylococcus saprophyticus</i>	JAFDPP000000000	SRR13530783	F5	Lab 3 overhead	BA, 37	25	2,663,767	711,481	1,176.36	32.99	20,216,888
F6_7S_P_5	<i>Staphylococcus saprophyticus</i>	JAFDQH000000000	SRR13530763	F6	Lab 3 overhead	BA, 37	23	2,664,922	711,479	1,502.54	32.99	25,822,574
F5_7S_P4	<i>Staphylococcus warneri</i>	JAFDPM000000000	SRR13530786	F5	Lab 3 overhead	BA, 37	26	2,558,875	420,301	813.75	32.46	13,169,560

^aWHC, waste and hygiene compartment; ARED, advanced resistive exercise device; PMM, permanent multipurpose module.

^bBA, blood agar.

for 7 days), potato dextrose agar (PDA) (25°C for 7 days), and blood agar (37°C for 2 days) using appropriate concentrations for microbial isolation. Isolated colonies were restreaked on tryptic soy agar (TSA) (25°C), and genomic DNA was extracted using the ZymoBIOMICS DNA MagBead kit according to the manufacturer's instructions. Libraries for whole-genome shotgun sequencing (WGS) were prepared using the Illumina Nextera DNA Flex library preparation kit as in previous studies (23) and were sequenced using the NovaSeq 6000 S4 flow cell paired-end 2 × 150-bp platform.

Sequencing reads were quality filtered and trimmed, and adapter sequences were removed, using FastQC v0.11.7 (24) and fastp v0.20.0 (25). Scaffolds were assembled with SPAdes v3.11.1 (26). QUAST v5.0.2 (27) was used to determine assembly quality, including the number of contigs, genome size, and N_{50} value. Default settings were used for all steps except for fastp, which included 512 adapters screening. OrthoANLu (28) was used to confirm the species identity for each strain against the species type strain sequence, with a minimum average nucleotide identity of 95% for identification. Genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (29).

Data availability. The WGS data and raw data have been deposited in GenBank under the BioProject accession number [PRJNA690512](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA690512). This project has also been deposited in the NASA GeneLab system (30) under the project number [GLDS-361](https://www.nasa.gov/genelab/BLDS-361). The versions described in this paper are the first versions.

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