

Parameters	Bacterial strain	
	CLCI03	CLCA07
Genus-level/species-level identification ^a	<i>Streptomyces</i> sp.	<i>Pseudomonas</i> sp.
Number of short paired reads (151 bp)	132,345,158	92,473,384
Number of long reads (average length, bp)	56,036 (7,482.5 bp)	33,842 (10,536.1 bp)
Average short-read coverage	294×	283×
Average long-read coverage (N ₅₀)	47× (8.83 kb)	52× (13.05 kb)
Chromosomal DNA size (bp)	8,678,721 ^c	6,733,244 ^d
Contig count	4	1
N ₅₀ (bp)	8,678,721	6,733,244
Contamination (%) ^b	0.70	4
G + C content (%)	71.75	58.53
Completeness (%) ^b	100	98.3
Coarse consistency (%)	98.9	99.0
Fine consistency (%)	95.7	97.0
Total CDSs ^e	7,878	6,072
CDSs with protein	7,690	5,928
tRNA	90	71
ncRNAs	3	4
rRNA (5S, 16S, and 23S)	21	22

^eCDS, coding sequence.[illegible]10.1128/mra.01375-25 **2**

respectively. The closest known species to strain CLCI03 is *Streptomycesnojiriensis* JCM 3382^T with 48.7% dDDH relatedness value, while strain CLCA07 exhibited the highest dDDH value of 42.5% with *Pseudomonas mucoide*s P154a^T. Phylogenomic analyses (20, 21) confirmed that these strains represent potential two novel lineages yet to be described (Fig. 1).

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Christian Larocque, Data curation, Formal analysis, Investigation, Methodology, Validation, Visualization, Writing – review and editing | Renlin Xu, Investigation, Methodology, Validation, Writing – review and editing | Mercy Akuma, Investigation, Methodology, Validation, Writing – review and editing | Cyr L. Doumbou, Conceptualization, Investigation, Resources, Supervision, Writing – review and editing | James T. Tambong, Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

This whole genome project has been deposited in GenBank under project number [PRJNA1357910](#); BioSample numbers [SAMN53096257](#) and [SAMN53096258](#); and accession numbers [JBSIFU000000000](#) and [JBSIFT000000000](#) for strains CLCI03 and CLCA07, respectively. The Illumina and Nanopore raw sequence reads were deposited in the Sequence Read Archive database under accession numbers [SRR36114699](#) and [SRR36114698](#) for CLCI03, and [SRR36114697](#) and [SRR36114696](#) for CLCA07, respectively.

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