



Draft Genome Sequences of Two Strains of a Newly Described Species, *Sphingobacterium cellulitidis*

Torsten Seemann,^{a,b} Dieter M. Bulach,^{a,b} Glen Carter,^b M. John Albert^c

Melbourne Bioinformatics, The University of Melbourne, Carlton, Australia^a; Doherty Applied Microbial Genomics, Department of Microbiology and Immunology, The University of Melbourne at The Peter Doherty Institute for Infection & Immunity, Melbourne, Australia^b; Department of Microbiology, Faculty of Medicine, Kuwait University, Jabriya, Kuwait^c

ABSTRACT The draft genome sequences of two strains of a newly described species, *Sphingobacterium cellulitidis*, have been determined. The type strain originated from cellulitis of a toe of a patient and the other strain from the environment. The sequences will provide the reference genomes of the new *Sphingobacterium* species.

The genus *Sphingobacterium* comprises Gram-negative, nonfermenting, non-spore-forming aerobic bacilli. These bacteria are catalase and oxidase positive. They can be cultivated on blood agar and MacConkey agar, where they produce colonies with a yellow color (1). They are ubiquitous in nature, being found in soil, plant material, and water bodies. They are characterized by the presence of menaquinone as the major respiratory quinone, as well as sphingolipids and polar lipids (2). There are 43 species of *Sphingobacterium*, and few are associated with human infection, with the exception of *S. spiritivorum* and *S. multivorum*. These two species are occasionally isolated from bloodstream infections, respiratory infections, cellulitis, and end-stage kidney disease (3–8). *Sphingobacterium* strain R-53603 was isolated from cellulitis of the right big toe of a female patient in Kuwait, and according to 16S rRNA gene sequence analysis, this strain is closely related to environmental strain R-53745 collected from an activated sludge isolate in Singapore. DNA-DNA hybridization and other analyses were used to provide evidence leading to the assignment of these strains to a new species, *Sphingobacterium cellulitidis* (9). Reported here are the annotated draft genome sequences for both R-53603 (the type strain for *S. cellulitidis*) and R-53745. Significantly, this is a third *Sphingobacterium* species associated with human disease.

Whole-genome sequencing of the strains was performed on an Illumina NextSeq 500 instrument using Nextera XT library preparation and paired-end 151-bp chemistry. Sequence reads were *de novo* assembled using Unicycler version 0.4 (10), with default parameters, and annotated using Prokka version 1.12 (11), with default parameters.

The characteristics of genome assembly and annotation of strains R-53603 and R-53745 are as follows: sequencing depths, 94× and 106×; sizes, 4.61 Mb and 4.40 Mb; numbers of contigs (≥ 200 bp), 32 and 51; contig N_{50} values, 438 kbp and 225 kbp; G+C contents, 37.5% and 37.4%; numbers of coding sequences (CDSs), 4,011 and 3,771; and numbers of tRNAs, 45 and 45, respectively. No antibiotic resistance genes (<http://cge.cbs.dtu.dk/services/ResFinder/>) or virulence factor genes (<http://www.mgc.ac.cn/VFs/>) were detected in the genome sequence of either *S. cellulitidis* strain.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession numbers [NOUX00000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=NOUX00000000) (strain R-53603) and [NOUY00000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=NOUY00000000) (strain R-53745). The versions described in this paper are the first versions, [NOUX01000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=NOUX01000000) and [NOUY01000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=NOUY01000000), respectively.

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Address correspondence to M. John Albert, john@hsc.edu.kw.

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