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Complete Genome Sequence of Staphylococcus pseudintermedius Type Strain LMG 22219

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Complete Genome Sequence of *Staphylococcus pseudintermedius* Type Strain LMG 22219

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ABSTRACT We report the first complete genome sequence of LMG 22219 (=ON 86[T] = CCUG 49543[T]), the *Staphylococcus pseudintermedius* type strain isolated from feline lung tissue. This sequence information will facilitate phylogenetic comparisons of staphylococcal species and other bacteria at the genome level.

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Here, we present the first complete genome sequence of LMG 22219 (=ON 86[T] = CCUG 49543[T]), the *Staphylococcus pseudintermedius* type strain isolated from lung tissue of a cat (1). *S. pseudintermedius* is a Gram-positive opportunistic bacterial pathogen (2) commonly associated with canine pyoderma and occasionally isolated from human infections (3–6). It was first defined as a unique species by Devriese et al. (1). This species is classified as a member of the *Staphylococcus intermedius* group, which also includes *S. intermedius* and *S. delphini*, as defined by Takahashi et al. (7). *S. pseudintermedius* is characterized by nonpigmented colonies surrounded by double-zone hemolysis on Columbia sheep blood agar. It is catalase-positive and coagulates rabbit plasma but is clumping-factor-negative in slide coagulase testing. *S. pseudintermedius* is positive for DNase, β-glucosidase, arginine dihydrolase, urease, nitrate reduction, pyrrolidonyl arylamidase, and ONPG (β-galactosidase). It does not produce β-glucuronidase and is susceptible to 8 μg ml^{-1} acriflavine and to novobiocin. It is also resistant to deferoxamine (1).

Whereas assays exist to differentiate *S. pseudintermedius* from other *Staphylococcus intermedius* group species, it may be misidentified in veterinary and human medicine (6, 8). Clinical treatment of infections relies upon accurate pathogen identification (9) and the availability of the complete genome for this organism may allow for genetic validation of phenotypic testing, as well as identification of new genetic targets for interspecies comparisons. Only genome sequences of *S. intermedius* and *S. delphini* (10) type strains are currently available, and consequently the elucidation of the genome sequence of the *S. pseudintermedius* type strain LMG 22219 will facilitate comparisons of different species and strains based on genetic analysis.

DNA was extracted and a library prepared using the Nextera XT library preparation kit in accordance with the manufacturer's protocol. Sequencing was performed using Illumina MiSeq version 2 (Illumina Inc., USA), and *de novo* assembly was performed using Geneious version 9.1.6 (11). Automated annotation of the assembled contigs was performed using the NCBI Prokaryote Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

A total of 1,432,416 MiSeq paired-end reads were used to generate 50 contigs with >100× average depth of coverage. The LMG 22219 genome comprises 2,523,112 bp with 37.6% GC content, 2,242 predicted coding sequences, and 81 RNAs.

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