JOURNAL OF BACTERIOLOGY, Mar. 2010, p. 1471–1472 Vol. 192, No. 5
0021-9193/10/$12.00 doi:10.1128/JB.01627-09

GENOME ANNOUNCEMENTS

Complete Genome Sequence of *Staphylococcus lugdunensis* Strain HKU09-01[▽]

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***Staphylococcus lugdunensis* is a member of the coagulase-negative staphylococci and commonly found as part of the human skin flora. It is a significant cause of catheter-related bacteremia and also causes serious infections like native valve endocarditis in previously healthy individuals. We report the complete genome sequence of this medically important bacterium.**

Staphylococcus lugdunensis is a member of the coagulase-negative staphylococci (CoNS) commonly colonizing the human skin and mucosal membranes. While the genus *Staphylococcus* contains 48 named species currently, only a few species, notably *S. aureus*, are coagulase positive. Thus, the phenotypic characteristic is routinely tested in the medical microbiological laboratory for rapid differentiation of the highly pathogenic *S. aureus* from the other staphylococci. Among the CoNS, only a few species are known to cause human disease, usually in the form of opportunistic infections only (6). However, *S. lugdunensis* is an important exception (3). Besides causing catheter-related bacteremia similar to other CoNS, it causes a variety of severe nosocomial and community-acquired infections, including native valve endocarditis, a devastating and potentially fatal disease that can affect previously healthy individuals. Another unusual feature are the susceptibilities of *S. lugdunensis* isolates to multiple antimicrobial agents even when the incidence of multiple-drug-resistant CoNS and *S. aureus* occurrences are increasing in both hospital and community settings (4, 5).

The genome sequence of *S. lugdunensis* strain HKU09-01 was determined by high-throughput sequencing performed on a GS FLX system (Roche Diagnostics, Basel, Switzerland), with approximately 45-fold coverage of the genome. This clinical strain was previously isolated from the culture of pus from a skin swab. Genome assembly was performed using the Newbler assembler, resulting in 30 large contigs (>500 bp in size). The contigs were then ordered and oriented into one scaffold using OSLay (11). The genome-finishing strategy for *S. lugdunensis* was similar to that employed for our previously sequenced *Laribacter hongkongensis* genome (12). Briefly, gap closures were performed by genomic PCR followed by DNA sequencing of amplification products on an ABI 3130xl sequencer (Applied Biosystems, CA). The finished sequence was validated by genome macrorestriction analysis using multiple rare-cutting enzymes and visualization by pulsed-field gel electrophoresis. Protein coding regions were predicted with Glimmer3 (2), and automatic genome annotation was performed on the RAST server (1). Additionally, annotation of tRNA and transfer-messenger RNA (tmRNA) genes was performed using tRNAScan-SE (10) and ARAGORN (9). Identification of rRNA genes was performed using RNAmmer (8).

The genome of *S. lugdunensis* strain HKU09-01 consists of a circular 2,658,366-bp chromosome with G+C content of 33.87%, similar to those of other staphylococci. No plasmids are present in the sequenced strain. The genome contains 61 tRNA genes for all amino acids and 2,489 predicted protein-coding genes. Eight putative genomic islands were identified, and one actually consists of a pair of duplicated 32-kb genomic regions. Similar to *Staphylococcus saprophyticus* (7), but different from the other staphylococci, the genome contains 6 rRNA operons, one of them having the unusual organization 5S-16S-23S-5S.

With the availability of the present genome sequence, *S. lugdunensis* now joins other staphylococcal species with human pathogenic potential, like *S. aureus*, *S. epidermidis*, *S. haemolyticus*, and *S. saprophyticus*, to have at least one reference genome available. Further in-depth analysis will be necessary to fully elucidate the genomic differences that may explain the variation in virulence of the staphylococcal species.

Nucleotide sequence accession number. The complete genome sequence has been deposited in NCBI GenBank under accession no. CP001837.

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▽ Published ahead of print on 4 January 2010.

We kindly acknowledge the assistance and advice provided by Nicholas J. Loman and Mark J. Pallen during genome finishing. We are grateful to the generous support of Hui Hoy and Hui Ming in the genomic sequencing platform.

This work is partly supported by the University Development Fund and Outstanding Young Researcher Award, The University of Hong

Kong, and the HKSAR Research Fund for the Control of Infectious Diseases of the Health, Welfare and Food Bureau.

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