JOURNAL OF BACTERIOLOGY, July 2011, p. 3411–3412 Vol. 193, No. 13
0021-9193/11/$12.00 doi:10.1128/JB.05135-11

Complete Genome Sequence of *Staphylococcus aureus* T0131, an ST239-MRSA-SCC*mec* Type III Clone Isolated in China▽

Yang Li,[1,2]† Boyang Cao,[2,3,4]† Yongfu Zhang,[1,2] Jiali Zhou,[2,3] Bin Yang,[1,2] and Lei Wang[1,2,4]*

Key Laboratory of Molecular Microbiology and Technology, Ministry of Education, People's Republic of China[1]; TEDA School of Biological Sciences and Biotechnology, Nankai University, 23 Hongda Street, TEDA, Tianjin 300457, People's Republic of China[2]; Tianjin Key Laboratory of Microbial Functional Genomics, Tianjin 300457, People's Republic of China[3]; and Tianjin Biochip Corporation, 23 Hongda Street, TEDA, Tianjin 300457, People's Republic of China[4]

Received 22 April 2011/Accepted 27 April 2011

We report here the complete genome sequence of *Staphylococcus aureus* T0131, which is a multiresistant clinical isolate recovered in China and the first sequenced epidemic ST239-MRSA-SCC*mec* type III strain obtained in Asia. Comparison with two published genomes of ST239 reveals the polymorphism among strains of this type from different continents.

Staphylococcus aureus is a ubiquitous bacterial pathogen and a leading cause of morbidity and mortality worldwide. The epidemiology of infections is influenced by rapid and widespread emergence of multidrug-resistant methicillin-resistant *S. aureus* (MRSA). ST239-MRSA-SCC*mec* type III is considered to be an epidemic strain of hospital-associated MRSA and is prevalent all over the world (2, 8, 10). *S. aureus* strain T0131, an ST239-MRSA-SCC*mec*III isolate, was recovered from an 87-year-old patient in 2006.

Whole-genome sequencing of *S. aureus* strain T0131 was performed with a combined strategy of 454 sequencing (11) and Solexa sequencing technology (1). A genomic library containing 8-kb inserts was constructed and 368,922 paired-end reads were generated using the GS FLX system, giving 27.3-fold coverage of the genome. Then, 94.0% of the reads were assembled into 10 scaffolds totaling 2.9 Mbp using Newbler version 2.3 (454 Life Sciences, Branford, CT). A total of 9,132,826 reads (2.1-kb library) were generated to reach a depth of 313-fold coverage with an Illumina Solexa Genome Analyzer IIx and mapped to the scaffolds using the Burrows-Wheeler alignment (BWA) tool (9). Gap closure was performed by sequencing PCR products using an ABI 3730 capillary sequencer. Prediction and annotation were performed as described previously (4).

The complete genome of *S. aureus* strain T0131 contains a single circular chromosome of 2,913,900 bp, with a GC content of 32.8% and no extrachromosomal elements. In all, 2,711 protein-encoding genes, 54 tRNA-encoding genes, 6 rRNA operons, and an SCC*mec*III were detected. Analyzing the seven housekeeping genes using the MLST database (http://www.mlst.net) confirmed T0131 as a member of the ST239 complex. Over 76% of genes were assigned to specific Clusters of Orthologous Groups (COG) functional groups, and 52% were assigned an enzyme classification number.

Comparison with the other two published genomes of *S. aureus* ST239 strains, JKD6008 (SCC*mec*III, NCBI GenBank accession number CP002120) and TW20 (SCC*mercury*, EMBL accession number FN433596), revealed that T0131 and JKD6008 share the highest average nucleotide identity, at 99.95%, and JKD6008 and TW20 share the lowest, at 99.89%. TW20 has two plasmids which are absent in the SCC*mec*III strains. T0131 shares 2,603 orthologous coding sequences (CDSs) with JKD6008 and 2,573 CDSs with TW20. T0131 has 85 specific genes compared with the other two genomes, and 65 of them form five pathogenic islands. It is worth noting that two copies of exfoliative toxin-encoding genes are present in two of the five pathogenic islands (13). T0131 possesses 21 copies of IS*256* found in JKD6008, as well as three sets of Tn*554* and a Tn*552* found in TW20. It also has 25 other types of IS elements and four sets of transposons. A locus containing a lantibiotic synthesis gene cluster (3) and a restriction modification system (12) was found in T0131 and TW20 but was absent in JKD008. JKD6008 harbors an integrated pSK1-like plasmid which is absent in the other two (6, 7). Strains JKD6008, TW20, and T0131 were isolated in New Zealand (6), England (5), and China, respectively, and the result indicated that the polymorphisms among ST239 strains are of different continental origins.

Nucleotide sequence accession number. The complete genome sequence has been deposited in NCBI GenBank under accession number CP002643.

This work was supported by the Chinese National Science Fund for Distinguished Young Scholars (30788001), the National 863 Program (2010AA10A203), the National 973 program of China grant 2009CB522603 and 2011CB504900, the National Natural Science Foundation of China (NSFC) Key Program Grant (31030002), and National Key Programs for Infectious Diseases of China 2009ZX10004-108.

* Corresponding author. Mailing address: TEDA School of Biological Sciences and Biotechnology, Nankai University, 23 Hongda St., TEDA, Tianjin 300457, China. Phone: 86-22-66229588. Fax: 86-22-66229596. E-mail: wanglei@nankai.edu.cn.

† The first two authors contributed equally to this paper.

▽ Published ahead of print on 6 May 2011.

REFERENCES

1. **Bentley, D. R., et al.** 2008. Accurate whole human genome sequencing using reversible terminator chemistry. Nature **456:**53–59.
2. **Chongtrakool, P., et al.** 2006. Staphylococcal cassette chromosome *mec* (SCC*mec*) typing of methicillin-resistant *Staphylococcus aureus* strains isolated in 11 Asian countries: a proposal for a new nomenclature for SCC*mec* elements. Antimicrob. Agents Chemother. **50:**1001–1012.

3. **Daly, K. M., et al.** 2010. Production of the Bsa lantibiotic by community-acquired *Staphylococcus aureus* strains. J. Bacteriol. **192:**1131–1142.
4. **Feng, L., et al.** 2008. A recalibrated molecular clock and independent origins for the cholera pandemic clones. PLoS One **3:**e4053.
5. **Holden, M. T., et al.** 2010. Genome sequence of a recently emerged, highly transmissible, multi-antibiotic- and antiseptic-resistant variant of methicillin-resistant *Staphylococcus aureus*, sequence type 239 (TW). J. Bacteriol. **192:** 888–892.
6. **Howden, B. P., et al.** 2010. Complete genome sequence of *Staphylococcus aureus strain* JKD6008, an ST239 clone of methicillin-resistant *Staphylococcus aureus* with intermediate-level vancomycin resistance. J. Bacteriol. **192:** 5848–5849.
7. **Jensen, S. O., et al.** 2010. Analysis of the prototypical *Staphylococcus aureus* multiresistance plasmid pSK1. Plasmid **64:**135–142.
8. **Ko, K. S., et al.** 2005. Distribution of major genotypes among methicillin-resistant *Staphylococcus aureus* clones in Asian countries. J. Clin. Microbiol. **43:**421–426.
9. **Li, H., and R. Durbin.** 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics **25:**1754–1760.
10. **Liu, Y., et al.** 2009. Molecular evidence for spread of two major methicillin-resistant *Staphylococcus aureus* clones with a unique geographic distribution in Chinese hospitals. Antimicrob. Agents Chemother. **53:**512–518.
11. **Margulies, M., et al.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437:**376–380.
12. **Waldron, D. E., and J. A. Lindsay.** 2006. SauI: a novel lineage-specific type I restriction-modification system that blocks horizontal gene transfer into *Staphylococcus aureus* and between *S. aureus* isolates of different lineages. J. Bacteriol. **188:**5578–5585.
13. **Watanabe, T., et al.** 2000. Cloning of the gene coding for *Staphylococcus hyicus* exfoliative toxin B and its expression in *Escherichia coli*. J. Bacteriol. **182:**4101–4103.