

Complete Genome Sequence of Linezolid-Susceptible *Staphylococcus haemolyticus* Sh29/312/L2, a Clonal Derivative of a Linezolid-Resistant Clinical Strain

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We report the whole-genome sequence (WGS) of an *in vitro* susceptible derivative revertant mutant from a bloodstream isolate involved in a nosocomial outbreak in Brazil. The WGS comprises 2.5 Mb with 2,500 protein-coding sequences, 16rRNA genes, and 60 tRNA genes.

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Staphylococcus haemolyticus, a commensal coagulase-negative staphylococcus (CoNS) species from the human skin microbiota, has also been increasingly associated with nosocomial infections and resistance to multiple antimicrobials (1, 2). We report the whole-genome sequence of *S. haemolyticus* strain Sh29/312/L2, which is an *in vitro* susceptible derivative from a bloodstream isolate of a linezolid-resistant *S. haemolyticus* clinical strain, Sh29/312. Sh29/312/L2 was isolated on day 7 from serial passages on antibiotic-free Mueller Hinton agar when the linezolid minimum inhibitory concentration (MIC) of Sh29/312 decreased from 64 to 1 µg/mL.

Genome sequencing was performed using the Ion Torrent PGM platform (Life Technologies) and 400-bp kit. The sequences were *de novo* assembled using Mira version 4.0.2 and SPAdes version 3.1.1. The scaffold was obtained using CLC Genomics Workbench version 7.5 and Geneious version 8.0.5 with the genome reference *S. haemolyticus* strain JCSC1435 (GenBank accession number AP006716.1) (3). The genome was annotated with Prokka (4) and curated using Artemis software (5).

The sequence analysis showed that *S. haemolyticus* strain Sh29/312/L2 has 2,561,368 bp with 2,417 protein-coding sequences, 16 rRNA genes, 60 tRNA genes, 39 pseudogenes, and 32.72% GC content. Sh29/312/L2 also harbors one intact and other incomplete phages.

The sequence of the *S. haemolyticus* Sh29/312/L2 genome will provide a reference for a comparative genome analysis with its ancestral linezolid-resistant *S. haemolyticus* clinical strain, which has some resistance mechanism other than those known target-site modifications that promote elevated MIC for linezolid. This research will help provide insight to the genomic background of an important CoNS species. After the important work of Takeuchi and colleagues (3), no whole-genome sequence of *S. haemolyticus* has yet been reported.

Nucleotide sequence accession number. The whole-genome sequence of *S. haemolyticus* strain Sh29/312/L2 has been deposited in DDBJ/ENA/GenBank under the accession number CP011116.

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Genomic DNA of *S. haemolyticus* strain Sh29/312/L2 was sequenced on the Ion Torrent PGM platform at the Section of Microbiology, Fleury Institute, São Paulo, Brazil.

REFERENCES

- Potoski BA, Adams J, Clarke L, Shutt K, Linden PK, Baxter C, Pasculle AW, Capitano B, Peleg AY, Szabo D, Paterson DL. 2006. Epidemiological profile of linezolid-resistant coagulase-negative staphylococci. *Clin Infect Dis* 43:165–171. <http://dx.doi.org/10.1086/505114>.
- Tewhey R, Gu B, Kelesidis T, Charlton C, Bobenchik A, Hindler J, Schork NJ, Humphries RM. 2014. Mechanisms of linezolid resistance among coagulase-negative staphylococci determined by whole-genome sequencing. *mBio* 5:e00894-14. <http://dx.doi.org/10.1128/mBio.00894-14>.
- Takeuchi F, Watanabe S, Baba T, Yuzawa H, Ito T, Morimoto Y, Kuroda M, Cui L, Takahashi M, Ankaï A, Baba S, Fukui S, Lee JC, Hiramatsu K. 2005. Whole-genome sequencing of *Staphylococcus haemolyticus* uncovers the extreme plasticity of its genome and the evolution of human-colonizing staphylococcal species. *J Bacteriol* 187:7292–7308. <http://dx.doi.org/10.1128/JB.187.21.7292-7308.2005>.
- Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <http://dx.doi.org/10.1093/bioinformatics/btu153>.
- Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B, Barrell B. 2000. Artemis: sequence visualization and annotation. *Bioinformatics* 16:944–945. <http://dx.doi.org/10.1093/bioinformatics/16.10.944>.