

Draft Genome Sequence of Linezolid-Resistant *Enterococcus faecalis* Clinical Isolate HS0914

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We report the draft genome sequence of linezolid-resistant *Enterococcus faecalis* strain HS-0914 isolated from a teaching hospital in Shanghai, China. The draft genome sequence is composed of 61 contigs for 2,816,079 bp. Ribosomal RNA mutations and *cfr*, which mediates linezolid resistance, are not present.

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Enterococcus faecalis is one of the most common causes of opportunistic infections. *E. faecalis* HS0914 was isolated from a urine sample collected from a patient at a teaching hospital in Shanghai, China. The clinical isolate was resistant to linezolid (MIC 32 mg/liter), although the patient had never been exposed to it. Five point mutations in the 23S rRNA (G2576T, U2500, G2447UA, C254U, and G2603U) and ribosomal protein (L3 and L4) genes could lead to linezolid resistance in Gram-positive cocci (1–3). The multidrug-resistant gene, *cfr*, could also result in linezolid resistance (4). However, neither the mutations previously reported nor the *cfr* gene was found in the linezolid-resistant clinical isolate HS0914 by PCR and Sanger sequencing. Whole-genome sequencing of the linezolid-resistant isolate could reveal novel mechanisms of linezolid resistance. In this paper, we describe the draft genome sequence of the linezolid-resistant isolate HS0914.

Genomic DNA was prepared using the QIAamp DNA MiniKit (Qiagen). Genome sequencing was performed using Illumina HiSeq 2000 technology (Illumina, Inc.). A total of 38,235,708 paired-end reads (insert size 300 bp) were obtained. BWA was used to filter the raw data for high quality (raw data: 3,861,806,508 bp, clean data: 3,670,009,615 bp) (5). Adaptor-free reads were used for assembly with SOAPdenovo (v1.05) (6). The final assembly contains 61 contigs, with a total size of 2,816,079 bp and an N_{50} contig length of 105,150 bp. The lengths of the contigs ranged from 236 bp to 452,383 bp, with a G+C mol% of 37.3%. The DNA sequences were annotated using GeneMark.hmm for Prokaryotes (7). The draft genome contains 3,023 genes, with 2,963 protein-coding genes and 63 structural RNAs.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JPDQ000000000](https://www.ncbi.nlm.nih.gov/nuccore/JPDQ000000000). The version described in this paper is version [JPDQ010000000](https://www.ncbi.nlm.nih.gov/nuccore/JPDQ010000000).

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