Genome Sequence of *Aerococcus viridans* LL1

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Aerococcus viridans is a catalase-negative Gram-positive bacterium and has been described as an airborne organism widely distributed in the hospital environment or in clinical specimens. We isolated *A. viridans* strain LL1 from indoor dust samples collected by a patient. Here, we prepared a genome sequence for this strain consisting of 31 contigs totaling 1,994,039 bases and a GC content of 39.42%.

Aerococcus viridans is described as an airborne organism prevalent in occupied rooms and has been reported to cause infective endocarditis, spondylodiscitis, and urinary tract infection (3, 9, 10). It is an organism having many characteristics that might cause it to be confused with streptococci or staphylococci (5). Here, we isolated *A. viridans* strain LL1 from indoor dust samples collected by a patient. The isolate was identified with the MicroFlex LT instrument (Bruker Daltonics) according to the manufacturer's suggested recommendations. Spectra were analyzed by Flexcontrol 3.0 software and the Biotyper 2.0 database (Bruker Daltonics) (11).

The sample was prepared for sequencing by growing the *A. viridans* LL1 strain aerobically overnight at 37°C in Mueller-Hinton broth (Oxoid, United Kingdom). Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Germany) according to the manufacturer's recommended protocol. The quantity of DNA obtained was determined using a Nanodrop spectrophotometer and Cubit. Typically, 5 µg of DNA was then sent to the State Key Laboratory for Diagnosis and Treatment of Infectious Disease at Zhejiang University for sequencing on a HiSeq2000 (Illumina, CA) sequencer.

Here, we present the whole genome sequence of *A. viridans* LL1, obtained using a whole-genome shotgun strategy by Illumina HiSeq2000 (totaling ~4,220,218 Mb; ~2,000-fold coverage of the genome). The Illumina paired-end reads were *de novo* assembled by Velvet (13). We obtained 31 contigs (length, >500 bp). The N_{50} of contig length is 239,692 bp.

The annotation was done by Glimmer (2) to predict the open reading frame (ORF), tRNAscan-SE 1.21 (7) to find tRNA, RNAmmer 1.2 (6) to search rRNA, and Tandem Repeats Finder 4.04 (1) to find 47 tandem repeat sequence in all contigs. In addition, the contigs were searched against the KEGG (4) and COGs (12) to annotate the genome. The draft genome includes 1,994,039 bases and contains 1,737 predicted coding sequences (CDSs), with a G+C content of 39.42%. There are single-copy genes predicted for 16S and 23S rRNA, 4 duplicated genes predicted for 5S rRNA, and 56 copies for tRNAs. An estimated 84.86% of 1,692,321 nucleotides are predicted to encode proteins. A total of 1,211 CDSs annotated by COGs can be classified into an extended 63 COG categories, including 986 COGs, and 761 CDSs can be annotated into 691 KEGG orthology by using KAAS (8).

In the NCBI database, the genome of *A. viridans* ATCC 11563 has been generated by the Human Genome Sequencing Center at Baylor College of Medicine as part of the Human Microbiome Project using 454 pyrosequencing technology. The genome assembly result of *A. viridans* LL1 is better than that of *A. viridans* ATCC 11563, and we are working on connecting the contigs together to reach a complete genome map and then do a comparison study between these two strains.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. [AJTG00000000](https://www.ncbi.nlm.nih.gov/nuclot/AJTG00000000). The version described in this paper is the first version, AJTG01000000.

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