

Draft Genome Sequence of *Streptococcus agalactiae* Serotype Ia Strain M19, a Multidrug-Resistant Isolate from a Cow with Bovine Mastitis

Feng Yang, Hongsheng Li, Shidong Zhang, Xurong Wang

Lanzhou Institute of Husbandry and Pharmaceutical Sciences of Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, People's Republic of China

***Streptococcus agalactiae* is a major contagious pathogen causing bovine mastitis worldwide. We report here the draft sequence of *S. agalactiae* Ia strain M19, a multidrug-resistant isolate from a bovine mastitis case in Ningxia Hui autonomous region, China.**

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Address correspondence to Xurong Wang, wxurong@126.com.

Streptococcus agalactiae is a major contagious pathogen causing bovine mastitis, which may have a substantial impact on the quantity and quality of produced milk (1). This bacterium is classified into 10 serotypes based on the antigenic diversity in the capsular polysaccharide (2). Strains of serotypes Ia and II are the most commonly encountered in bovine mastitis in China (data not shown). Here, we report the draft genome sequence of *S. agalactiae* Ia strain M19, a multidrug-resistant isolate from a cow with bovine mastitis in Ningxia Hui autonomous region, China.

The draft genome sequence of *S. agalactiae* strain M19 was performed using Illumina HiSeq 2000 sequencing platform at the Beijing Genomics Institute (BGI) (Shenzhen, China). Draft assemblies were based on 382-Mb clean data. All reads provided about 177-fold coverage of the genome. The paired-end reads were assembled into four contigs in three scaffolds with the SOAPdenovo program (3, 4). Putative open reading frames were predicted using Glimmer (5). Tandem repeats were selected using Tandem Repeat Finder (6). tRNAs and rRNAs were identified using tRNAscan-SE (7) and RNAmmer (8), respectively. The functions of encoding genes were annotated by using the NCBI nr, Kyoto Encyclopedia of Genes and Genomes (KEGG), and Cluster of Orthologous Groups of proteins (COG), as well as the Antibiotic Resistance Genes Database (ARDB).

The circular chromosome of *S. agalactiae* M19 is composed of 2,111,437 nucleotides with an overall G+C content of 35.61%. It contains 2,056 coding sequences (CDSs) that account for 88.45% of the genome, 1,707 of which (83.0%) were annotatable with known proteins with biological function or a functional domain and 349 of which (17.0%) were annotated as conserved hypothetical proteins. The genome also harbors 68 tandem repeat sequences, including loci for 34 minisatellite DNAs and 3 microsatellite DNAs, as well as 57 tRNAs and 15 rRNAs. ARDB annotated 11 genes conferring resistance to chloramphenicol (one), vancomycin (four), bacitracin (three), tetracycline (one), penicillin (one), and multidrug resistance to ciprofloxacin and norfloxacin (one).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [LKPA01000000](https://www.ncbi.nlm.nih.gov/nuclink/LKPA01000000) with the scaffold accession number [KV757177](https://www.ncbi.nlm.nih.gov/nuclink/KV757177).

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