

Complete Genome Sequence of *Streptococcus agalactiae* ZQ0910, a Pathogen Causing Meningoencephalitis in the GIFT Strain of Nile Tilapia (*Oreochromis niloticus*)

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***Streptococcus agalactiae* (group B streptococcus [GBS]) is a pathogen that causes meningoencephalitis in Nile tilapia (*Oreochromis niloticus*). Here, we reported the complete genome sequence of *S. agalactiae* strain ZQ0910, which was isolated from the GIFT strain of Nile tilapia in Guangdong, China.**

Streptococcus agalactiae (Lancefield group B; group B streptococcus [GBS]) is an important pathogen frequently associated with meningoencephalitis in fish (7). In aquaculture, *S. agalactiae* is an emerging pathogen that has been associated with considerable morbidity and mortality in fish farms worldwide (5, 6, 12, 14). *S. agalactiae* has been associated with illness in many other hosts, such as mastitis in cows and neonatal meningitis in humans. However, almost all studies have been conducted with *S. agalactiae* isolated from cows and humans. Until now, little was known about *S. agalactiae* isolated from Nile tilapia (*Oreochromis niloticus*). The *S. agalactiae* strain, ZQ0910, which was isolated from diseased fish in Guangdong Province, China, was chosen for sequencing.

The draft genome sequence of *S. agalactiae* strain ZQ0910 was determined using Illumina Genome Analyzer II (GAII) at the Beijing Genomics Institute (BGI) (Shenzhen, China). Draft assemblies were based on 500-Mb reads. All reads provided about 98-fold coverage of the genome. The GAI paired-end reads were assembled into 54 contigs in 14 scaffolds with the SOAPdenovo program. Gaps were closed by primer walking and sequencing of PCR products. Putative open reading frames with more than 30 amino acid residues were predicted using Glimmer 3.0 (4). tRNAs and rRNAs were identified using tRNAscan-SE (10) and RNAmmer (9), respectively. The scaffolds were searched against the KEGG (Kyoto Encyclopedia of Genes and Genomes) and COG (Clusters of Orthologous Groups) databases to annotate the gene descriptions.

The genome of strain ZQ0910 contains 1,814,715 nucleotides and has a GC content of 36.02%. There are 2,022 coding sequences (CDSs) that account for 89.18% of the genome, 28 tRNAs, 1 rRNA loci.

It has been thought that capsular polysaccharides (CPS) elicit protective immunity for the virulence of the bacterium and serve as an antigen to identify the serotype. CpsB to CpsJ, CpsL, and CpsM genes were also found in the *cps* locus of the ZQ0910 genome, which may play a common role in different serotypes (2). CDSs for a few virulence-associated factors, such as fibronectin/fibrinogen-binding protein (8, 15), Sip protein (1), sortase A (13), serine peptidase (HtrA) (11), and ATP-binding cassette (ABC) transporters (3), which have been confirmed to contribute to the virulence of *S. agalactiae*, were also found in the genome of ZQ0910. Learning more about these factors would strengthen our understanding of the virulence of *S. agalactiae* strain ZQ0910, and

analysis of the complete genome sequence of *S. agalactiae* strain ZQ0910 will open new avenues for the identification of novel potential vaccine targets.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [AKAP00000000](https://www.ncbi.nlm.nih.gov/nuccore/AKAP00000000). The version described in this paper is the first version and has been assigned accession number [AKAP01000000](https://www.ncbi.nlm.nih.gov/nuccore/AKAP01000000).

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