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Unveiling Complete Genome of *Streptococcus agalactiae* from Malaysian Aquaculture: A Closer Look at Molecular Characteristics and Phylogenomic

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Abstract

Streptococcus agalactiae (Group B *Streptococcus*, GBS) is a significant pathogen in aquaculture worldwide and is responsible for high mortality in farmed fish. Despite its regional impact, complete genome data from Malaysian isolates remain scarce. In this study, we report the first complete genome of a Malaysian *S. agalactiae* isolate, SA2BKE, derived from infected tilapia. Using Oxford Nanopore long-read sequencing, we assembled a 2.03 Mb circular complete genome of *S. agalactiae*. The functional annotation revealed 1,970 protein-coding genes and 108 RNA genes. Several antimicrobial resistance genes, including *tet(M)*, *mreA*, and *mprF*, are associated with resistance to tetracyclines, macrolides, and peptides, respectively. Notably, there are 15 virulence-associated proteins involved in cell wall/membrane/envelope biogenesis. Multilocus sequence typing (MLST) identified SA2BKE as sequence type ST283, which has the potential to infect both fish and humans. Comparative phylogenomic analysis revealed 215 global strains positioned SA2BKE within a clade of other ST283 isolates from Asia and South America, suggesting potential transregional transmission. Pan-genome analysis identified 555 core genes shared among the analysed genomes, highlighting substantial genomic diversity within the species. Additionally, 14 mobile genetic element-associated regions were detected in SA2BKE, indicating potential

genome plasticity and horizontal gene transfer events. These findings expand the genomic reference data for *S. agalactiae* isolates from Malaysia, contributing to regional surveillance efforts across Southeast Asia and supporting integrated disease management strategies in aquaculture. © The Author(s), under exclusive licence to Springer Science+Business Media, LLC, part of Springer Nature 2026.

Author keywords

Multilocus sequence typing (MLST); Phylogenomics; *Streptococcus agalactiae*; Whole-genome sequencing (WGS)

Indexed keywords

MeSH

Animals; Aquaculture; Drug Resistance, Bacterial; Fish Diseases; Genome, Bacterial; Malaysia; Multilocus Sequence Typing; Phylogeny; Streptococcal Infections; *Streptococcus agalactiae*; Tilapia; Whole Genome Sequencing

Regional Index

Malaysia

Engineering controlled terms

Aquaculture; Gene transfer; Genes; Genome; Proteomics

Engineering uncontrolled terms

Complete genomes; Group B *Streptococcus*; Malaysians; Molecular characteristics; Multi-loci sequence typing; Multilocus sequence typing; Phylogenomics; *Streptococcus agalactiae*; Whole genome sequencing; Whole-genome sequencing

GEOBASE Subject Index

aquaculture; bacterium; comparative study; genome; molecular analysis; protein; RNA

EMTREE medical terms

animal; antibiotic resistance; aquaculture; bacterial genome; fish disease; genetics; isolation and purification; Malaysia; microbiology; multilocus sequence typing; pathogenicity; phylogeny; *Streptococcus agalactiae*; *Streptococcus* infection; Tilapia; veterinary medicine; whole genome sequencing

Engineering main heading

Fish

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