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agalactiae from Malaysian Aquaculture: A Closer Look at Molecular Characteristics and Phylogenomic

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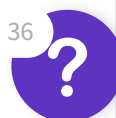
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Abstract	Streptococcus agalactiae (Group B Streptococcus, GBS) is a significant pathogen in aquaculture worldwide and is responsible for high mortality in farmed fish. Despite its regional impact, complete genome data from Malaysian isolates remain scarce. In this study, we report the first complete genome of a Malaysian <i>S. agalactiae</i> isolate, SA2BKE, derived from infected tilapia. Using Oxford Nanopore long-read sequencing, we assembled a 2.03 Mb circular complete genome of <i>S. agalactiae</i>. 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 <i>S. agalactiae</i> isolates from Malaysia, contributing to regional surveillance efforts across Southeast Asia and supporting integrated disease management strategies in aquaculture.
Keywords	Author Keywords: Streptococcus agalactiae; Whole-genome sequencing (WGS); Multilocus sequence typing (MLST); Phylogenomics Keywords Plus: SEQUENCE TYPE 283; GOLDEN POMPAÑO; FISH; OUTBREAK; INFECTION; IDENTIFICATION; CONSUMPTION; PATHOGEN
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Data availability statement

The data supporting the findings of this study are available within the article and further inquiries can be directed to the corresponding author.

Conflict of interest statement

The authors declare no competing interests.

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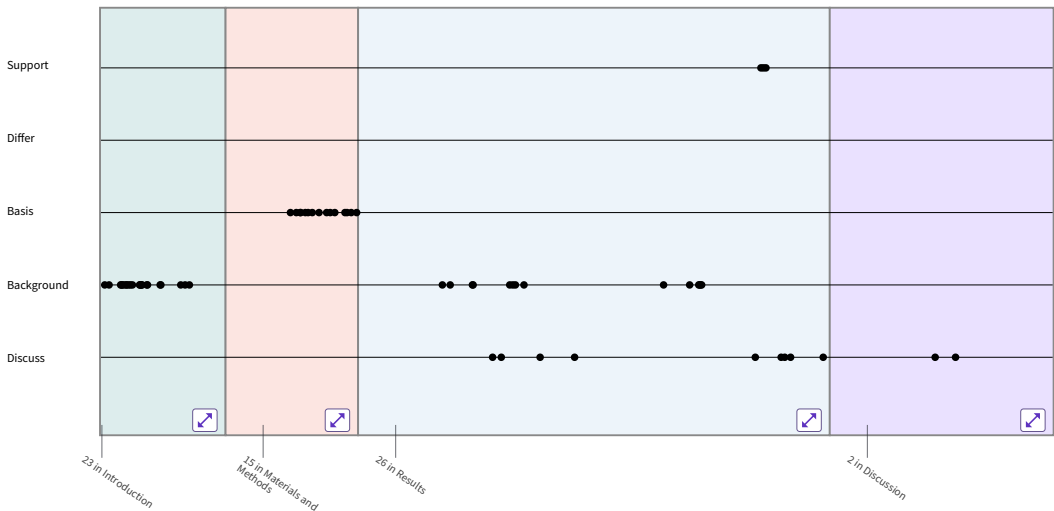
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