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GENOME ANNOUNCEMENT

Draft Genome Sequence of a Nonhemolytic Fish-Pathogenic *Streptococcus agalactiae* Strain

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***Streptococcus agalactiae* is a significant Gram-positive bacterial pathogen of terrestrial and aquatic animals. A subpopulation of nonhemolytic strains which appear to be pathogenic only for poikilotherms exists. We report here the first draft genome sequence of a nonhemolytic *S. agalactiae* isolate recovered from a diseased fish.**

Streptococcus agalactiae is a Gram-positive bacterium that can cause a variety of diseases in a wide range of host species, including humans, cattle, and fish (5, 7, 8). To date, 3 complete genome sequences and 7 draft genome sequences of *S. agalactiae* have been made publicly available (3, 10, 12, 13); these include 8 isolates of human origin and 2 of bovine origin. Significantly, comparative analysis of these sequences has permitted the identification of virulence determinants and genes involved in host adaptation (1, 10).

The *S. agalactiae* STIR-CD-17 genome is the first submission to NCBI of a nonhemolytic strain isolated from fish. The strain was isolated from the heart of a moribund fish during a disease outbreak affecting farmed tilapia (*Oreochromis* sp.) in Honduras in 2008 and was selected for further analysis based on the outcome of epidemiological, phenotypic, and genotypic characterization (C. M. J. Delannoy, M. Crumlish, M. C. Fontaine, J. Pollock, G. Foster, M. Dagleish, J. F. Turnbull, and R. N. Zadoks, submitted for publication). The strain is nonhemolytic and belongs to serotype Ib. Based on multilocus sequence typing (MLST) (4), it belongs to the sequence type (ST) 260 and clonal complex (CC) 552, corresponding to a cluster of nonhemolytic strains that have been associated exclusively with disease in aquatic poikilotherms (2). Moreover, based on a standardized 3-set genotyping analysis (6), STIR-CD-17 is negative for all surface protein genes and mobile genetic elements screened, further supporting that it is not closely related to other described *S. agalactiae* strains of human or bovine origin. Experimental intraperitoneal infection of tilapia also revealed that STIR-CD-17 is highly pathogenic for fish (our unpublished data).

Genome sequencing was performed with an Illumina Solexa Genome Analyzer at the GenePool sequencing core facility (University of Edinburgh). *De novo* assembly of Solexa reads was achieved using Velvet 0.6 (14), and the resulting 96 contigs were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (9).

The draft genome contains 1,805,303 bp, with an average G+C content of 35%. Altogether, a total of 1,697 protein-encoding genes were predicted, with 505 (29.8%) being annotated as hypothetical proteins. In addition, 102 pseudogenes, in which frameshift and nonsense mutations introduce multiple stop codons throughout the gene, were identified. The predicted genes were sorted on the basis of clusters of orthologous groups (COG) classification (11). A total of 352 (20.7%) genes were associated with information storage and processing, 268 (15.8%) were associated with cellular processes and signaling, and 548 (32.3%) were associated with metabolism. Finally, 529 (31.2%) residual genes, which were not able to be categorized into COG classes, have poorly characterized functions and features. We anticipate that the comparison of the STIR-CD-17 genome with other published *S. agalactiae* genomes from strains of bovine and human origin will provide further insights into the molecular basis of the host adaptation and pathogenicity of this important bacterial pathogen.

Nucleotide sequence accession number. The draft genome sequence of *S. agalactiae* STIR-CD-17 has been deposited in GenBank under the accession number ALXB00000000.

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