



Draft Genome Sequence of *Francisella noatunensis* subsp. *orientalis* STIR-GUS-F2f7, a Highly Virulent Strain Recovered from Diseased Red Nile Tilapia Farmed in Europe

José Gustavo Ramírez-Paredes,^a Pär Larsson,^{b,*} Stefanie Wehner,^a Michaël Bekaert,^a Caroline Öhrman,^b Matthijs Metselaar,^c Kimberly Dawn Thompson,^d Randolph Harvey Richards,^a David James Penman,^a Alexandra Adams^a

Institute of Aquaculture, Faculty of Natural Sciences, University of Stirling, Stirling, United Kingdom^a; Swedish Defence Research Agency (FOI), CBRN Defence and Security, Umeå, Sweden^b; The Fish Vet Group, Inverness, United Kingdom^c; Aquaculture Research Group, Moredun Research Institute, Edinburgh, United Kingdom^d

ABSTRACT A highly virulent strain of *Francisella noatunensis* subsp. *orientalis*, STIR-GUS-F2f7, was isolated from moribund red Nile tilapia (*Oreochromis niloticus*) farmed in Europe. In this communication, the complete genome sequencing of this bacterium is reported.

Francisella noatunensis subsp. *orientalis* is a Gram-negative, nonmotile, nonsporulating, aerobic, intracellular, fastidious, and pleomorphic coccobacillus (size, 0.2 to 1.7 μm) associated with systematic granulomatous disease in tropical farmed and ornamental fish, for which currently no prophylactic treatment exists (1). In November 2012, a highly virulent strain of *F. noatunensis* subsp. *orientalis*, STIR-GUS-F2f7, was recovered from diseased red Nile tilapia (~10 g/5.5 cm) farmed in a recirculating system in Europe, where mortality rates were around 60% (2).

The genomic DNA of STIR-GUS-F2f7 was extracted as outlined by Seward et al. (3). The purity and concentration of the DNA were assessed by electrophoresis using a 1% agarose gel stained with ethidium bromide at 0.001%, and 260/280-to-260/230 ratios were determined using a NanoDrop ND1000 (Thermo Scientific, DE). The final DNA concentration was adjusted to 2 μg and assessed with a Qubit 2.0 fluorometer (Invitrogen Life Technologies, Inc., CA). Libraries were prepared from 1 μg of DNA with the TruSeq 100-bp cycle paired-end DNA sample prep kit, and the genome was sequenced using the HiSeq 2500 platform (Illumina, CA, USA) with version 3 sequence chemistry. The parallel paired-end sequence assembler ABySS version 1.3.5 (4) was used for *de novo* assembly, which resulted in a total of 10 contigs, all of which had a length longer than 200 bp, an N_{50} of 482,249 bp, and a coverage of 11 \times . The genome of STIR-GUS-F2f7 consists of 1,887,094 bp, with no plasmids and a G+C content of 32.4%. RNAmmer version 1.2 (5) predicted 19 copies of rRNA genes: seven 5S and six of 16S and 23S. The genome annotation performed with the NCBI Prokaryotic Genome Annotation Pipeline version 3.1 (6) predicted a total of 1,892 genes, of which 1,451 were protein-coding sequences, 45 were tRNA, four were noncoding RNAs (ncRNA), and 373 were pseudogenes. Of the protein-coding genes, the RAST server (7) predicted 239 as being involved in protein metabolism; 199 in the synthesis of amino acids and derivatives; 122 in carbohydrate catabolism; 116 in cofactors, vitamins, prosthetic groups, or pigment production; 100 in RNA metabolism; 95 in fatty acid, lipid, and isoprenoid synthesis; 82 in DNA metabolism; 79 in respiration; 74 in capsule and cell

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Address correspondence to José Gustavo Ramírez-Paredes, jgr1@stir.ac.uk.

* Present address: Pär Larsson, Laboratory Medicine, Clinical Genetics/Pathology, Umeå University Hospital, Umeå, Sweden.

wall synthesis; 71 in stress response; 59 in nucleoside and nucleotide synthesis; 54 in membrane transport; 32 in virulence, disease, and defense mechanisms; 24 in cell division and cell cycle; 17 in potassium metabolism; 16 in regulation and cell signaling; 11 in phosphorus metabolism; 10 in iron acquisition and metabolism; 10 in sulfur metabolism; six in the metabolism of aromatic compounds; five in secondary metabolism; five in nitrogen metabolism; one in dormancy; and 34 as miscellaneous proteins.

At present, no *F. noatunensis* subsp. *orientalis* genomes from Europe are available in public databases. The genome sequence of STIR-GUS-F2f7 will facilitate comparative analyses with less virulent *F. noatunensis* subsp. *orientalis* strains from different geographical origins.

Accession number(s). This whole-genome assembly has been deposited at DDBJ/EMBL/GenBank databases under the BioProject PRJNA297804. The genome accession number is [LTDO00000000](https://www.ncbi.nlm.nih.gov/assembly/LTDO00000000/), and the version described in this paper is LTDO01000000. The raw sequences have been submitted to the Sequence Read Archive (SRA) database under the accession number SRP080830.

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