



Complete Genome Sequence of *Francisella endociliophora* Strain FSC1006, Isolated from a Laboratory Culture of the Marine Ciliate *Euplotes raikovi*

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A strain of *Francisella endociliophora* was isolated from a laboratory culture of the marine ciliate *Euplotes raikovi*. Here, we report the complete genome sequence of the bacterial strain FSC1006 (*Francisella* Strain Collection, Swedish Defence Research Agency, Umeå, Sweden).

Received 13 October 2014 Accepted 17 October 2014 Published 26 November 2014

Citation Sjödin A, Öhrman C, Bäckman S, Lärkeryd A, Granberg M, Lundmark E, Karlsson E, Vallesi A, Tellgren-Roth C, Stenberg P, Thelaus J. 2014. Complete genome sequence of *Francisella endociliophora* strain FSC1006, isolated from a laboratory culture of the marine ciliate *Euplotes raikovi*. Genome Announc. 2(6):e01227-14. doi:10.1128/ genomeA.01227-14.

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n 2011, Schrallhammer and colleagues (1) published a 16S RNA gene sequence from a bacterium associated with the marine ciliate Euplotes raikovi that was phylogenetically positioned within the genus Francisella and described as "Candidatus F. noatunensis subsp. endociliophora subsp. nov." (1). The genus Francisella includes several species with little genetic variation but with diverse environmental niches spanning from marine fish pathogens, potential endosymbionts of protozoa, and human pathogens, viz. Francisella tularensis subsp. tularensis, the causative agent of tularemia included among the tier 1 agents on the United States Select Agents list (2-4). The laboratory culture of E. raikovi was used to isolate strain FSC1006 (Francisella Strain Collection, Swedish Defence Research Agency, Umeå, Sweden). Briefly, the sample was bead beaten and acid treated (5) before being serially diluted in phosphate-buffered saline (PBS) and spread on Thayer-Martin agar culture plates (6). The culture plates were incubated at room temperature (20°C) for 1 to 2 weeks and monitored for bacterial growth. The strain FSC1006 grows in nutrient broth (NB) and McLeod medium at room temperature (RT) but not at 37°C.

DNA was extracted as previously described by Larsson et al. (7) and sent for sequencing to the Uppsala Genome Center (Uppsala, Sweden). A Pacific Biosciences RSII system (10-kb library, 2-h movie length) generated a total of 144,357 PacBio reads, with an average read length of 3.9 kb, using two single-molecular real-time (SMRT) cells. The SMRT Analysis system version 2.2.0.p3 was used to assemble a draft genome consisting of a single contig. Finally, the contig ends were aligned to determine the joining point of the circular genome. The complete genome consists of 2,015,987 nucleotides and has a mean G+C content of 32.4%. Annotation was performed using the NCBI annotation service.

F. endociliophora FSC1006 contains 1,831 predicted protein-

coding sequences and 49 predicted noncoding RNAs. The average nucleotide identity (ANI) was calculated by pairwise genome comparisons for the publicly available genomes within *Francisella* clades I and II (8), using the MUMmer and BLAST algorithms with JSpecies version 1.2.1 (9). The similarities between *F. endo-ciliophora* and the clade I and clade II genomes were 78.4 to 77.5% and 78.3 to 77.6%, respectively. Commonly, a threshold of >95 to 96% identity is used to classify genomes as belonging to the same species (10). Multiple genome alignments were computed using progressiveMauve, with default parameters (11), and a phylogenetic tree was generated using the neighbor-joining method. The phylogeny shows that *F. endociliophora* does not belong to any of the two previously known *Francisella* clades and instead forms a new separate branching clade in the *Francisella* genus.

This complete genome sequence is of great importance for the understanding of the environmental diversity of *Francisella* species. A broadening of our understanding is needed in order to further explore the ecology and epidemiology of *Francisella* spp. (12). We argue, based on the phylogeny and low similarity, that this isolate should be classified as a new species, *F. endociliophora*, instead of being a subspecies of *Francisella noatunensis*.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. CP009574. The version described in this paper is the first version, CP009574.1.

ACKNOWLEDGMENTS

This work was supported by the Swedish Ministry of Defence (A4042) and the Swedish Ministry of Foreign Affairs (A4052). We acknowledge the support of the National Genomics Infrastructure (NGI)/Uppsala Genome Center and UPPMAX for providing assistance in massive parallel sequencing and computational infrastructure. The work performed at NGI/Uppsala Genome Center was funded by RFI/VR and Science for Life Laboratory, Sweden.

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