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Genome Sequence of the Filamentous Bacterium *Fibrisoma limi* BUZ 3^T

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***Fibrisoma limi* strain BUZ 3^T, a Gram-negative bacterium, was isolated from coastal mud from the North Sea (Fedderwardersiel, Germany) and characterized using a polyphasic approach in 2011. The genome consists of a chromosome of about 7.5 Mb and three plasmids.**

Fibrisoma limi BUZ 3^T is a member of the genus *Fibrisoma* (*Bacteroidetes*, *Sphingobacteriales*, *Cytophagaceae*), was characterized in 2011 (1), and produces multicellular filaments during growth, reaching up to 90 μm in length after 1 day of growth in liquid culture. This bacterium does not produce flagella, and gliding motility was not observed.

Bacteria were grown overnight in SM broth (DSMZ medium 7) at 28°C. DNA was isolated using the Genomic 500 DNA kit (Qiagen, Hilden, Germany) following the instructions of the manufacturer. Based on its phylogenetic relationship to *Spirosoma linguale* (2), the cell lysis modification procedure and prolonged incubation time for that bacterium were applied as well.

The genome was sequenced at the Functional Genomics Center Zurich (Zurich, Switzerland) with Roche 454 GS FLX Titanium chemistry. Two libraries were prepared: half a plate with an 8-kb insert paired-end library and half a plate with a shotgun library. This strategy yielded 1,325,215 reads with an average size of 378 nucleotides (nt) for the shotgun library and 330 nt for the paired-end library. Both sets of reads were assembled using the GS DeNovo Assembler version 2.5.3 (Roche) with various parameter settings. The two best assemblies were merged using Minimus 2 version 3.00 (5) and scaffolded using Oslay software version 1.0 (4). The assembly was further improved by repeatedly mapping the paired-end reads against the assembly and manually checking the gap regions, which allowed the closure of most gaps. The final genome sequence of *F. limi* BUZ 3^T is composed of 11 scaffolded contigs representing the chromosome (N_{50}, 2,007,105), a large plasmid (pFLIM01), and two small plasmids (pFLIM02 and pFLIM03). The total size of the chromosomal contigs is 7,454,326 bp, with a G+C content of 52.7%. The size of pFLIM01 is 151,932 bp with a G+C content of 49.8%, while the two small plasmids are 14,391 bp (pFLIM02; G+C content, 47.03%) and 8,321 bp (pFLIM03; G+C content, 37.4%). The average coverage ranged between 38.3-fold (pFLIM03) and 58.6-fold (pFLIM01), with the chromosome having 44.4-fold average coverage.

The GenDB annotation platform (3) was employed for the genome annotation. A total of 6,710 protein-coding genes (CDSs) and 49 structural RNAs on the chromosome and 197 CDSs on the three plasmids were annotated.

Members of the phylum *Bacteroidetes* are widely distributed in aquatic environments and have several interesting metabolic (e.g., degradation of complex polymers) and morphological (e.g., multicellular filamentation) features. Therefore, increasing the number of genomes sequenced for this phylum will improve knowledge of these organisms. A comprehensive comparative genome analysis is under way.

Nucleotide sequence accession numbers. The 11 contigs of the chromosome of *F. limi* BUZ 3^T were deposited at EBI under the accession numbers CAIT01000001 through CAIT01000011 (project number CAIT01000000), and the plasmids were deposited under accession numbers HE805916 (pFLIM01), HE805917 (pFLIM02), and HE805918 (pFLIM03).

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REFERENCES

1. **Filippini M, Kaech A, Ziegler U, Bagheri HC.** 2011. *Fibrisoma limi* gen. nov., sp nov., a filamentous bacterium isolated from tidal flats. Int. J. Syst. Evol. Microbiol. **61**:1418–1424.
2. **Lail K, et al.** 2010. Complete genome sequence of *Spirosoma linguale* type strain (1T). Stand. Genomic Sci. **2**:176–185.
3. **Meyer F, et al.** 2003. GenDB: an open source genome annotation system for prokaryote genomes. Nucleic Acids Res. **31**:2187–2195.
4. **Richter DC, Schuster SC, Huson DH.** 2007. OSLay: optimal syntenic layout of unfinished assemblies. Bioinformatics **23**:1573–1579.
5. **Schatz MC, et al.** 23 December 2011, posting date. Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. Brief. Bioinform. doi:10.1093/bib/bbr074.

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