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Complete Genome Sequence of *Neisseria weaveri* Strain NCTC13585

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Neisseria weaveri is a commensal organism of the canine oral cavity and an occasional opportunistic human pathogen which is associated with dog bite wounds. Here we report the first complete genomic sequence of the _N. weaveri_ NCTC13585 (CCUG30381) strain, which was originally isolated from a patient with a canine bite wound.

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Neisseria weaveri is a Gram-negative, nonmotile, aerobic, rod-like bacterium that is a commensal of the canine oral flora (1–3). It is an infrequent opportunistic pathogen of dog bite wounds and there are also isolated reports of *N. weaveri* causing lower respiratory tract and septic infection (4, 5). There is a paucity of information on *N. weaveri* within the literature and historically there has been confusion with its taxonomy, with two different type strains being described (1–3). To date there are only two draft genomes available for *N. weaveri*, LMG 5135 and ATCC 51223 (both the proposed type strains), which have been assembled into 46 and 40 contigs, respectively (6, 7). Here we report the first complete genome for *N. weaveri* strain NCTC13585, which was isolated from a human dog bite wound in Danderyd, Sweden, in 1982.

High-molecular-weight genomic DNA was extracted from a pure culture using the Masterpure DNA extraction kit (Epicentre, WI, USA) and the quality was confirmed (>50 kb) using the Agilent 2200 TapeStation. Whole-genome sequencing (WGS) was performed using the PacBio single-molecule real-time (SMRT) DNA sequencing technology utilizing C4/P6 chemistry followed by genome assembly using an automated assembly pipeline and annotation with Prokka.

The genomic size of NCTC13585 was determined to be 2,188,497 bp. The average G+C content of the sequence was 49.0%. No plasmids were identified in this strain. In total there were 2,060 coding sequences, four rRNA operons, and 55 tRNA genes identified.

Accession number(s). The complete genome sequence has been deposited in the European Nucleotide Archive under the BioSample accession number SAMEA3174300 and the assembly accession number LT571436.

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