



Twelve Complete Reference Genomes of Clinical Isolates in the *Capnocytophaga* Genus

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ABSTRACT We report here 1 near-complete genome sequence and 12 complete genome sequences for clinical *Capnocytophaga* isolates. Total read coverages ranged from 211× to 737×, and genome sizes ranged from 2.41 Mb to 3.10 Mb. These genomes will enable a more comprehensive taxonomic evaluation of the *Capnocytophaga* genus.

Species of the *Capnocytophaga* genus are commensal organisms that are most commonly found as naturally occurring microbiota in human, dog, and cat oral cavities (1–3). Six of the nine recognized species are associated with periodontal disease in humans (1, 4–7). *C. canis*, *C. canimorsus*, and *C. cynodegmi* are opportunistic zoonotic pathogens that inhabit the oral cavities of cats (*Felis catus*) and dogs (*Canis familiaris*) (8, 9). Severe complications from cat and dog bite wound infections in humans can include sepsis, meningitis, and endocarditis, which are often fatal to immunocompromised individuals. We sequenced 13 clinical *Capnocytophaga* isolates from infections associated with bite wounds to generate clinically relevant reference genome sequences of the *Capnocytophaga* genus.

All isolates were grown on heart infusion agar with 5% rabbit blood at 35°C with 5% CO₂ for 48 h. Genomic DNA was extracted using the MasterPure DNA purification kit (Epicentre, Madison, WI, USA), and quality was assessed with a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA). Either 10-kb or 20-kb libraries were generated with the SMRTbell template prep kit version 1.0. The libraries were bound to polymerase using the DNA/polymerase P6v2 binding kit (Pacific Biosciences, Menlo Park, CA, USA) and then loaded on single-molecule real-time cells and sequenced with C4v2 chemistry (Pacific Biosciences) for movie times of 270 min (10-kb libraries) or 360 min (20-kb libraries) on the RSII instrument (Pacific Biosciences). All 20-kb libraries were size selected with Blue Pippin (Sage Science, Beverly, MA, USA). Paired-end sequencing (2 × 250 bp) was performed on NEBNext ultra DNA libraries with the Illumina MiSeq platform.

The PacBio reads were assembled in Canu version 1.4 with “errorRate=0.013,” “minReadLength=5000,” “corMinCoverage=3,” and “corOutCoverage=500” options, and circularization was attempted for each chromosome with Circlator version 1.4.0, which relied on MUMmer version 3.1 and SPAdes version 3.9.0 (10–13). Illumina read sets were cleaned with BBDUK version 37.02 and Trimmomatic version 0.36 before they were mapped onto their corresponding assemblies with BWA-MEM version 0.7.15-r1140 with the “-x intractg” option (14, 15). Both indel and single-nucleotide polymorphism errors were corrected with Pilon version 1.21 using the “--mindepth 0.5” option (16). For a subset of isolates, the resulting assemblies were verified, and in some cases corrected, by comparing their predicted Afill maps with Afill whole-genome optical maps and with contigs generated by CLC Genomics Workbench version 10.1. Reads were trimmed within CLC Genomics Workbench using a quality limit of 0.02 prior to assembly; contigs were then

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TABLE 1 Features of the 13 sequenced genomes of *Capnocytophaga* strains

Species	Strain	GenBank accession no.	Total no. of genes	Sequencing depth (×)	Genome size (bp)	Sequencing technologies
<i>C. canimorsus</i>	7120	CP022382	2,136	531.8	2,414,275	PacBio, Illumina, OpGen
<i>C. canimorsus</i>	H3936	CP022389	2,173	422.9	2,455,405	PacBio, Illumina, OpGen
<i>C. canimorsus</i>	H5594	CP022388	2,269	731.6	2,493,828	PacBio, Illumina, OpGen
<i>C. canis</i>	H2931	CP022381	2,231	523.3	2,632,967	PacBio, Illumina, OpGen
<i>C. canis</i>	H4358	CP022380	2,224	452.9	2,633,192	PacBio, Illumina
<i>C. cynodegmi</i>	G7591	CP022378	2,329	422.2	2,640,475	PacBio, Illumina
<i>C. gingivalis</i>	H1496	CP022386	2,724	211.3	2,838,633	PacBio, Illumina, OpGen
<i>C. leadbetteri</i>	H6253	CP022384	2,243	643.3	2,504,023	PacBio, Illumina, OpGen
<i>C. sputigena</i>	D1179	CP022379	2,563	737.4	2,855,148	PacBio, Illumina
<i>C. sputigena</i>	H4486	CP022383	2,821	503.7	3,098,616	PacBio, Illumina, OpGen
<i>C. sputigena</i>	H6490	NIBW00000000	2,671	343.5	2,963,948	PacBio, Illumina
<i>C. sputigena</i>	KC1668	CP022385	2,822	263.6	3,074,746	PacBio, Illumina, OpGen
<i>C. stomatis</i>	H2177	CP022387	2,519	449.3	2,831,350	PacBio, Illumina, OpGen

corrected by mapping PacBio reads to them with a mismatch cost of two, and they were further polished by remapping the Illumina reads with a mismatch cost of 3. Discrepancies between the Canu assemblies and the whole-genome optical maps were detected using MapSolver version 3.2 (OpGen, Inc., Gaithersburg, MD, USA) and corrected using the BioEdit version 7.1.9 sequence-editing tool (17). All final assemblies were submitted to NCBI for archiving and annotation with Prokaryotic Genome Annotation Pipeline (PGAP) version 4.2.

Accession number(s). The genome sequences of the *Capnocytophaga* isolates reported here have been deposited in DDBJ/ENA/GenBank under the accession numbers listed in Table 1.

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