Chelonobacter oris 1662T is a type strain of the recently described species of the Pasteurellaceae family. The strain was isolated from the choanae of a captive tortoise with signs of respiratory tract infection. The genome reported here is approximately 2.6 Mb in size and has a G+C content of 47.1%.

Pasteurellaceae, with few exceptions, are primarily opportunistic pathogens. Until 2011, the Pasteurellaceae family included 15 genera (1); however, new genera isolated from various animal species are continuously added to the family Pasteurellaceae (2–6).

Most Pasteurellaceae species are host-specific and only occasionally may be transmitted between different hosts (7).

Chelonobacter oris, currently the only species in the Chelonobacter genus, was described in 2009 (8). Based on the phylogeny inferred from analyzing 16S rRNA, rpoB, infB, and recN gene sequences, C. oris clusters together with [Pasteurella] testudinis, a species also found in captive tortoises (9). The two taxa form a distinct cluster distantly related to all other species within the Pasteurellaceae family (3).

The genomic DNA from C. oris strain 1662T was isolated using a blood and tissue kit (catalog no. 69506; Qiagen). The draft genome sequencing was performed at the National High-Throughput DNA Sequencing Center of the University of Copenhagen. The MiSeq instrument (Illumina) was used for the genome sequencing with a 150-bp paired-end-read format. The CLC Genomic Workbench version 6.5.1 software package (CLC, Denmark) was used to perform quality trimming and de novo assembly of the reads. The run yielded 1,156,558 high-quality filtered sequences in pairs containing 134,646,107 bases, which provided an average of 50-fold coverage of the genome. The assembly resulted in 35 contigs ranging from 1,370 bp to 447,435 bp in size. Prediction of protein-coding sequences and annotation was performed by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The total estimated size of the genome was 2,610,727 bp with a G+C content of 47.1%. The genome contained 2,284 coding DNA sequences (CDSs), 3 rRNAs, and 48 tRNA sequences. In comparison to other Pasteurellaceae members, C. oris has one of the largest genomes reported and a relatively high G+C content (10).

All C. oris strains are β-hemolytic on calf-blood agar. To identify the potential hemolysins, we compared the assembled genome to a local database built from RTX-like proteins present in different gammaproteobacteria (11), and to the MVirDB database (12) with BLASTp. RTX toxins are the most abundant toxins among Pasteurellaceae bacteria, where they often act as the primary virulence factor (7). Although several proteins (locus tags: OA57_07455, OA57_11040, OA57_08905, and OA57_11380) harboring RTX repeats were identified in C. oris, none of these showed significant sequence similarity to known RTX toxins. Interestingly, another possible hemolysin (locus tag OA57_07415), together with a channel-forming transporter protein (locus tag OA57_07410) was identified. Both proteins showed significant sequence similarity to the HpmA (accession no. P16466.1) and HpmB (accession no. P16465.1) proteins, respectively, of Proteus mirabilis (13). The HpmA protein belongs to the family of the pore-forming calcium-independent cytolysins described previously (14). Homologs of these proteins were not detected in other members of Pasteurellaceae, and thus their role in the pathogenicity of C. oris remains to be investigated.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JSUM0000000. The version described in this paper is version JSUM0100000.

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