Draft Genome Sequences of *Porphyromonas crevioricanis* JCM 15906<sup>T</sup> and *Porphyromonas cansulci* JCM 13913<sup>T</sup> Isolated from a Canine Oral Cavity

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Here, we report the draft genome sequences of *Porphyromonas crevioricanis* JCM 15906<sup>T</sup> and *Porphyromonas cansulci* JCM 13913<sup>T</sup>, which were isolated from a canine oral cavity and were recently united under the single species *P. crevioricanis*. These two genome sequences are very similar, and yet a high degree of genome rearrangements is observed.

*Porphyromonas crevioricanis* (1) and *Porphyromonas cansulci* (2) have been isolated from canine oral cavities. *P. crevioricanis* is one of the predominant bacterial species in subgingival plaque in dogs (3). It has been reported that *P. crevioricanis* strain JCM 15906<sup>T</sup> shows a very high *hsp60* gene sequence similarity (100%) with that of *P. cansulci* JCM 13913<sup>T</sup>, as well as with a very high 16S rRNA gene sequence similarity (99.9%) (4). Recently, *P. crevioricanis* and *P. cansulci* were found to be a single species, *P. crevioricanis*, based on the relatedness of their DNA (>91%) (5). Therefore, the genome sequences of two strains are expected to provide new insights into this species concept.

Chromosomal DNA was extracted from *P. crevioricanis* JCM 15906<sup>T</sup> and *P. cansulci* JCM 13913<sup>T</sup> using a Genomic-tip 100/G (Qiagen). Whole-genome sequencing was performed using Illumina genome analyzer IIx, which produced paired-end reads of 101 bp with an insert size of 500 bp. De novo assemblies were performed using Velvet v1.1.02 (6), with parameters optimized as assemblies were performed using Velvet v1.1.02 (6), with parameters optimized by the VelvetOptimiser (http://www.vichioinformatics.com/software.velvetoptimiser.shtml), resulting in 118 contigs with an N<sub>50</sub> of 49,631 bp for *P. crevioricanis* JCM 15906<sup>T</sup>, comprising 2,044,812 bp, with an average G+C content of 45.3%, and 89 contigs with an N<sub>50</sub> of 69,079 bp for *P. cansulci* JCM 13913<sup>T</sup>, comprising 2,108,435 bp with an average G+C content of 45.4%. The draft genomes were annotated by the Genome-to-Genome Distance Calculator (GGDC) web server (GGDC 2.0; http://ggdc.dsmz.de/distcalc2.php). BLAST dot plot analysis comparison in the SEED viewer (http://www.theseed.org) indicated a high degree of genome rearrangements between *P. crevioricanis* JCM 15906<sup>T</sup> and *P. cansulci* JCM 13913<sup>T</sup> genome sequences. *P. cansulci* JCM 13913<sup>T</sup> contains large numbers of conjugative transposon proteins, which are frequently associated with genomic rearrangements. This might have contributed to rearrangement of the genomic structure and led to the diversification of *P. crevioricanis*. Further genome analyses will improve our understanding of this species.

Nucleotide sequence accession numbers. The draft genome sequences of *P. crevioricanis* JCM 15906<sup>T</sup> and *P. cansulci* JCM 13913<sup>T</sup> have been deposited in DDBJ/EMBL/GenBank under the accession nos. BAOU00000000 and BAOV00000000.

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