Dear Editor,

*Pasteurella canis* is a gram-negative coccobacillus mainly resides in the oral cavity, nasopharynx, or intestine of domestic animals. It is an important bacterial pathogen in both animals and humans. *P. canis* can cause a variety of infections that lead to osteomyelitis, keratitis, peritonitis, and bacteraemia. In humans, dog bites are a potential risk of infection caused by this pathogen. There are reports of *P. canis* infection in humans following a scratch or bite from a domestic animal. These studies have been carried out mainly on the phenotype of the bacteria, with little genomic research. The genomic characteristics of this bacterial pathogen still need to be better elucidated. Here, we report the first genome sequence of a clinical *P. canis* strain isolated from a patient diagnosed with index finger osteomyelitis in China. Genotypic characterization of this strain was further analyzed.

A 76-year-old male patient was diagnosed with index finger osteomyelitis and hospitalized in the department of hand surgery in a teaching hospital in Zhejiang Province in August 2019. This patient was accidentally bitten by a dog, which injured his right hand and led to bleeding and pain, 20 days prior to his hospitalization. He immediately went to the community hospital for treatment, which included debridement, suture bandaging, and rabies vaccine injection. Ten days prior to his hospitalization, his right hand showed redness, swelling, pain, and suppuration. The patient used to be physically fit. There was no history of diabetes, coronary heart disease, or infectious disease except for hypertension. The results of initial routine blood tests were as follows: white blood cells (WBCs), $9.41 \times 10^9$/L (neutrophils 73.9% and lymphocytes 18.2%); platelets, $228 \times 10^9$/L; and hemoglobin, 148 g/L. The patient underwent two rounds of debridement of osteomyelitis while in the hospital. The patient’s right index finger was infected from the distal segment to the proximal segment with tendon infection, tendon necrosis, tendon sheath infection, soft tissue infection, and bone defect. The wound was thoroughly debrided. Necrotic bone, tendons, and necrotic tissue

| Antimicrobial resistance gene | Contig | Identity (%) | Position | Antimicrobial resistance category |
|-------------------------------|--------|--------------|----------|----------------------------------|
| qnrS1                         | contig00021 | 99.85     | 454-1110 | quinolone                        |

| Virulence gene | Contig | Identity (%) | Position | Functional annotation               |
|----------------|--------|--------------|----------|-------------------------------------|
| gmhA/lpcA      | contig00003 | 85.32       | 175625-176135 | Phosphoheptose isomerase            |
| hitA           | contig00002 | 83.65       | 259731-260562 | Periplasmic iron-binding protein    |
| inv            | contig00024 | 93.06       | 1037-1180 | Invasin                            |
| kdsA           | contig00001 | 83.17       | 96418-97148 | 2-dehydro-3-deoxyphosphoconate aldolase |
| lpxC           | contig00003 | 82.18       | 198819-199688 | UDP-3-O-(R-3-hydroxymyristoyl)N-acetylglucosamine deacetylase |

| Plasmid replicon | Contig | Identity (%) | Position | Annotation                   |
|------------------|--------|--------------|----------|------------------------------|
| CoIRNAI          | contig00019 | 92.23     | 1062-1164 | Gram-negative                |
The isolate was preliminarily identified using the VITEK MS system (bioMérieux, France) and was further confirmed by calculating the average nucleotide identity (ANI), one of the bacterial whole-genome similarity metrics. The ANI results revealed that the genome of *P. canis* strain QBSD was over 99.89% identical to the type strain *P. canis* NCTC11621. Antimicrobial susceptibility testing was conducted using the Etest method following the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Piperacillin, ceftazidime, ceftriaxone, cefepime, imipenem, levofloxacin, and tetracycline were used in the test. The whole-genome sequence of the strain was determined using the Illumina NovaSeq 6000 platform (Illumina Inc). The short reads generated were de novo assembled into contigs using SPAdes 3.13.0. The whole-genome sequence was automatically annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) server. Antimicrobial resistance genes, virulence genes, and plasmid replicons of the isolate were analyzed using the BacWGSTdb server.9,10

The whole-genome sequence of *P. canis* strain QBSD consisted of 30 contigs that comprised 2,231,959 bp, and the PGAP server predicted a total of 2,033 protein-coding sequences. The overall G + C content of this isolate amounted to 36.7%. In total, 52 tRNA genes, 11 rRNA genes, and 4 ncRNA operons were identified. The genome contained several IS elements, the majority of which belong to the IS1595, IS3, and IS200 families. Two confirmed CRISPR sequences and one putative secondary metabolite gene cluster bacteriocin could also be predicted. The antimicrobial resistance genes, virulence genes, and plasmid replicons of *P. canis* strain QBSD are presented in Table 1. One quinolone resistance gene, *qnrS1*, and one plasmid replicon, ColRNAI, could be identified in the genome. Five virulence genes were identified in *P. canis* strain QBSD, which were *gmhA/lpcA*, *hitA*, *inv*, *kdsA*, and *lpxC*.

A total of two *P. canis* strains could be found in the NCBI GenBank database. Orthologous genes between QBSD and these two strains were identified using Roary and OrthoVenn, and phylogenetic relationships were determined by NJ/UPGMA phylogeny based on core genome single nucleotide polymorphism analysis. Comparative genomic analyses of the three *P. canis* isolates revealed that they shared a large number of genes. However, phylogenetic analysis showed that these strains were not epidemiologically related (Figure 1).

In summary, we report the first genome sequence of a clinical *P. canis* strain isolated from a patient diagnosed with index finger osteomyelitis in China. Our data may help to understand the genomic features of this bacterial pathogen.

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number WUMP00000000.

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