

Complete Genome Sequence of *Trueperella pyogenes*, an Important Opportunistic Pathogen of Livestock

Vinicius S. Machado, Rodrigo C. Bicalho

Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, New York, USA

Here, we report the complete genome sequence of *Trueperella pyogenes* TP6375, a strain isolated from the uterus of a dairy cow affected with metritis. The complete circular genome is 2,338,390 bp and contains several genes needed for pathogenicity.

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Address correspondence to Rodrigo C. Bicalho, rcb28@cornell.edu.

Trueperella pyogenes, a Gram-positive, nonmotile, non-spore-forming, short, rod-shaped bacterium (1), is a common inhabitant of the urogenital, gastrointestinal, and upper respiratory tracts of many animal species (2–4). However, a physical or microbial insult to the host can lead to a variety of suppurative *T. pyogenes* infections, such as mastitis and uterine diseases in dairy cows (5, 6), liver abscesses in feedlot cattle (7) and high-producing dairy cows (8), pneumonia in pigs (9), and abscesses in various species of wildlife, such as musk deer (10). Infections caused by *T. pyogenes* are uncommon in humans and are usually linked to occupational exposure, because the organism is not part of the human normal flora (11). *T. pyogenes* can grow under aerobic or strictly anaerobic conditions, but it optimally grows in a CO₂-enriched (7% CO₂) atmosphere (1).

T. pyogenes is equipped with several known and putative virulence factors that are important for its pathogenic potential. Its primary virulence factor, pyolysin, is a potent cholesterol-dependent cytolysin and is associated with the tissue damage caused by *T. pyogenes* infection (1, 12). *T. pyogenes* also expresses a number of surface-exposed proteins, such as fimbriae, neuraminidases, and extracellular matrix-binding proteins, which are involved in adherence and mucosal colonization (1, 6, 13).

Here, we report the complete chromosome sequence of *T. pyogenes* strain TP6375. The strain was isolated from the uterus of a dairy cow affected with metritis and was subjected to whole-genome sequencing. The genomic DNA was extracted from an overnight culture using a PowerSoil DNA isolation kit, according to the manufacturer's instructions. A library for sequencing was prepared with 2 μg of the extracted genomic DNA using a TruSeq DNA PCR-free LT sample preparation kit (Illumina), and paired-end sequencing was performed using the MiSeq reagent kit version 3 (600 cycles) with the Illumina MiSeq platform. The sequences were *de novo* assembled using the DNASTar SeqMan NGen (version 11.2.1.25) assembler. Genome annotation was done by the NCBI Prokaryotic Genome Annotation Pipeline.

The complete circular genome is 2,338,390 bp long, with a G+C content of 59.5% and 2,082 predicted genes; of those genes,

1,984 are coding sequences (CDS), 45 are pseudogenes, 1 is a clustered regularly interspaced short palindromic repeat (CRISPR) array, 6 are rRNAs, 46 are tRNAs, 1 is a noncoding RNA (ncRNA), and 15 are frameshifted genes. The genome encodes several known and putative virulence factors, including adhesion factors (1 collagen adhesion and 4 fimbrial proteins) and toxins (pyolysin, cytotoxin, and one other toxin). The complete genome sequence presented here will serve as a platform for identifying new genes that may contribute to pathogenicity, will advance our knowledge regarding the evolution, metabolism, and antibiotic resistance of this strain, and will serve as a template for future transcriptomic work.

Nucleotide sequence accession number. The annotated chromosome sequence of *T. pyogenes* strain TP6375 has been deposited in GenBank under the accession no. CP007519.

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We declare no conflicts of interest.

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