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Draft Genome Sequence of *Trueperella pyogenes*, Isolated from the Infected Uterus of a Postpartum Cow with Metritis

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*Trueperella pyogenes* is a common commensal bacterium and an opportunistic pathogen associated with chronic purulent disease, particularly in ruminants. We report here the genome sequence of a *T. pyogenes* isolate from a severe case of bovine metritis. This is the first full record of a *T. pyogenes* genome.

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Recently, the genus *Trueperella* was proposed to encompass 5 species previously classified as belonging to *Arcanobacterium* (1). Among these reclassified species is *T. pyogenes*, previously known as *Arcanobacterium pyogenes*, *Actinomyces pyogenes*, and *Corynebacterium pyogenes*. *T. pyogenes* has long been recognized as a mucosal membrane resident in many animal species and as an opportunistic pathogen (2). *T. pyogenes* is particularly associated with suppurative infections, such as mastitis, septic arthritis, liver abscessation, pneumonia, endometritis, and metritis. *T. pyogenes* is recognized as a key etiological agent in bovine endometritis and abscessation, pneumonia, endometritis, and metritis.

*M. Tetraena* is a common commensal bacterium and an opportunistic pathogen associated with chronic purulent disease, particularly in ruminants. We report here the genome sequence of a *T. pyogenes* isolate from a severe case of bovine metritis. This is the first full record of a *T. pyogenes* genome.

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Resistance to antibiotics often used in veterinary practice is common in *T. pyogenes*. A gene encoding resistance to tetracycline (*tetW*) was identified in the genome of strain MS249. Although resistance to macrolides, chloramphenicol, and β-lactam antibiotics among *T. pyogenes* strains has been reported (16–20), no specific resistance elements were identified in strain MS249, consistent with its sensitivity to these antibiotics.

This is the first reported genome sequence for *T. pyogenes*. This sequence will be used to extend the understanding of this novel bacterial opportunistic pathogen and form the basis for systematic studies of its pathogenicity and physiology, as well as to perform a comparative genomic analysis among *Actinobacteria*.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JALQ0000000. The version described in this paper is version JALQ01000000.

**ACKNOWLEDGMENTS.** This work is a component of the project "Integrated systems approach for preventing uterine disease in dairy cattle (iPUD)," funded by BBSRC through the EMIDA ERA-NET initiative, project reference BB/1017240/1 and BB/BB/1017283/1.

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