

Draft Genome Sequences of 113 *Escherichia coli* Strains Isolated from Intramammary Infections in Dairy Cattle

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ABSTRACT *Escherichia coli* is one of the most common etiological agents responsible for clinical bovine mastitis. Here, we report the draft genome sequences and annotations of 113 *E. coli* strains that were isolated from Holstein cows with intramammary infections in Canada.

Escherichia coli is a major pathogen that is responsible for clinical mastitis in dairy cows. Dairy cows with intramammary *E. coli* infections result in economic losses for the dairy industry due to reductions in milk yield, premature culling, and treatment costs (1). Bovine mastitis cases caused by *E. coli* have increased, relative to contagious mastitis, over the past few decades (2–5). However, the etiology of *E. coli* mastitis is not fully understood. Several attempts have been made to define a specific mammary pathogenic *E. coli* pathotype, but a set of core virulence factors has not yet been defined (6–10). Therefore, this sequencing project was conducted to sequence additional *E. coli* isolates from intramammary infections to better define the molecular characteristics and pangenomic composition of mammary pathogenic *E. coli*.

The Canadian Bovine Mastitis Research Network maintains a culture collection of mastitis isolates that were collected from 91 dairy farms across Canada over a 2-year period (2007 and 2008) (11). All strains sequenced in this project were obtained from this collection. Each isolate was collected from cows experiencing clinical mastitis, either on the day of diagnosis or during subsequent post-clinical mastitis follow-up sampling.

Here, we present the draft genome sequences of 113 *E. coli* isolates from bovine mastitis cases in Canada. Briefly, the isolates were cultured from raw milk samples plated on biplates containing a 1:1 mixture of Columbia agar with 5% sheep blood and MacConkey agar. Standard biochemical tests were performed to confirm that the isolates were *E. coli* (lactose and indole positive and oxidase and citrate negative) (11). To extract DNA for sequencing, *E. coli* was grown overnight on tryptic soy agar (TSA) and a well-isolated single colony was selected for DNA isolation. DNA was extracted using DNAzol reagent (Invitrogen, Carlsbad, CA) and the Maxwell RSC blood DNA kit (Promega, Madison, WI) following the manufacturer's instructions. The short-read sequence data were generated by preparing paired-end libraries with the Nextera Flex DNA library preparation kit (Illumina, San Diego, CA) and Nextera DNA CD indexes (96 indexes and 96 samples), with sequencing on a MiSeq benchtop sequencer (Illumina) for 301 cycles in each direction. The reads were assembled *de novo* into high-quality draft genomes with ProkaryoteAssembly v0.1.6 (<https://github.com/bfssi-forest-dussault/ProkaryoteAssembly>). This pipeline consists of quality control and trimming of low-quality sequences (Q value, <20) using BBduk (BBMap v38.79), error correction using Tadpole (BBMap v38.79), assembly using SKESA v2.4, alignment of error-corrected reads against the draft assembly (BBMap v38.79), and polishing of the

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performed by the National Center for Biotechnology Information (NCBI) through the Prokaryotic Genome Annotation Pipeline (PGAP) (15, 16).

Data availability. These nucleotide sequences have been deposited in DDBJ/ENA/GenBank as BioProject [PRJNA612640](#) under the accession numbers provided in Table 1.

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