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GENOME SEQUENCES

Draft Genome Sequence of a *Campylobacter coli* WL22 Isolate Possessing *erm*(B) with *gyrA* Mutations, Isolated from Poultry in China

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ABSTRACT *Campylobacter coli* is a major foodborne pathogen worldwide that causes campylobacteriosis cases in humans and is an emerging threat in developing countries. The rapid dissemination of the macrolide resistance gene *erm*(B) poses a significant threat to the clinical therapy of campylobacteriosis. Here, we report the draft genome sequences of one *Campylobacter coli* strain possessing *erm*(B), isolated from the cecal contents of poultry in Jinhua, China.

Campylobacter coli is a common foodborne pathogenic bacterium that causes bacterial gastroenteritis in humans (1). Poultry are believed to be the most important source of *C. coli* human infections. The rapid dissemination of the macrolide resistance gene *erm*(B) will likely compromise the efficacy of macrolides as the treatment of choice for campylobacteriosis (2). We describe here the draft genome sequences of one *Campylobacter coli* WL22 strain (GONG3) possessing *erm*(B) with *gyrA* mutations.

Campylobacter sp. isolation from the cecal contents of poultry in slaughterhouses was performed using the *Campylobacter* isolation kit incorporating a membrane filter method (ZC-CAMPY-002; Qingdao Sinova Biotechnology Co., Ltd., Qingdao, China), according to the manufacturer's instructions. Species identification of *C. coli* strain GONG3 was conducted with the matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) system at the Department of Medical College of Jinhua Polytechnic in Jinhua, China in 2019. To isolate the genome DNA, the strains were preenriched for 24 h at 42°C in Bolton broth containing *Campylobacter* growth supplements, under microaerobic conditions (5% O_2, 10% CO_2, and 85% N_2). One-hundred-microliter drops of the preenrichment were plated onto the surface of a Columbia blood agar plate. These plates were further cultured overnight at 42°C under microaerobic conditions.

Genomic DNA of strain GONG3 was extracted using a DNeasy blood and tissue kit (Qiagen, Germany), according to the manufacturer's instructions. Genomic DNA purity and concentration were evaluated by NanoDrop spectrophotometer and measured by a fluorometer (Qubit; ThermoFisher). The DNA library was prepared using a Nextera XT DNA library preparation kit (Illumina, Inc., Cambridge, UK), and genomic DNA was sequenced on an Illumina NovaSeq instrument with a 150-bp paired-end approach at a depth of approximately 200×, which yielded 3,287,640 paired-end raw reads. The quality of sequencing and trimming were verified with FastQC v0.11.7, while low-quality sequences and Illumina PCR adapter sequences were removed with Trimmomatic v0.36 (3). All good-quality paired reads of *C. coli* GONG3 were assembled using the SPAdes genome assembler v3.12.0 with default settings (4), which yielded 38 contigs with an N_{50} value of 269,170 bp, and the total number of assembled bases was 1,680,364 bp. The overall GC content of the *C. coli* GONG3 strain was 31.44%. Rapid

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Annotations using Subsystems Technology (RAST) showed that 1,764 coding sequences (CDS) and 42 RNAs were observed in the genome (5).

Whole-genome sequence data analyses were performed using bioinformatics tools (MLST v2.0 and PathogenFinder v1.1) with default parameters available from the Center for Genomic Epidemiology (6). MLST v2.0 demonstrated that *C. coli* GONG3 belongs to multilocus sequence typing (MLST) sequence type 872 (ST872). The PathogenFinder analysis revealed a pathogenic potential for *C. coli* GONG3 as a human pathogen. This strain matched 66 pathogenic families (90.8%) indicating a high risk for human infections. *C. coli* GONG3 carried cytolethal distending toxin (CDT) composed of *cdtA*, *cdtB*, and *cdtC* genes.

Resistance genes in strain GONG3 were screened using RGI 5.1.1 (7), which showed that it contained the resistance genes to a macrolide [*erm*(B)], beta-lactam ($bla_{OXA-451}$), aminoglycosides [*aac(6')-aph(2')*, *ant(6)-Ia*, *aph(2')-If*, and *aph(3')-III*], and tetracycline (*tetO*) and the fluoroquinolone resistance-related Thr-86-Ile substitution in *gyrA*. It is alarming that *erm*(B) is always associated with multidrug resistance genomic islands (MDRGIs), which confer resistance to multiple classes of antibiotics, including aminoglycosides, fosfomycin, and tetracyclines (8).

The presented genome sequences of *erm*(B)-positive *Campylobacter coli* strain WL22 could provide valuable knowledge for understanding the macrolide resistance and genetic characteristics of *C. coli*.

Data availability. The complete genome sequences of the *C. coli* WL22 isolate reported here have been deposited at DDBJ/ENA/GenBank under the accession no. JACZZI000000000. The raw data have been deposited at the SRA under the accession no. SRR12762486.

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