Complete Genome Sequence of the Campylobacter cuniculorum Type Strain LMG 24588

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ABSTRACT Campylobacter cuniculorum is a thermotolerant species isolated from farmed rabbits (Oryctolagus cuniculus). Although C. cuniculorum is highly prevalent in rabbits farmed for human consumption, the pathogenicity of this organism in humans is still unknown. This study describes the whole-genome sequence of the C. cuniculorum type strain LMG 24588 (=CCUG 56289T).

Campylobacter cuniculorum is a thermotolerant species isolated from farmed rabbits (Oryctolagus cuniculus) (1, 2). Although rabbit meat is consumed by humans, there have been no reported cases of C. cuniculorum-related human illness. The pathogenicity of this organism is unknown; however, similar to Campylobacter jejuni, the C. cuniculorum type strain was shown to adhere to and invade Vero, HeLa, and COLO205 cells (3). The C. cuniculorum type strain LMG 24588 (=150BT = CCUG 56289T) was isolated in Italy from the cecal contents of a farmed rabbit (2). In this study, we report the first closed genome sequence of the C. cuniculorum type strain.

The Roche GS-FLX, Illumina HiSeq, and PacBio RS next-generation sequencing platforms were used to complete the genome of the C. cuniculorum type strain LMG 24588. Shotgun and paired-end Roche 454 reads were assembled (using Newbler version 2.6) into a single array of 200 unique and repeat chromosomal contigs. Most of the contig gaps were closed using Illumina HiSeq reads (SeqWright, Houston, TX) and/or PCR amplification/Sanger sequencing. However, the repeat topography of the LMG 24588T chromosome required PacBio sequencing for both genome closure and assembly validation. Two single-contig plasmid scaffolds were closed/circularized, and all base calls were validated using Illumina HiSeq reads (913× coverage). The final coverage across the genome was 1,363×.

C. cuniculorum strain LMG 24588T has a circular genome of 1,931 kbp, with an average G+C content of 31.6%. Protein-, rRNA- and tRNA-coding genes were identified as described previously (4). The genome contains 1,786 putative protein-coding genes, 63 pseudogenes, and 2 sets of rRNA genes. The LMG 24588T chromosome contains six putative genetic islands: one encodes a putative type VI secretion system, and another encodes a putative type IV secretion system. The chromosome also contains 89 G+C tracts ≥8 bp. Seventy-seven of these tracts were demonstrated to be hypervariable; thus, the C. cuniculorum type strain is predicted to encode at least 60 contingency genes. Two small plasmids, pCUN1 (4,923 bp) and pCUN2 (1,834 bp), were identified in the LMG 24588T genome.

The Embden-Meyerhof-Parnas glycolytic pathway is incomplete in Campylobacter spp.; therefore, these organisms cannot utilize sugars as a carbon source, with the exception of fucose for some strains (5, 6). However, some C. jejuni and Campylobacter coli strains encode a complete set of enzymes for the alternative Entner-Doudoroff
pathway (7–9), which has been shown to be functional (9). Similar to C. jejuni and C. coli, strain LMG 24588T is also predicted to encode a complete Entner-Doudoroff pathway; however, unlike C. jejuni and C. coli, this gene cluster is not embedded within an rRNA locus.

Another noteworthy locus contained in C. cuniculorum is tcuABC, which is involved in tricarboxylate utilization (10). Within Campylobacter spp., these genes were also identified in the reptile-associated C. fetus subsp. testudinum and C. iguaniorum (11, 12) and the swine-associated C. hyointestinalis subsp. lawsonii (11). Tricarboxylate utilization was proposed to be associated with the hindgut niche potentially inhabited by these organisms (11). Rabbits, like pigs and reptiles, are also hindgut fermenters; thus, tricarboxylate utilization may be used by C. cuniculorum to more efficiently colonize their hosts.

Accession number(s). The complete genome sequence of C. cuniculorum strain LMG 24588T has been deposited in GenBank under the accession numbers CP020867 (chromosome) and CP020868 and CP020869 (plasmids pCUN1 and pCUN2, respectively).

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