Complete Genome Sequence of the Hippuricase-Positive Campylobacter avium Type Strain LMG 24591

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ABSTRACT  Campylobacter avium is a thermotolerant Campylobacter species that has been isolated from poultry. C. avium was also the second hippuricase-positive species to be identified within Campylobacter. Here, we present the genome sequence of the C. avium type strain LMG 24591 (=CCUG 56292T), isolated in 2006 from a broiler chicken in Italy.

Campylobacter spp., primarily C. jejuni and C. coli, are commonly associated with acute bacterial gastroenteritis in humans (1), and transmission is often via contaminated poultry products (1, 2). In 2006, hippuricase-positive Campylobacter strains were isolated from poultry on three farms in Italy (3). Although initially identified as C. jejuni, based on their hippuricase activity, additional molecular and phenotypic tests identified these organisms as a novel species, termed Campylobacter avium (3). In this study, we present the first closed genome sequence of the C. avium type strain LMG 24591.

The genome of C. avium strain LMG 24591T was completed using the Roche 454, Illumina HiSeq, and PacBio next-generation sequencing platforms, as previously described (4). Illumina HiSeq reads for strain LMG 24591T were obtained from SeqWright (Houston, TX). The final coverage across the genome was 1,191 x. The LMG 24591T assembly was additionally verified using a bacterial optical restriction map (XbaI; OpGen, Gaithersburg, MD). Putative coding sequences (CDSs) were identified using GeneMark (5). Final annotation, including manual start codon curation, determination of homopolymeric GC tract variability, and the identification of rRNA- and tRNA-coding genes and pseudogenes, was performed as described previously (6).

C. avium strain LMG 24591T has a circular genome of 1,738.6 kbp, with a GC content of 34.2%. The genome contains 1,645 putative protein-coding genes, 48 pseudogenes, 2 rRNA loci, and 3 putative genetic islands, with one encoding a partial type VI secretion system. Forty-four GC tracts of 8 bp were identified in the LMG 24591T genome; 40 of these were determined to be hypervariable. No plasmids were identified in LMG 24591T.

Noteworthy in C. avium is the absence of the selenocysteinyl tRNA and genes encoding selenium-associated proteins, e.g., selenocysteine insertion proteins, selenoproteins, and selenoprotein-associated chaperones. The absence of selenium metabolism was reported previously for Campylobacter larienae and related taxa (7). An ortholog of the C. jejuni fibronectin-binding protein CadF is also not encoded by C. avium. Because CadF is required for C. jejuni host cell invasion and colonization (8, 9), its absence might indicate reduced virulence in C. avium. Other proteins that are not encoded by C. avium include the ferredoxins FdxA and FdxB, methionine sulfoxide reductase (MsrA, MsrB, or MsrAB), and the globin Cgb, suggesting that, when compared...
to *C. jejuni*, *C. avium* might have a lower aerotolerance and is more sensitive to oxidative and nitrosative stress (10–12).

Prior to the identification of *C. avium*, *C. jejuni* was unique among Campylobacter spp. in its ability to hydrolyze hippuric acid (13). Hippuric acid (*hippurase* positive, the *hipA* gene was not detected in strain LMG 24591\(^\text{T}\)). Thus, it is likely that *C. avium* encodes an alternate hippocrusc with low similarity to HipO. *C. jejuni hipO* contains a peptidase M20 domain and encodes a predicted zinc-dependent aminoacylase/carboxypeptidase. Analysis of the *C. avium* LMG 24591\(^\text{T}\) genome identified a candidate hippocrusc gene with a similar domain structure, which we have termed *hipA*.

**Accession number(s).** The complete genome sequence of *C. avium* strain LMG 24591\(^\text{T}\) has been deposited in GenBank under the accession number CP022347.

**ACKNOWLEDGMENTS**

This work was funded by the United States Department of Agriculture, Agricultural Research Service, under CRIS projects 2030-42000-230-047, 2030-42000-230-051, and 3040-42000-015-00D.

We thank Sandy Fryda-Bradley for excellent technical assistance.

**REFERENCES**