



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 56292^T), 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 24591^T was completed using the Roche 454, Illumina HiSeq, and PacBio next-generation sequencing platforms, as previously described (4). Illumina HiSeq reads for strain LMG 24591^T were obtained from SeqWright (Houston, TX). The final coverage across the genome was 1,191×. The LMG 24591^T assembly was additionally verified using a bacterial optical restriction map (Xbal; 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 previously described (6).

C. avium strain LMG 24591^T 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 24591^T genome; 40 of these were determined to be hypervariable. No plasmids were identified in LMG 24591^T.

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 lanienae* 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

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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 (*N*-benzoylglycine) is cleaved by HipO (14) to produce glycine and benzoic acid, with glycine production measured by a simple colorimetric assay (15). Although we confirmed that *C. avium* is hippuricase positive, the *hipO* gene was not detected in strain LMG 24591^T. Thus, it is likely that *C. avium* encodes an alternate hippuricase 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^T genome identified a candidate hippuricase gene with a similar domain structure, which we have termed *hipA*.

Accession number(s). The complete genome sequence of *C. avium* strain LMG 24591^T has been deposited in GenBank under the accession number [CP022347](https://doi.org/10.1093/gbe/evx112).

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