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Complete Genome Sequence of *Campylobacter iguaniorum* Strain 1485E^T, Isolated from a Bearded Dragon (*Pogona vitticeps*)

Maarten J. Gilbert,[a] William G. Miller,[b] Emma Yee,[b] Marja Kik,[c] Jaap A. Wagenaar,[a,d,e] Birgitta Duim[a,e]

Department of Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands[a]; Produce Safety and Microbiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Albany, California, USA[b]; Department of Pathobiology, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands[c]; Central Veterinary Institute of Wageningen UR, Lelystad, The Netherlands[d]; WHO Collaborating Center for Campylobacter/OIE Reference Laboratory for Campylobacteriosis, Utrecht, The Netherlands[e]

Campylobacter iguaniorum has been isolated from reptiles. This **Campylobacter** species is genetically related to **Campylobacter fetus** and **Campylobacter hyointestinalis.** Here we present the first whole-genome sequence for this species.

Address correspondence to Maarten J. Gilbert, m.j.gilbert@uu.nl, or William G. Miller, william.miller@ars.usda.gov.

*C*ampylobacter iguaniorum is genetically related to, but distinct from, the species *Campylobacter fetus* and *Campylobacter hyointestinalis* and has recently been proposed as a novel *Campylobacter* species (Gilbert et al., submitted for publication). Reptiles, chelonians, and lizards in particular appear to be the primary reservoir of this *Campylobacter* species [1]. The pathogenicity of this species is unknown; strains have been recovered from reptiles with and without clinical signs of disease [1, 2]. Here, we report the first whole-genome sequence of the *C. iguaniorum* type strain 1485E^T (LMG 28143^T), isolated from a bearded dragon (*Pogona vitticeps*).

Sequencing was performed using shotgun and paired-end reads obtained on a Roche 454 FLX genome sequencer. Using the Newbler assembler (v. 2.6), we assembled a total of 220,914 454 reads into a single chromosomal scaffold of 12 contigs and a single megaplasmid contig, providing a draft genome sequence with a coverage of 68×. All 454 base calls were validated using 1,570,644 Illumina MiSeq reads, providing an additional 178× coverage. Scaffold gaps were filled as described [3]. Sequences across the contig junctions were confirmed with Sanger sequencing. Homopolymeric GC tracts were characterized using the high-depth MiSeq reads.

The circular genome size of *C. iguaniorum* strain 1485E^T is 1,684,608 bp, with an average G+C content of 35.9%. A 70,030-bp megaplasmid is present. Protein-, rRNA-, and tRNA-encoding genes were identified as described [3]. The genome was annotated based on *C. fetus* subsp. *testudinum* strain 03-427^T (accession number CP006833) [4, 5], with further annotation using Artemis [6], the identification of Pfam domains [v.26.0 [7]], and BLASTP comparisons to proteins in the NCBI nonredundant (nr) database. The chromosomal genome encodes 1663 putative protein-coding genes (including 18 probable pseudogenes), 43 tRNA genes, and 3 rRNA operons. The megaplasmid encodes an additional 111 putative protein-coding genes. A total of 34 homopolymeric GC tracts (≥8 bp) were identified, of which 23 were hypervariable. Many of these hypervariable GC tracts reside in surface-structure-related genes, as in other campylobacters; notably, however, eight are located within autotransporter domain-containing genes, whose role in *C. iguaniorum* biology remains to be determined.

In contrast to *C. fetus*, strain 1485E^T does not encode an S-layer. Also, a defined lipooligosaccharide (LOS) region, bounded by *waa* genes and containing multiple glycosyltransferases, is absent from strain 1485E^T; instead, five separate predicted glycosylation regions were identified. One of these regions is >50 kb and has a deviant G+C content (30.0%), suggesting possible acquisition via lateral transfer. A clustered regularly interspaced short palindromic repeats (CRISPR)-Cas system is present. Multiple genes encoding respiratory enzymes not identified to date within the *C. fetus* group are also present. Interestingly, as in reptile-associated *C. fetus* subsp. *testudinum*, a putative tricarballylate catabolism pathway was identified.

The whole-genome sequence of strain 1485E^T supports the proposal of *C. iguaniorum*. Further genome analysis and comparison can provide valuable insights into host adaptation, virulence, taxonomic structure, and evolution of this novel reptile-associated *Campylobacter* species.

Nucleotide sequence accession numbers. The complete genome sequence of *C. iguaniorum* strain 1485E^T has been deposited in GenBank under accession numbers CP009043 and CP009044.

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