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

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*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.

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*Campylobacter 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 1485ET (LMG 28143T), 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 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 68X. All 454 base calls were validated using 1,570,644 Illumina MiSeq reads, providing an additional 178X 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 1485ET 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 03-427T (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 tRNA 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 1485ET does not encode an S-layer. Also, a defined lipooligosaccharide (LOS) region, bounded by waa genes and containing multiple glycosyltransferases, is absent from strain 1485ET; 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 tricarboxylate catabolism pathway was identified.

The whole-genome sequence of strain 1485ET 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 1485ET has been deposited in GenBank under accession numbers CP009043 and CP009044.

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**REFERENCES**


