



# Complete Genome Sequence of *Campylobacter jejuni* RM1246-ERRC, Which Exhibits Resistance to Quaternary Ammonium Compounds

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**ABSTRACT** *Campylobacter jejuni* strain RM1246-ERRC is a clinical isolate. In laboratory experiments, RM1246-ERRC exhibited greater resistance to the antimicrobial effects of quaternary ammonium compounds than other *C. jejuni* strains. The chromosome of RM1246-ERRC is 1,659,694 bp with a G+C content of 30.56%. The strain also possesses a 45,197-bp plasmid.

Bacteria in the genus *Campylobacter* are nutritionally fastidious organisms that depend on microaerobic conditions for growth (1). However, *Campylobacter* spp. are also the cause of the largest annual number of foodborne bacterial gastrointestinal infections in the developed world (2, 3). A path by which *Campylobacter* spp. can come into contact with humans is through cross-contamination events mediated by kitchen surfaces during food preparation (4). For this reason, materials that will properly sanitize preparation surfaces and eliminate *Campylobacter* spp. are desirable, as is identifying the genetic mechanisms that are employed by the bacteria to circumvent these sanitization efforts.

*Campylobacter jejuni* strain RM1246-ERRC was originally isolated by the California State Public Health Laboratory (S. Abbott, Berkeley, CA, USA) from a case of human disease and designated strain 92A3120. The strain was renamed RM1246 before it was provided to our laboratory by Robert Mandrell (ARS, Albany, CA, USA) (5, 6). The RM1246-ERRC designation was added when the organism was entered into our strain collection. During research on the performance of a novel group of quaternary ammonium compounds (QACs) against *Campylobacter* strains, RM1246-ERRC was observed to be more resistant to the antimicrobial effects of the QACs compared to other *C. jejuni* strains (our unpublished results).

The single chromosome and plasmid of RM1246-ERRC was sequenced using a PacBio system consistent with previous whole-genome sequencing efforts (7, 8). The Celera Assembler version 8.1, along with the SMRT Analysis software suite, was used for error correction, assembly, and subread filtering (9, 10). Quiver was used to polish contigs, and Geneious version 7.1.5 (Biomatters, Auckland, New Zealand) was used to trim overlapping ends and to reorient contigs, which was followed by a second application of the Quiver program (9). The resulting assembly had a consensus accuracy of 99.9999% with 20× coverage. The RM1246-ERRC assembly yielded a circular, 1,659,694-bp single chromosome that was accompanied by a 45,197-bp plasmid.

Since RM1246-ERRC was observed to have a higher degree of resistance to QACs compared to other *C. jejuni* strains, the genome was scanned for genes that could account for this behavior. The RM1246-ERRC chromosome contains four orthologs to known multidrug-resistant proteins that belong to the QacE SMR transporter family (locus tags: CFK74\_01430, CFK74\_01435, CFK74\_05950, and CFK74\_05955). These sequences produce membrane-based transporters that are capable of effluxing QACs.

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However, this set of genes was also found in other *C. jejuni* strains that did not exhibit increased resistance to QACs, and with only minor variations in the gene sequences, this would suggest that other genetic elements may be responsible for the observed antimicrobial resistance.

**Accession number(s).** The genome sequence of *C. jejuni* strain RM1246-ERRC chromosome has been deposited in GenBank under the accession no. [CP022470](#) (chromosome) and [CP022471](#) (plasmid).

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