



# Draft Genome Sequence of *Clostridium estertheticum*-like Strain FP4, Isolated from Spoiled Uncooked Lamb

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**ABSTRACT** In order to improve the phylogenetic resolution of the genus *Clostridium* and our limited knowledge of meat spoilage caused by *Clostridium estertheticum*, the genome of *C. estertheticum*-like strain FP4 was sequenced. Here, we describe the 4.1-Mb draft genome sequence of *C. estertheticum*-like strain FP4, isolated from vacuum-packaged refrigerated spoiled lamb.

*Clostridium estertheticum*-like strain FP4 is a Gram-positive, spore-forming, and slow-growing psychrotrophic bacterium that requires strict anaerobic conditions to grow (1). Contamination with different *Clostridia* species has been recognized as a major cause of blown-pack spoilage (BPS) in vacuum-packed meat products associated with a variety of animal types, including cattle, sheep, and deer (2). Recent amplified rRNA gene restriction analysis (ARDRA) profiling and a positive real-time *C. estertheticum*-like-specific PCR assay (3, 4) placed strain FP4 into the nontoxigenic *C. estertheticum*-like cluster with >89% similarity. This paper presents the draft genome sequence of *C. estertheticum*-like strain FP4 to facilitate future investigations into meat spoilage caused by psychrotrophic *Clostridium* species.

Strain FP4 was originally isolated in 2017 at AgResearch Ltd., Palmerston North, New Zealand, from a slightly distended package of vacuum-packed refrigerated spoiled lamb in which the meat had no discoloration. FP4 was originally isolated and cultured anaerobically from the meat drip at 10°C in 10-fold suspensions of prereduced peptone-yeast extract-glucose-starch (PYGS) broth (4), and phenol-chloroform genomic DNA extraction was conducted in accordance with a previously described method (5). Paired-end (PE) sequencing libraries were generated with a TruSeq Nano DNA library prep kit (Illumina, San Diego, CA, USA), followed by whole-genome sequencing on the MiSeq platform with a MiSeq reagent kit v2 (2 × 250 bp). Trimmomatic v0.39 (<http://www.usadellab.org/cms/?page=trimmomatic>) was used to filter the raw reads (Q score, >15 in a sliding window of 4 nucleotides [nt]; minimum length, >36 nt), yielding a total of 4,534,616 PE raw sequences. *De novo* assembly was conducted with A5-miseq v20169825 (6). Default parameters were used for all software unless otherwise specified.

*In silico* analysis of FP4 yielded 251 scaffolds with an overall genome coverage of 242×, a total length of 4,093,822 bp, and a G+C content of 31.2%. The FP4 assembly produced an  $N_{50}$  value of 43,169 bp, with the largest scaffold being 133,780 bp long. The genome sequence of FP4 reported here is a useful resource for the future development of strategies for early identification of the presence of clostridial spoilage and reduction in the onset of BPS.

**Data availability.** The draft genome sequence of *Clostridium estertheticum*-like strain FP4 has been deposited in GenBank under accession number [JAAMNG000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAAMNG000000000) and BioProject accession number [PRJNA574489](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA574489). The raw sequence reads were deposited in the Sequence Read Archive (SRA) under accession number [SRR11113220](https://www.ncbi.nlm.nih.gov/sra/SRR11113220).

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