Draft Genome Sequences of Nine \textit{Campylobacter hyointestinalis} subsp. \textit{lawsonii} Strains

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\textbf{ABSTRACT} 
With increasing reports of \textit{Campylobacter hyointestinalis} species associated with human diseases, more genome sequences are required to understand the virulence mechanisms of this emerging pathogen. Here, we describe the genome sequences of nine \textit{C. hyointestinalis} subsp. \textit{lawsonii} strains.

\textit{Campylobacter jejuni} is one of the major causes of gastrointestinal illness worldwide \cite{1–4}, and other \textit{Campylobacter} species are increasingly reported to be associated with diarrheal burden \cite{5,6}. \textit{C. hyointestinalis} is among these emerging pathogens and is commonly isolated from farm animals and associated with diarrhea, gastric adenocarcinomas, proliferative enteritis, and inflammatory bowel disease in humans through zoonotic infection \cite{7–11}. The complete genome sequences of two subspecies, \textit{C. hyointestinalis} subsp. \textit{hyointestinalis} and \textit{C. hyointestinalis} subsp. \textit{lawsonii}, were first published in 2016 \cite{12}, but additional \textit{C. hyointestinalis} subsp. \textit{lawsonii} genome sequences have not been published since then. Additional genome sequences are required for understanding the virulence mechanisms and developing molecular detection methods for this emerging pathogen. Here, we report the draft genome sequences of nine \textit{C. hyointestinalis} subsp. \textit{lawsonii} strains.

Nine \textit{C. hyointestinalis} subsp. \textit{lawsonii} strains, representing eight multilocus sequence typing (MLST) sequence types (STs) \cite{13}, including the type strain of the subspecies (CHYS = LMG 14432 = NCTC 12901 = CCUG 34538), were selected for sequencing (Table 1). Single colonies from each strain were grown microaerobically for 48 h at 37°C on anaerobe basal agar supplemented with 5% laked horse blood. Genomic DNA was extracted from a loop (~5 µl) of cells using the Wizard genomic DNA kit.

Genome sequencing was performed using the Illumina MiSeq platform (Table 1). For each genome, the 2 × 250-bp paired-end trimmed MiSeq reads (average length = 237 bp) were assembled using the Newbler assembler version 2.6. An average of 75 contigs were obtained for the nine \textit{C. hyointestinalis} subsp. \textit{lawsonii} genomes, with approximately 96 to 98% of each genome represented by large contigs of ≥5,000 bp. Nearly every base in these contigs had a quality score of ≥40. The coverage for each genome ranged from 124× to 241×. All sequencing reads were deposited in the NCBI Sequence Read Archive (SRA; Table 1).

The average total sequence length for the nine \textit{C. hyointestinalis} subsp. \textit{lawsonii} genomes was 1.796 Mb (Table 1), and the G+C contents for the nine genomes ranged from 33.3 to 33.5%. These data are consistent with the previously sequenced genome of \textit{C. hyointestinalis} subsp. \textit{lawsonii} strain LMG 15993 (1.753 Mb, 33.6% G+C content) \cite{12}. Each genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and the RAST (Rapid Annotations using Subsystem Technology) version 2.0.

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| Strain   | ST | Source     | BioSample no. | BioProject no. | SRA no. | GenBank accession no. | Reads | Contigs | % of genome in large contigs (Q40%) | Total sequence length (Mb) |
|----------|----|------------|----------------|----------------|---------|------------------------|-------|---------|----------------------------------|--------------------------|
| CHY5     | 8  | Pig, stomach | SAMN09274393   | PRJNA473765    | SRP150729 | QMAE000000000         | 1,572,688 238.5 209 | 86 | 57 | 97.7 (100) | 1.786 |
| RM9004   | 97 | Pig, feces  | SAMN09274394   | PRJNA473766    | SRP150725 | QMAF000000000         | 1,060,682 237 143 | 68 | 38 | 97.9 (100) | 1.747 |
| RM9426   | 20 | Pig, feces  | SAMN09274395   | PRJNA473767    | SRP150727 | QMAG000000000         | 1,179,661 237.2 153 | 76 | 47 | 97.7 (100) | 1.823 |
| RM9752   | 21 | Pig, feces  | SAMN09274396   | PRJNA473771    | SRP150726 | QMAH000000000         | 1,809,534 238 241 | 71 | 43 | 97.6 (100) | 1.785 |
| RM9767   | 22 | Pig, feces  | SAMN09274397   | PRJNA473772    | SRP150728 | QMAI000000000         | 1,184,803 237.3 155 | 82 | 49 | 97.3 (100) | 1.808 |
| RM10071  | 23 | Pig, feces  | SAMN09274398   | PRJNA473773    | SRP150732 | QMAJ000000000         | 1,580,942 235.6 202 | 91 | 43 | 95.8 (100) | 1.836 |
| RM10074  | 22 | Pig, feces  | SAMN09274399   | PRJNA473774    | SRP150734 | QMAK000000000         | 1,409,722 233.5 181 | 82 | 47 | 96.8 (100) | 1.809 |
| RM10075  | 24 | Pig, feces  | SAMN09274400   | PRJNA473775    | SRP150736 | QMAL000000000         | 941,976 236.3 124 | 67 | 40 | 97.7 (100) | 1.786 |
| RM14416  | 37 | Cow, feces  | SAMN09274401   | PRJNA473776    | SRP150737 | QMAM000000000         | 940,690 241.2 127 | 54 | 33 | 98.1 (100) | 1.786 |
2 server ([http://rast.nmpdr.org](http://rast.nmpdr.org)) (14, 15). PGAP analysis identified an average of 1,814 putative protein-coding genes and 39 to 44 tRNAs per genome.

All strains possess genes encoding factors for bacterial defense, antimicrobial resistance, virulence, and DNA exchange, including homologs of colicin V bacteriocins, the *Campylobacter* multidrug efflux (Cme) pump, a macrolide efflux (MacAB) transporter, systems for heavy metal resistance, group II capsular polysaccharides, nonulosonic acid biosynthesis, N-linked protein glycosylation, DNA transfer mechanisms (Tra, Trb, T4SS), and the cytotochalins distending toxin (CdtABC), while some strains produce homologs of zonula occludens toxin, prophage remnants, and tetracycline resistance proteins. All these features should be examined in greater detail to understand the pathogenesis of this emerging *Campylobacter* species.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers QMAE00000000 to QAMM00000000. The versions described in this paper are the first versions, QMAE01000000 to QMAM01000000.

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