



Draft Genome Sequences of Two *Listeria monocytogenes* Strains Isolated from Raccoon Feces in Japan

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ABSTRACT *Listeria monocytogenes* serotype 4b strains RF01 and RF06 were isolated from raccoon feces in Japan. Here, we report the draft genome sequences of the two isolated strains; the genome sizes were 2,918,024 and 2,872,491 bp, with 535× and 510× coverage, for the RF01 and RF06 strains, respectively.

L *isteria monocytogenes* is a causative foodborne pathogen of listeriosis and is widespread in the environment. This bacterium has also been isolated from raccoons (*Procyon lotor*), which are free-living animals; therefore, raccoons have been suspected to transmit *L. monocytogenes* by direct contact and/or indirect contamination of the environment via invasion of human residential areas (1, 2). In Japan, *L. monocytogenes* isolates from raccoons belong to serotype 4b, which is highly pathogenic for humans (3, 4). Furthermore, their pulsed-field gel electrophoresis (PFGE) patterns are highly similar to those of strains in humans (3). These strains may influence human health; however, the relevant information is limited. To characterize this genetic trait, in this study we sequenced *L. monocytogenes* isolates from raccoon feces.

Two strains of *L. monocytogenes* from raccoon feces, RF01 and RF06, were isolated in our previous study; samples collected from raccoons in cage traps were incubated in Fraser broth and *Listeria* Oxford medium (both from Becton Dickinson) at 35°C for 24 to 48 h (3). Genomic DNA was extracted from bacterial cultures that had been incubated on brain heart infusion agar at 37°C for 18 h using a Maxwell RSC blood DNA kit (Promega). After verification of the concentration and purity of DNA extracts using the TapeStation 4150 system (Agilent Technology), the genomic library was prepared using the NEBNext Fast DNA fragmentation and library prep set for Ion Torrent kit (New England Biolabs). Genome sequencing was performed using the Ion Chef/GeneStudio S5 system (Life Technologies). Raw reads were trimmed and assembled *de novo* using CLC Genomics Workbench v.21.0 (Qiagen) and annotated using the DDBJ Fast Annotation and Submission Tool (DFAST) v.1.1.4 (5). All analyses were conducted using the default parameters for the software programs unless otherwise specified.

In total, 7,061,058 and 6,820,342 raw reads (total lengths of 1,562,322,790 and 1,465,878,468 bp) were obtained from the RF01 and RF06 strains, respectively. These strains were assembled into 45 and 35 contigs, with accumulated lengths of 2,918,024 and 2,872,491 bp at 535× and 510× coverage, for RF01 and RF06, respectively (GC content, each 37.9%).

Their sequence types (STs) were identified as ST6 (RF01) and ST4 (RF06) via multilocus sequence typing (MLST) v.2.0 (6). *L. monocytogenes* ST6 has been reported to be a hypervirulent clone and is increasingly being associated with outbreaks (7); moreover, ST4 has been associated with meat products and is considered to highly contribute to listeriosis cases (8). The virulence factors of these strains were determined *in silico* using VirulenceFinder v.2.0. In total, 82 and 81 genes in RF01 and RF06, respectively, were identified (9). The data provide the genome sequence information for *L.*

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The authors declare no conflict of interest.

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TABLE 1 Genome sequences of the isolated *Listeria monocytogenes* strains

Parameter	Data for strain:	
	RF01	RF06
Sequencing analysis		
No. of reads	7,061,058	6,820,342
Total read length (bp)	1,562,322,790	1,465,878,468
No. of contigs	45	35
Size (bp)	2,918,024	2,872,491
N_{50} (bp)	145,649	193,605
GC content (%)	37.9	37.9
Coverage depth (×)	535	510
No. of coding sequences	2,946	2,845
No. of rRNAs	3	4
No. of tRNAs	38	53
DDBJ accession no.	BRCB01000001 to BRCB01000045	BRCC01000001 to BRCC01000035
DRA accession no.	DRR362389	DRR362390
<i>In silico</i> analysis		
MLST ST	6	4
No. of virulence genes	82	81

monocytogenes strains from raccoons and suggest that these strains carried by raccoons may potentially adversely affect human health. Further accumulation of data is needed for the epidemiological monitoring of the virulence potential of this pathogen.

Data availability. Draft genomes were deposited in DDBJ/ENA/GenBank under the accession numbers provided in Table 1. Raw sequence data were deposited in the DRA under the BioProject accession number [PRJDB13507](#).

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