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GENOME SEQUENCES

Draft Whole-Genome Sequences of Seven *Listeria monocytogenes* Strains with Variations in Virulence and Stress Responses

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ABSTRACT *Listeria monocytogenes* is an important foodborne pathogen that causes listeriosis. Here, we report the draft genome sequences of seven *L. monocytogenes* strains isolated from food, environmental, and clinical sources. Sequence differences at the genome level may help in understanding why these strains displayed different virulence and stress response characteristics.

Listeria monocytogenes is a Gram-positive bacterial pathogen that is present ubiquitously in the environment. *L. monocytogenes* is often associated with foods such as ready-to-eat meats, raw produce, and dairy products (1). It is a foodborne pathogen that can cause listeriosis with a high mortality rate. *L. monocytogenes* is very difficult to control in the food industry since it can survive under very harsh conditions, such as high salt, low pH, and low temperature (2, 3). Strains of *L. monocytogenes* isolated from food, environmental, and clinical sources have displayed different serotypes, stress responses, and virulence potentials. In the current study, isolates from food were serotypes 1/2a, 1/2b, or 1/2c, whereas the clinical isolate was serotype 4b (Table 1), similar to many other reported clinical isolates (4).

Here, we report the draft genome sequences of seven *L. monocytogenes* strains isolated from food, environmental, and clinical samples (Table 1) which belong to different serotypes and have shown different stress response and virulence profiles. For example, both strains LMB33029 and LMB33868 displayed sensitivity to salt (10% NaCl) treatment, whereas strain LMB33029 was more sensitive to nisin (125 μg/ml) treatment than is strain LMB33868. LMB33761, LMB57147, and LMB33724 displayed weak ability to form biofilms as shown by biofilm assays (5). However, as determined by a plaque assay, strains LMB33761 and LMB57147 had strong virulence potential compared to that of strain LMB33724 (6). LMB33922 and LMB33123 had a strong biofilm-forming ability and a virulence potential similar to that of LMB33724 but less than that of LMB33761 and LMB57147 (our unpublished data).

For whole-genome sequencing, genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Valencia, CA) from 1 ml of overnight culture grown in tryptic soy broth (TSB), and the concentrations of genomic DNA were measured using a Qubit 3.0 fluorometer (Life Technologies, Carlsbad, CA). Library preparation was carried out using the Nextera DNA Flex library prep kit (Illumina, San Diego, CA) according to the manufacturer's instructions. Libraries generated with 600-bp frag-

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TABLE 1 Characteristics of seven *L. monocytogenes* strains

Characteristic[c]	Data for strain:						
	LMB33029	**LMB33123**	**LMB33724**	**LMB33761**	**LMB33868**	**LMB33922**	**LMB57147**
Original strain name	OB001124	NRRL B-33123	OB060053	OB050399	OB070080	OB050075	FSL F2-407
Serotype	1/2c	1/2b	1/2c	1/2c	1/2b	1/2a	4a
Origin	Food (hot dog)	Environmental (floor drain)	Food (chicken corn dogs)	Food (chili-cheese corn dog)	Environmental (food contact surface)	Food (smoked ham, water added)	Clinical (human sporadic, blood isolate)
GenBank accession no.	QGLY00000000	QGLZ00000000	QGMB00000000	QGMA00000000	QGMC00000000	QGMD00000000	QGME00000000
BioProject no.	PRJNA472364	PRJNA472366	PRJNA472369	PRJNA472372	PRJNA472380	PRJNA472385	PRJNA472388
SRA accession no.	SRP155875	SRP155874	SRP155872	SRP155871	SRP155869	SRP155868	SRP155873
Genome coverage (×)[a]	530	380	382	305	151	234	336
Size (bp)	3,066,724	3,050,559	3,040,623	3,046,742	3,080,573	2,976,439	2,764,284
GC content (%)[a]	37.8	37.8	37.8	37.8	37.9	37.8	37.9
No. of contigs	252	293	136	161	102	120	92
Total no. of genes	3,266	3,229	3,182	3,198	3,178	3,078	2,866
No. of pseudogenes	78	77	51	46	40	59	73
N_{50} (bp)[b]	50,9571	476,743	496,777	496,777	378,293	545,582	541,112
No. of CDSs	3,102	3,075	3,055	3,087	3,070	2,938	2,718
No. of tRNAs	58	58	57	56	57	58	57
No. of rRNAs	24	15	15	5	7	19	14
No. of ncRNAs	4	4	4	4	4	4	4

[a]The genome coverage was calculated via the Coverage/Read Count Calculator (http://apps.bioconnector.virginia.edu/covcalc/) (9).
[b]The N_{50} value is the size of the shortest contig in the set of longest contigs that together cover at least 50% of the total genome size.
[c]ncRNA, noncoding RNA; CDS, coding sequence.

ments were quantified by a Qubit 3.0 fluorometer (Life Technologies), and the denatured pooled libraries were loaded onto a flow cell for cluster generation. Sequencing was performed using the Illumina MiniSeq platform with a 2 × 150-bp paired-end read protocol with more than 151× coverage. The quality of the sequences was assessed by FastQC and assembled using the SPAdes genome assembler (version 3.9.0) (7), available on the BaseSpace cloud platform (BaseSpace software version 2.0.2018) from Illumina. Virulence factors, multilocus sequence types (MLST), rRNA, tRNA, genes, pseudogenes, and coding sequences (CDSs) were determined using the Illumina Bacterial Analysis Pipeline (version 1.0.4) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 4.3 (8). A description of the characteristics of the seven *L. monocytogenes* strains is presented in Table 1. Whole-genome sequence information can be used to identify the sequence differences among these strains and assist in understanding why these strains have displayed different virulence potentials and stress responses.

Data availability. The draft genome sequences reported here have been deposited in DDBJ/ENA/GenBank under the accession and BioProject numbers listed in Table 1. The versions described in this paper are the first versions.

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