

# Complete Genome Sequences of vB\_LmoS\_188 and vB\_LmoS\_293, Two Bacteriophages with Specificity for *Listeria monocytogenes* Strains of Serotypes 4b and 4e

Aidan Casey,<sup>a,b</sup> Kieran Jordan,<sup>a</sup> Aidan Coffey,<sup>b</sup> Olivia McAuliffe<sup>a</sup>

Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland<sup>a</sup>; Department of Biological Sciences, Cork Institute of Technology, Bishopstown, Co. Cork, Ireland<sup>b</sup>

***Listeria monocytogenes* is responsible for the rare disease listeriosis, which is associated with the consumption of contaminated food products. We report here the complete genome sequences of vB\_LmoS\_188 and vB\_LmoS\_293, phages isolated from environmental sources and that have host specificity for *L. monocytogenes* strains of the 4b and 4e serotypes.**

Received 15 January 2015 Accepted 6 March 2015 Published 9 April 2015

**Citation** Casey A, Jordan K, Coffey A, McAuliffe O. 2015. Complete genome sequences of vB\_LmoS\_188 and vB\_LmoS\_293, two bacteriophages with specificity for *Listeria monocytogenes* strains of serotypes 4b and 4e. *Genome Announc* 3(2):e00040-15. doi:10.1128/genomeA.00040-15.

**Copyright** © 2015 Casey et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Olivia McAuliffe, [olivia.mcauliffe@teagasc.ie](mailto:olivia.mcauliffe@teagasc.ie).

*Listeria monocytogenes* is a Gram-positive facultative anaerobe and the causative agent of listeriosis, a disease associated with the consumption of contaminated food products. Its psychotropic nature, coupled with its ability to persist in the environment (1, 2), make it a serious food safety threat, manifested by the high mortality rates (20 to 30%) associated with listeriosis (3). Three serotypes of the species (1/2a, 1/2b, and 4b) are responsible for >90% of listeriosis cases, with serotype 4b strains associated with the greatest number of outbreaks (4). While the genomic diversity of *L. monocytogenes* has been well studied (5, 6), less is known about the genomic diversity of *L. monocytogenes* phages and, in particular, the genetic determinants responsible for the specific interactions between *Listeria* phages and their hosts.

Two *L. monocytogenes* bacteriophages were isolated from mushroom compost (vB\_LmoS\_293) and wild mushroom (vB\_LmoS\_188) samples. The genomes were sequenced by MWG Eurofins (Eurofins MWG Operon, Germany) on an Illumina MiSeq next-generation sequencing (NGS) system to >100× coverage. For each, sequencing yielded approximately 3 million reads, with an average length of 148 bp and an average quality score of 37. The removal of low-quality reads was undertaken using Trimmomatic (7), and overlapping paired-end reads were segregated using FLASH (8). The reads were assembled using the DNASTar LaserGene SeqMan NGen software (DNASTar, Inc., USA). Open reading frames (ORFs) were predicted using Glimmer version 3.02 (9) and RAST (10), and RAST was utilized in subsequent genome annotations. The annotations were verified and curated using BLASTp (11) and Artemis (12), while functional domains were predicted using InterPro (<http://www.ebi.ac.uk/interpro>).

The vB\_LmoS\_188 genome is 38,392 bp in length (G+C content, 35.9%), while bacteriophage vB\_LmoS\_293 is 40,759 bp in length (G+C content, 36.9%). PCR analyses confirmed that both genomes contain linear circularly permuted double-stranded DNA (dsDNA) with terminal redundancy. Sixty ORFs were detected in vB\_LmoS\_188, while 72 ORFs were detected in vB\_LmoS\_293. The ORFs predominantly begin with the ATG start codon (91.6% in vB\_LmoS\_188 and 87.5% in vB\_LmoS\_293). No

tRNAs were detected. No function was assigned to 34/60 ORFs detected in vB\_LmoS\_188 or for 41/72 ORFs in vB\_LmoS\_293. The genomes are ordered in a modular fashion, consistent with previous observations for *Listeria* bacteriophages (13). Despite their similar host ranges and modular arrangements, the genomes of these two bacteriophages share only 37% nucleotide sequence identity and a maximum of 65% nucleotide identity with any other published *Listeria* phage genome in the NCBI database. These phages belong to a recently defined group of *Listeria* bacteriophages denoted orthocluster IV, along with phages A500, A118, A006, and LP-030-3 (14). Their specificity for *L. monocytogenes* strains of serotypes 4b and 4e is likely attributed to a small cluster of putative tail fiber genes, namely, ORFs 18 to 22 in vB\_LmoS\_188 and ORFs 19 to 23 in vB\_LmoS\_293, which are thought to function in bacterial host recognition.

**Nucleotide sequence accession numbers.** The genome sequences of these two phages have been deposited in GenBank under the accession numbers [KP399677](https://ncbi.nlm.nih.gov/nucl/KP399677) (vB\_LmoS\_188) and [KP399678](https://ncbi.nlm.nih.gov/nucl/KP399678) (vB\_LmoS\_293).

## ACKNOWLEDGMENTS

This work was supported by the EU 7th Framework projects PROMISE (project no. 265877) and FOODSEG (project no. 266061) and by a safe-food mini-project.

A.C. was the recipient of a Teagasc Walsh Fellowship.

## REFERENCES

1. Carpentier B, Cerf O. 2011. Review—persistence of *Listeria monocytogenes* in food industry equipment and premises. *Int J Food Microbiol* 145:1–8. <http://dx.doi.org/10.1016/j.ijfoodmicro.2011.01.005>.
2. Casey A, Fox EM, Schmitz-Esser S, Coffey A, McAuliffe O, Jordan K. 2014. Transcriptome analysis of *Listeria monocytogenes* exposed to biocidal stress reveals a multi-system response involving cell wall synthesis, sugar uptake, and motility. *Front Microbiol* 5:68. <http://dx.doi.org/10.3389/fmicb.2014.00068>.
3. Vázquez-Boland JA, Kuhn M, Berche P, Chakraborty T, Domínguez-Bernal G, Goebel W, González-Zorn B, Wehland J, Kreft J. 2001. *Listeria* pathogenesis and molecular virulence determinants. *Clin Microbiol Rev* 14:584–640. <http://dx.doi.org/10.1128/CMR.14.3.584-640.2001>.

4. Pan Y, Breidt F, Gorski L. 2010. Synergistic effects of sodium chloride, glucose, and temperature on biofilm formation by *Listeria monocytogenes* serotype 1/2a and 4b strains. *Appl Environ Microbiol* 76:1433–1441. <http://dx.doi.org/10.1128/AEM.02185-09>.
5. Orsi RH, den Bakker HC, Wiedmann M. 2011. *Listeria monocytogenes* lineages: genomics, evolution, ecology, and phenotypic characteristics. *Int J Med Microbiol* 301:79–96. <http://dx.doi.org/10.1016/j.ijmm.2010.05.002>.
6. Hain T, Ghai R, Billion A, Kuenne CT, Steinweg C, Izar B, Mohamed W, Mraheil MA, Domann E, Schaffrath S, Kärst U, Goesmann A, Oehm S, Pühler A, Merkl R, Vorwerk S, Glaser P, Garrido P, Rusniok C, Buchrieser C. 2012. Comparative genomics and transcriptomics of lineages I, II, and III strains of *Listeria monocytogenes*. *BMC Genomics* 13: 144. <http://dx.doi.org/10.1186/1471-2164-13-144>.
7. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <http://dx.doi.org/10.1093/bioinformatics/btu170>.
8. Magoč T, Salzberg SL. 2011. FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics* 27:2957–2963. <http://dx.doi.org/10.1093/bioinformatics/btr507>.
9. Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with Glimmer. *Nucleic Acids Res* 27: 4636–4641. <http://dx.doi.org/10.1093/nar/27.23.4636>.
10. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
11. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* 215:403–410. [http://dx.doi.org/10.1016/S0022-2836\(05\)80360-2](http://dx.doi.org/10.1016/S0022-2836(05)80360-2).
12. Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream M-A, Barrell B. 2000. Artemis: sequence visualization and annotation. *Bioinformatics* 16:944–945. <http://dx.doi.org/10.1093/bioinformatics/16.10.944>.
13. Dorscht J, Klumpp J, Biemann R, Schmelcher M, Born Y, Zimmer M, Calendar R, Loessner MJ. 2009. Comparative genome analysis of *Listeria* bacteriophages reveals extensive mosaicism, programmed translational frameshifting, and a novel prophage insertion site. *J Bacteriol* 191: 7206–7215. <http://dx.doi.org/10.1128/JB.01041-09>.
14. Denes T, Vongkamjan K, Ackermann H-, Moreno Switt AI, Wiedmann M, den Bakker HC. 2014. Comparative genomic and morphological analyses of *Listeria* phages isolated from farm environments. *Appl Environ Microbiol* 80:4616–4625. <http://dx.doi.org/10.1128/AEM.00720-14>.