

UCC Library and UCC researchers have made this item openly available. Please [let us know](#) how this has helped you. Thanks!

<b>Title</b>	Draft genome sequences of <i>Listeria monocytogenes</i> serotype 4b strains 944 and 2993 and serotype 1/2c strains 198 and 2932.
<b>Author(s)</b>	Casey, Aidan; McAuliffe, Olivia; Fox, Edward M.; Leong, Dara; Gahan, Cormac G.; Jordan, Kieran
<b>Publication date</b>	2016-06-02
<b>Original citation</b>	Casey, A., McAuliffe, O., Fox, E. M., Leong, D., Gahan, C. G. M. and Jordan, K. (2016) 'Draft genome sequences of <i>Listeria monocytogenes</i> serotype 4b strains 944 and 2993 and serotype 1/2c strains 198 and 2932', <i>Genome Announcements</i> , 4(3), e00482-16 (2pp). doi:10.1128/genomeA.00482-16
<b>Type of publication</b>	Other
<b>Link to publisher's version</b>	<a href="http://dx.doi.org/10.1128/genomeA.00482-16">http://dx.doi.org/10.1128/genomeA.00482-16</a> Access to the full text of the published version may require a subscription.
<b>Rights</b>	© 2016, the Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license. <a href="https://creativecommons.org/licenses/by/4.0/">https://creativecommons.org/licenses/by/4.0/</a>
<b>Item downloaded from</b>	<a href="http://hdl.handle.net/10468/3740">http://hdl.handle.net/10468/3740</a>

Downloaded on 2019-04-23T18:32:10Z

# Draft Genome Sequences of *Listeria monocytogenes* Serotype 4b Strains 944 and 2993 and Serotype 1/2c Strains 198 and 2932

Aidan Casey,<sup>a</sup> Olivia McAuliffe,<sup>a</sup> Edward M. Fox,<sup>b</sup> Dara Leong,<sup>a,c</sup> Cormac G. M. Gahan,<sup>d,d</sup> Kieran Jordan<sup>a</sup>

Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland<sup>a</sup>; CSIRO Animal Food and Health Sciences, Victoria, Australia<sup>b</sup>; School of Microbiology, University College Cork, Co. Cork, Ireland<sup>c</sup>; School of Pharmacy, University College Cork, Co. Cork, Ireland<sup>d</sup>

***Listeria monocytogenes* is a foodborne pathogen and the causative agent of listeriosis among humans and animals. The draft genome sequences of *L. monocytogenes* serotype 4b strains 944 and 2993 and serotype 1/2c strains 198 and 2932 are reported here.**

Received 18 April 2016 Accepted 21 April 2016 Published 2 June 2016

**Citation** Casey A, McAuliffe O, Fox EM, Leong D, Gahan CGM, Jordan K. 2016. Draft genome sequences of *Listeria monocytogenes* serotype 4b strains 944 and 2993 and serotype 1/2c strains 198 and 2932. *Genome Announc* 4(3):e00482-16. doi:10.1128/genomeA.00482-16.

**Copyright** © 2016 Casey et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Olivia McAuliffe, olivia.mcauliffe@teagasc.ie

*Listeria monocytogenes* is a Gram-positive pathogen responsible for the bacterial infection listeriosis. Listeriosis, which is associated with the consumption of contaminated foods, primarily affects the young, the old, and the immunocompromised, who are most susceptible to the infection (1). At least 95% of strains isolated from food and clinical samples are members of the 1/2a, 1/2b, 1/2c, or 4b serotype (2). Four *L. monocytogenes* strains, identified as either 4b or 1/2c, were isolated during screening of foods and food-processing environments. Strains 198 and 944 were isolated from cheese products in Ireland, while strains 2932 and 2993 were isolated from Australian meat and dairy production facilities, respectively. Pulsed-field gel electrophoresis analysis demonstrated that while strains 198 and 2932 were closely related, differing only by a single band, the pulsotypes of strains 944 and 2993 were indistinguishable.

DNA was prepared from each of the isolates using the DNeasy blood and tissue kit (Qiagen, The Netherlands), as per the manufacturer's instructions. Library preparation and 300-bp paired-end sequencing were performed using the Illumina MiSeq platform. Raw reads were preprocessed to remove adapter sequences and low-quality reads using the Trimmomatic (version 0.22) software (3). *De novo* assembly of strains 944, 2932, and 2993 was performed using the SPAdes genome assembler tool (version 2.5.1) (4), while *de novo* assembly of strain 198 was performed using the DNASTar Lasergene SeqMan NGen software (DNASTar, Inc., Madison, WI). Open reading frames (ORFs) were predicted using RAST (5), with subsequent annotations verified and manually curated using BLASTp (6) and Artemis (7).

The resulting assemblies generated a total of 10, 12, 13, and 9 contigs (all >40× average coverage) for *L. monocytogenes* strains 944, 2932, 2993, and 198, respectively, with maximum contig sizes of 816,575 bp, 640,274 bp, 562,372 bp, and 605,673 bp, and a contig  $N_{50}$  of 388,885 bp, 482,234 bp, 420,755 bp, and 516,594 bp, respectively. The draft genome sizes varied from 2.85 to 2.99 Mb, all with a G+C content of 37.9%. RAST annotation identified 2,877, 2,829, 2,876, and 2,986 protein-coding genes in strains 944, 2932, 2993, and 198, respectively. In addition, strain 198 contained a plasmid of 58,536 bp. Genome comparisons revealed 157

ORFs in strain 198 that were absent in the closely related strain 2932, many of which had phage-related or unknown functions. Also, strain 198 harbored genes potentially conferring resistance to vancomycin (AOA13\_1524c) and fosfomicin (AOA13\_1530c), as well as an aminoglycoside 3-N-acetyltransferase (AOA13\_1536c), previously reported to confer resistance to antibiotics, such as tobramycin, gentamicin, and streptomycin (8). The results suggest that strain 198 in particular may have a considerably higher tolerance to the effects of antibiotic treatment than the other strains, consistent with previous research indicating a high prevalence for antibiotic and antimicrobial resistance genes among *L. monocytogenes* dairy isolates (9).

**Nucleotide sequence accession numbers.** The whole-genome shotgun projects for these *L. monocytogenes* strains have been deposited at DDBJ/EMBL/GenBank under the accession numbers LJPD00000000 (strain 944), LJPE00000000 (strain 2932), LJPF00000000 (strain 2993), and LJOZ00000000 (strain 198). The versions described in this paper are versions LJPD01000000, LJPE01000000, LJPF01000000, and LJOZ01000000, respectively.

## FUNDING INFORMATION

This work, including the efforts of Kieran Jordan, was funded by EC Seventh Framework Programme (FP7) (265877 and 266061).

## REFERENCES

- De Noordhout CM, Devleeschauwer B, Angulo FJ, Verbeke G, Haagsma J, Kirk M, Havelaar A, Speybroeck N. 2014. The global burden of listeriosis: a systematic review and meta-analysis. *Lancet Infect Dis* 14: 1073–1082. [http://dx.doi.org/10.1016/S1473-3099\(14\)70870-9](http://dx.doi.org/10.1016/S1473-3099(14)70870-9).
- Lahuerta A, Westrell T, Takkinen J, Boelaert F, Rizzi V, Helwigh B, Borck Høg B, Korsgaard H, Ammon A, Mäkelä P. 2011. Zoonoses in the European Union: origin, distribution and dynamics the EFSA-ECDC summary report 2009. *Euro Surveill* 16:5–8. <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19832>.
- 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>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.

5. 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: <http://dx.doi.org/10.1186/1471-2164-9-75>.
6. 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).
7. 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>.
8. Morar M, Wright GD. 2010. The genomic enzymology of antibiotic resistance. *Annu Rev Genet* 44:25–51. <http://dx.doi.org/10.1146/annurev-genet-102209-163517>.
9. Srinivasan V, Nam H, Nguyen L, Tamilselvam B, Murinda S, Oliver S. 2005. Prevalence of antimicrobial resistance genes in *Listeria monocytogenes* isolated from dairy farms. *Foodborne Pathog Dis* 2:201–211.