



# Draft Genome Sequences of *Listeria monocytogenes*, Isolated from Fresh Leaf Vegetables in Owerri City, Nigeria

Ogueri Nwaiwu,<sup>a</sup> Alexandra Moura,<sup>b,c</sup> Pierre Thouvenot,<sup>b</sup> Catherine Rees,<sup>a</sup>  
Alexandre Leclercq,<sup>b</sup> Marc Lecuit<sup>b,c,d,e</sup>

University of Nottingham, Sutton Bonington Campus, Loughborough, Leicestershire, United Kingdom<sup>a</sup>;  
Institut Pasteur, National Reference Center and WHO Collaborating Center for *Listeria*, Paris, France<sup>b</sup>; Institut  
Pasteur, Biology of Infection Unit, Paris, France<sup>c</sup>; Inserm U1117, Paris, France<sup>d</sup>; Paris Descartes University,  
Sorbonne Paris Cité, Institut Imagine, Necker-Enfants Malades University Hospital, Division of Infectious  
Diseases and Tropical Medicine, APHP, Paris, France<sup>e</sup>

**ABSTRACT** Here, we report the draft genome sequences of three *Listeria monocytogenes* isolates from fresh leaves collected in Nigeria, belonging to sequence types ST5 and ST155 (sublineages SL5 and SL155, respectively).

*Listeria monocytogenes* is a foodborne Gram-positive bacterium that can cause listeriosis, a severe infection in humans and animals. Recent genomic studies have demonstrated the international circulation of *L. monocytogenes*, highlighting the urgent need to monitor strains at the global level (1).

Here, we report the draft genome of three isolates isolated in Owerri City, south-eastern Nigeria, from fresh leaves of *Gnetum africanum*, *Gongronema latifolium*, and *Vernonia amygdalina* vegetables (2).

DNA was purified using the DNeasy blood and tissue extraction kit (Qiagen), from 5 mL of liquid culture grown overnight at 35°C in brain heart infusion medium (BD Difco) under aerobic conditions. DNA quantity and purity was assessed using Qubit (Thermo Fisher Scientific). Library preparation was carried out using the Nextera XT DNA sample kit according to the manufacturer's protocol (Illumina). Whole-genome sequencing was performed on an Illumina NextSeq 500 platform using 2 × 150 bp runs (Illumina, San Diego, CA, USA), at an estimated average read coverage of 130× (Table 1). FqCleaner v3.0 was used to eliminate adapter sequences (3), reduce redundant or over-represented reads (4), correct sequencing errors (5), merge overlapping paired reads (6), and discard reads with Phred scores of ≤20. Assemblies were generated with SPAdes v3.1.0 (7), with different k-mer values ranging from 21 to 127. The draft genome sizes varied from 2.93 to 3.06 Mb, with a G+C content of 37.9% (Table 1). Multilocus sequence typing (MLST) and core genome MLST (cgMLST) allelic profiles were performed from the assemblies using the BIGSdb-*Lm* database (<http://bigsdb.pasteur.fr/listeria>), as described previously (1). Isolates belonged to MLST ST5 and ST155 (8) and cgMLST profiles were defined as new cgMLST types (CT2050 and CT2051) (1). Gene prediction and annotation were performed by the RAST tool (9).

These isolates constitute the first *L. monocytogenes* genome sequences from Nigeria and will contribute to a better knowledge of the diversity of this species in Africa (10).

**Accession number(s).** The draft assemblies reported here were deposited at DDBJ/EMBL/GenBank under the accession numbers provided in Table 1.

Received 24 March 2017 Accepted 6 April 2017 Published 1 June 2017

**Citation** Nwaiwu O, Moura A, Thouvenot P, Rees C, Leclercq A, Lecuit M. 2017. Draft genome sequences of *Listeria monocytogenes*, isolated from fresh leaf vegetables in Owerri City, Nigeria. *Genome Announc* 5:e00354-17. <https://doi.org/10.1128/genomeA.00354-17>.

**Copyright** © 2017 Nwaiwu 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 Alexandra Moura, [amoura@pasteur.fr](mailto:amoura@pasteur.fr), or Marc Lecuit, [marc.lecuit@pasteur.fr](mailto:marc.lecuit@pasteur.fr).

**TABLE 1** Genome features of the three *L. monocytogenes* isolates reported in this study

| Isolate (genotype <sup>a</sup> ) | No. of reads | Avg coverage | No. of contigs | N <sub>50</sub> contig length (bp) | Genome size (bp) | % G+C | No. of genes | Accession no.                  |
|----------------------------------|--------------|--------------|----------------|------------------------------------|------------------|-------|--------------|--------------------------------|
| LmNG1 (L1-SL5-ST5-CT2050)        | 1,112,112    | 111          | 25             | 412,544                            | 2,968,175        | 37.86 | 2,996        | FWPO01000001 to FWPO01000025   |
| LmNG2 (L1-SL5-ST5-CT2050)        | 1,172,506    | 117          | 30             | 237,962                            | 3,060,847        | 37.86 | 3,106        | FWPRO10000001 to FWPRO10000030 |
| LmNG3 (L2-SL155-ST155-CT2051)    | 1,310,101    | 131          | 30             | 510,628                            | 2,933,139        | 37.86 | 2,983        | FWPS01000001 to FWPS01000030   |

<sup>a</sup>The genotype is indicated as a string of phylogenetic lineage (L), sublineage (SL), sequence type (ST), and cgMLST type (CT).

## ACKNOWLEDGMENTS

We thank the P2M platform (Institut Pasteur, Paris, France) for genome sequencing. This work was supported by Institut Pasteur.

## REFERENCES

- Moura A, Criscuolo A, Pouseele H, Maury MM, Leclercq A, Tarr C, Björkman JT, Dallman T, Reimer A, Enouf V, Larssonneur E, Carleton H, Bracq-Dieye H, Katz LS, Jones L, Touchon M, Tourdjman M, Walker M, Stroika S, Cantinelli T, Chenal-Francisque V, Kucerova Z, Rocha EPC, Nadon C, Grant K, Nielsen EM, Pot B, Gerner-Smidt P, Lecuit M, Brisse S. 2016. Whole genome-based population biology and epidemiological surveillance of *Listeria monocytogenes*. *Nat Microbiol* 2:16185. <https://doi.org/10.1038/nmicrobiol.2016.185>.
- Nwaiwu O. 2016. Molecular serotype and evolutionary lineage of *Listeria monocytogenes* isolated from different Nigerian food items. *Afr J Biotechnol* 15:696–705. <https://doi.org/10.5897/AJB2015.15125>.
- Criscuolo A, Brisse S. 2013. AlienTrimmer: A tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. *Genomics* 102:500–506. <https://doi.org/10.1016/j.ygeno.2013.07.011>.
- Crusoe MR, Alameldin HF, Awad S, Boucher E, Caldwell A, Cartwright R, Charbonneau A, Constantinides B, Edverson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, González I, Guermond S, Guo J, Gupta A, Herr JR, Howe A, Hyer A, Härpfer A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McA'Nulty P, McDonald E, Mizzi J, Murray KD, Nahum JR, Nanlohy K, Nederbragt AJ, Ortiz-Zuazaga H, Ory J, Pell J, Pepe-Ranney C, Russ ZN, Schwarz E, Scott C, Seaman J, Sievert S, Simpson J, Skennerton CT, Spencer J, Srinivasan R, Standage D, Stapleton JA, Steinman SR, Stein J, Taylor B, Trimble W, Wiencko HL, Wright M, Wyss B, Zhang Q, Zyme E, Brown CT. 2015. The Khmer software package: enabling efficient nucleotide sequence analysis. *F1000Res* 4:900.
- Liu Y, Schröder J, Schmidt B. 2013. Musket: A multistage k-mer spectrum-based error corrector for Illumina sequence data. *Bioinformatics* 29:308–315. <https://doi.org/10.1093/bioinformatics/bts690>.
- Magoč T, Salzberg SL. 2011. FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics* 27:2957–2963. <https://doi.org/10.1093/bioinformatics/btr507>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski 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. <https://doi.org/10.1089/cmb.2012.0021>.
- Ragon M, Wirth T, Hollandt F, Lavenir R, Lecuit M, Le Monnier A, Brisse S. 2008. A new perspective on *Listeria monocytogenes* evolution. *PLoS Pathog* 4:e1000146. <https://doi.org/10.1371/journal.ppat.1000146>.
- 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, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST Server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Leclercq A, Charlier C, Lecuit M. 2014. Global burden of listeriosis: the tip of the iceberg. *Lancet Infect Dis* 14:1027–1028. [https://doi.org/10.1016/S1473-3099\(14\)70903-X](https://doi.org/10.1016/S1473-3099(14)70903-X).