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Draft Genome Sequences of 25 Listeria monocytogenes Isolates Associated with Human Clinical Listeriosis in Ireland

Amy O’Callaghan,a,b Amber Hilliard,a,b Ciara A. Morgan,a,b Eamonn P. Culligan,a,b* Dara Leong,c Niall DeLappe,d Colin Hill,a,b Kieran Jordan,c Martin Cormican,e Cormac G. M. Gahan,a,b,f

APC Microbiome Institute, University College Cork, Cork, Ireland; School of Microbiology, University College Cork, Cork, Ireland; Teagasc Food Research Centre, Moorepark, Fermoy, Cork, Ireland; National Salmonella, Shigella and Listeria Reference Laboratory, Galway University Hospitals, Galway, Ireland; School of Medicine, National University of Ireland, Galway, Ireland; School of Pharmacy, University College Cork, Cork, Ireland

ABSTRACT Listeria monocytogenes is a Gram-positive opportunistic pathogen that is the causative agent of listeriosis. Here, we report the draft genome sequences of 25 L. monocytogenes strains isolated from patients with clinical listeriosis in the Republic of Ireland between 2013 and 2015.

Listeria monocytogenes is a Gram-positive, intracellular foodborne pathogen that causes listeriosis. Contaminated foods, in particular, ready-to-eat foods, are the primary vehicle of transmission to humans. Infections can result in mild gastroenteritis in otherwise healthy individuals. However, more common presentations of the disease are invasive infections such as bloodstream infection, meningitis, and meningoencephalitis. These conditions are typically associated with pregnancy, the newborn, the elderly, and those that are otherwise immunocompromised (1, 2). Although disease incidence is uncommon, mortality is as high as 30% (1). Given the severity of the disease, epidemiological surveillance and control of L. monocytogenes is important to ensure early detection of linked cases allowing timely intervention to protect public health and ensure the safety of the food chain. Whole-genome sequencing of L. monocytogenes is emerging as the primary means of molecular typing of isolates and allows epidemiological surveillance of strains from food sources and from clinical disease, thus facilitating detection of previously undetected links. This underpins the investigation of mechanisms that may influence disease pathogenesis (1, 3). To aid in the molecular epidemiological surveillance of the pathogen, the draft genome sequences of 25 L. monocytogenes isolates have been determined. The isolates were obtained from clinical cases of disease in Ireland between 2013 and 2015 and were submitted to the National Salmonella, Shigella and Listeria (human health) Reference Laboratory service at Galway University Hospital.

Whole-genomic DNA was extracted using the GenElute bacterial genomic DNA kit (Sigma Aldrich) per the manufacturer’s instructions. Library preparation and 250-bp paired-end sequencing was performed using the Illumina HiSeq 2500 platform (Microbes NG, University of Birmingham, UK). Raw reads were mapped to a reference genome using BWA-mem and de novo assembly was performed using SPAdes genome assembler. Contigs were reordered using Mauve aligner (v2.4.0). Prediction of putative open reading frames (ORFs) was performed using PRODIGAL prediction software (http://prodigal.ornl.gov/) and supported by BLASTx (4) alignments. Results of Prodigal/BLASTx were combined manually and a preliminary identification of ORFs was performed on the basis of BLASTp (4) analysis against a nonredundant protein database.

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Address correspondence to Cormac G. M. Gahan, c.gahan@ucc.ie.

* Present address: Eamonn P. Culligan, Department of Biological Sciences, Cork Institute of Technology, Bishopstown, Cork, Ireland.

A.O. and A.H. contributed equally to this work.
Using the ORF finding outputs and associated BLASTp results, Artemis (5) was employed for visualization and manual editing in order to verify and, where necessary, redefine the start of every predicted coding region, or to remove or add coding regions.

The assignment of protein function to predicted coding regions was performed manually. In addition, the individual members of the revised gene/protein data set were searched against the protein family (Pfam) (6) and Clusters of Orthologous Groups (COG) (7) databases.

rRNA and tRNA genes were detected using RNAMMER (http://www.cbs.dtu.dk/services/RNAmmer/) and tRNA-scanSE (http://lowelab.ucsc.edu/tRNAscan-SE/), respectively.

COG category assignment (7) was performed by means of BLASTp (4) analysis against the COG database (8) for deduced proteins of all identified ORFs contained by the genomes of both L. monocytogenes strains that were sequenced as part of the current study, and of all publicly available L. monocytogenes strains.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank. Accession numbers and basic genome information are presented in Table 1.

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