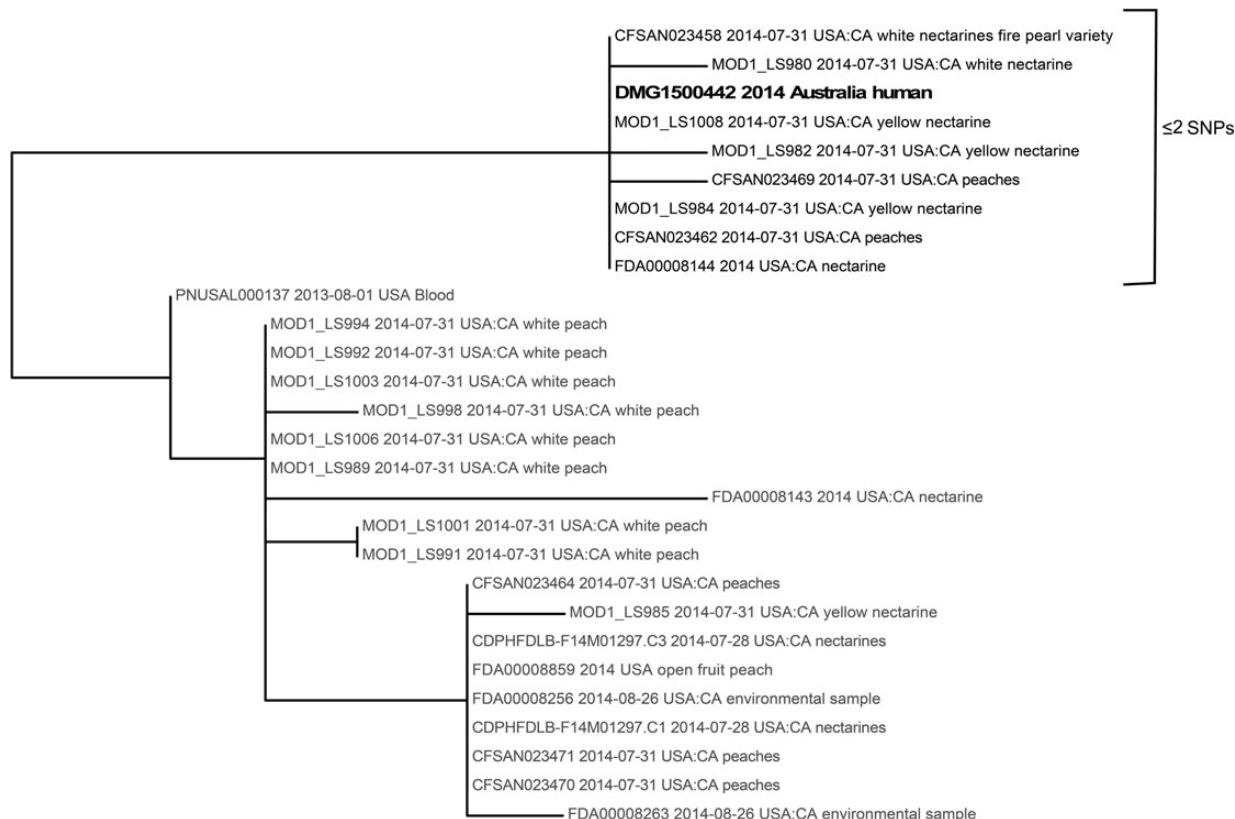


**Sharing Is Caring: International Sharing of Data Enhances Genomic Surveillance of *Listeria monocytogenes***

TO THE EDITOR—We read with interest the 2 recent reports by Jackson et al and Jensen et al on the use of whole-genome sequencing (WGS) for surveillance and outbreak investigation of *Listeria monocytogenes* [1, 2]. We have also used WGS in Australia for this purpose [3] and, on the basis of our experience, we wish to highlight the importance of international collaborations and real-time data exchange.

An elderly man presented with confusion and fever for investigation and was subsequently admitted to hospital. Blood cultures were positive for *L. monocytogenes*, with the case notified to the state department of health, and the isolate was referred to state and national *Listeria* reference laboratories. The isolate underwent molecular typing and WGS (European Nucleotide Archive accession number ERS946910) in accordance with a national *Listeria* surveillance program [3], and epidemiologic information was obtained using a standardized case questionnaire. As the isolate was not epidemiologically or genomically linked to any other Australian isolate, the case was deemed to be sporadic.

WGS data were also submitted to the US Food and Drug Administration Genome-Trakr network, an enhanced real-time surveillance program, for comparison with international isolates [1]. Upon analysis, the isolate was found to be almost identical to a US cluster of isolates from stone fruit,



**Figure 1.** Phylogenetic tree based on core genome single-nucleotide polymorphisms (SNPs) showing the genomic relationship of the Australian *Listeria monocytogenes* isolate to the US cluster associated with stone fruit. Fewer than or equal to 2 SNPs separated the isolates within the cluster, indicating a high degree of genomic relatedness. The phylogeny was inferred using the US Food and Drug Administration Center for Food Safety and Applied Nutrition SNP Pipeline (<http://snp-pipeline.readthedocs.io/en/latest/>).

reported by Jackson et al [1] (Figure 1). Unconsumed stone fruit imported into Australia from the United States was subsequently recalled, and no other clinical cases linked to the fruit were detected.

A history of nectarine and peach consumption after local purchase was noted on review of the case, with no recent international travel reported. Although the fruit was no longer available for testing, given stone fruit were out of season in Australia and significant quantities were being imported from the United States at the time, it is highly plausible that the fruit consumed by the patient was derived from the contaminated US batch.

Similar to our study [3], Jackson et al also demonstrated the superior resolution of WGS over other typing methods for discrimination of isolates. This case of listeriosis also illustrates the ease of using WGS to compare international isolates.

In addition, the case emphasizes the benefits of international sharing of microbial genomic data from pathogen surveillance programs, as others have previously advocated [4]. With this data exchange, the use of WGS was able to link a seemingly sporadic case to an outbreak cluster—a critical step in limiting the early spread of outbreaks in new jurisdictions.

We note that sequencing data from the study by Jensen et al has not been made publicly available at this time [2]. Although we acknowledge there may be sensitivity related to the public release of data, we believe that this data would also facilitate interjurisdiction comparison of outbreaks.

In an age in which both hosts and pathogens frequently cross international boundaries, surveillance systems need to be adaptable to these movements, accurately identifying related isolates, while maintaining confidentiality of patient information.

Although WGS provides the means, only with sharing of data in real time can we hope to maintain pace with the international spread of pathogens.

#### Note

**Potential conflicts of interest.** All authors: No reported conflicts. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

**Jason C. Kwong,<sup>1,2</sup> Russell Stafford,<sup>3</sup> Errol Strain,<sup>4</sup> Timothy P. Stinear,<sup>1,2</sup> Torsten Seemann,<sup>1,5</sup> and Benjamin P. Howden<sup>1,2,6</sup>**

<sup>1</sup>Doherty Applied Microbial Genomics, Doherty Institute, Melbourne, <sup>2</sup>Department of Microbiology and Immunology, University of Melbourne, Parkville, and <sup>3</sup>OzFoodNet, Communicable Diseases Branch, Queensland Health, Brisbane, Australia; <sup>4</sup>US Food and Drug Administration, College Park, Maryland; <sup>5</sup>Victorian Life Sciences Computation Initiative, University of Melbourne, Carlton, and <sup>6</sup>Microbiological Diagnostic Unit Public Health Laboratory, Doherty Institute, Melbourne, Australia

#### References

1. Jackson BR, Strain E, Tarr C, et al. Implementation of nationwide real-time whole-genome sequencing to

- enhance listeriosis outbreak detection and investigation. *Clin Infect Dis* **2016**; 63:380–6.
2. Jensen AK, Nielsen EM, Björkman JT, et al. Whole-genome sequencing used to investigate a nationwide outbreak of listeriosis caused by ready-to-eat delicatessen meat, Denmark, 2014. *Clin Infect Dis* **2016**; 63:64–70.
  3. Kwong JC, Mercoulia K, Tomita T, et al. Prospective whole-genome sequencing enhances national surveillance of *Listeria monocytogenes*. *J Clin Microbiol* **2016**; 54:333–42.
  4. Gardy JL, Loman NJ, Rambaut A. Real-time digital pathogen surveillance. *Genome Biol* **2015**; 16:155.

Correspondence: B. P. Howden, Microbiological Diagnostic Unit Public Health Laboratory, Doherty Institute for Infection and Immunity, 792 Elizabeth Street, Melbourne, VIC 3000, Australia (bhowden@unimelb.edu.au).

**Clinical Infectious Diseases® 2016;63(6):846–8**

© The Author 2016. Published by Oxford University Press for the Infectious Diseases Society of America. All rights reserved. For permissions, e-mail journals.permissions@oup.com. DOI: 10.1093/cid/ciw359