A multinational listeriosis outbreak and the importance of sharing genomic data

Our globalised food supply presents immense challenges to ensuring food safety, as shown by outbreaks of foodborne illnesses associated with imported foods.[1] The speed with which such outbreaks are resolved often depends on how rapidly public health scientists communicate and disseminate actionable data. One such data source is whole-genome sequencing, which is the newest method of molecular subtyping and has superior discriminatory power compared with previous methods.[2] Consequently, whole-genome sequencing has been and continues to be adopted by countries across the world as a tool to combat foodborne pathogens.[3] Sequence data can be made publicly available through numerous databases (eg, the European Nucleotide Archive, the National Center for Biotechnology Information [NCBI] Sequence Read Archive, and the DNA Data Bank of Japan Sequence Read Archive). Laboratories are encouraged to share the genomes they have sequenced[4] and, as new genomes are made public, isolates can be clustered into genetically similar groups to facilitate the detection of potential outbreaks and sources of contamination.

Here we discuss a recent case of how international collaboration and sharing of whole-genome sequencing data facilitated the identification of a novel food associated with outbreaks caused by *Listeria monocytogenes* in Australia, Canada, and the USA. We hope that the events we describe will encourage all public health, food safety, and other authorities to contribute their whole-genome sequencing data to public databases in as close to real-time as possible.

By the end of 2019, cluster PDS000011550 in the NCBI *L monocytogenes* Pathogen Detection database contained 36 clinical isolates with a distinct genetic pattern. The associated illnesses, which included four deaths and six pregnancy-associated infections, began in 2016 and a suspected food vehicle could not be identified from available food exposure histories.

In February, 2020, the Canadian Food Inspection Agency (CFIA) uploaded whole-genome sequencing data for a 2016 isolate from a food sample from its pathogen archives to the NCBI Pathogen Detection database. This Canadian domestic mushroom matched the outbreak cluster. Subsequently, another Canadian isolate from an imported enoki mushroom sample was uploaded to the NCBI Pathogen Detection database that matched the outbreak cluster. These isolates provided the first evidence of what contaminated food might be causing human illnesses and deaths.

In late February to early March, 2020, US state and federal partners collected enoki mushroom product samples, which yielded 12 isolates whose sequences were uploaded into the NCBI Pathogen Detection database and were found to match the outbreak cluster.[5]

In the middle of March, 2020, US public health officials learned via the EU Epidemic Intelligence Information System that French authorities had collected five *L monocytogenes* isolates from enoki mushrooms originating from South Korea in 2017. Genomic analyses showed these five food isolates were highly related to the outbreak, but those sequence data are not publicly available.

In late March, 2020, further testing by the CFIA identified five samples of enoki mushroom product from South Korea that were positive for *L monocytogenes*; whole-genome sequencing data was a match to the outbreak cluster. Additionally, through the Food and Agriculture Organization and WHO International Food Safety Authorities Network, US federal officials were notified of six clinical isolates collected in Australia between October, 2017, and March, 2020. These isolates were uploaded to NCBI Pathogen Detection database and found to match the outbreak cluster.

In April, 2020, as part of the US domestic outbreak investigation, additional imported enoki mushrooms from South Korea were sampled and *L monocytogenes* isolates were found that matched the outbreak.

This outbreak investigation shows how international sharing of whole-genome sequencing data can decrease the time required to resolve foodborne outbreaks and reduce the burden to public health (appendix pp 1–2). None of the insights described here would have been possible without effective surveillance and international cooperation based on shared genomic data. A common cause of illness over several years and continents would not have been recognised,

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For the **European Nucleotide Archive** see https://www.ebi.ac.uk/ena/browser/home

For the **National Center for Biotechnology Information Sequence Read Archive** see https://www.ncbi.nlm.nih.gov/sra

For the **DNA Data Bank of Japan Sequence Read Archive** see https://www.ddbj.nig.ac.jp/dra/index-e.html

See **Online** for appendix

contaminated products would have remained in the food supply chain, and more people would have been at risk from contaminated food. Delays in aggregating and disseminating data internationally can result in the continued exposure of consumers to potentially contaminated products, whereas routine real-time data sharing can halt this exposure and save lives. We hope this case study provides incentive to all nations doing whole-genome sequencing of foodborne pathogens to upload and share their whole-genome sequencing data in real-time. By doing so, we can reduce the time a foodborne pathogen is present within the global food chain.

We declare no competing interests. The findings and conclusions in this Comment are those of the authors and do not necessarily represent the official position of the US Centers for Disease Control and Prevention.

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