

# The Impact of Prospective Whole Genome Sequencing for *Listeria monocytogenes* on Outbreak Detection and Response: A Canadian Perspective



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## BACKGROUND

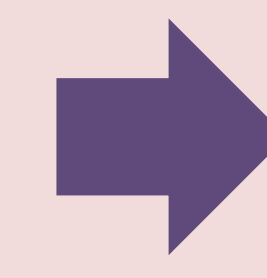
*Listeria monocytogenes* (LM) is a nationally notifiable disease in Canada and is under enhanced surveillance. When clusters of genetically related illness meeting defined criteria are identified, epidemiologic investigations are initiated to determine the potential source of illness. These investigations involve information requests to provincial/territorial partners and the review of case level exposure information collected through the Enhanced National Listeriosis Surveillance Program. In January 2017, Canada began prospective whole genome sequencing (WGS) for clinical isolates of LM, replacing Pulsed Field Gel Electrophoresis (PFGE) as the standard molecular typing technique used for detecting clusters of LM illness.

## OBJECTIVE

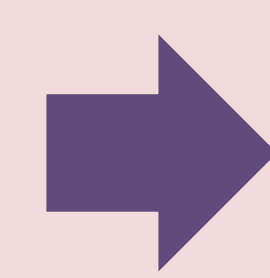
To describe how the transition from PFGE to WGS affected outbreak detection and response activities for multi-jurisdictional clusters of LM in Canada.

## METHODS

Multi-jurisdictional clusters of LM identified



Clusters reviewed and prioritized for follow-up using defined criteria\*

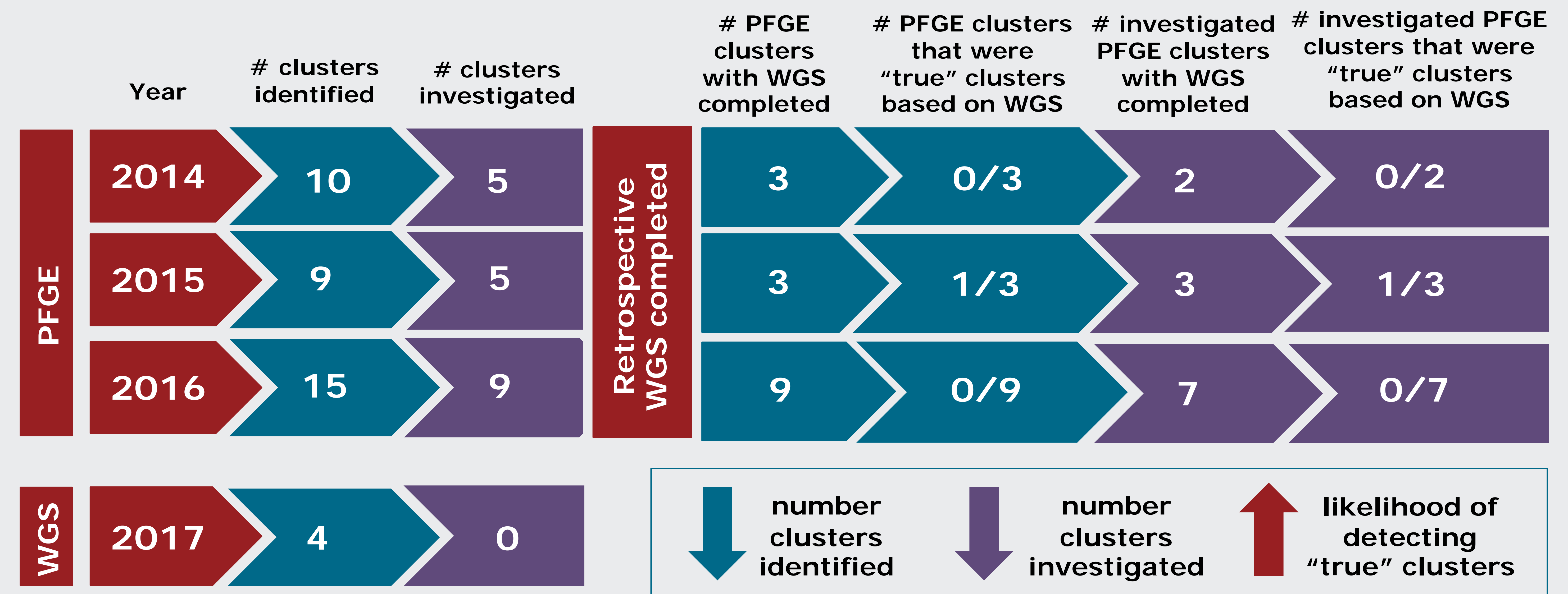


Epidemiological information collated and analyzed

The number of PFGE clusters identified and investigated each year between January 1, 2014 and December 31, 2016 was compared to the number of WGS clusters identified and investigated in 2017 during the same time period. Retrospective sequencing was completed on select PFGE clusters to determine “true” relatedness based on WGS.

## RESULTS

Epidemiological investigations were initiated for 19 of 34 multi-jurisdictional PFGE clusters identified between 2014 and 2016. Retrospective WGS was completed for 15 of these PFGE clusters and only one cluster from 2015 was confirmed to be genetically related. This was the only cluster for which a source was identified. There were 4 multi-jurisdictional LM clusters detected by WGS in 2017 but none resulted in epidemiological investigations as they did not meet the criteria for follow-up\*.



\* **LM Criteria for Follow-up:** 3 or more isolates in 120 days, with at least 2 human isolates OR 4 or more isolates in the last 5 years, with at least 2 human isolates and at least 1 human isolate in the last 120 days.

## CONCLUSIONS

WGS has demonstrated greater discriminatory power than PFGE for the detection of LM clusters in Canada. Previous unsuccessful attempts to identify sources of illness within PFGE clusters were likely due to the investigation of genetically unrelated cases. The implementation of WGS has resulted in a decrease in the number of LM clusters identified, resulting in fewer epidemiological investigations and more efficient use of resources for outbreak response.

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