NML SCIENCE STORY

WEEK OF FEBRUARY 10, 2020

TRACKING CHANGES IN WHOOPING COUGH

Laboratory surveillance Of vaccinepreventable diseases is important for public health as it helps us understand the dynamics of infectious agents and how vaccines affect them. This research is one of the ongoing example vigilance necessary to monitor and understand how able to persist despite widespread vaccination efforts.

What was known about this area prior to your work, and why was the research done?

Pertussis (whooping cough) is a highly contagious, vaccine-preventable bacterial disease caused by *Bordetella pertussis*



The evolving nature of Bordetella pertussis in Ontario, Canada, 2009-2017: strains with shifting genotypes and pertactin deficiency. Tsang RSW*, Shuel M*, Cronin K*, Deng S*, Whyte K*, Marchand-Austin A, Ma J, Bolotin S, Crowcroft N, Schwartz K, Van Domselaar G*, Graham M*, Jamieson FB. Can J Microbiol 2019 Nov;65(11):823-30. doi: https://doi.org/10.1139/cjm-2019-0128

(*B. pertussis*) and infects between 1000 and 3000 Canadians each year. Most developed countries, including Canada, have infant immunization programs. The most common type of pertussis vaccine contains only parts of the bacteria cell, such as pertactin (PRN) and fimbriae (FIM3) antigens, rather than the whole bacteria. These components are also used to distinguish and classify pertussis strains into distinct Sequence Types (ST). Despite high vaccination rates, increases in pertussis have been reported in recent years. One reason for this increase could be changes in the bacterium that create a mismatch with components of the current vaccine. Identifying and understanding these changes in the circulating pertussis strains is important and a key function of a national reference laboratory.

What are your most significant findings from this work?

In collaboration with Public Health Ontario, a collection of *B. pertussis* cultures recovered from patients over a nine-year period (2009-2017) were analysed. Many of these clinical isolates did not match with two important vaccine components (FIM3 and PRN). Also, two predominant genotypes (ST-1 and ST-2), appeared to alternate in prevalence over the study period. When the presence of ST-1 increased, ST-2 decreased and vice versa. This is likely due to the bacteria adapting to the vaccine. Of note, two newer STs (ST-21 and ST-22) lacking PRN function have emerged since 2015. Their infection rates appear to be increasing (3% of 2015 isolates to 15% of 2017 isolates). These changes in the *B. pertussis*



bacterium may be a result of strain selection brought about by natural and/or vaccinedriven immunity.

What are the implications or impact of the research?

This study showed that some clinical isolates of *B. pertussis* did not match important vaccine components. The current vaccine may become less and less effective in the future if this trend continues. Laboratory surveillance studies with detailed strain characterization are important to monitor circulating strains. When circulating strains begin to deviate from vaccine targets, vaccine efficacy can diminish and infection risk increases. Understanding vaccine effectiveness aids in preparedness efforts to create and update vaccines to control this common childhood disease. The representative strains collected at the NML will serve as an important bio-bank of materials for future reference. The knowledge acquired from this study will be helpful to consider in the development of new vaccines

* PHAC-NML researcher