



# Infectious laryngotracheitis (ILT) Outbreak Investigation

**Final Report**

## Why do this investigation?



- BC poultry flocks have experienced an increasing number of ILT outbreaks over the last decade. ILT outbreaks can result from naturally occurring ILT viruses or from viruses originating from certain ILT vaccines that subsequently mutate to spread and cause disease.
- **The goal of this project was to determine if genomics (i.e., DNA sequencing-based) technologies can help shed light on the source(s) of ILT viruses circulating in BC.**

## What did we do?



- In collaboration with the BC Centre for Disease Control, **we developed a new ILT sequencing technology.**
- That technology was used to sequence a selection of samples from ILT cases submitted to the Animal Health Centre between 2015 to 2023. For the purpose of this project, each 'ILT positive detection' represents a specific BC farm at a specific point in time, with birds that have either i) ILT-compatible histopathology lesions or ii) PCR positive without compatible lesions or iii) PCR positive but have not been examined microscopically.

## What did we learn?



- There was a total of 256 ILT positive detections between 2015 and 2023, with the peak number of detections occurring in 2022. ILT positive detections came from 165 farms, with 49 farms having 2 or more detections up to a maximum of 6 per farm.
- A total of 104 viruses were successfully sequenced, making this the **single largest genomic study of ILT viruses ever conducted in North America.**
- All ILT virus sequences were very similar to one another. It means that viral sequences cannot be used to track chains of transmission among farms.
- BC ILT viruses were very similar to those from other Canadian provinces, including ILT viruses from Alberta, Ontario and Quebec detected during the same time range.
- All BC ILT viruses are descendants of CEO vaccine revertants. However, the genomic evidence suggests that this reversion most likely occurred at least a decade ago and that **ongoing vaccine reversion is not contributing to ILT cases that have occurred since 2015. This means that ILT prevention should include maintaining good biosecurity practices and continuing to prioritize vaccine products that are less prone to reversion.**

## What is next?



- It was not possible to identify risk factors for ILT outbreaks due to a lack of epidemiological information in historic cases.
- Because of the high level of genetic similarity between ILT viruses circulating in BC, genomics alone is not sufficient to understand how ILT is transmitted in the Fraser Valley.
- **A collaborative project to identify farm-specific risk factors would provide data to strengthen ILT prevention recommendations for BC poultry flocks.**