



An Investigation of HPAI H5N1 in BC, Fall 2023 – A Synopsis

Objectives:

The purpose of this investigation was to understand the genomic, spatiotemporal, and epidemiological trends from the fall 2023 'wave' of the Highly Pathogenic Avian Influenza (HPAI) outbreak in poultry and wild birds in BC. The findings from this investigation can be used to develop and prioritize HPAI monitoring and mitigation activities being conducted by the BC Ministry of Agriculture and Food and the BC poultry industry and to identify knowledge gaps that can guide future investigations.

Outbreak Summary:

The third 'wave' of HPAI H5N1 in BC occurred from October 20, 2023, to January 22, 2024. During this period, a total of 54 poultry farms were infected (Infected Premises [IPs] 105-158). A total of 134 HPAI-infected wild birds were detected between September and December 2023. The majority of these infected wild birds and poultry farms were concentrated in the Fraser Valley.

Analytical Focus and Genomic Evolution:

The genetic sequence of HPAI viruses can be determined in laboratories, and then used to understand how HPAI viruses isolated from different individual animals or groups of animals (e.g. flocks) are related to one another, and therefore what transmission networks are most likely. HPAI sequence data is initially used to understand big picture relationships, and subsequently investigated in more detail to explore linkages between more closely related viruses.

For this investigation, HPAI viruses from poultry and wild birds isolated in BC between October, 2023 and January, 2024 were sequenced¹, and sequences were compared to determine how viruses from different sources were related to each other. Groups of related viruses were categorized into 'genomic clusters'. In the fall 2023 'wave', wild birds and poultry were infected with viruses belonging to three distinct HPAI H5N1 genomic clusters: Cluster 3A-NP-A (9 poultry farms and 24 wild birds), Cluster 3A-NP-B (38 poultry farms and 26 wild birds), and Cluster 6A (7 poultry farms and 24 wild birds) (Figure 1).

Only poultry and wild birds within the same genomic cluster could have transmitted HPAI to one another. Therefore, within each genomic cluster, potential connections among farms and wildlife were assessed using detailed sequence data, detection dates, locations, and ownership details for farms.



Figure 1 - Two genomic clusters were detected in wild birds and poultry in Wave 3 of the HPAI H5N1 – Cluster 6A and 3A. Cluster 3A was further divided into two subclusters (3A-NP-A and 3A-NP-B) based on two distinct reassortments of the NP gene.

HPAI H5NI Wave 3 Transmission Investigation – Key Findings:

Due to producer confidentiality, this synopsis does not include any specific IP information ; rather, a high-level example is used to illustrate the major findings relevant to the transmission network.

¹ HPAI viruses from domestic poultry were sequenced at the CFIA NCFAD laboratory, and HPAI viruses from wildlife were sequenced at the BCCDC laboratory.

Within genomic clusters 3A-NP-A and 3A-NP-B, there were at least seven groups of farms, encompassing a total of 35 of the 47 total IPs, that showed strong genetic, geographic, and temporal evidence of local transmission or farm-to-farm spread. The remaining ten farms appeared to be independent incursions.

Within Cluster 3A-NP-B specifically, there were a total of 38 poultry farms and 26 wild birds (Figure 2). Of the 38 farms, there were 28 farms that could be clearly grouped into one of five groups based on strong genetic, geographic, and temporal evidence. This finding is supportive for local and/or farm-to-farm spread within each group (Figure 3).

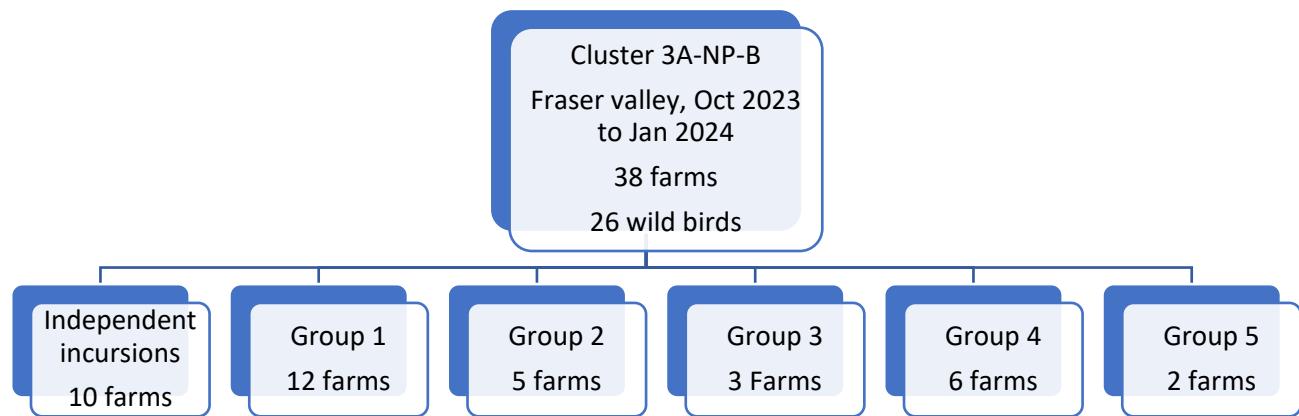


Figure 2 – Details of number of farms in each genetic-geographic- temporal group in cluster 3A-NP-B.

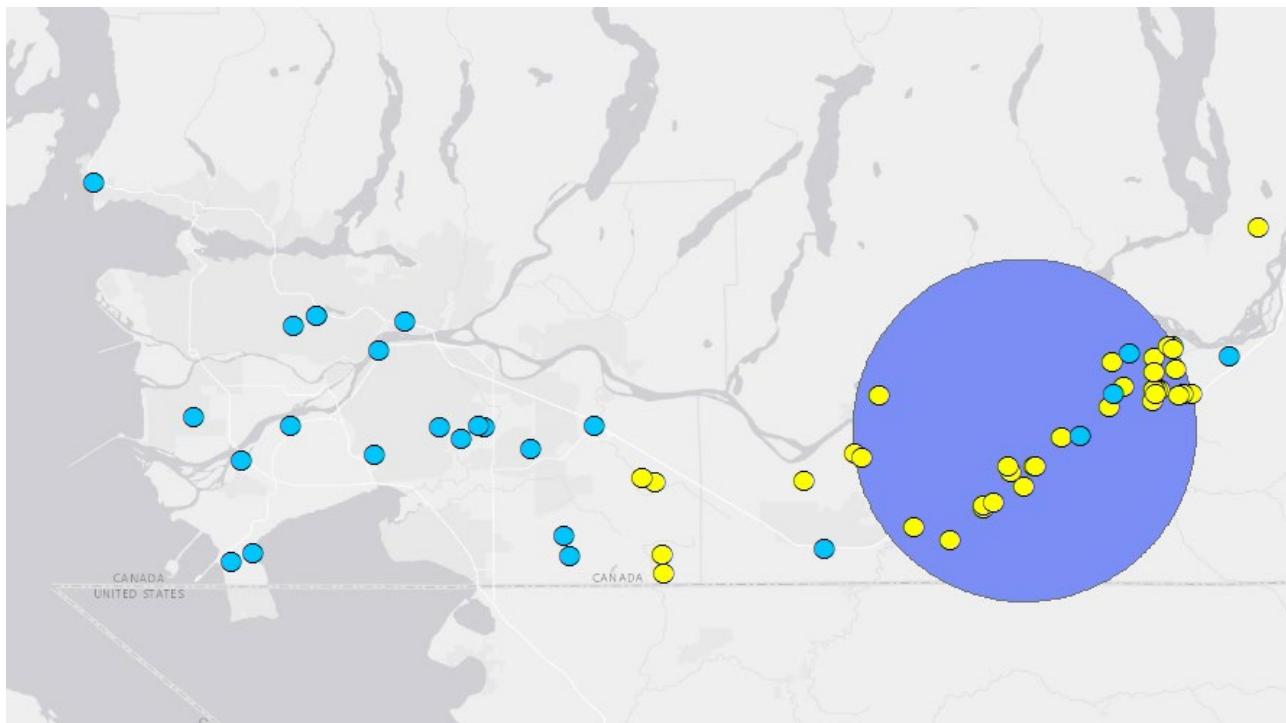


Figure 3 - Geographic distribution of wild birds (blue) and poultry farms (yellow) infected with Cluster 3A-NP-B with statistically significant geographic cluster of infected farms (large circle).

Full Report and Next Steps:

The full descriptive epidemiology report provides comprehensive genomic, temporal, and spatial analyses for each wild bird and IP. Since the report includes potentially identifying information, sharing the full report will require affected producers to provide consent. If all producers in a cluster consent, there is an opportunity to share the identity of farms within a cluster with all producers in that cluster, allowing them to further consider potential avenues of farm-to-farm transmission. Distribution of the report and associate information would be strictly limited to producers, producer associations, marketing boards and government agencies involved in the response, with the explicit goal of working collaboratively to reduce the risk of transmission, protect flock health and a stable supply chain.

This analysis was completed independently and in parallel with the CFIA analysis. Findings have not been validated by the CFIA in its role as competent veterinary authority for Canada. We will continue to work closely with the CFIA on epidemiological investigations and reports.

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