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Wave 2 - highly pathogenic avian influenza (HPAI)  
H5N1 clade 2.3.4.4b in B.C. and the Yukon, Canada,  
September 2022 to April 2023

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# Why do we still care about HPAI?!

- Longest and largest outbreak North America has ever experienced
- AIVs spread globally via wild bird migrations
- Major implications for the commercial poultry sector
- Unprecedented impacts on wild birds
  - Large die offs
- Global, unprecedented non-human mammalian spillover
- Human pandemic potential

# Data Collection for HPAI Detection & Surveillance

## *Passive surveillance*

- *Collection of wild bird and mammal carcasses*

## *Active surveillance*

- Hunter harvest
- Live bird capture
- Wetland sediment surveillance

## *Domestic birds*

- Canadian Food Inspection Agency (CFIA)



Michelle Coombe

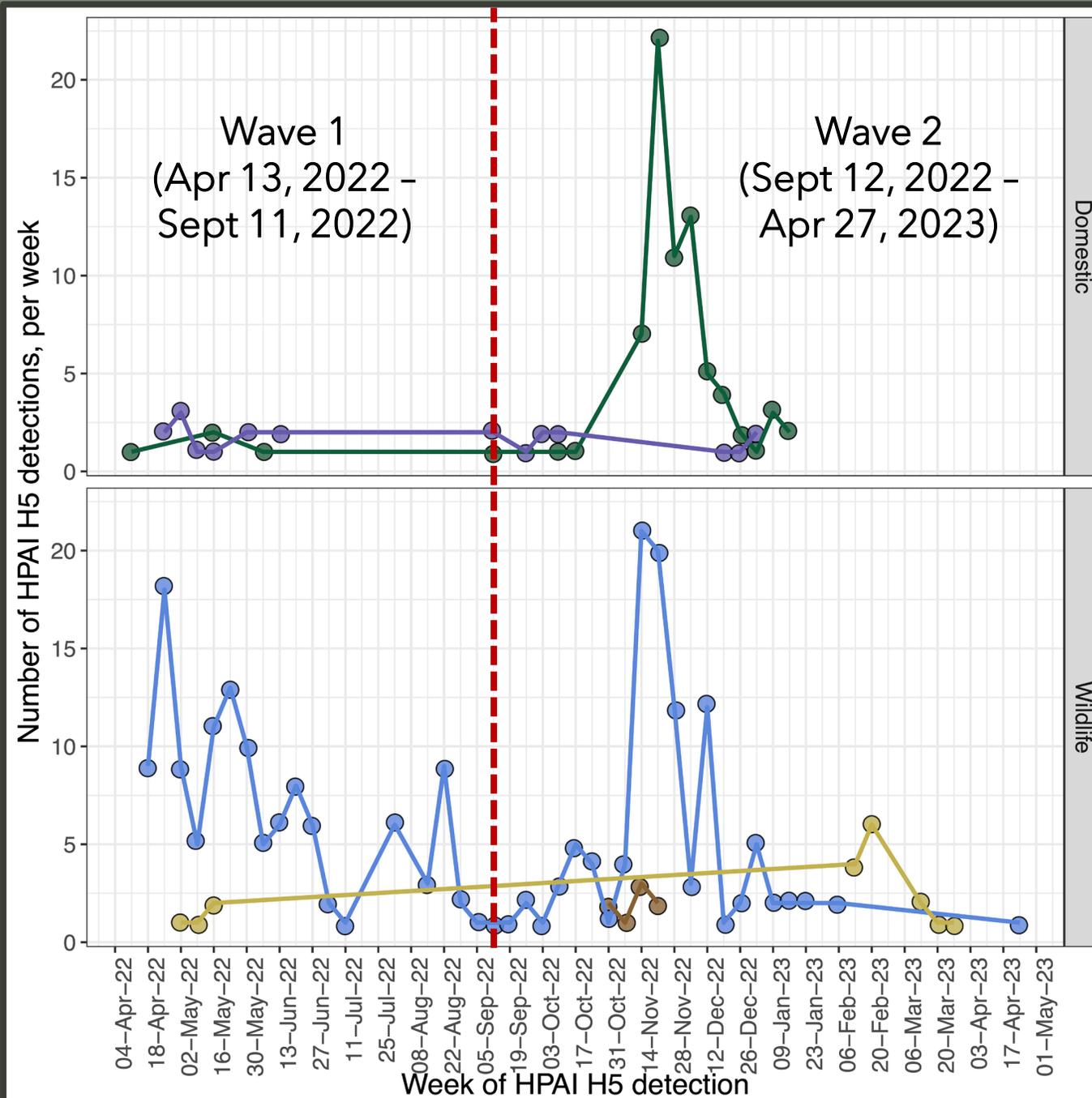


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# Epidemic curve of HPAI H5N1 in B.C. and the Yukon



- Animal Type**
- Domestic - Commercial
  - Domestic - Non-commercial
  - Wild - Passive bird
  - Wild - Passive mammal
  - Wild - Active hunted

# Taxonomic (descriptive) epidemiology

## *BC Passive wild bird surveillance (n = 394)*

- 67 different species
- **134 birds (34%) positive on PCR**

## *YT Passive wild bird surveillance (n = 23)*

- 14 different species
- **2 birds (9%) positive on PCR**

## *Active surveillance (hunting) (n = 87)*

- 6 species
- **11 birds (11.5%) positive on PCR**

## *Active surveillance (live capture) (n = 50)*

- 2 species
- **No positives**

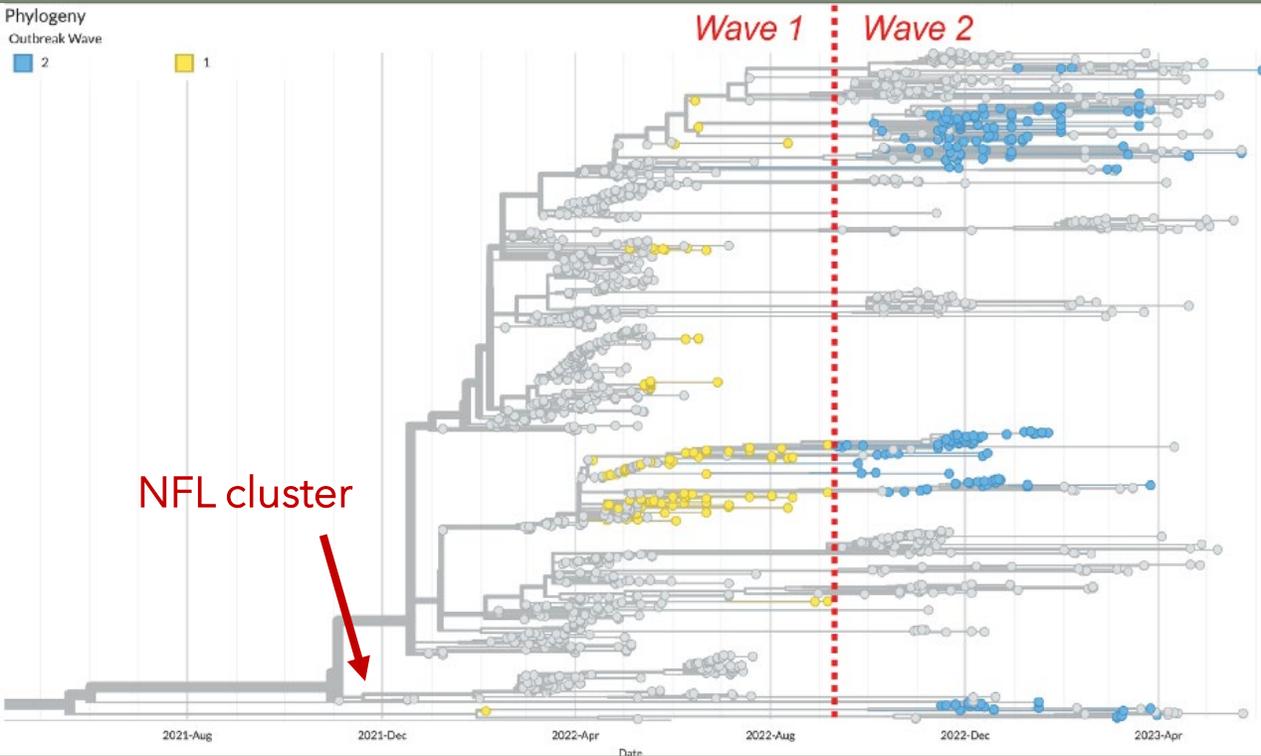
## *Domestic premises*

- 85 B.C. poultry farms, 73 commercial and 12 non-commercial

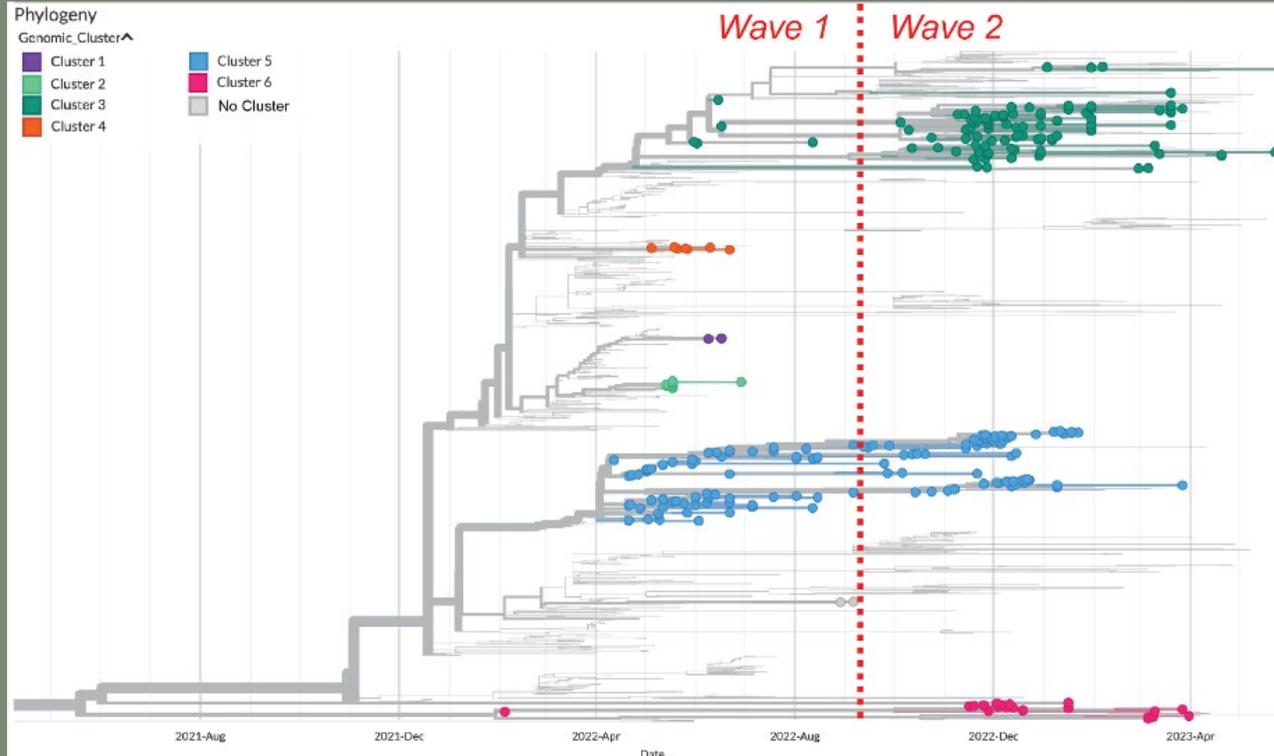


# 6 distinct genetic clusters – multiple introductions of HPAI H5N1 2.3.4.4b

A.

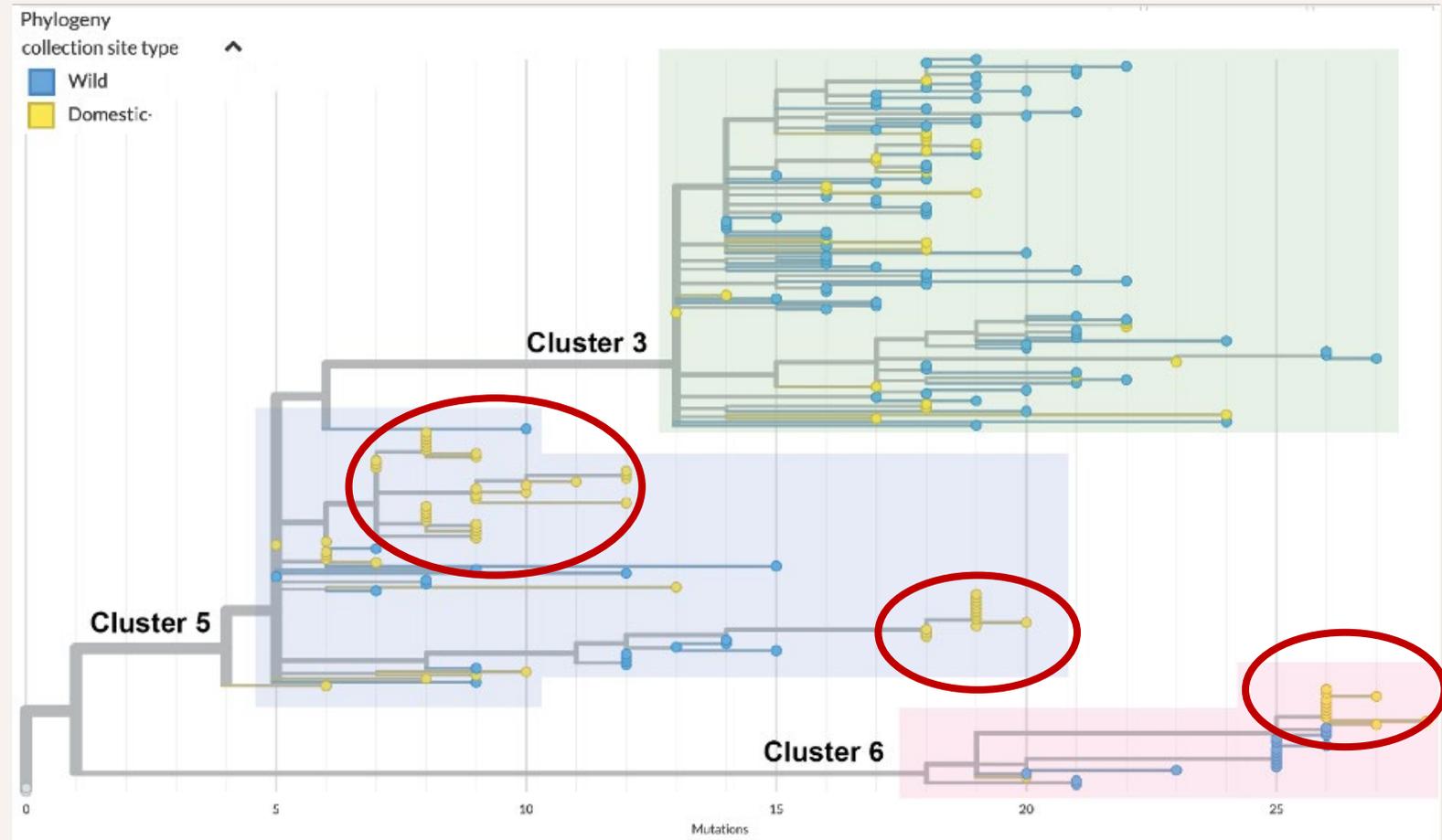


B.

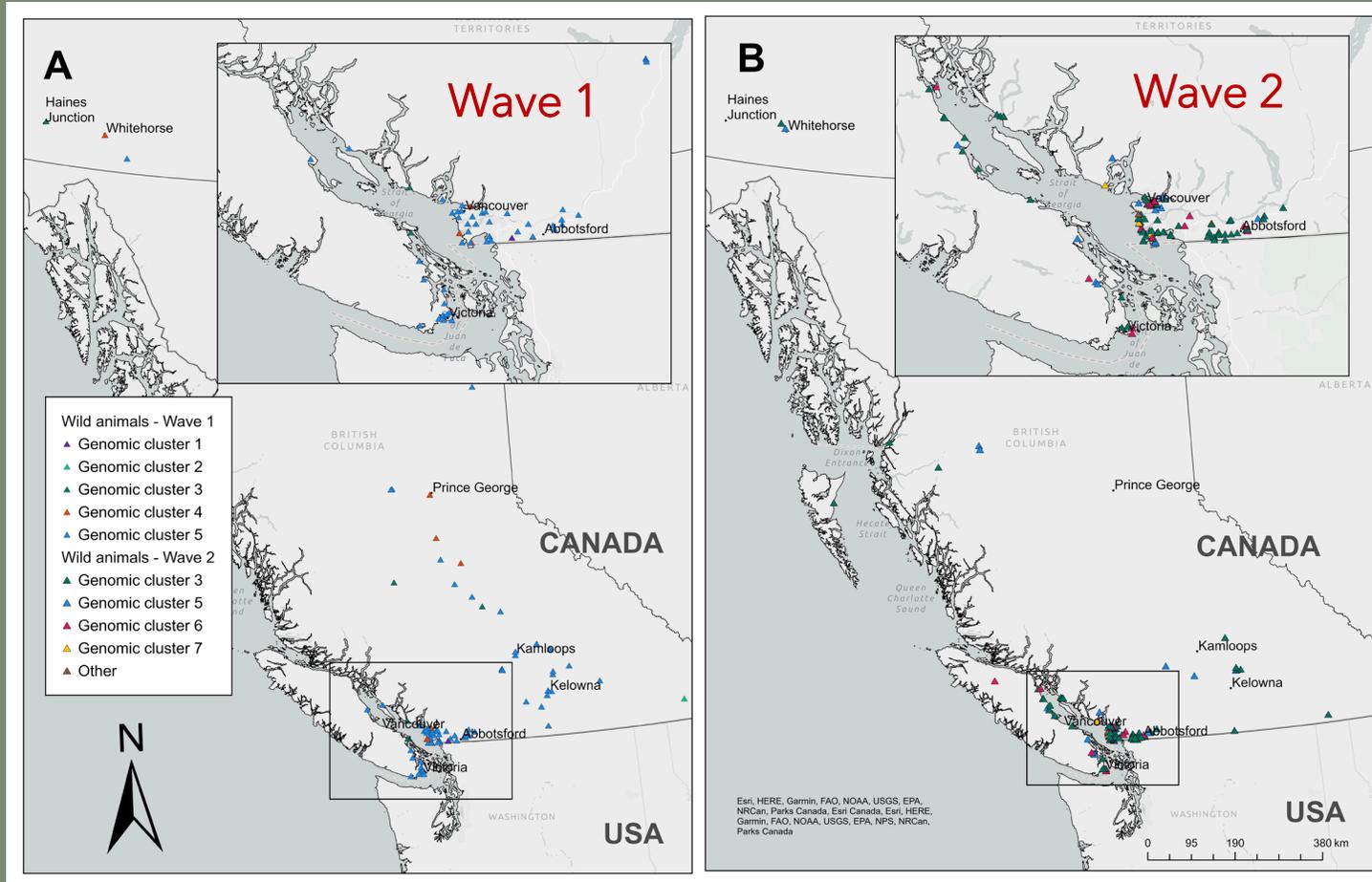


Hemagglutinin (HA)-specific phylogenetic analysis of H5N1 detections in British Columbia (B.C.) and the Yukon

Examining the genetic relationships between domestic and wild birds suggest multiple modes of transmission contributed to spread



# Temporospatial analysis (Wave 1 vs Wave 2)



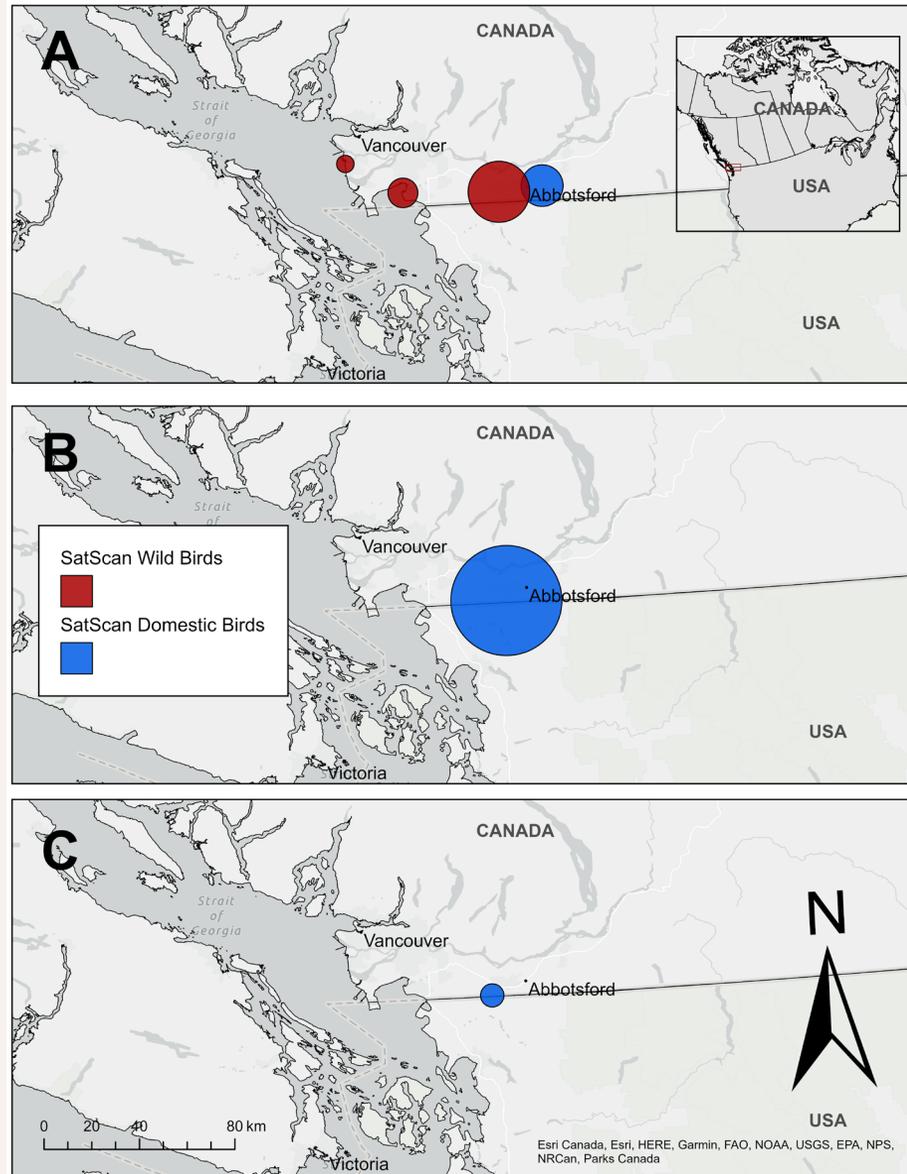
- More cases in interior B.C. in W1 than W2
- Cases more concentrated within southwestern B.C. W2 vs W1
- Generally widespread genetic clusters and bird species over time

# SatScan analysis

## Geospatial clustering

Statistically significant ( $p \leq 0.05$ ) spatial clustering for genetic Clusters 3, 5 and 6

- *Cluster 3* - three spatial clusters in wild birds, one in poultry, **none of which directly coincided spatially**
- *Cluster 5* - One large spatial cluster for poultry farms
- *Cluster 6(B)* - one smaller spatial cluster



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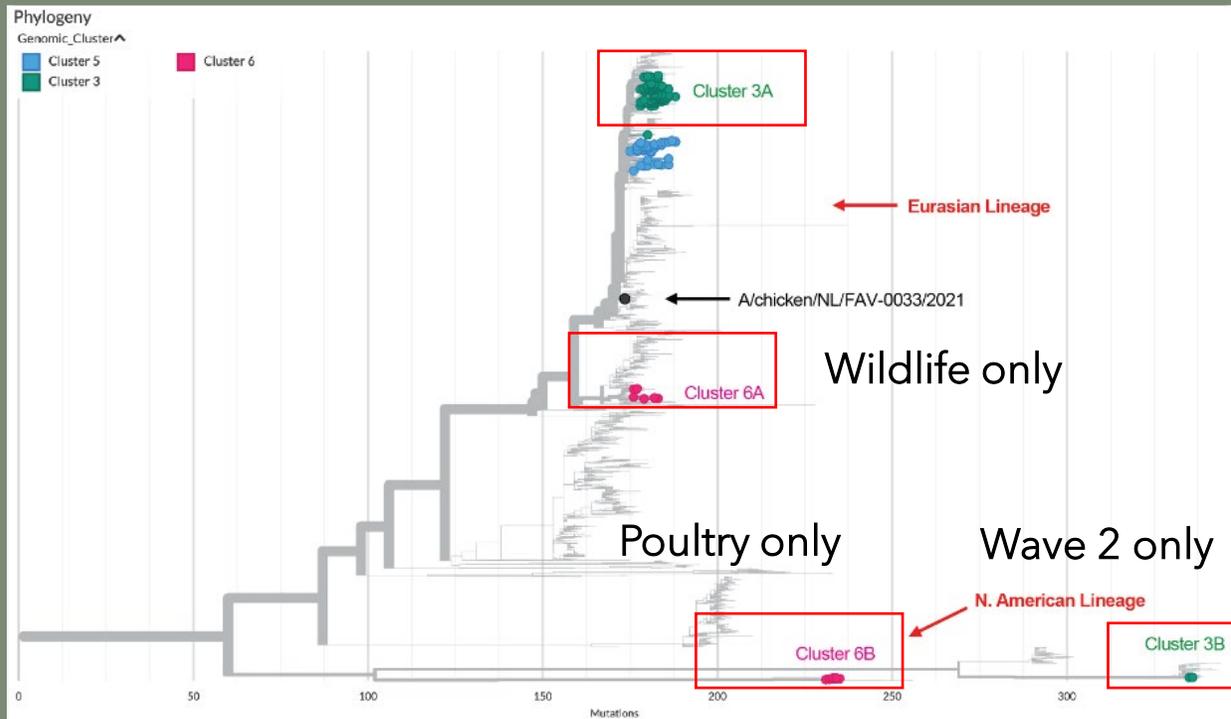
5 different reassortment patterns were observed in the H5N1 viruses detected in the B.C./Yukon outbreak, illustrating the diversity of strains that were in circulation

Genetic Cluster	Influenza A Segment*								Genome Constellation	Total wildlife samples (N (%))	Total poultry samples (N (%))
	HA	NA	M	NP	NS	PA	PB1	PB2			
Cluster 3A	EA	EA	EA	NAm	NAm	EA	NAm	NAm	A	78 (67%)	24 (28%)
Cluster 3B	EA	EA	EA	NAm	NAm	NAm	NAm	NAm	B	0 (0%)	2 (2%)
Cluster 5	EA	EA	EA	NAm	EA	EA	EA	NAm	C	21 (18%)	50 (59%)
Cluster 6A	EA	EA	EA	EA	EA	EA	EA	EA	D	17 (15%)	0 (0%)
Cluster 6B	EA	EA	EA	EA	EA	NAm	NAm	EA	E	0 (0%)	9 (11%)

\*EA = Eurasian lineage; NAm = North American lineage

Cluster 6B has North American origin gene segments for both PA and PB, whereas 6A is entirely Eurasian in origin  
*Cluster 6A - wildlife only, Cluster 6B - poultry only*  
Cluster 6A was detected in bald eagle in March 2022, and not again until November 2023

### C. PA



### D. PB1



# Conclusions

Complex and quickly changing disease ecology in wild birds

- Combination of migration and resident bird effects

Widespread dissemination of six genomic strains of the virus

Rapid viral evolution

Multiple spillover events into poultry, but cannot rule out lateral transmission



Hans Isaacson (Unsplash)

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## Provincial Health Services Authority



BC Centre for Disease Control

