Wild bird surveillance for avian influenza in BC

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BC Centre for Disease Control
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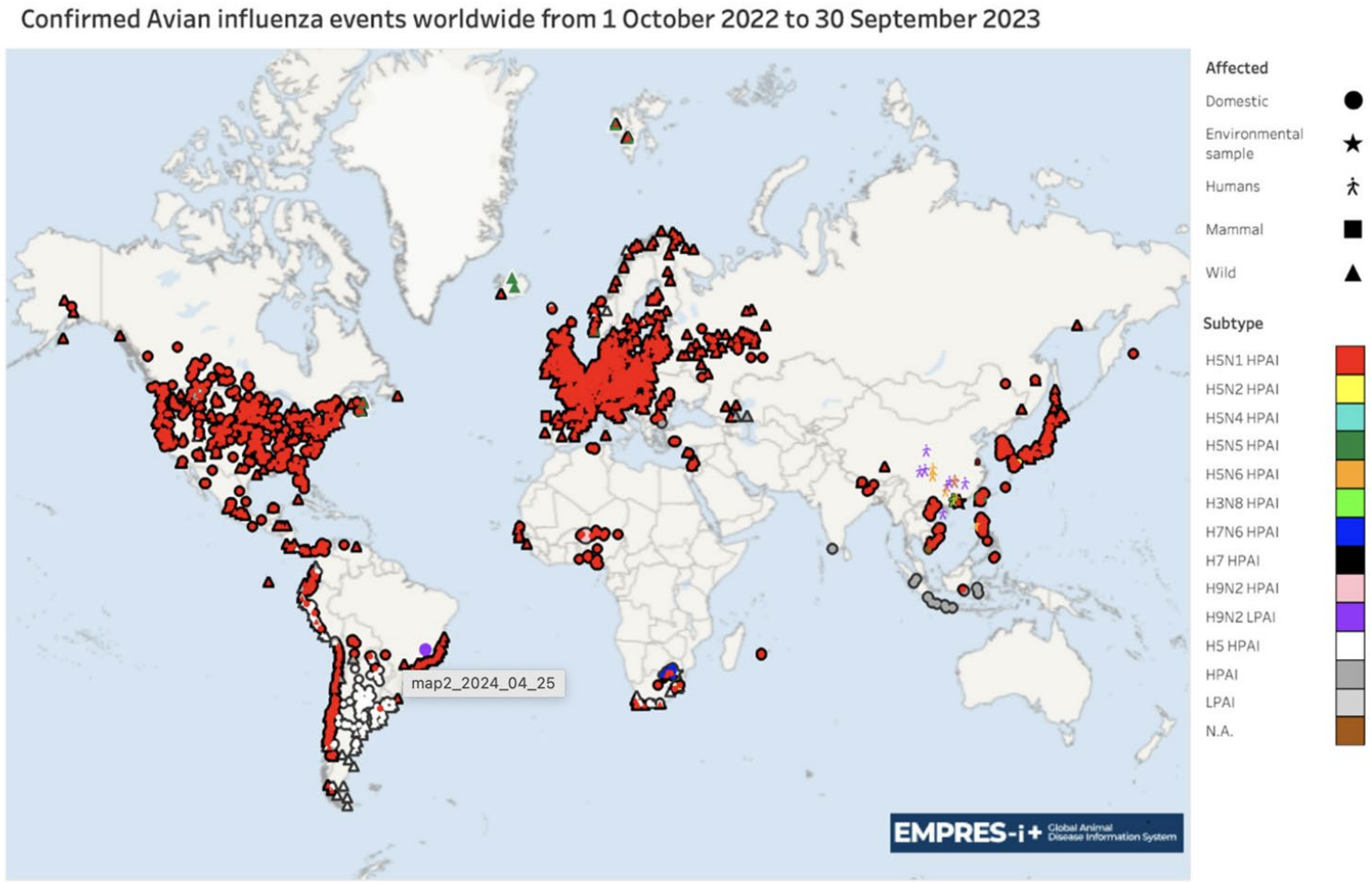
Global impact of HPAI H5N1 Clade 2.3.4.4b outbreak

Map 2. *Global distribution of AIV with zoonotic potential* observed in the period 1 October 2022 to 30 September 2023 (i.e. previous wave)*



https://www.fao.org/animal-health/situation-updates/global-aiv-with-zoonotic-potential/en

Emergence of H5N1 in cattle, swine and non-avian wildlife suggests the virus may be adapting to mammalian hosts

USDA announces first H5N1 avian flu detection in US pigs

Lisa Schnirring, October 30, 2024

B.C. has had more poultry flocks destroyed due to HPAI than any other province

Province	Number of infected premises (current IPs)	Number of previously infected premises (released IPs)	Estimated numbe impacted (as of
Alberta	3	82	1,862,000
British Columbia	41	158	6,562,000
Manitoba	0	23	400,000
New Brunswick	0	2	Under 100
Newfoundland and Labrador	0	2	400
Nova Scotia	0	8	12,000
Ontario	0	49	899,000
Quebec	1	54	1,411,000
Saskatchewan	1	44	751,000
Total	**46**	**422**	**11,897,000**

https://inspection.canada.ca/en/animal-health/terrestrial-animals/diseases/reportable/avian-influenza/latest-bird-flu-situation/status-ongoing-avian-influenza-response

TODAY IN BC

6 poultry farms in Fraser Valley hit with avian influenza in October

3 Chilliwack farms, 3 Abbotsford farms with avian influenza breaks 8-month streak in Canada

Jennifer Feinberg
about 24 hours ago

VANCOUVER | News

'My tears will not stop': B.C. family farm forced to kill all chickens and ducks after avian flu outbreak

B.C. has had more poultry flocks destroyed due to HPAI than any other province

Province	Number of infected premises (current IPs)	Number of previously infected premises (released IPs)	Estimated number of birds impacted (as of 2024-11-13)
Alberta	3	82	1,86
British Columbia	41	158	6,5
Manitoba	0	23	400
New Brunswick	0	2	Un
Newfoundland and Labrador	0	2	400
Nova Scotia	0	8	12,0
Ontario	0	49	899
Quebec	1	54	1,4
Saskatchewan	1	44	751
Total	**46**	**422**	**11,**

BRITISH COLUMBIA | BC Gov News

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Health

First presumptive positive case of H5 avian influenza detected in B.C.

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News Release

Victoria
Saturday, November 9, 2024 3:37 PM

Media Contacts

Andy Watson
Director of Communications
Office of the Provincial Health Officer
236 475-3094

An individual in British Columbia has tested presumptive positive for avian influenza (also known as bird flu) caused by the H5 influenza virus, the first detection of avian influenza due to the H5 virus in a person in B.C.

This is also the first detection of a presumed human case of H5 avian influenza acquired in Canada. The positive test for H5 was performed at the BC Centre for Disease Control's Public-Health Laboratory. Samples are being sent to the National Microbiology Laboratory in Winnipeg for confirmatory testing.

The individual is a teenager from the Fraser Health region who is receiving care at BC Children's Hospital. A public-health investigation has been initiated to determine the source of exposure and identify any contacts.

https://inspection.canada.ca/en/animal-health/terrestrial-animals/diseases/reportable/avian-influenza/latest-bird-flu-situation/status-ongoing-avian-influenza-response

https://news.gov.bc.ca/releases/2024HLTH0152-001583

Environmental Surveillance

Active Surveillance

Passive Surveillance

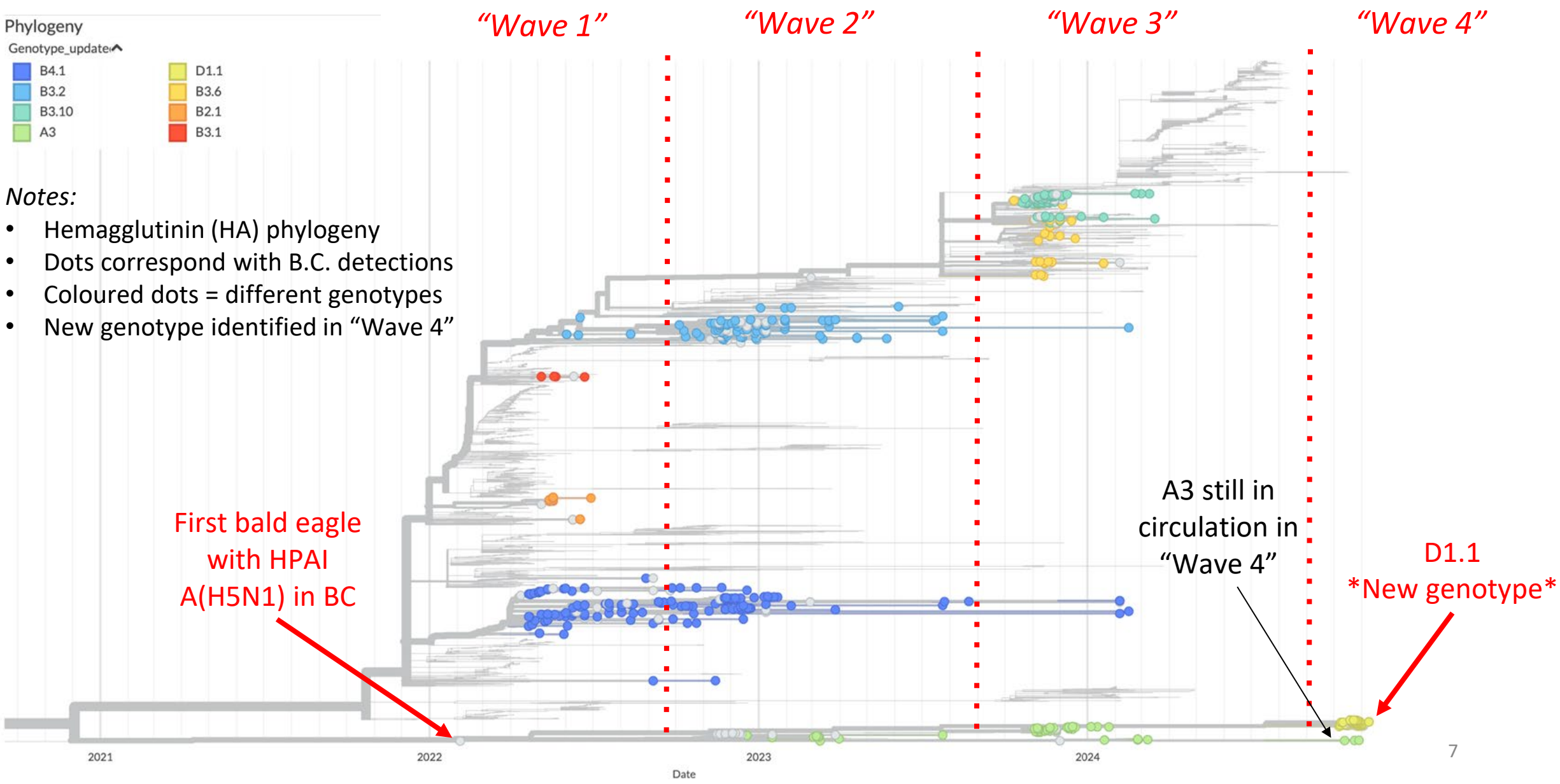
Sources of wildlife surveillance for HPAI in BC

Adapted from a slide by Michelle Coombe, Ministry of Agriculture and Food

Goals of HPAI genomic surveillance in B.C.

- To understand sources of HPAI in B.C. wild birds (where is it coming from in the wild?)
- To resolve transmission patterns between wild birds and poultry, and *between* poultry premises (how is HPAI being transmitted?)
- To determine whether genomic signals can inform risks to animal/human health (what is the risk to wild birds, commodities, mammals?)

Context: the predominant circulating A(H5N1) clade 2.3.4.4b lineages have changed over time in the B.C. outbreak



Wave 4: New genotype detected in wild/domestic BC birds

- Majority of recent B.C. H5 detections belong to D1.1 genotype:
  - Contains 4 Eurasian lineage segments (HA, M, NS, PB1), resembling A3 lineage virus previously identified B.C.
  - Contains 4 reassorted segments associated with N. American LPAI lineage viruses (NA, NP, PA, PB2), not previously identified in B.C.
  - First instance of a non-Eurasian lineage NA segment detected in B.C. outbreak
  - HA segment contains HPAI motif

Table 1. H5N1 genotype classification identifying overall genotype and individual segment genotypes identified in B.C. outbreak, as defined by GenoFlu tool (USDA). (Note: B3.13 genotype from U.S. dairy cattle added for context.)

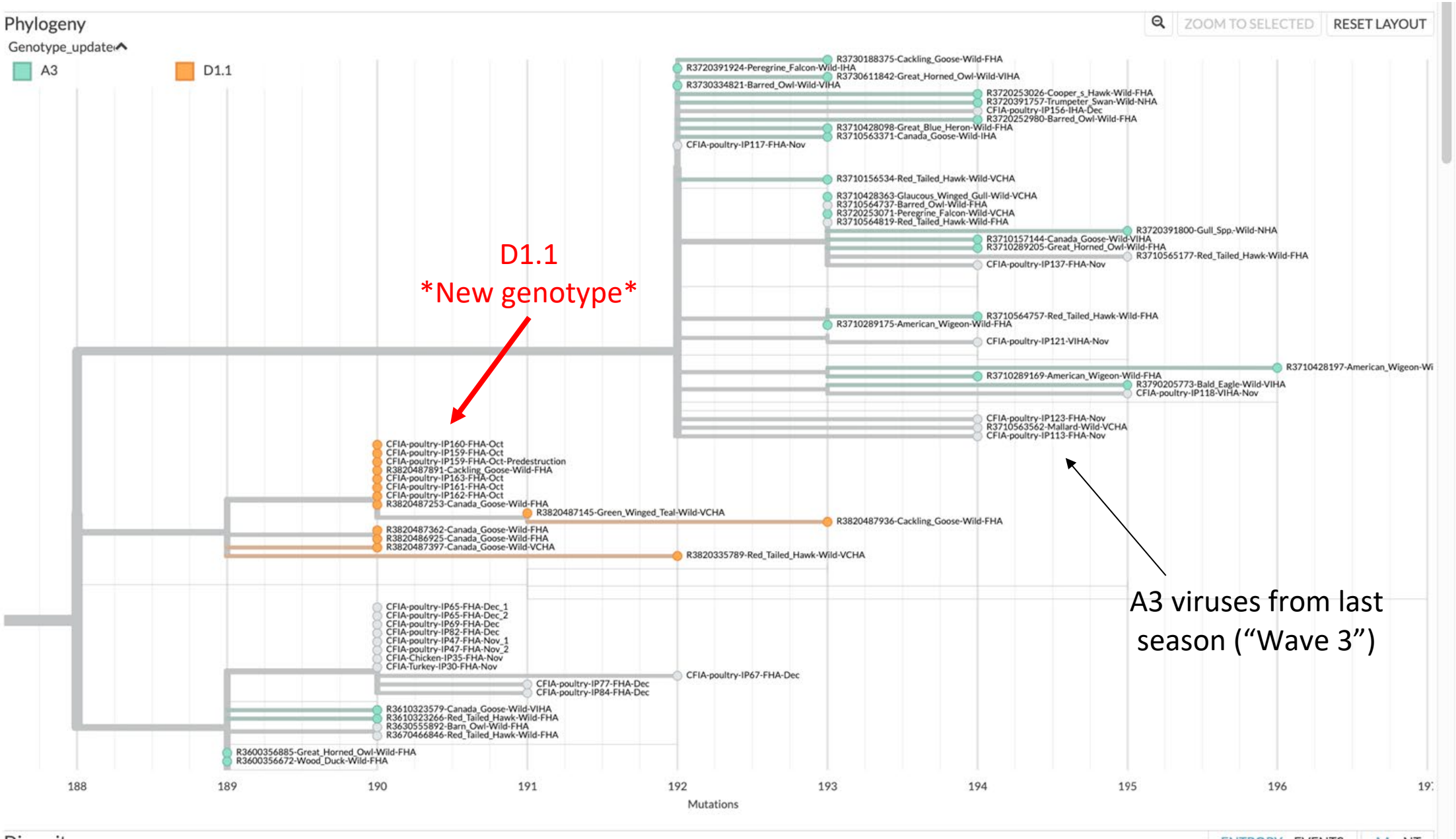
Genotype*	Influenza A Segment*							
	HA	NA	M	NP	NS	PA	PB1	PB2
B2.1	EA1	EA1	EA1	Am1.1	EA1	EA1	EA1	Am1.2
B2.1	EA1	EA1	EA1	Am1.1	EA1	EA1	EA1	Am1.2
B3.2	EA1	EA1	EA1	Am1.4.1	Am1.1	EA1	Am1.2	Am2.1
B3.6	EA1	EA1	EA1	Am1.4.1	Am1.1	EA1	Am4	Am5
B3.10	EA1	EA1	EA1	Am4	Am1.1	EA1	Am4	Am5
B3.1	EA1	EA1	EA1	Am1.4.1	EA1	EA1	EA1	Am1.2
B4.1	EA1	EA1	EA1	Am1.3	EA1	EA1	EA1	Am2.2
A3	EA3	EA3	EA3	EA3	EA3	EA3	EA3	EA3
D1.1	EA3	Am4N1	EA3	Am13	EA3	Am4	EA3	Am24
B3.13	EA1	EA1	EA1	Am8	Am1.1	EA1	Am4	Am2.2

New B.C. genotype → D1.1

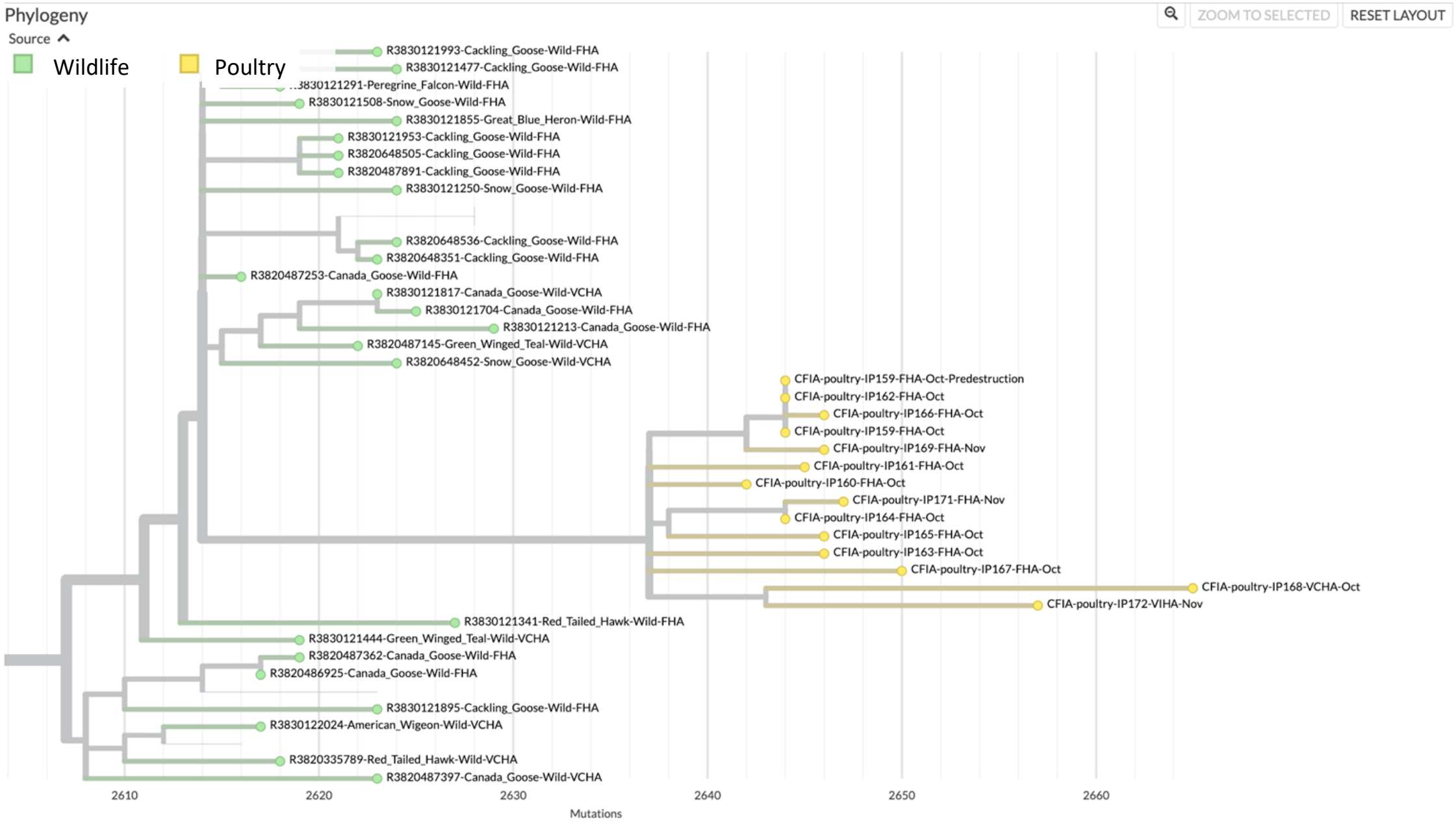
U.S. Dairy Cattle virus → B3.13 (for context)

*EA = Eurasian lineage; Am = North American lineage

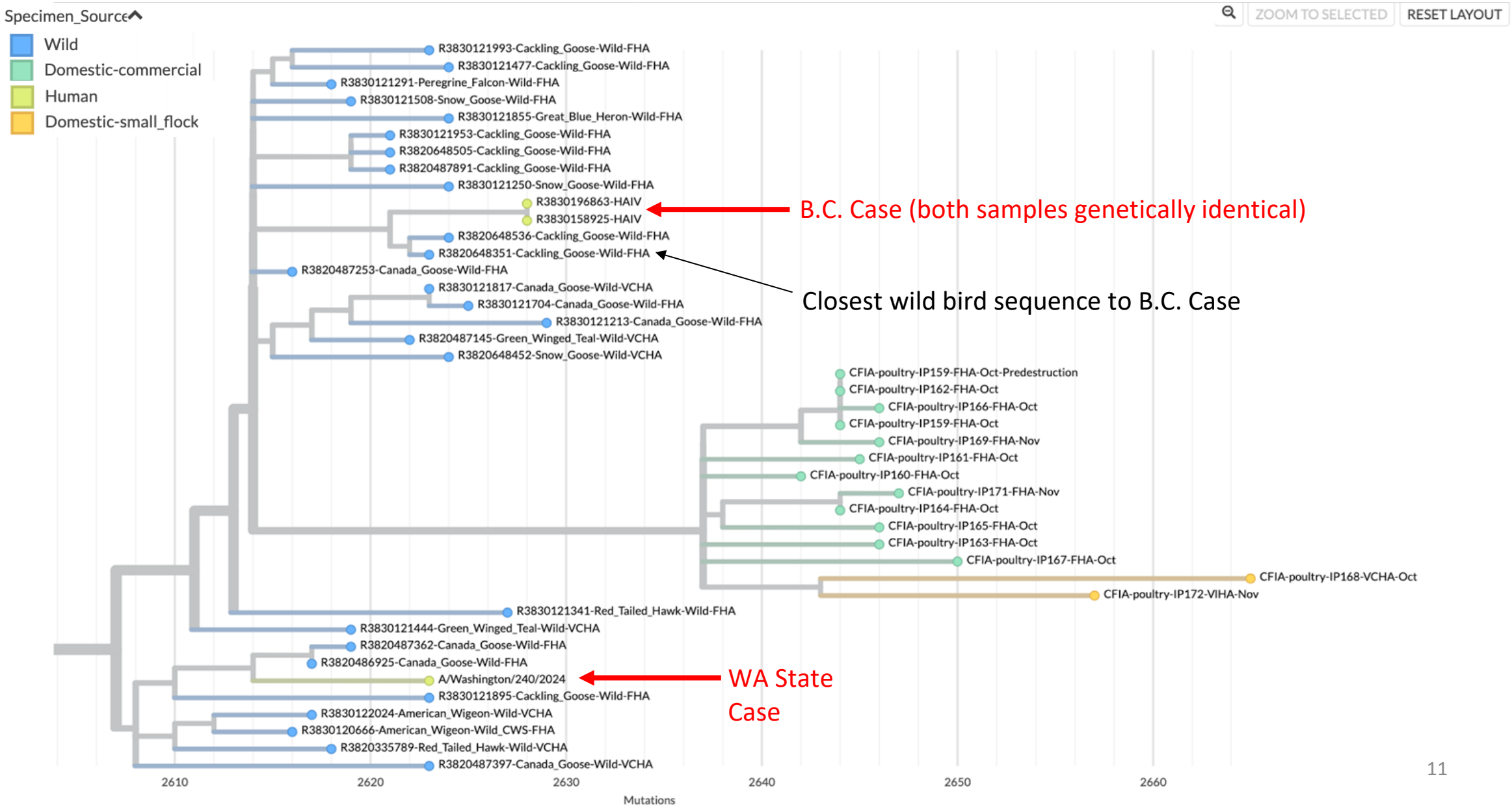
Intriguingly, the HA segment in the D1.1 viruses is “under-diverged”. Why?



Wild birds and poultry form distinct genetic clusters, within D1.1 lineage



B.C. human case considered related to viruses circulating in B.C. wild birds from the Fraser Valley



Limitations of the interpretation

- Wild bird samples represent birds collected through passive surveillance (sick/found dead), requiring a bird to be:
  1. Showing clinical signs of illness
  2. Identified by members of the public or a wildlife rehab center and flagged for testing
- This surveillance system vastly underrepresents the frequency/distribution of HPAI circulating among asymptomatic carriers such as wild waterfowl
- Caution is needed when making inferences about relationships between wildlife detections and spillover into poultry or humans.

What have we learned from sequencing HPAI H5N1 in B.C.?

- **Multiple viral incursions** occurred in B.C. across three consecutive “waves” of the outbreak (2022-2024), likely introduced by wild bird migratory flyways
- **9 genetically distinct lineages** were characterized: 1 fully Eurasian virus, and 8 reassortants containing N. American lineage gene segments
- There were dramatic **shifts in the dominant lineages** over time (ecological factors? fitness factors?)
- **Multiple modes of transmission** were likely contributing to HPAI persistence in B.C.
- Linking **genomic data** with animal surveillance data **enhances** our understanding of the **ecology and epidemiology of HPAI**, informing disease mitigation and risk assessment strategies

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