



Animal and Plant Health Inspection Service
U.S. DEPARTMENT OF AGRICULTURE

U.S. HPAI Update (H5 2.3.4.4b)

USDA APHIS VS D&B National Veterinary Services Laboratories, Diagnostic Virology Laboratory
SEPTEMBER 2023 Mia Kim Torchetti and Kristina Lantz NVSL.DVL.Heads@USDA.GOV

2022-2023 U.S. H5N1 clade 2.3.4.4b Event

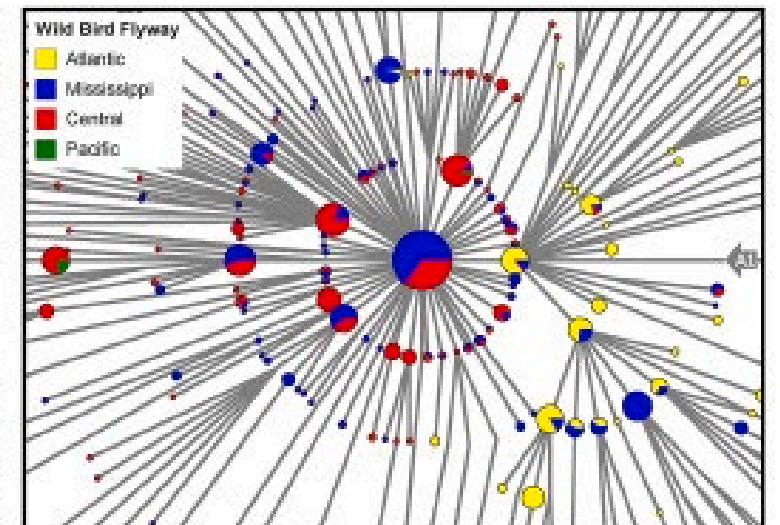
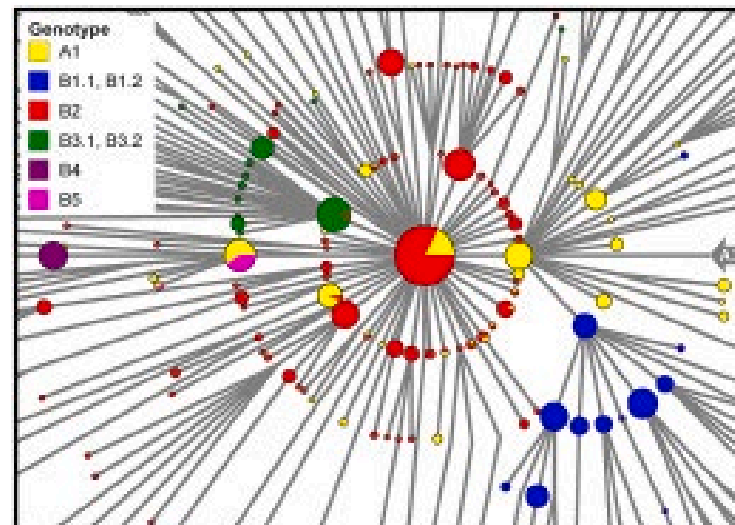
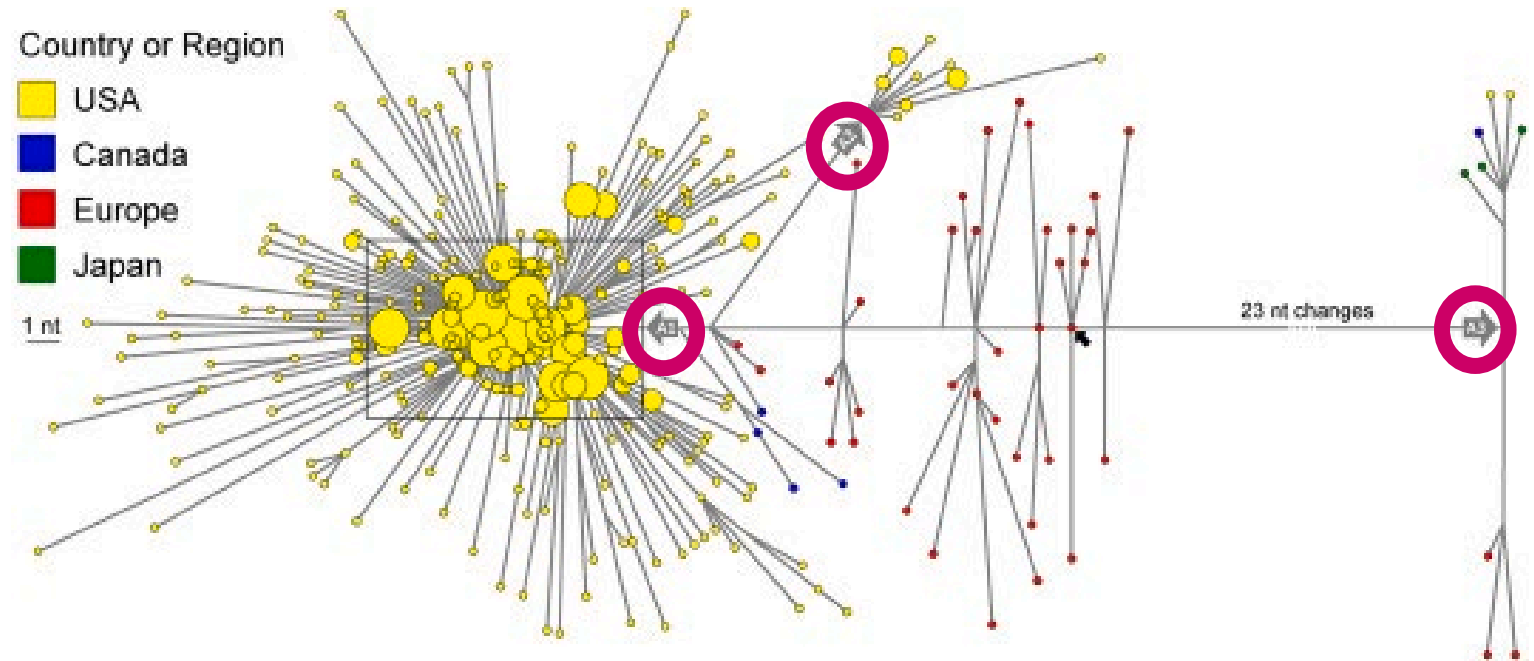
Summary

This work is being conducted in collaboration with APHIS Wildlife Services and ARS Southeast Poultry Research Laboratory

- Near real-time analysis of over 7000 full genome sequences; poultry, mammal, and representative wild bird sequences uploaded to public databases
- The H5N1 clade 2.3.4.4b genotype **A1** was first identified in wild birds collected December 2021. This virus spread across all four flyways and has reassorted with North American (AM) wild bird avian influenza viruses. Several introductions have since been identified: genotype **A2** was detected in February 2022 in the northeastern US; **A3** was likely introduced via the Pacific flyway April 2022; and three additional introductions have since been identified in wild bird samples collected from October through December of 2022 (**A4** via the Pacific flyway in wild birds in Alaska, and **A5** and **A6** via Atlantic flyway [of note, A6 is a fully Eurasian virus with a reassorted neuraminidase (H5N5)]).

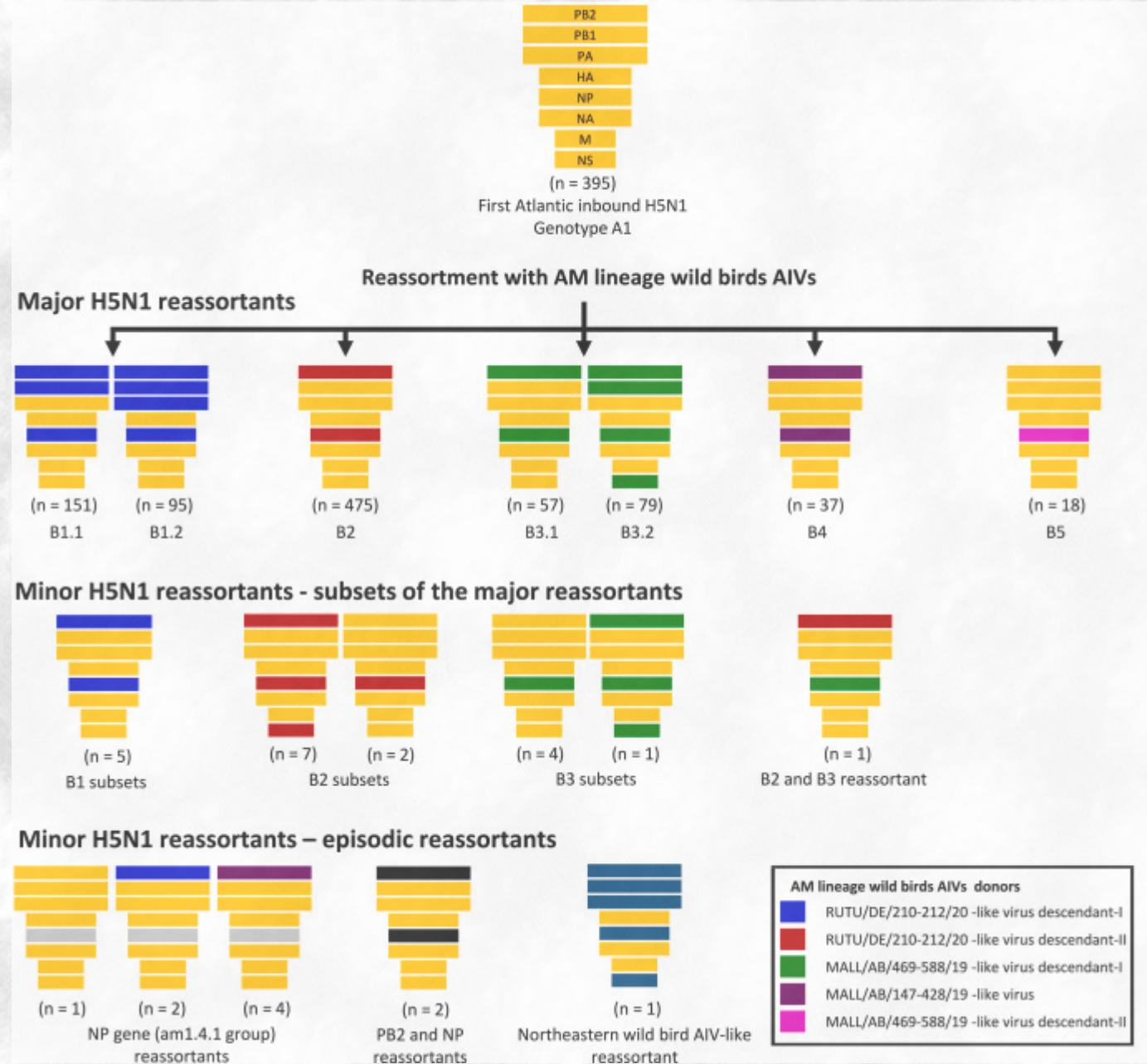
Introductions into North American flyways

H5N1 highly pathogenic avian influenza clade 2.3.4.4b in wild and domestic birds: Introductions into the United States and reassortments, December 2021–April 2022 - ScienceDirect



Reassortment of H5N1 2022 (A1) with North American lineage wild bird influenza A viruses

[H5N1 highly pathogenic avian influenza clade 2.3.4.4b in wild and domestic birds: Introductions into the United States and reassortments, December 2021–April 2022 - ScienceDirect](#)



Major genotypes as determined by **GenoFlu**

Genotype	Segment group							
	PB2	PB1	PA	HA	NP	NA	M	NS
A1	ea1	ea1	ea1	ea1	ea1	ea1	ea1	ea1
B1.1	am1.1	am1.1	ea1	ea1	am1.2	ea1	ea1	ea1
B1.2	am1.1	am1.1	am1	ea1	am1.2	ea1	ea1	ea1
B2	am1.2	ea1	ea1	ea1	am1.1	ea1	ea1	ea1
B3.1	am2.1	ea1	ea1	ea1	am1.4.1	ea1	ea1	ea1
B3.2	am2.1	am1.2	ea1	ea1	am1.4.1	ea1	ea1	am1.1
B4	am2.2	ea1	ea1	ea1	am1.3	ea1	ea1	ea1
B5	ea1	ea1	ea1	ea1	am1.4.2	ea1	ea1	ea1

“A” genotypes are unreassorted or fully Eurasian (EA)

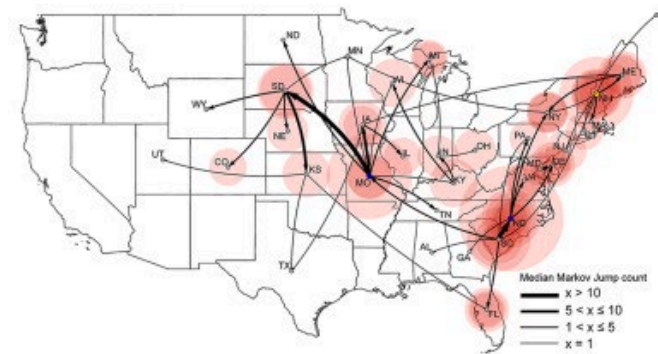
“B” genotypes are A1 reassortments with North American (AM) lineage viruses

[GitHub - USDA-VS/GenoFLU: Influenza data pipeline to automate genotyping assignment](#)

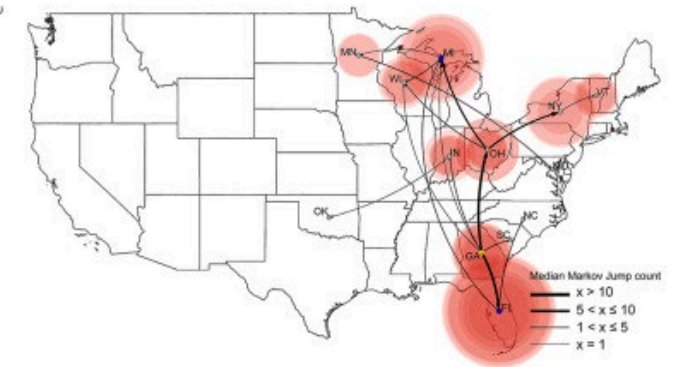
Spatial diffusion of US H5N1 clade 2.3.4.4b viruses by genotype

H5N1 highly pathogenic avian influenza clade 2.3.4.4b in wild and domestic birds: Introductions into the United States and reassortments, December 2021–April 2022 - ScienceDirect

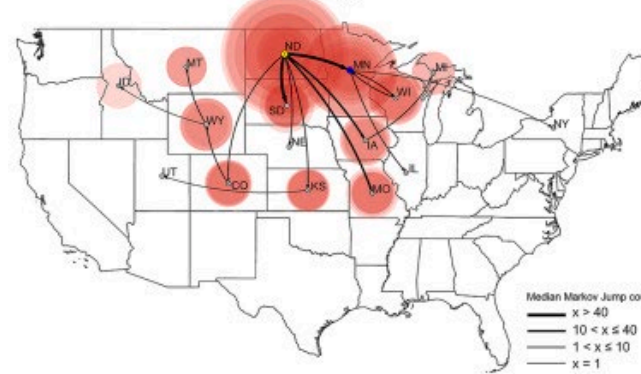
Genotype A1



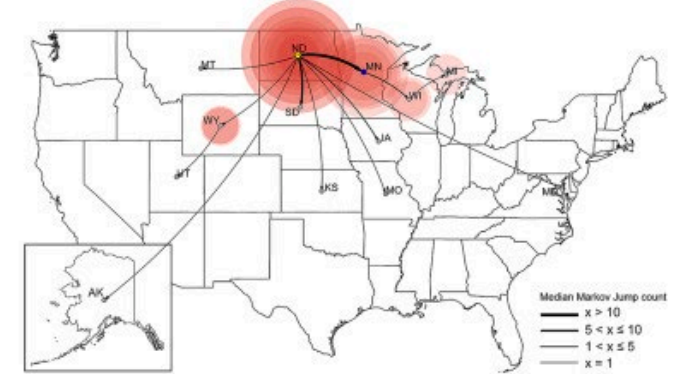
Genotype B1.1 and B1.2



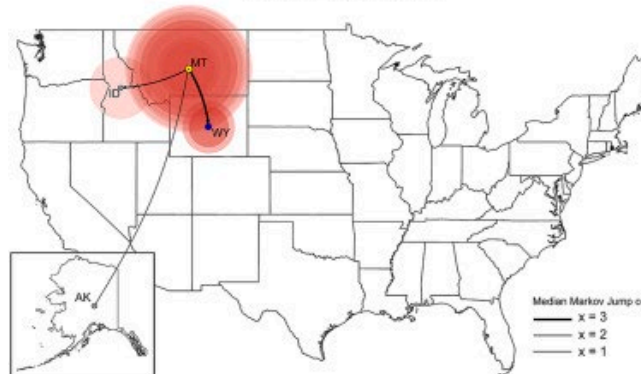
Genotype B2



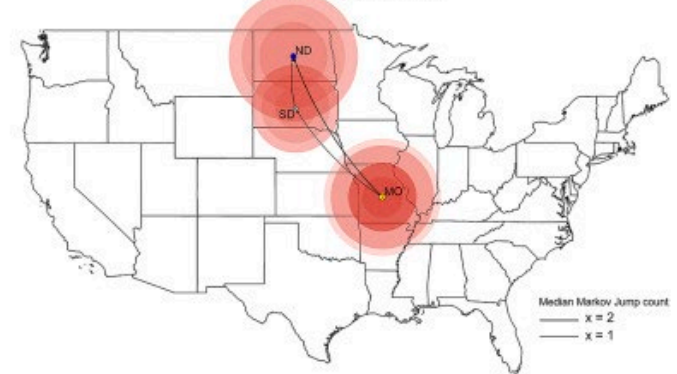
Genotype B3.1 and B3.2



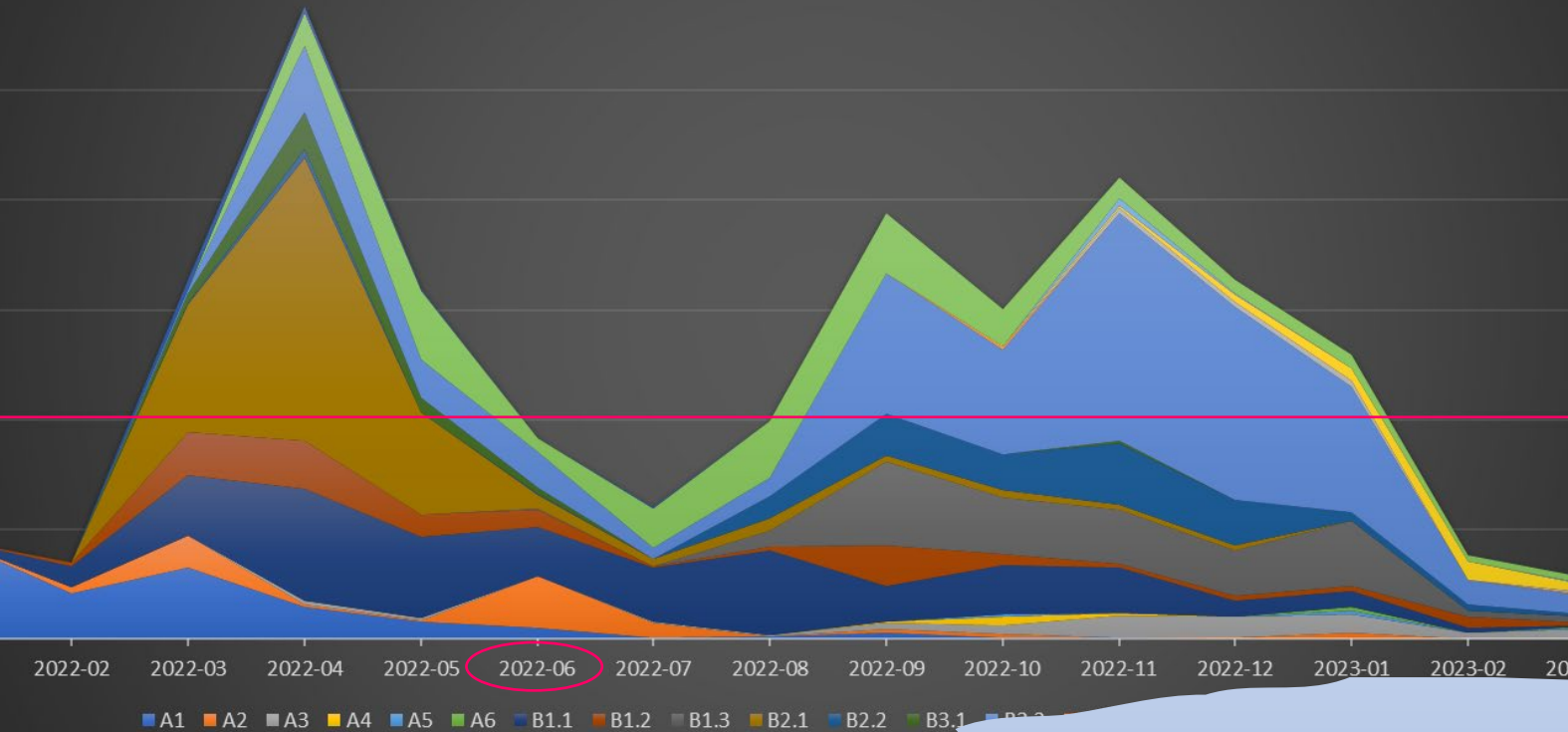
Genotype B4



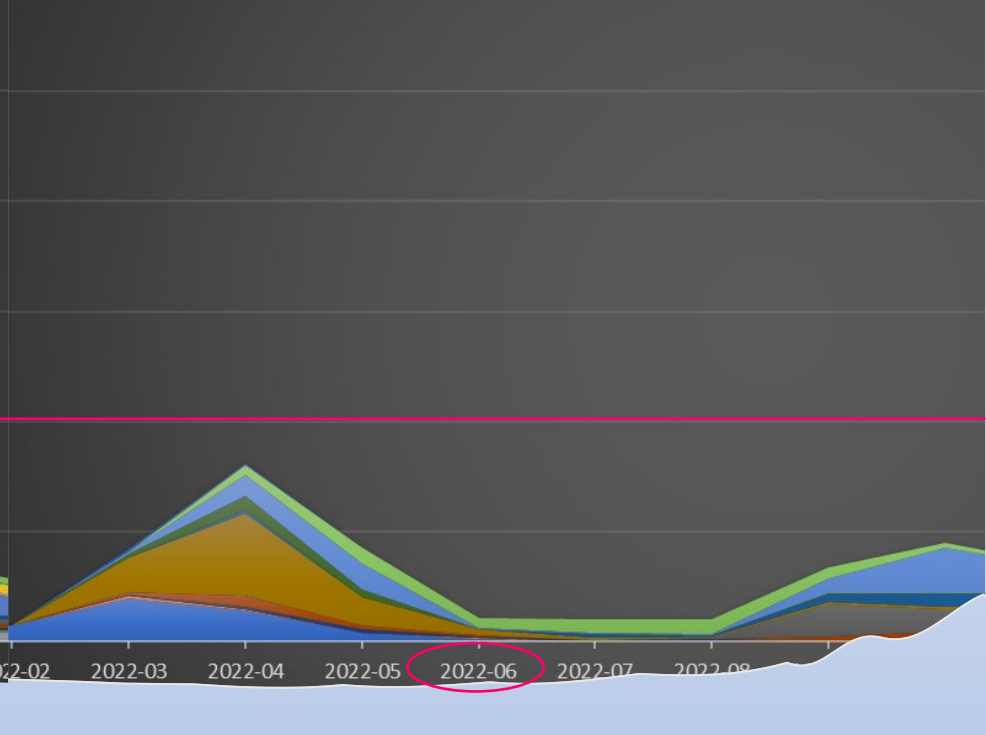
Genotype B5



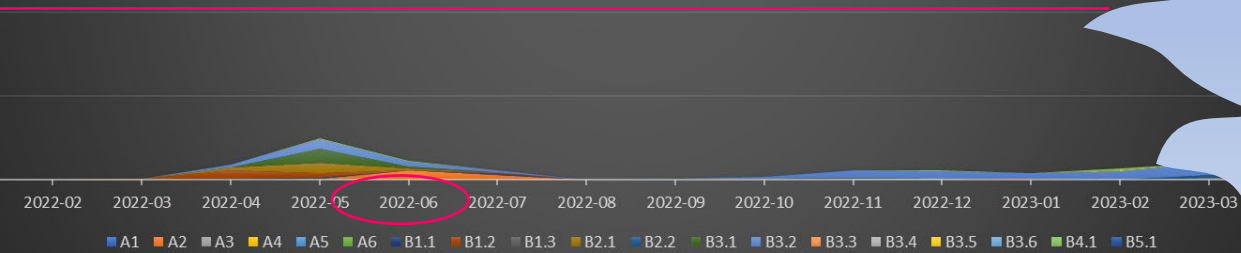
Wild Birds by Genotype



Poultry by Genotype



Mammals by Genotype



Genotype Distribution December 2021 to May 2023

(same scale across wild birds, poultry and mammals)

Counts are per virus; marker set at 200 viruses

Current Status for U.S. Poultry



HPAI 2022/2023 Confirmed Detections

as of September 22, 2023
 Last reported detection Friday, September 15, 2023
 Data updated weekdays by 12pm Eastern

[Download Data](#)

840 Confirmed Flocks

1 confirmed last 30 days
 Birds tested and confirmed having HPAI

47 Affected States

1 states last 30 days
 States with at least one confirmed infected flock

Commercial Flocks

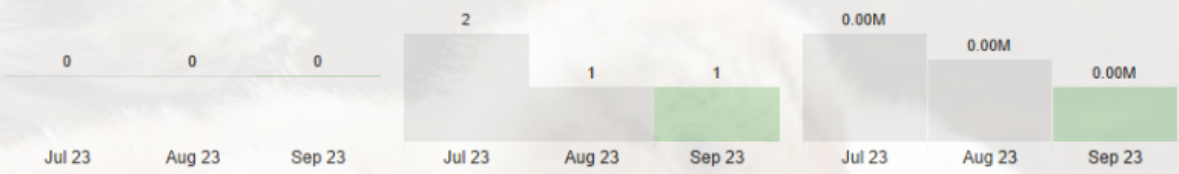
325

Backyard Flocks

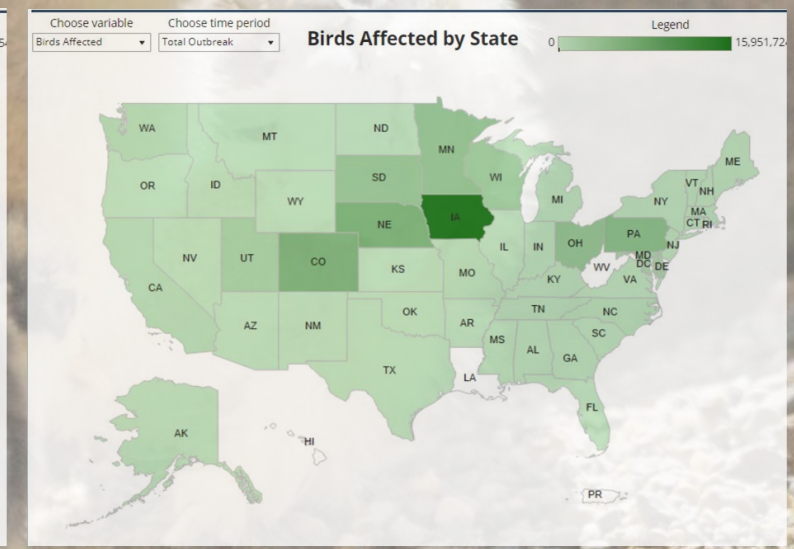
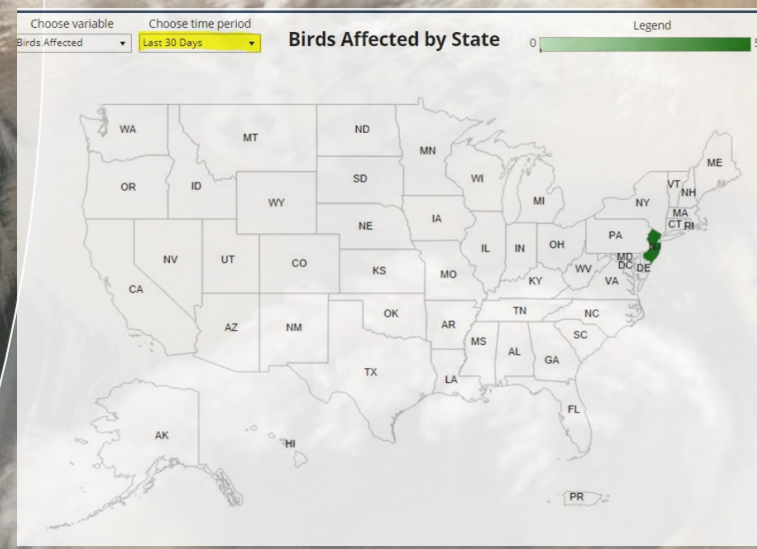
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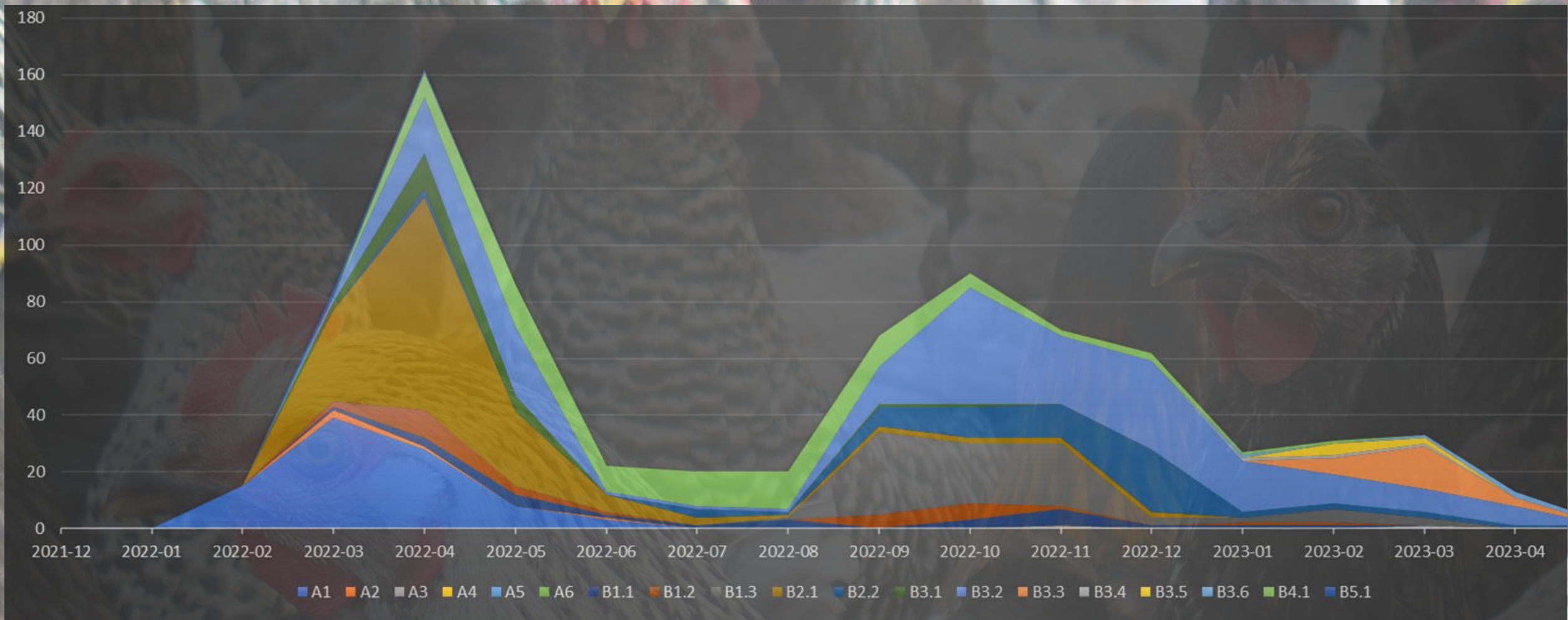
Birds Affected*

58.79M



*Number of birds on confirmed infected premises.
 Bars reflect most recent 4 months (numbers may not add up to total).





Genotype Distribution for Poultry
December 2021 to May 2023

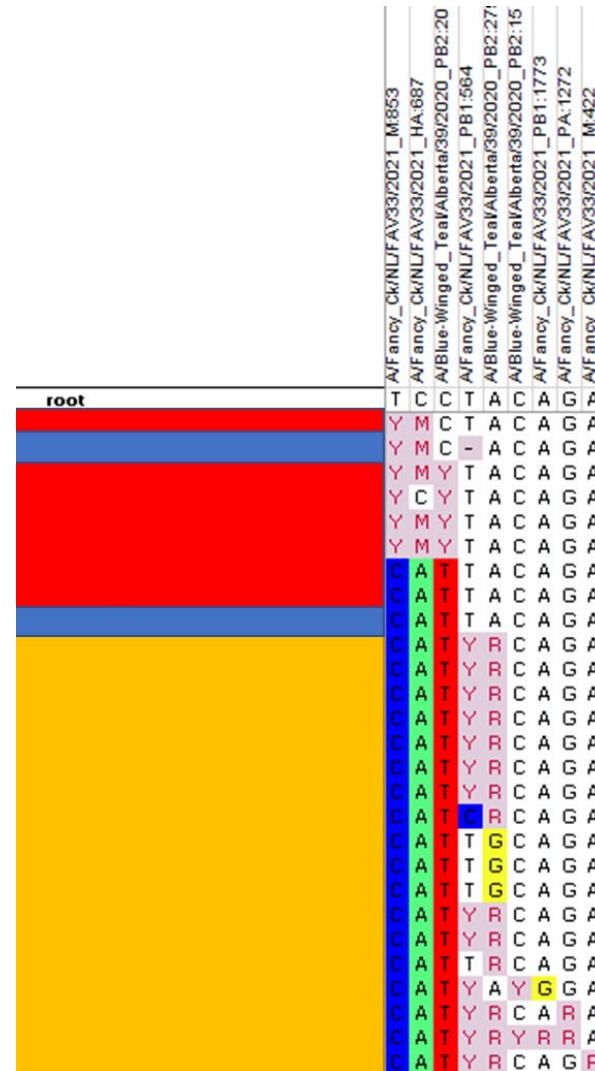
Genomic analysis

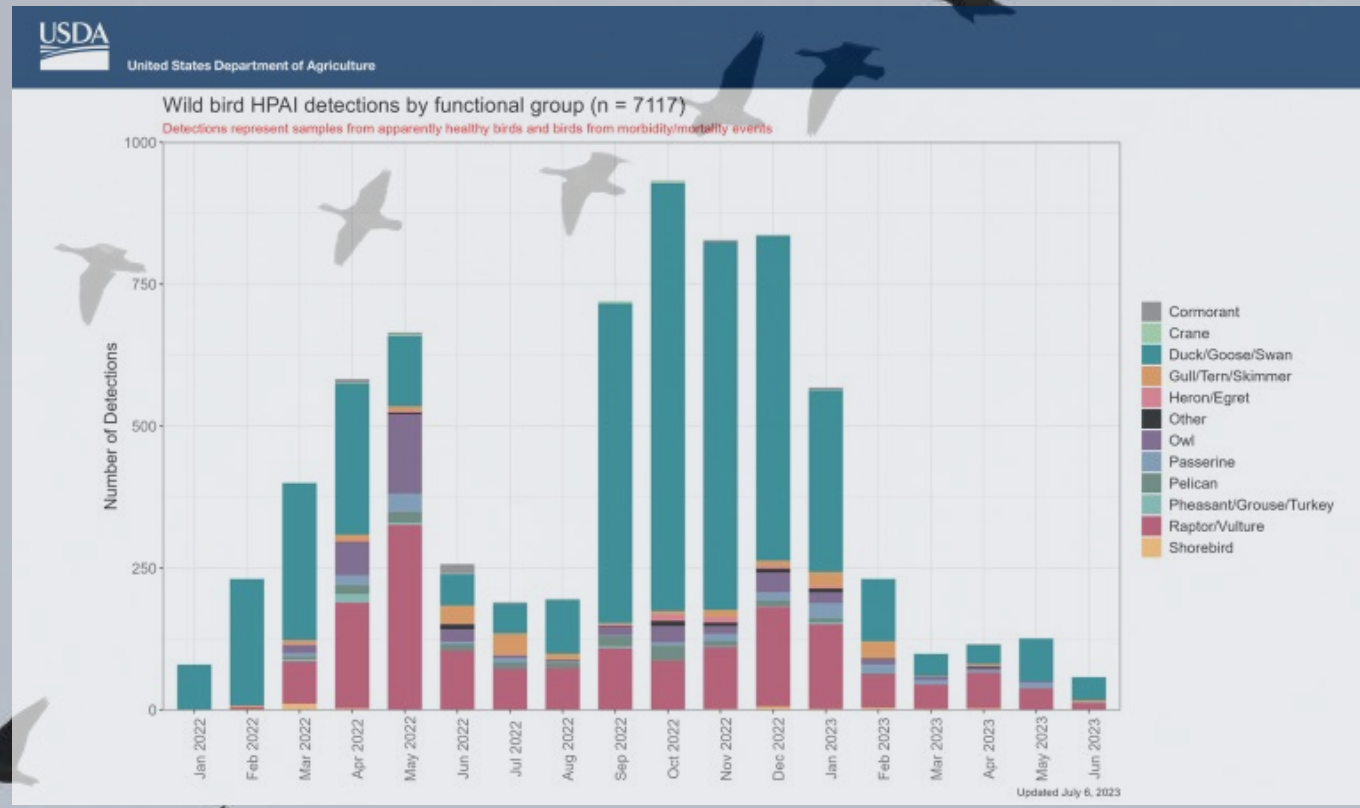
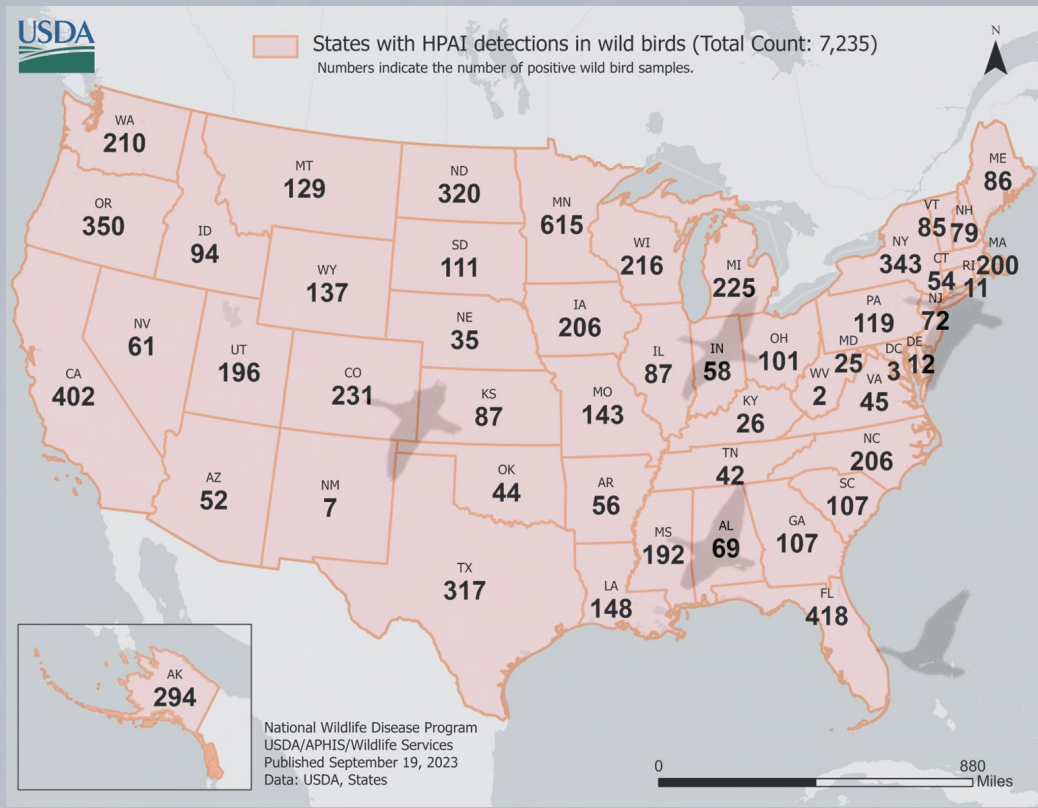
The outcomes of phylogenetic analysis should be interpreted in context of all available virus and epidemiologic information and should not be used directly to infer transmission

- The entire genome is used for analysis (not only HA gene)
- Single Nucleotide Polymorphism (SNP)
 - A single genetic change in the virus, compared to other related viruses
- Ancestral genotype/common ancestor
 - The (often theoretical) virus that is the last common ancestor between two viruses
- Directionality
 - Once a SNP is acquired and fixed in a population it is unlikely to revert
 - Stepwise acquisition of SNPs may indicate directionality (e.g., movement of virus from one population to another)

Common Source/ Lateral Transmission Example Genotype B3.3 PB2 PB1 NP NS

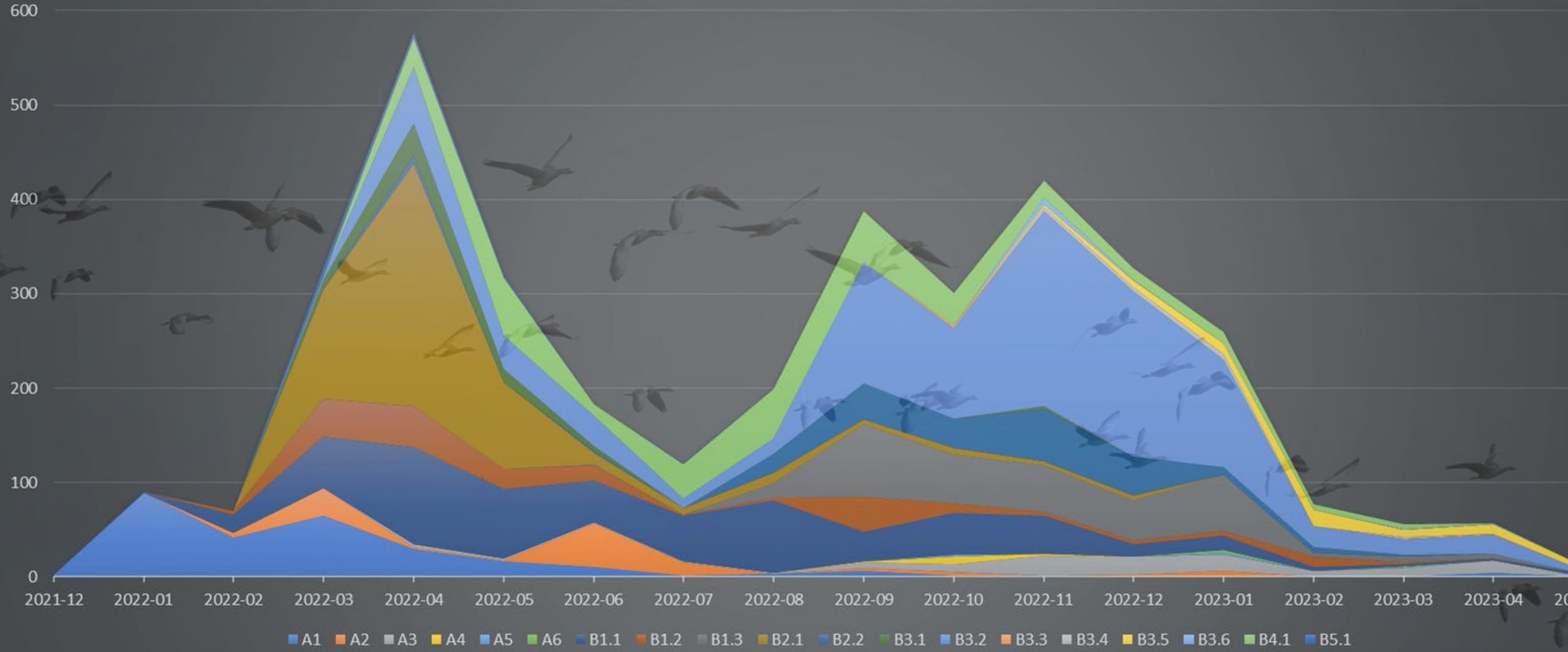
- GOLD shaded viruses are closely related to BLUE and RED shaded viruses that are ancestral
 - Three mixed/fixed SNPs in the ancestral viruses are fixed in the GOLD viruses
 - Additionally, there are 2-5 more SNPs in GOLD, moderate diversity may be indicative of longer circulation or a diverse virus source
 - Potential for lateral transmission from either the RED or BLUE premises or a common source to all three





Wild Bird Detections

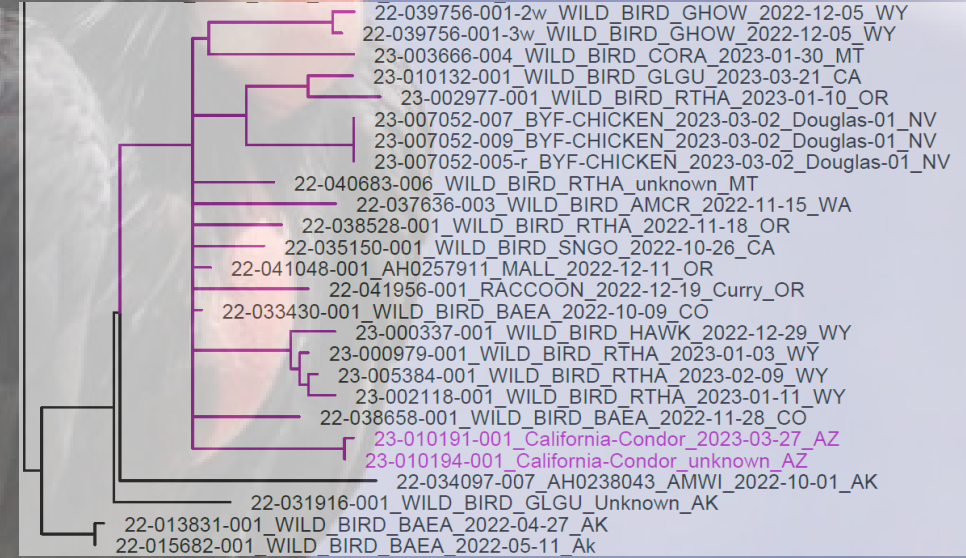
(slides courtesy of APHIS-WS)



Genotype Distribution for Wild Birds
 December 2021 to May 2023

AZ: California Condors Genotype A3

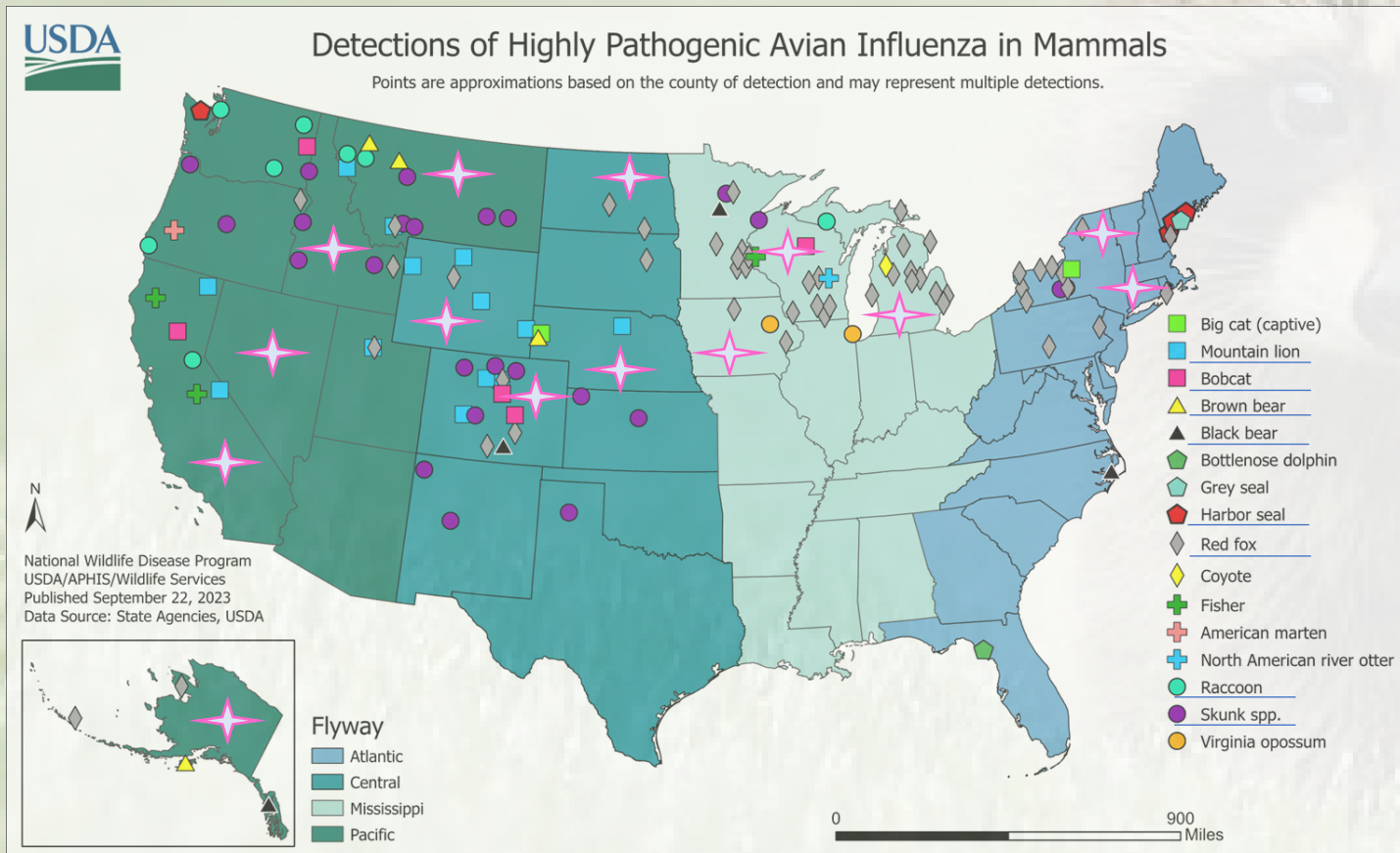
- A3 is fully Eurasian, no AM genes
- Pacific flyway introduction, initially detected in AK
- Spread to lower 48 in fall 2022
- Located on a branch of A3 with other detections in the Southeastern US




	A	F	N	L	C	A	G	A	C	C	T	G	C	T	G	G	C	A	C	T	C	T	A	G	G	A	G	C	A	A	C	T	T	G	A	A	C	C	G	A	A	A	C		
root	G	T	C	A	A	G	G	A	C	C	T	G	C	T	G	G	C	A	C	T	C	T	A	G	G	A	G	C	A	A	C	T	T	G	A	A	C	C	G	A	A	A	C		
22-033430-001_WILD_BIRD_BAEA_2022-10-09_CO	R	G	C	A	A	G	G	A	A	C	C	T	G	C	T	G	G	C	A	C	T	C	T	A	G	G	A	G	C	A	A	C	T	T	G	A	A	C	C	G	A	A	A	C	
23-000337-001_WILD_BIRD_HAWK_2022-12-29_WY	A	T	T	G	T	A	A	C	C	A	T	C	G	C	T	A	G	C	C	A	C	T	C	T	A	G	G	A	G	C	A	A	C	T	T	G	A	A	C	C	G	A	A	A	C
23-000979-001_WILD_BIRD_RTHA_2023-01-03_WY	A	T	T	G	T	A	A	C	C	A	T	C	G	C	T	A	G	C	C	A	C	T	C	T	A	G	G	A	G	C	A	A	C	T	T	G	A	A	C	C	G	A	A	A	C
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22-038658-001_WILD_BIRD_BAEA_2022-11-28_CO	G	T	C	A	A	G	A	A	C	C	T	C	G	C	T	G	A	T	G	C	A	T	T	G	A	T	G	A	T	C	C	T	C	A	G	A	A	A	G	G	G	A	A	A	C
23-010191-001_California-Condor_2023-03-27_AZ	G	T	C	A	A	G	A	A	C	C	T	C	G	C	T	G	A	T	G	C	C	A	C	T	C	T	A	G	G	A	T	G	G	T	C	C	A	G	A	A	A	G	G	G	A
23-010194-001_California-Condor_unknown_AZ	G	T	C	A	A	G	A	A	C	C	T	C	G	C	T	G	A	T	G	C	C	A	C	T	C	T	A	G	G	A	T	G	G	T	C	C	A	G	A	A	A	G	G	G	A

Mammal Detections (Sept 2023)

[USDA APHIS | 2022-2023 Detections of Highly Pathogenic Avian Influenza](#)

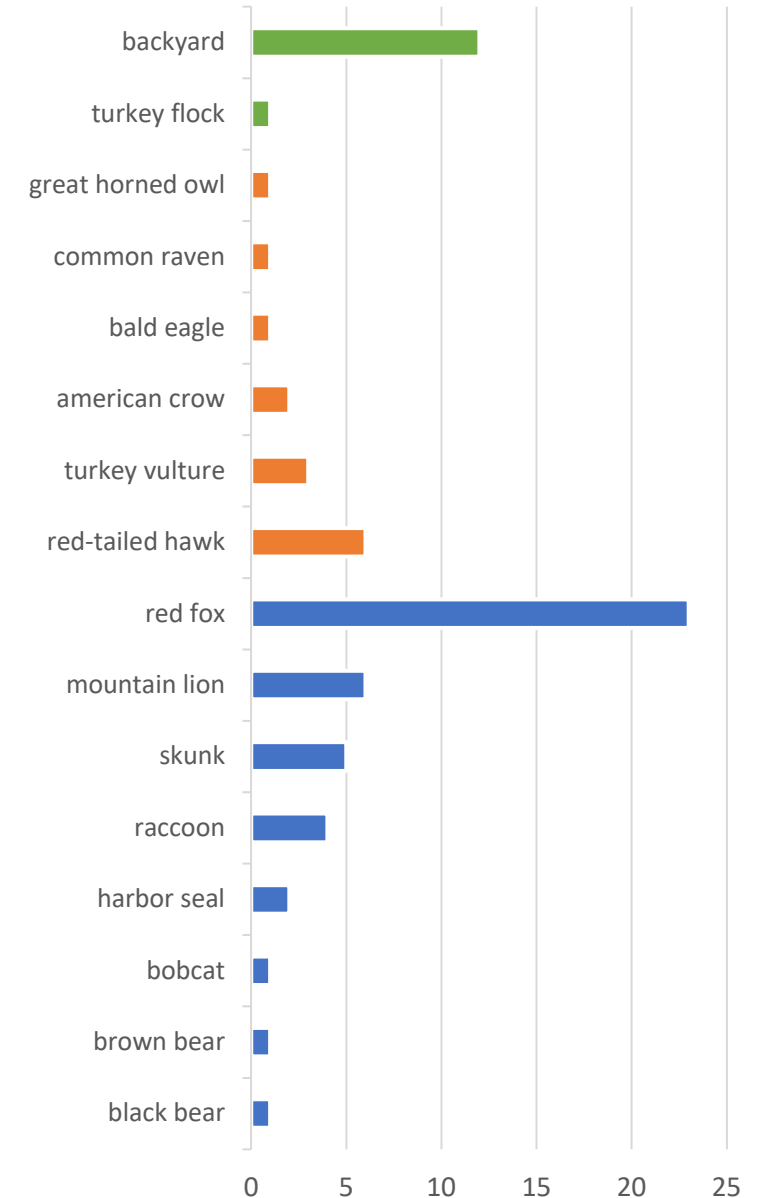


- Over **200** animals across **18** species (terrestrial and marine) in **26** states have been confirmed including a Florida dolphin that was collected in March 2022.
- The confirmations include several domestic/outdoor cats in 3 states.
- A molecular marker (E627K)  previously associated with adaptation in mammals has been identified in ~19% (37/200) across all 4 flyways and multiple genotypes. NVSL continues to monitor viruses for known mammalian mutations.

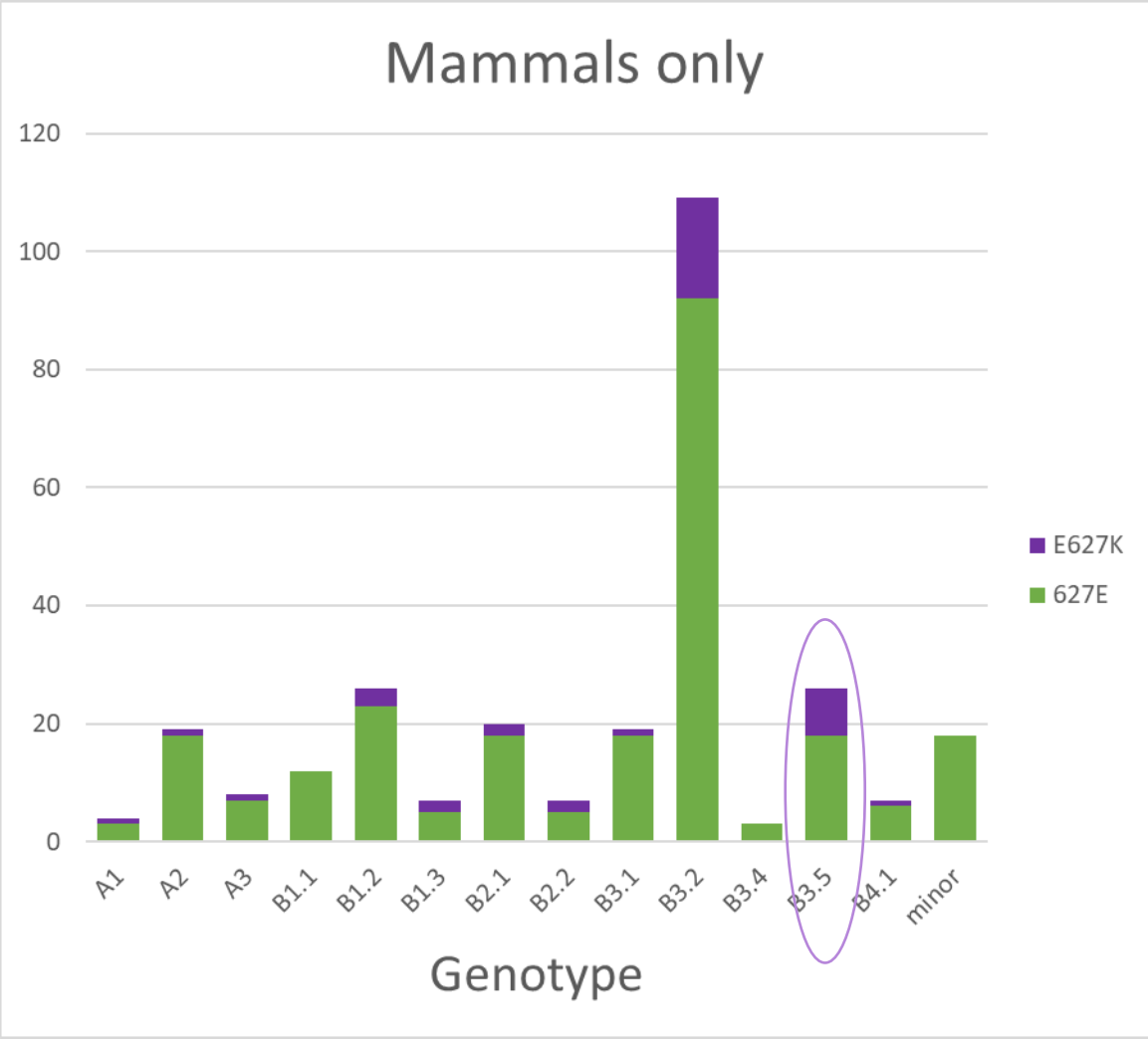
E627K detections

Findings span all four flyways, & represent multiple species and genotypes

- 12 backyard findings and one turkey flock across 10 states and several genotypes; no evidence of onward transmission
- Wild bird species affected are those that may predate or scavenge on small mammals
- Red fox are most frequently detected and also the most frequently sampled (nearly half of all mammals)
- D701N rare detections in pheasants, raptors, and single detections in cat, fox, mountain lion, and captive leopard



Spontaneous emergence of E627K



Mammal E627K
 Wild Bird E627K
 No E627K



- We are grateful for the dedicated people and institutions working hard to combat this virus including the DVL team!
- Many thanks to our NAHLN and state partners as well as other academic institutions and states that continue to contribute to surveillance in wildlife.
- This analysis is possible thanks to our collaboration with Wildlife Services, ARS Southeast Poultry Research Laboratory, and our colleagues at the Center for Epidemiology and Animal Health.



World Organisation
for Animal Health
Founded as OIE

