



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

Leveraging the real time whole genome together with available epidemiologic information allows understanding of how the virus is moving and when spillovers to poultry occur, insight into how the virus is spreading.

With thousands of wild bird detections across at least 144 species and 49 U.S. states, reassortments of the H5 2.3.4.4b virus with North American viruses continue to predominate at $^{\sim}86\%$ of detections.





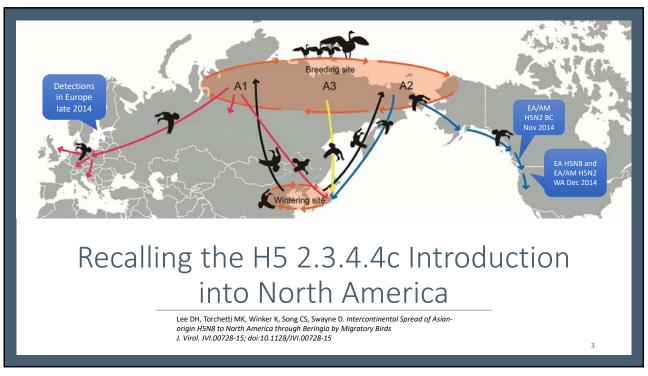


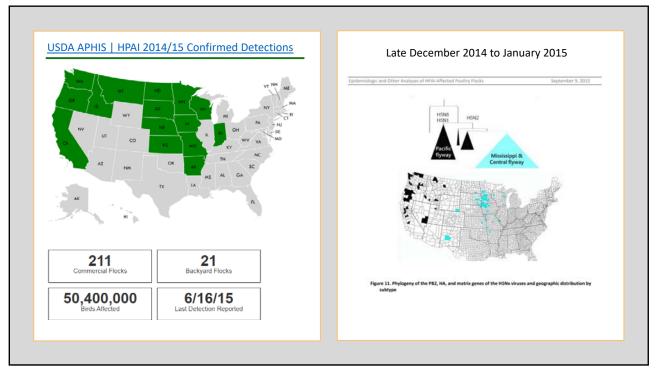


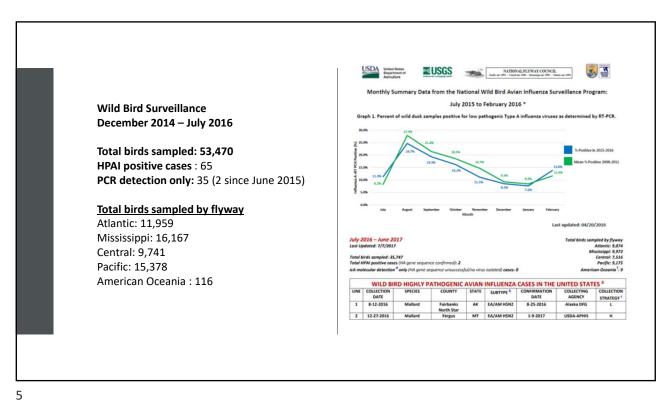






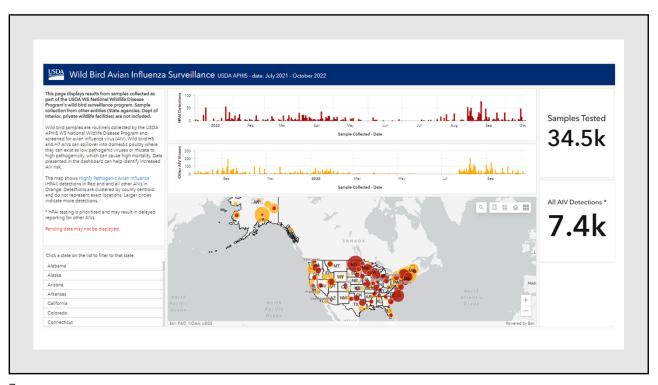


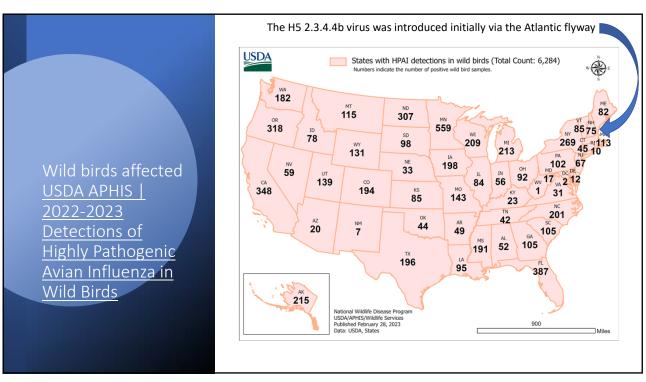


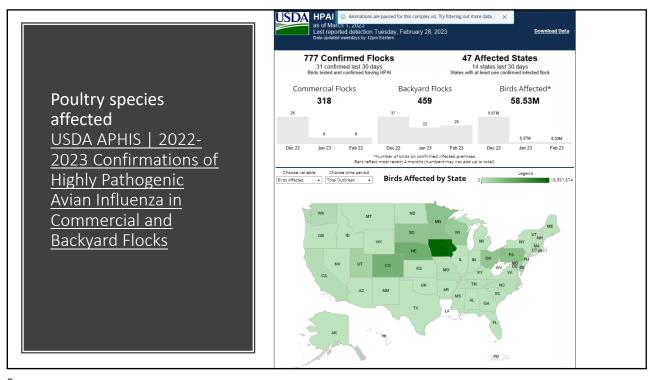


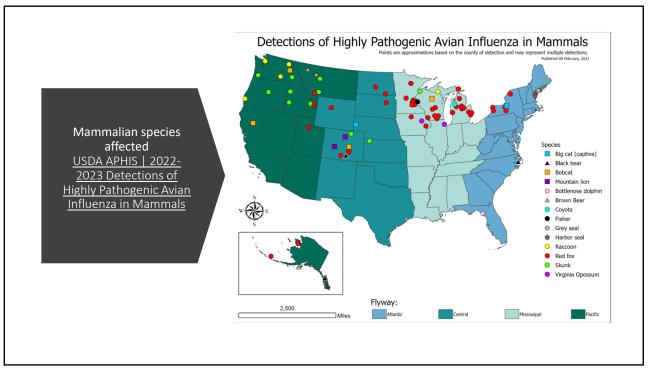
2022 H5N1 2344b Introduction

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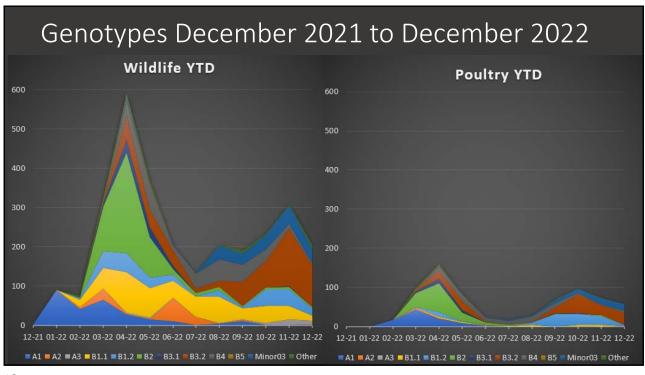


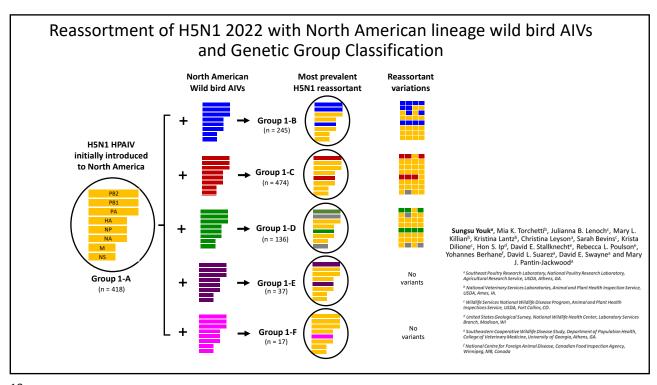


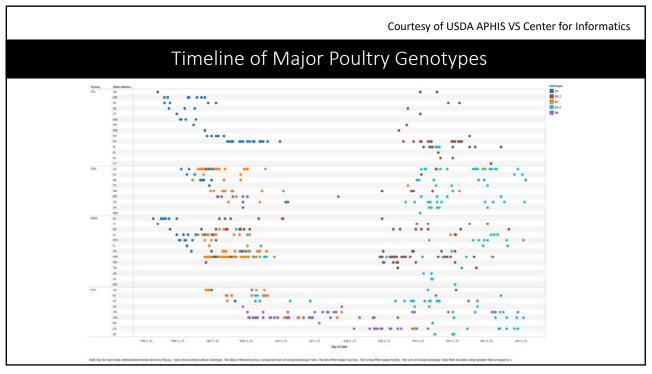


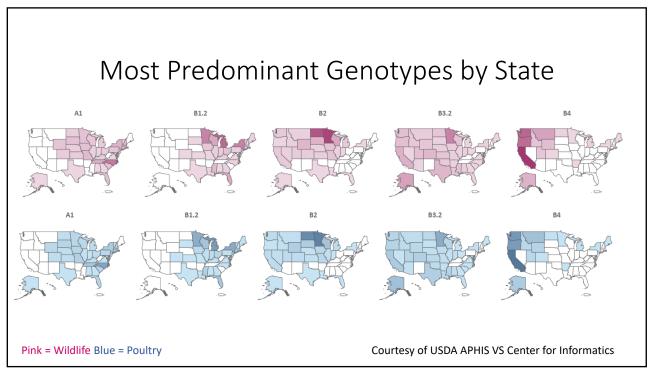


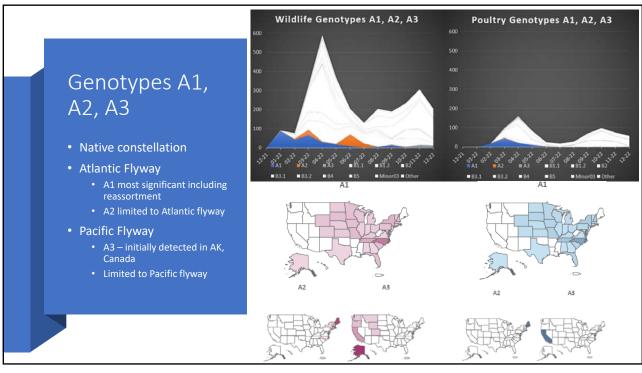


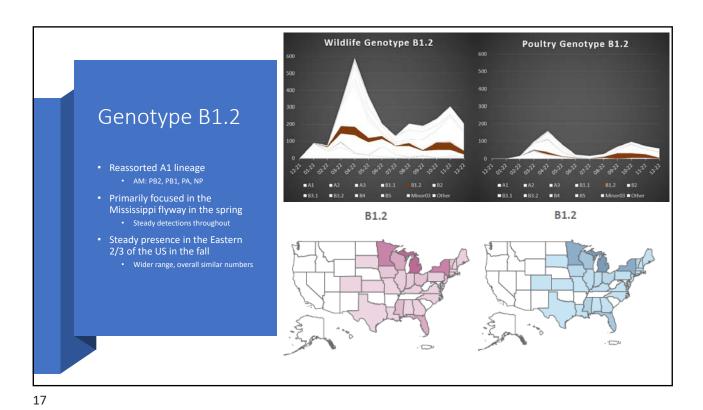












Wildlife Genotype B2

Poultry Genotype B2

Reassorted A1 lineage

AMP B2, NP

Very dominant in the upper Midwest in the spring

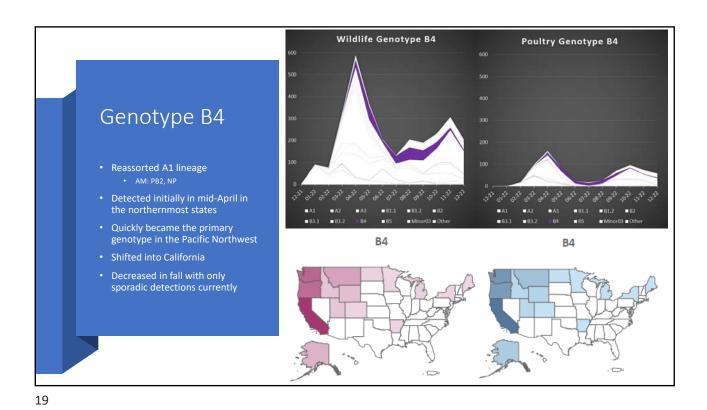
Wild bird mortalities

Poultry detections in MN, ND, SD, ID

Dropped significantly by June 2022

Sporadic ongoing detections

Low prevalence but wider distribution in the fall



Wildlife Genotypes B3.1, B3.2

Poultry Genotypes B3.1, B3.2

Reassorted A1 lineage

AM: PB2, PB1, NP, NS

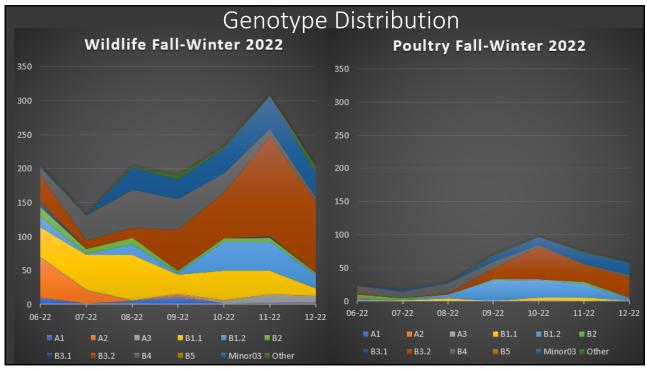
Steady detections in the spring along the northern tier of states

Expanded down into ID and Utah

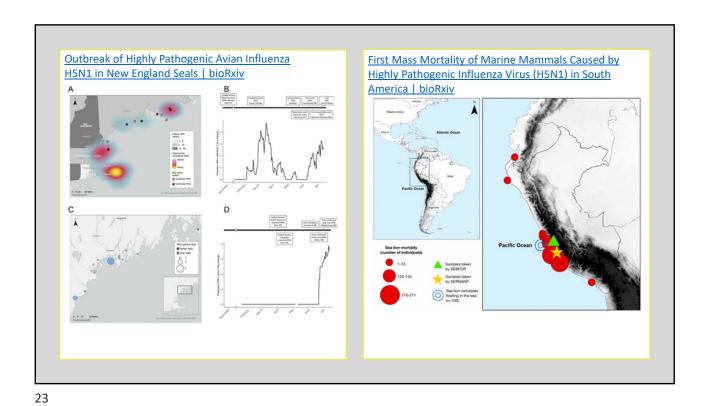
New branch emerged in the fall

Detected in AK and ID in June

Detected in







Acknowledgments



- 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



