

# Surveillance for Respiratory pathogens in Ghana



Ivy Asantewaa Asante, Laboratory Lead

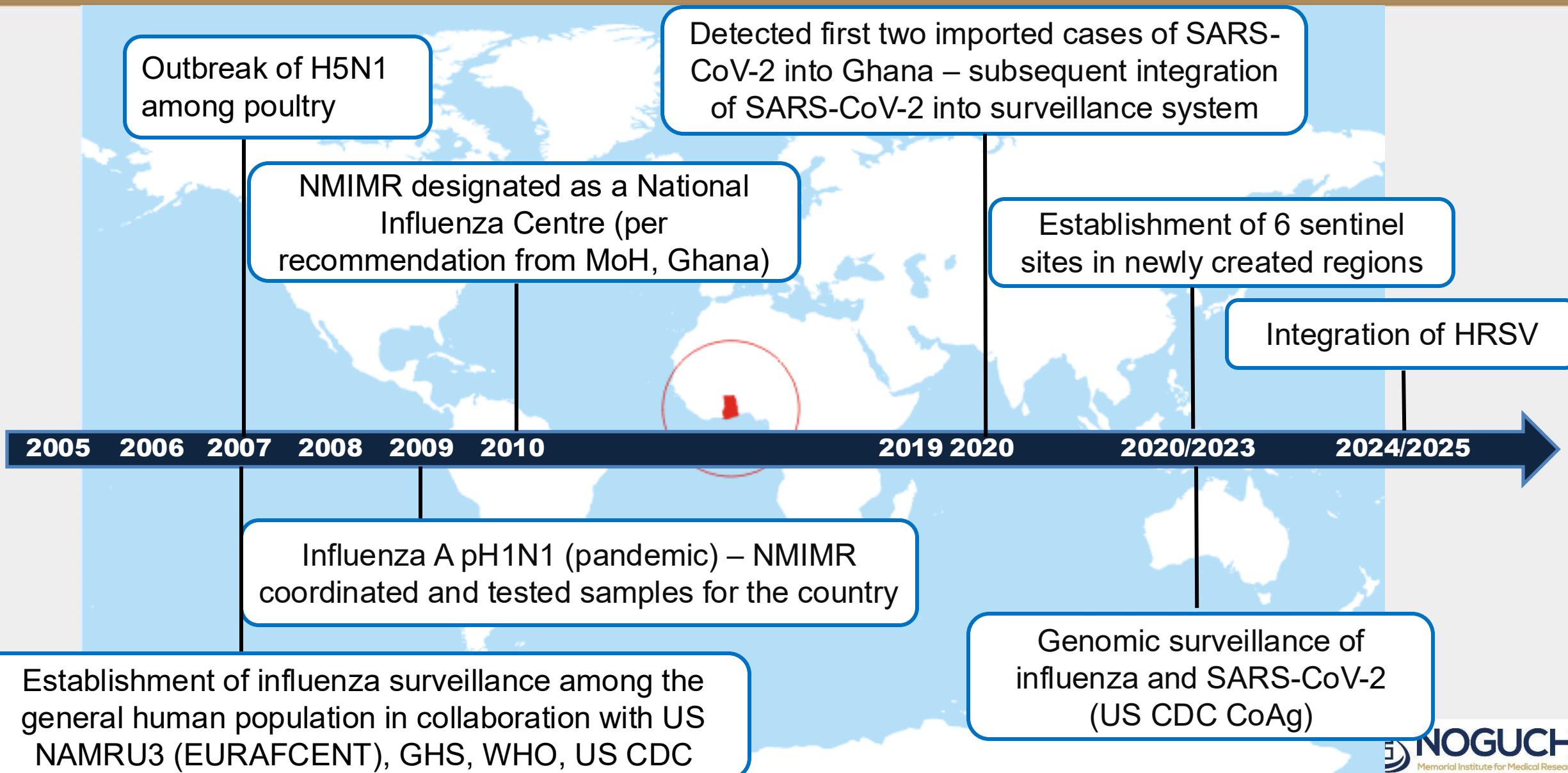


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# Timeline of events for respiratory pathogen surveillance in Ghana



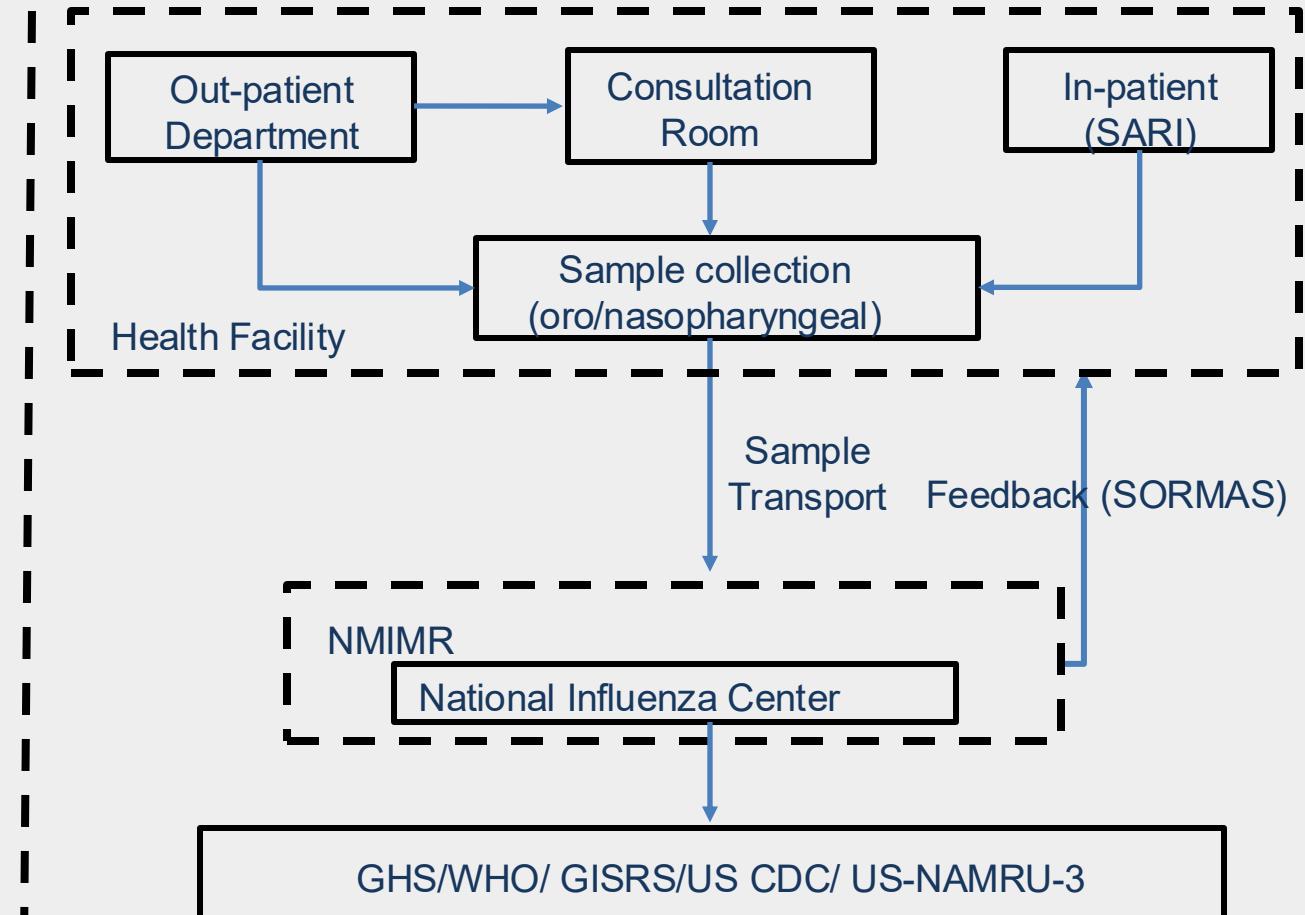
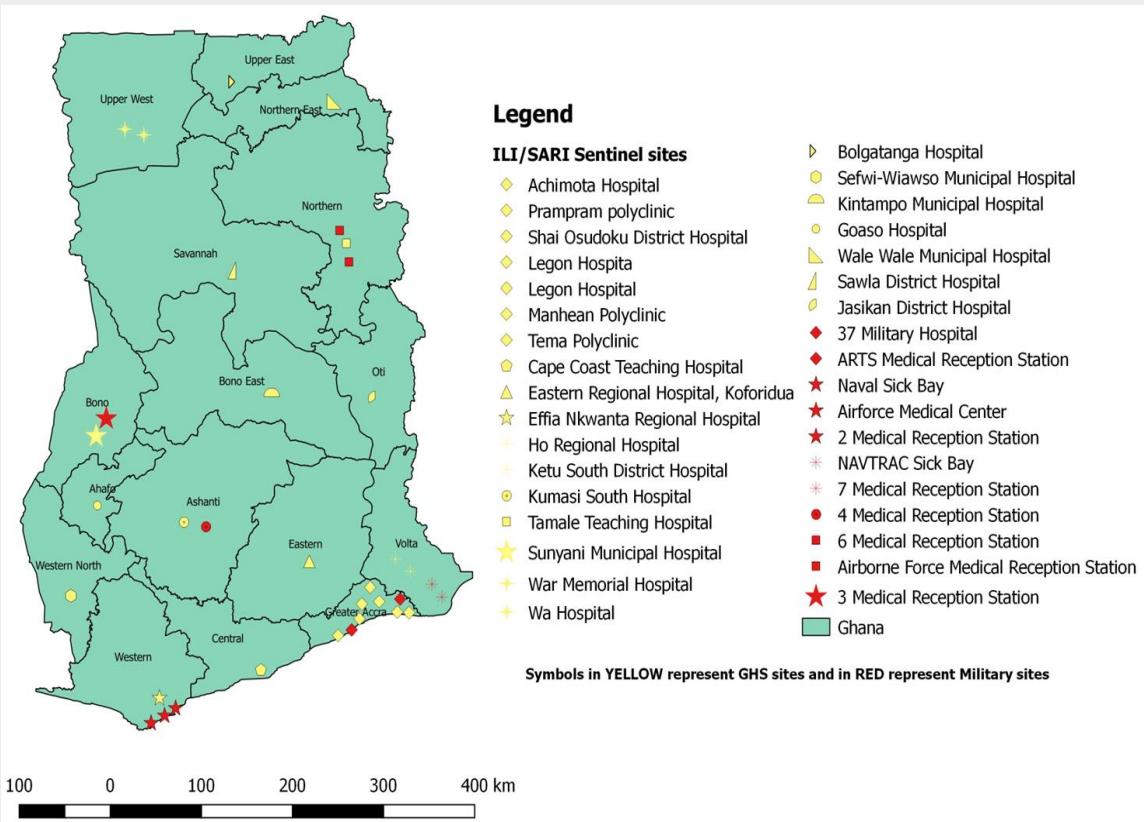
# Objectives

## Specific Objectives (Revised, 2021)

- ❖ Identify locally circulating influenza strains, coronaviruses and other respiratory pathogens
- ❖ Monitor trends in morbidity and mortality associated with respiratory pathogens in humans
- ❖ Report emerging and re-emerging respiratory infections
- ❖ Monitor the health of people exposed to infected animals



# Sample collection and processing



## Sentinel sites

## Surveillance procedure

Source: Asante IA et al.,. Epidemiology of influenza in Ghana, 2011 to 2019. *PLOS Global Public Health*, 2022.

# Sample collection: modified WHO case definitions (per IDSR)

## Case definitions

An acute respiratory infection with:

### Influenza-Like Illness (ILI)

Fever (measured/history) fever of  $\geq 38 C^\circ$

Cough/other respiratory signs

with onset within the last 10 days.

- First 15 ILI cases/site are collected

### Severe Acute Respiratory Illness (SARI)

Measured/ history of fever of  $\geq 38 C^\circ$

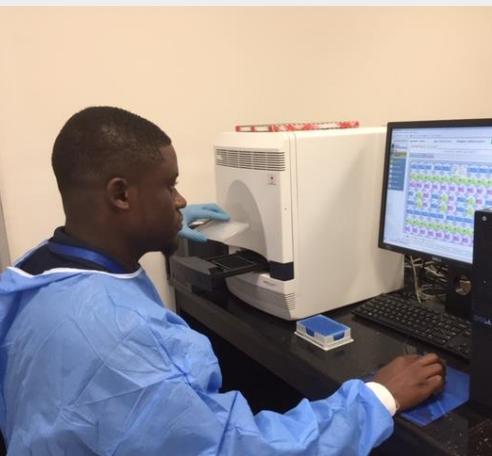
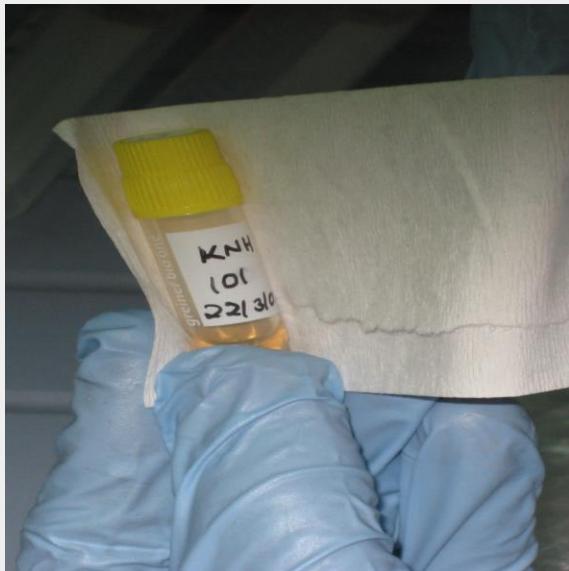
Cough/other respiratory signs

with onset within the last 10 days.

**Requires hospitalization**

- All SARI cases/ site are collected

# Samples are processed at the NIC - NMIMR



Data from surveillance system is shared with the **Global Influenza Surveillance and Response System (GISRS)**. Isolates are also shared with GISRS labs (WHO CC in London and Atlanta)

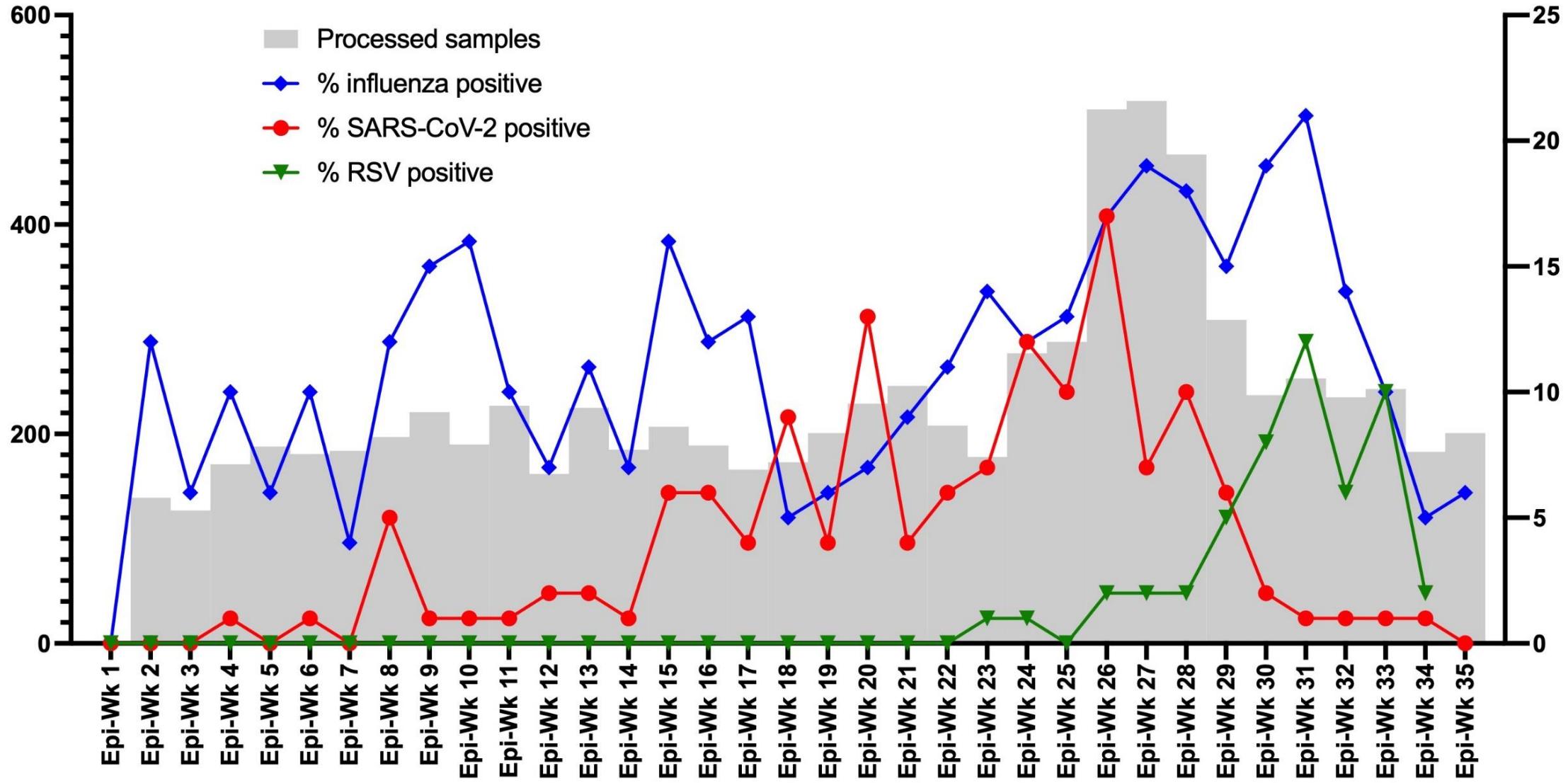
Genomic surveillance for Influenza and SARS-CoV-2

Samples are transported at +4°C to the National Influenza Centre at the NMIMR for processing

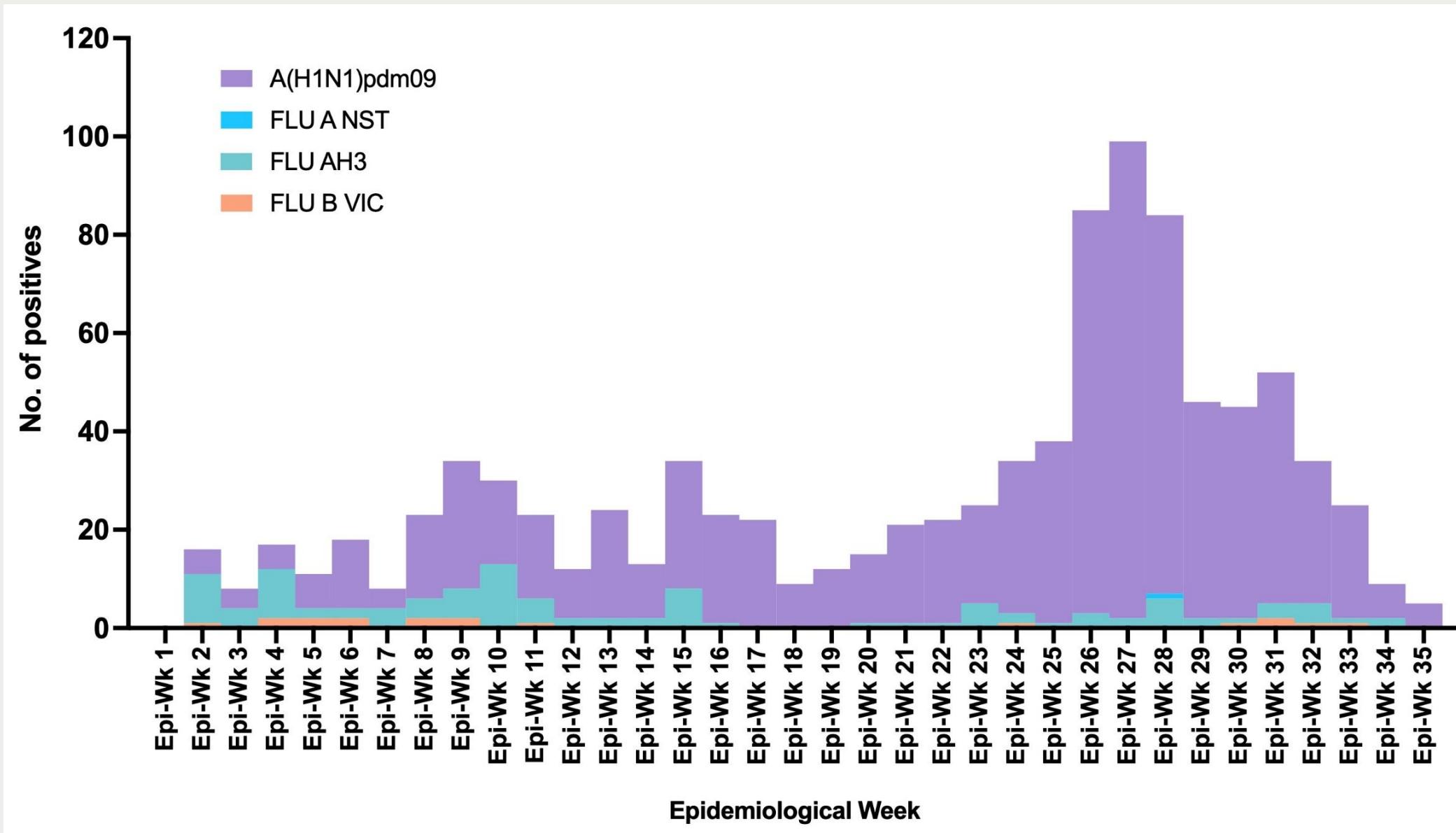
# Respiratory pathogen summary, 2025

Syndrome	Total number of samples processed	Influenza positives				SARS-CoV-2 positives	RSV positives
		A(H1N1) pdm09	FLU A not subtypable	FLU AH3	FLU B VIC		
ILI	6751	735	1	107	16	375	125
SARI	1164	119	0	3	2	38	19
<b>Total</b>	<b>7915</b>	<b>854</b>	<b>1</b>	<b>110</b>	<b>18</b>	<b>413</b>	<b>144</b>
<b>Positives (%)</b>		<b>983 (12.42%)</b>				<b>413 (5.22%)</b>	<b>144 (1.82%)</b>

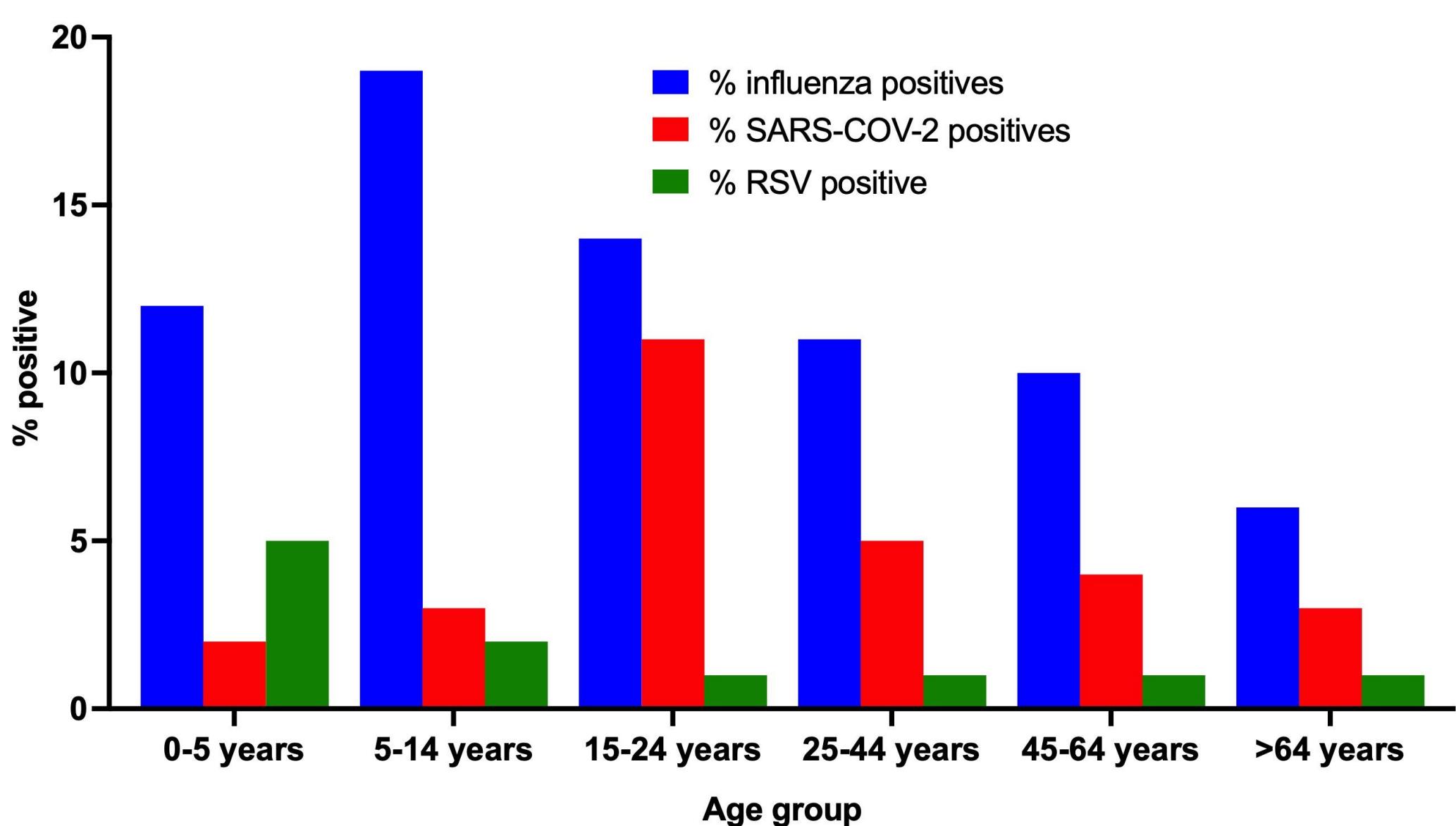
# Influenza, RSV, and SARS-CoV-2 trend per week



# Circulating influenza subtypes by epi-weeks

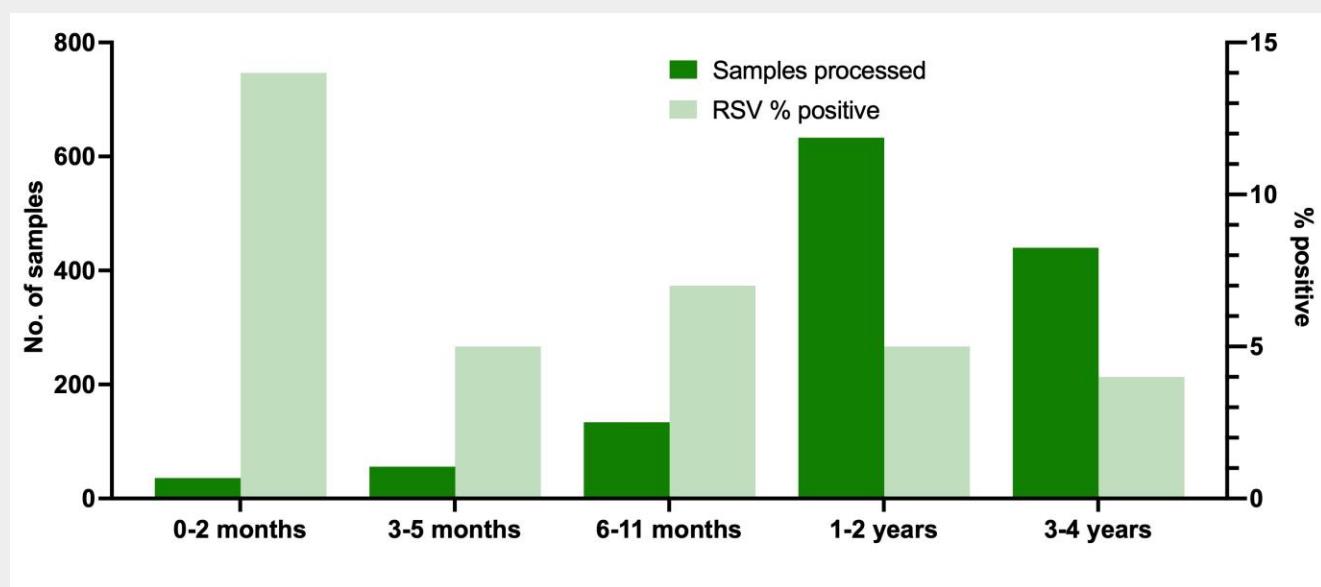


# Influenza and SARS-CoV-2 positivity by Age group



# RSV detection in children under 5 years

Age group	Samples processed	RSV Positive	RSV % Positive
0-2 months	36	5	14%
3-5 months	56	3	5%
6-11 months	134	9	7%
1-2 years	633	31	5%
3-4 years	440	19	4%
<b>Total</b>	<b>1299</b>	<b>67</b>	<b>5.58%</b>



# HRSV Under 5 years, ILI and SARI

## ILI syndrome

Age group	No. of samples processed	HRSV positive
0-2 months	32	5
3-5 months	45	2
6-11 months	117	8
1-2 years	541	26
3-4 years	382	17
<b>Total</b>	<b>1117</b>	<b>58 (5.19%)</b>

## SARI syndrome

Age group	No. of samples processed	HRSV positive
0-2 months	4	0
3-5 months	11	1
6-11 months	17	1
1-2 years	92	5
3-4 years	58	2
<b>Total</b>	<b>182</b>	<b>9 (4.94%)</b>



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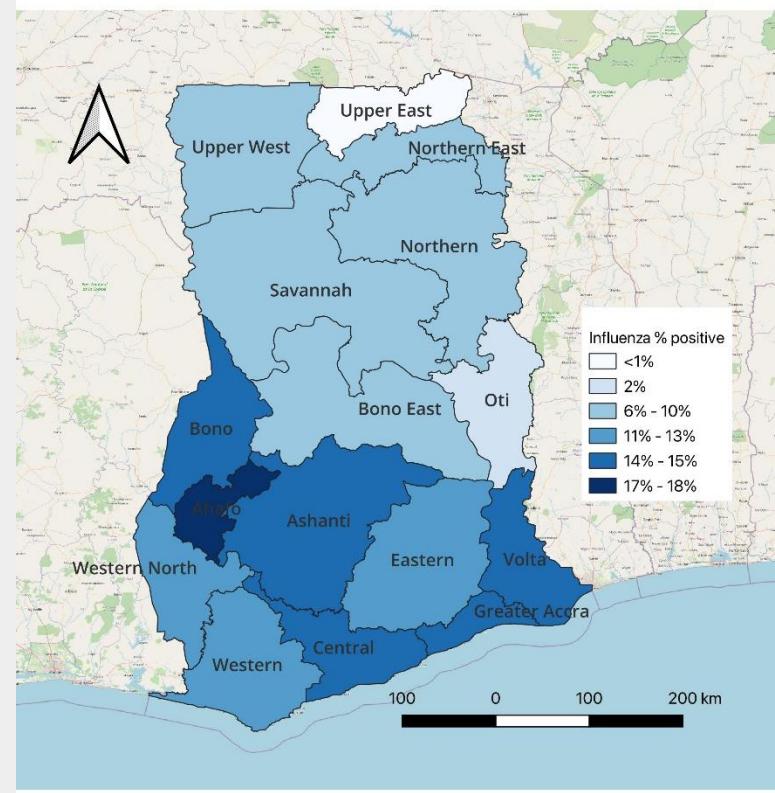
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# Regional detection of influenza, SARS-CoV-2 and HRSV

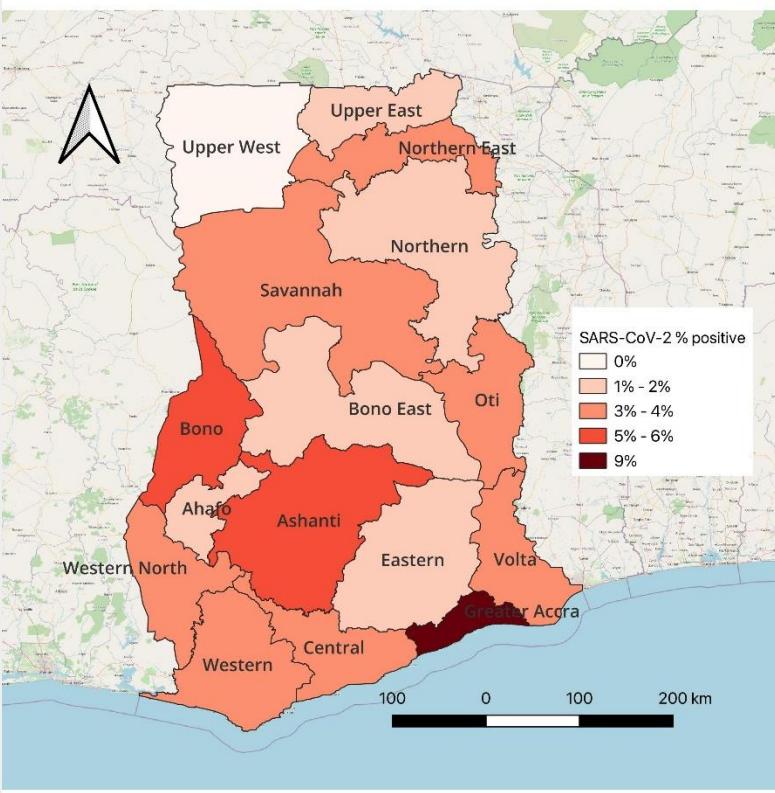
Region	No. of samples received	NO. of influenza positives	No. of SARS-CoV-2 positives	No. of HRSV positives
Ahafo	137	24	3	2
Ashanti	491	71	23	8
Bono	274	38	15	2
Bono east	323	20	2	8
Central	252	35	8	5
Eastern	414	54	6	9
Greater accra	3052	447	267	68
North east	124	8	3	1
Northern	402	28	14	4
Oti	117	3	4	0
Savannah	144	14	5	5
Upper east	467	1	5	3
Upper west	30	3	0	0
Volta	881	139	29	21
Western	539	67	19	7
Western north	268	31	10	1
<b>Total</b>	<b>7915</b>	<b>983</b>	<b>413</b>	<b>144</b>

# Regional distribution of influenza and SARS-CoV-2

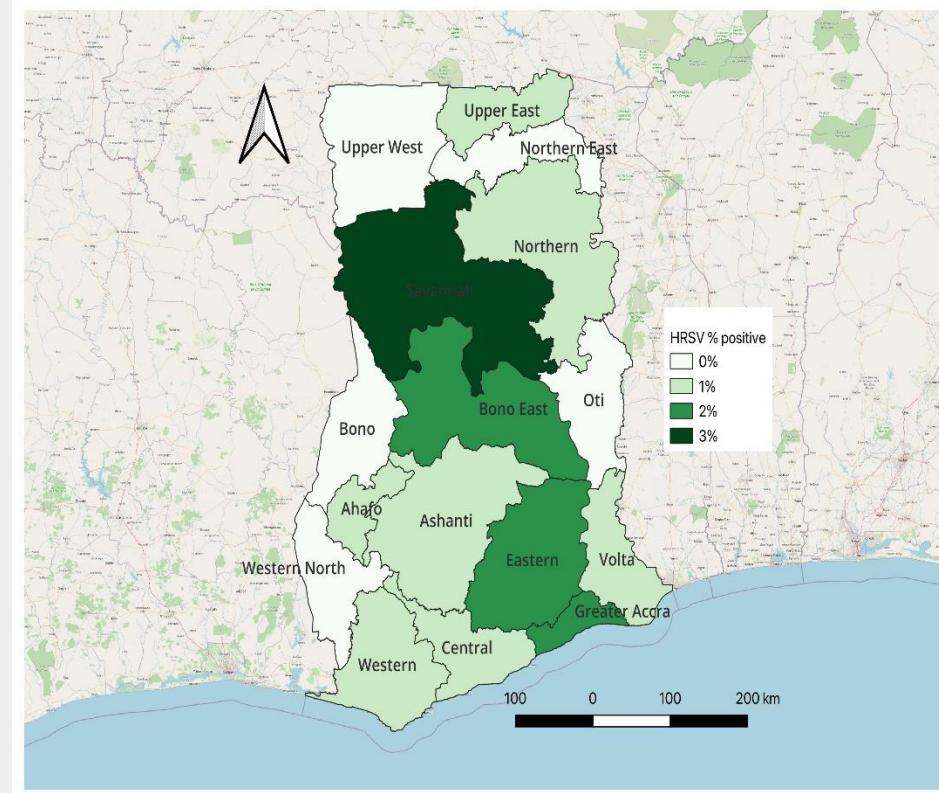
Influenza



SARS-CoV-2



HRSV

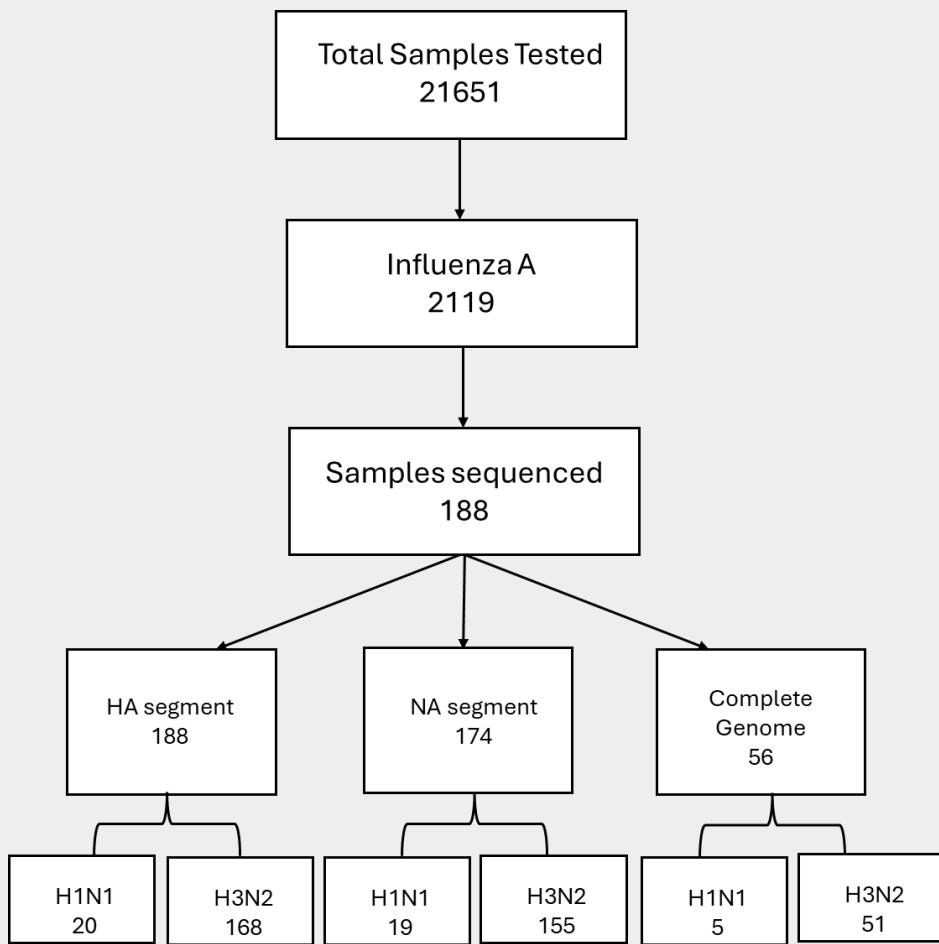


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# Genomic surveillance: Influenza

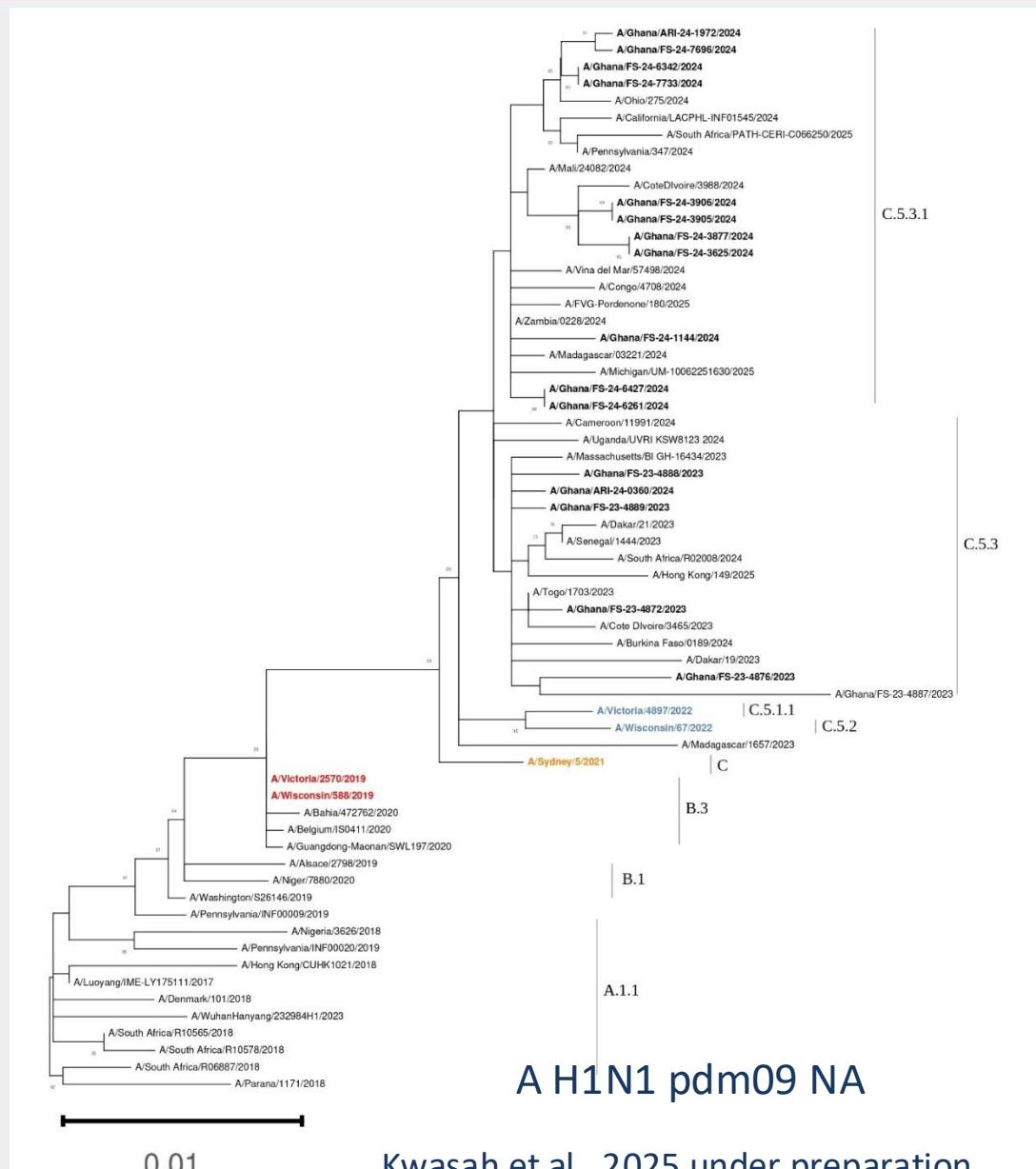
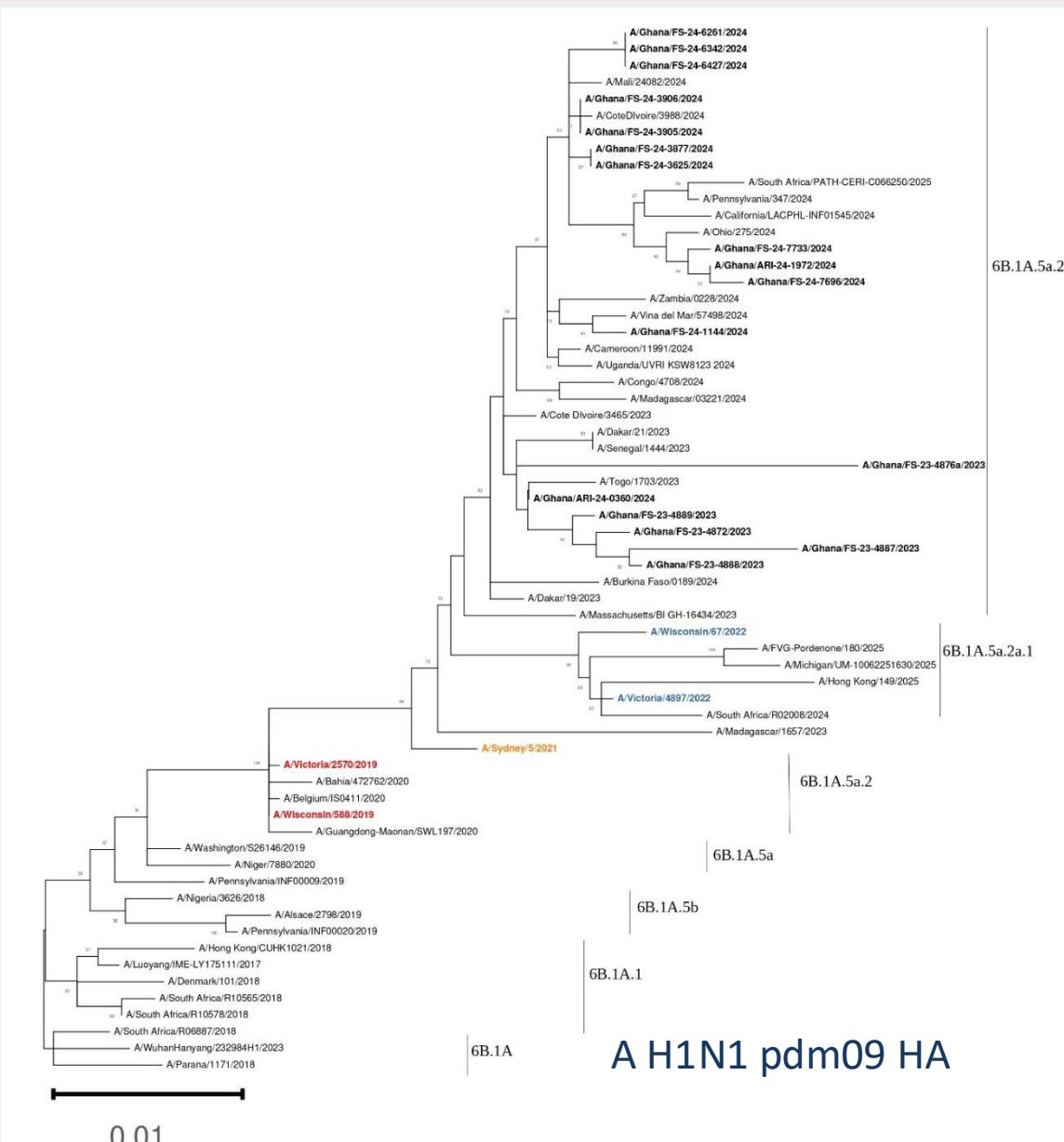


**Fig. 2** Flow chart showing the number of samples selected for whole genome sequencing (2023 to 2024)

**Table 2:** Distribution of Influenza A Virus Clades and Subclades among sequenced samples

Total samples sequenced (188)	Number of samples (%Cohort)	% of Type or clade
<b>H1N1 pdm09</b>		
<b>Total</b>	<b>20</b>	<b>10.64%</b>
<b>6B1A.5a.2a</b>		
C.1	9	45%
C.1.9	7	35%
C.1.9.2	1	5%
C.1.9.3	3	15%
<b>H3N2</b>		
<b>Total</b>	<b>168</b>	<b>89.36%</b>
<b>3C.2a1b.2</b>		
E	1	1%
<b>3C.2a1b.2a.2a.3a</b>	<b>53</b>	<b>31.55%</b>
G.1.3.1	53	100%
<b>3C.2a1b.2a.2a.3a.1</b>	<b>110</b>	<b>65.48%</b>
J	1	0.91%
J.2	108	98.18%
J.4	1	0.91%
<b>3C.2a1b.2a.2a.3b</b>	<b>4</b>	<b>2.38%</b>
G.1.3.2	4	100%

# Genomic surveillance: Influenza



# Characterization of the first detected Avian Influenza A(H9N2) human case in Ghana

B

FS-24-2641 (our specimen)  
FS-24-2641 (our specimen)  
WF10/99 (H9N2) Hong Kong  
MF 510852.1  
MK 287785.1  
MT 501620.1  
MW 159162.1  
MZ150645.1  
OR133281.1

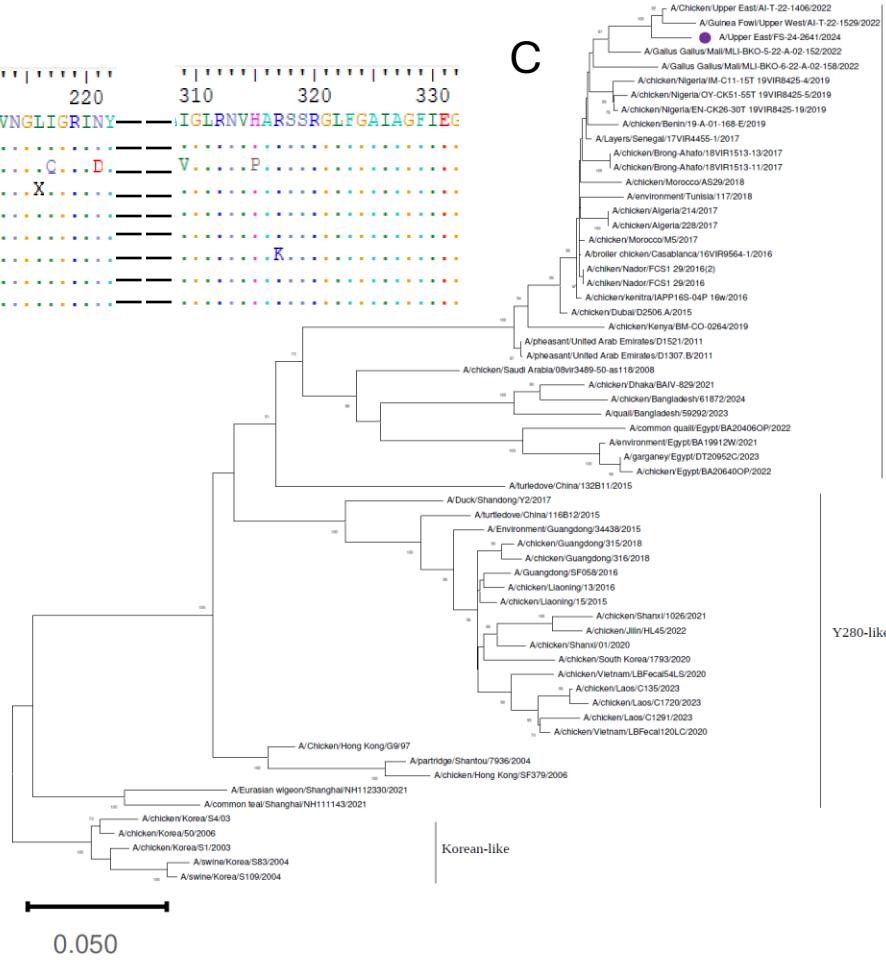


A



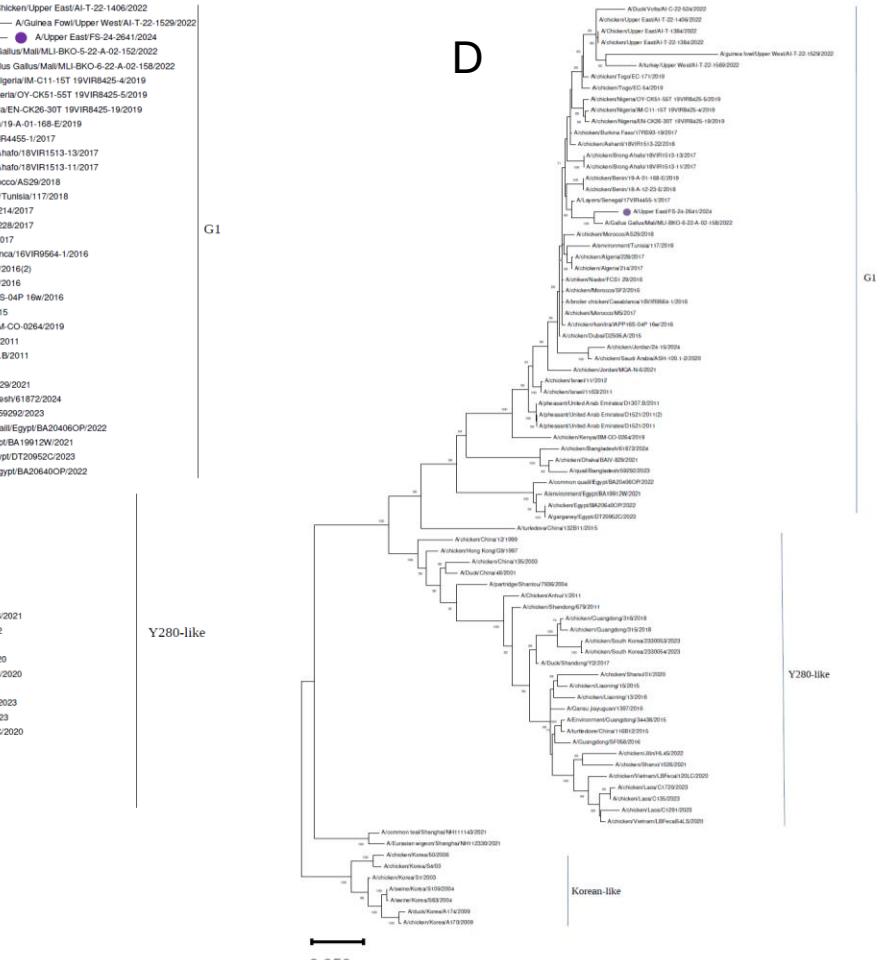
Accepted for publication: Asante et al., 2025,  
Emerging Microbes and Infections,

C



Y280-like

G1



Y280-like

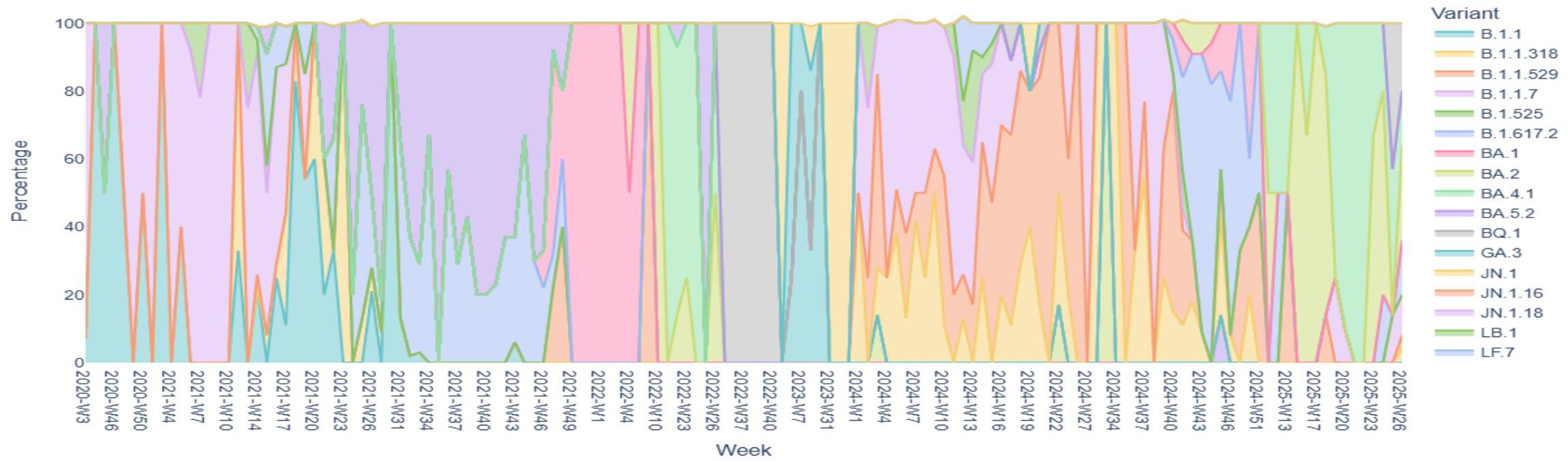
G1

Korean-like

Figure 1: Characterization of the first human case of avian influenza virus infection in human detected in Ghana. A. Map of Africa showing Ghana, in West Africa. Yellow highlight shows the region where the case was detected. B. Genetic analyses of HA showing RSSR/GLF at cleavage site, an indication of low pathogenicity and 145T and 216L mammalian adaptive motifs (mature H9 numbering) C. Phylogenetic analysis of the Neuraminidase gene from AIV A(H9N2) isolated from a child in Ghana D. Phylogenetic analysis of the Haemagglutinin gene from AIV A(H9N2) isolated from a child in Ghana. Sequence from this case is shown with a purple dot. Sequences belong to the G1 A(H9N2) lineage and closely clusters with other A(H9N2) sequences circulating among poultry in West Africa and North Africa. Accepted for publication: Asante et al., 2025, Emerging Microbes and Infections,

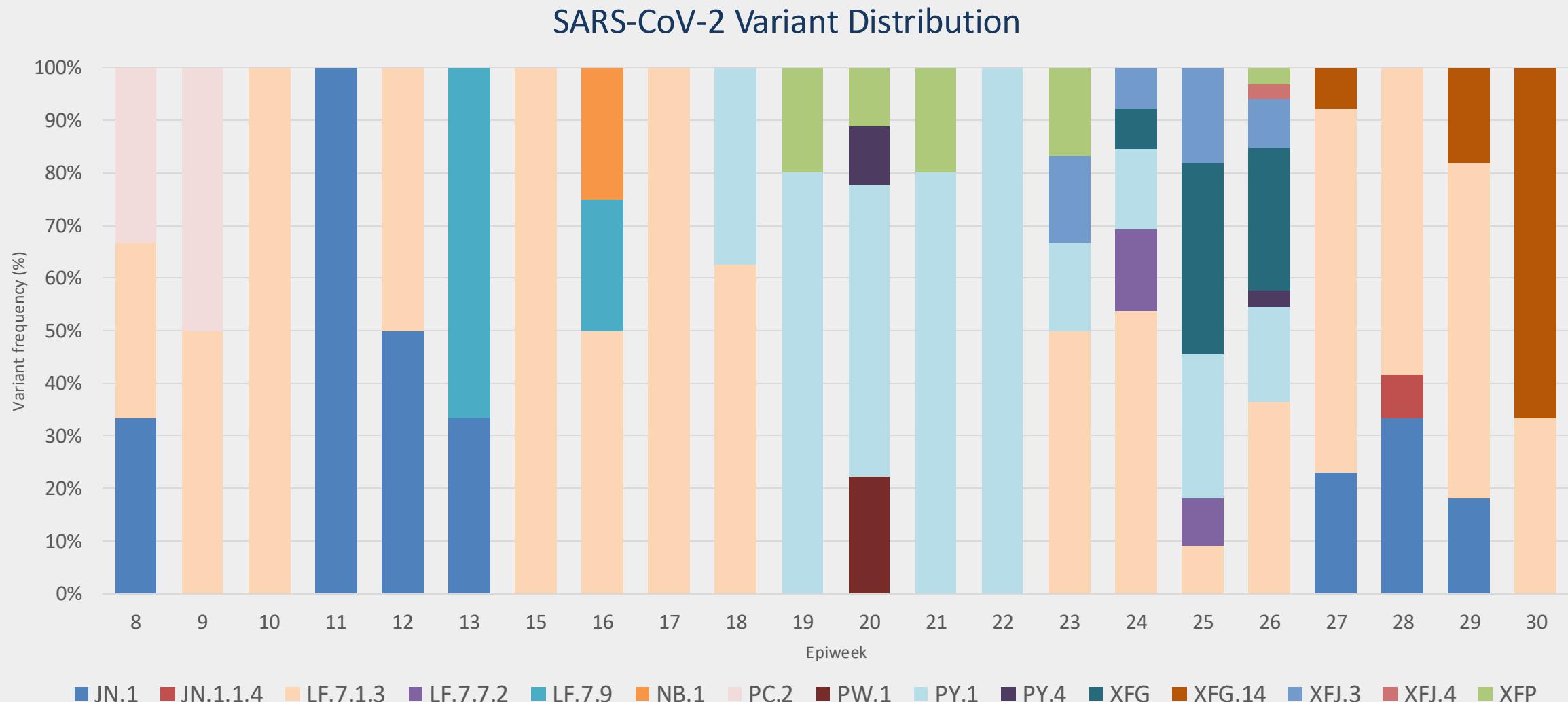
# Genomic surveillance: SARS-CoV-2

SARS-CoV-2 sequences from Ghana since 2020.



**B.1.1.7 (Alpha)** was dominant in early 2021. **B.1.617.2 (Delta)** in mid to late 2021. **B.1.1.529 (Omicron)** emerged strongly in late 2021 and remained prevalent throughout 2022. From 2022 to 2024, various **Omicron sub lineages** such as **BA.1**, **BA.2**, **BA.4.1**, **BA.5.2**, **BQ.1**, and **XBB.1.5** were periodically dominant. Emerging lineages such as **JN.1**, **LF.7**, **LF.7.1**, and **LB.1** began to dominate in 2024 and continued into mid-2025.

# Sequencing results SARS-CoV-2, 2025



# Animal sampling activities

**2022**

Implementation of the one health approach in nationwide avian influenza sampling



**2011**



Animal surveillance in barracks of the Ghana Armed Forces

**2010**

Designation of NMIMR as NIC in Ghana

**2009**

H1N1 pdm09 outbreak

**2007**

H5N1 Outbreak



Establishment of Influenza surveillance in Ghana

## FIELD ACTIVITIES

- Troop education/farmers
- Sampling (farmers, animals and environment)

## LAB WORK & DATA ANALYSIS

- Molecular detection
- Sequencing
- Data analysis

## COMMUNICATION & PUBLICATION



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# Sampling – troop/farmers education

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# Sampling – farmers

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# Sampling – Animals



# Sampling – Environment

25



Magnusen et al., 2025 under preparation

# Supporting VSD with avian influenza outbreak response (2021)



NIC-NMIMR supports with sample collection from farmers and contacts

# Results - Farmers

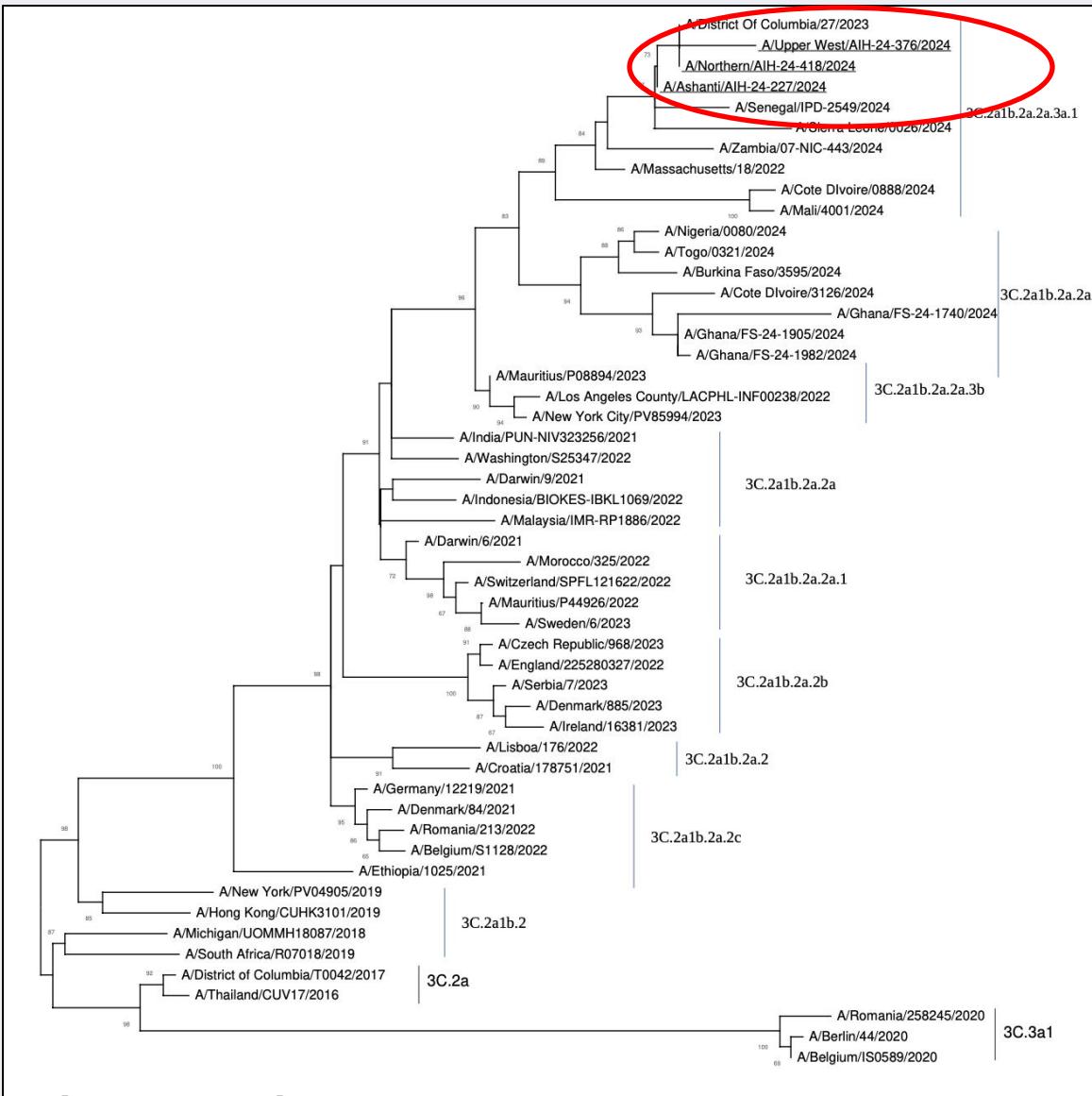
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Influenza and SARS-CoV-2 positivity among sampled farmers in Ghana, 2024

Sex	No. Samples Processed	Influenza	SARS-CoV 2
Male	344 (75%)	5	2
Female	113 (25%)	4	0
Total	457	9 (1.97%)	2(0.44%)

Magnusen et al., 2025 under preparation

# AH3 phylogeny - Farmers

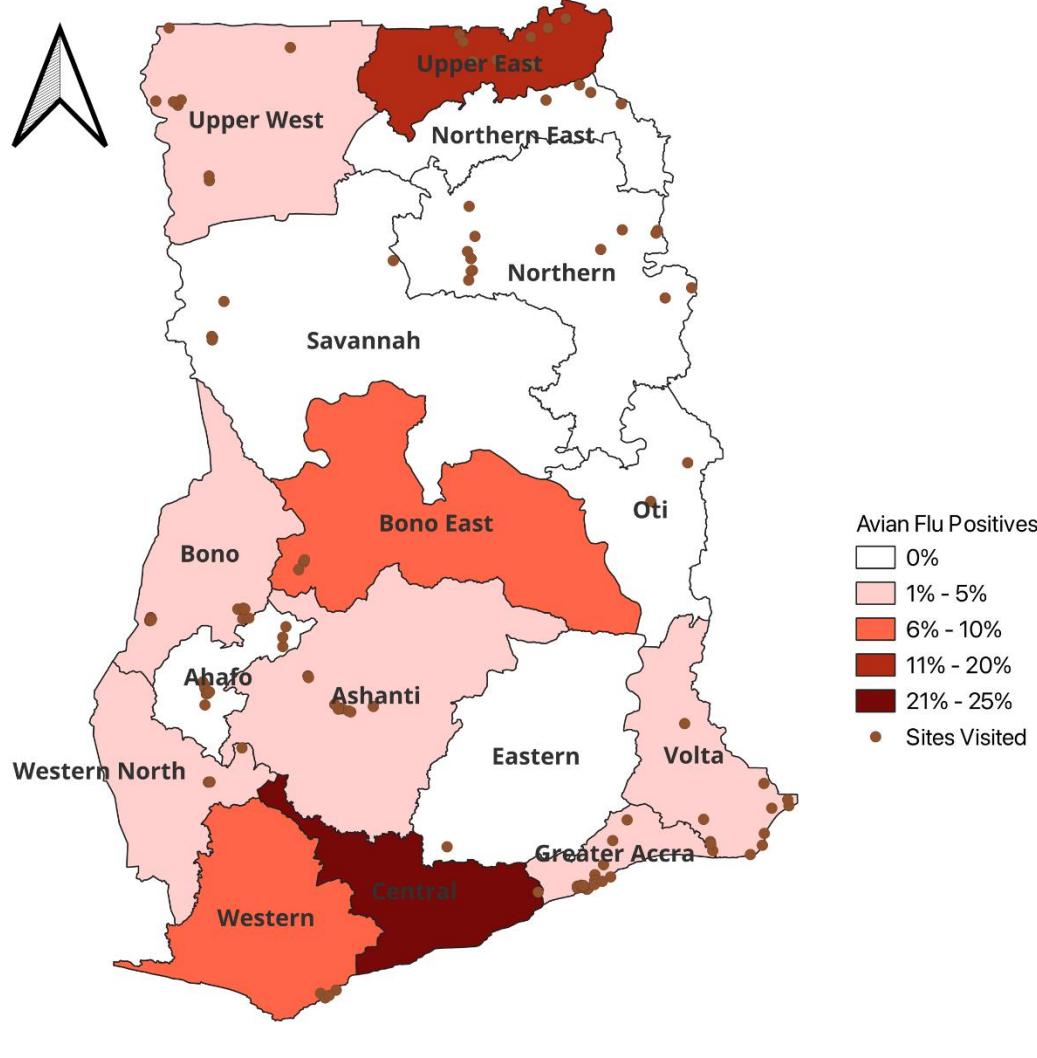


Clustering within seasonal clades  
(3C.2a1b.2a.2a.3a.1)

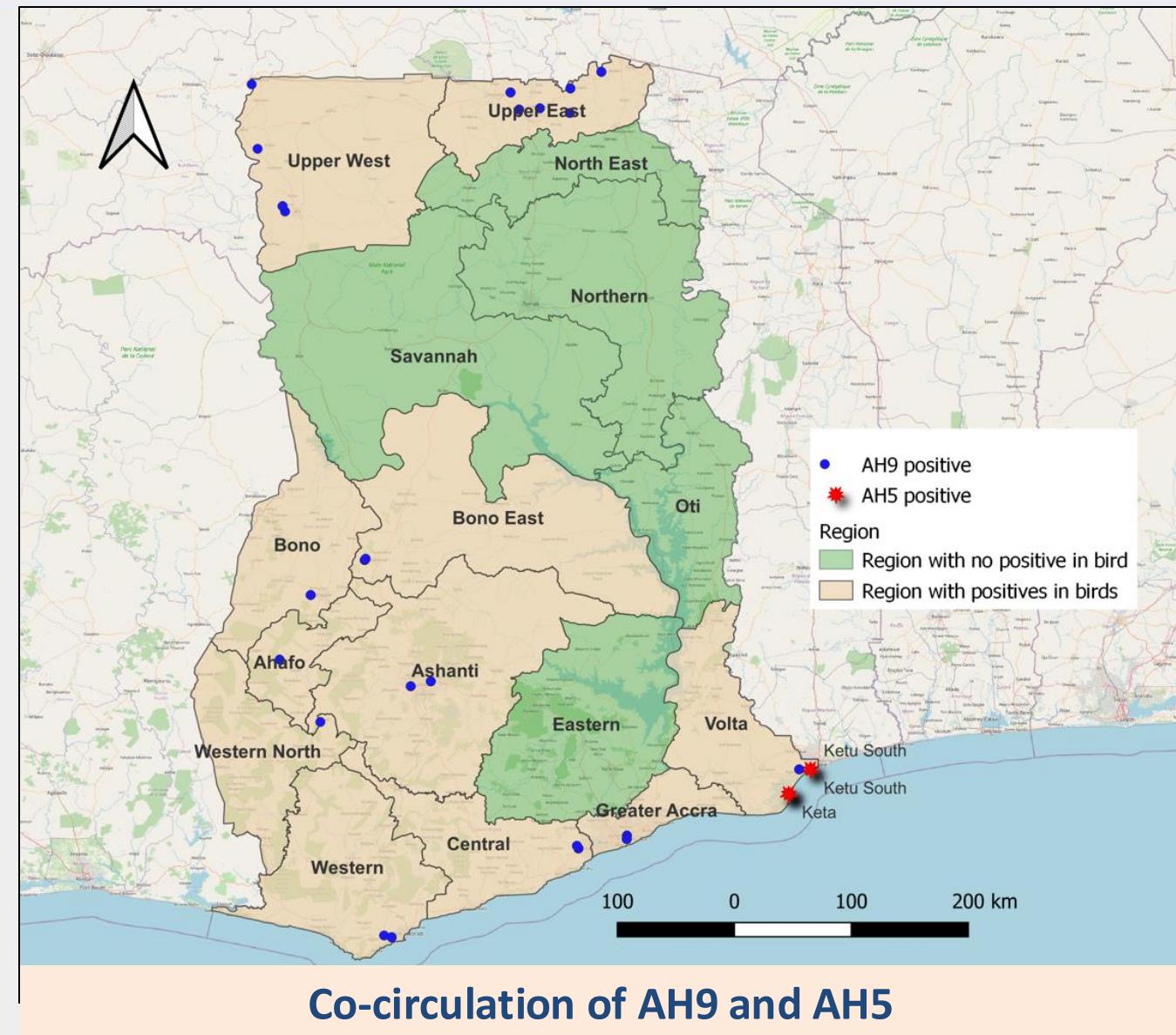
Magnusen et al., 2025 under preparation

# Distribution of AIJs in Ghana, 2024

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Magnusen et al., 2025 under preparation



NMIMR University of Ghana

# Results - Animals

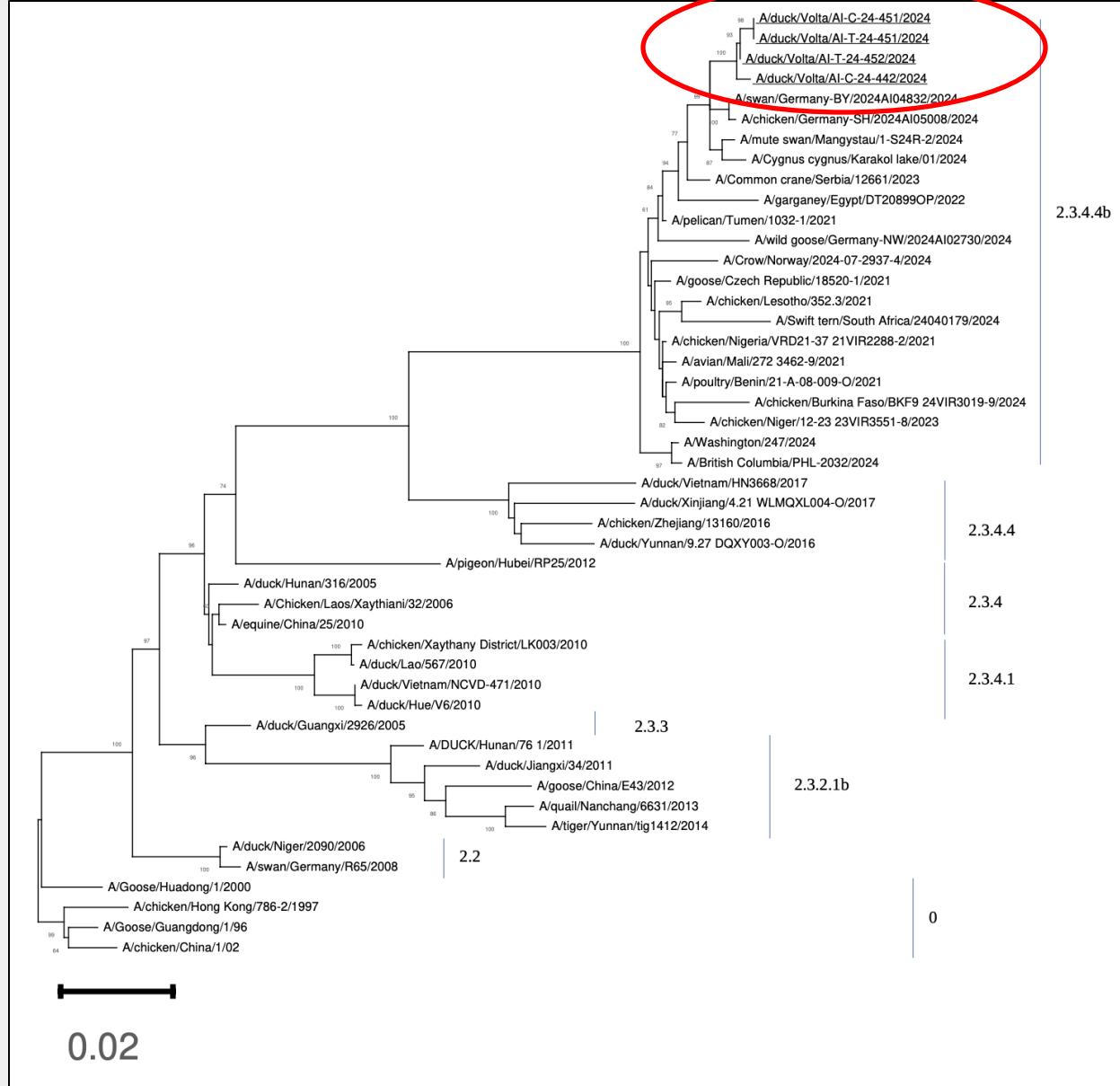
Characteristic	No Samples Tested	H5N1	[(n/N),%]	H9N2	[(n/N),%]
Total	1932	5	0.26%	78	4.04%
<b>Farm Animals</b>					
Avian	1821	5	0.27%	78	4.28%
Mammal	111	-	-	-	-
<b>Animal Sampled</b>					
Cattle	5	0	-	0	-
Chicken	1329	1	0.08%	63	4.74%
Dove	44	0	-	2	4.55%
Duck	173	4	2.31%	4	2.31%
Goat	4	0	-	0	-
Goose	18	0	-	0	-
Guinea fowl	157	0	-	9	5.73%
Quail	6	0	-	0	-
Swine	102	0	-	0	-
Turkey	84	0	-	0	-
<b>Health Status</b>					
Healthy	1806	5	0.28%	77	4.26%
Sick	119	0	-	1	0.84%
Dead	7	0	-	0	-

Avian influenza was detected in 4.30% (83/1932) of animal samples

Magnusen et al., 2025 under preparation



# Phylogeny – Animals AH5



- ❖ Phylogenetic analysis confirmed that all H5N1 isolates belonged to clade 2.3.4.4b. A globally dominant, highly pathogenic lineage known for frequent reassortment and zoonotic potential
- ❖ These isolates clustered closely with other German strains
- ❖ Regional transmission possibly linked to wild bird migration, trade, and informal farming

Magnusen et al., 2025  
under preparation

# Genetic Analysis of AH5N1 viruses

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Mutations in the HA segment of AH5 duck isolates compared with (A/chicken/Nigeria/VRD21-37\_21VIR2288-2/2021)

Study Isolates	Connecting peptide sequences								
	323-329	53	83	95	134	136	184	503	532
A/duck/Volta/AI-C-442/2024	REKRRKR		A83D	L95F	S134A	P136S	A184E	S503N	M532I
A/duck/Volta/AI-C-451/2024	REKRRKR	K53R	A83D	L95F	S134A	P136S	A184E	S503N	M532I
A/duck/Volta/AI-T-451/2024	REKRRKR	K53R	A83D	L95F	S134A	P136S	A184E	S503N	M532I
A/duck/Volta/AI-C-442/2024	REKRRKR		A83D	L95F	S134A	P136S	A184E	S503N	M532I

HPAI  
Characteristic

Mammalian  
adaptation

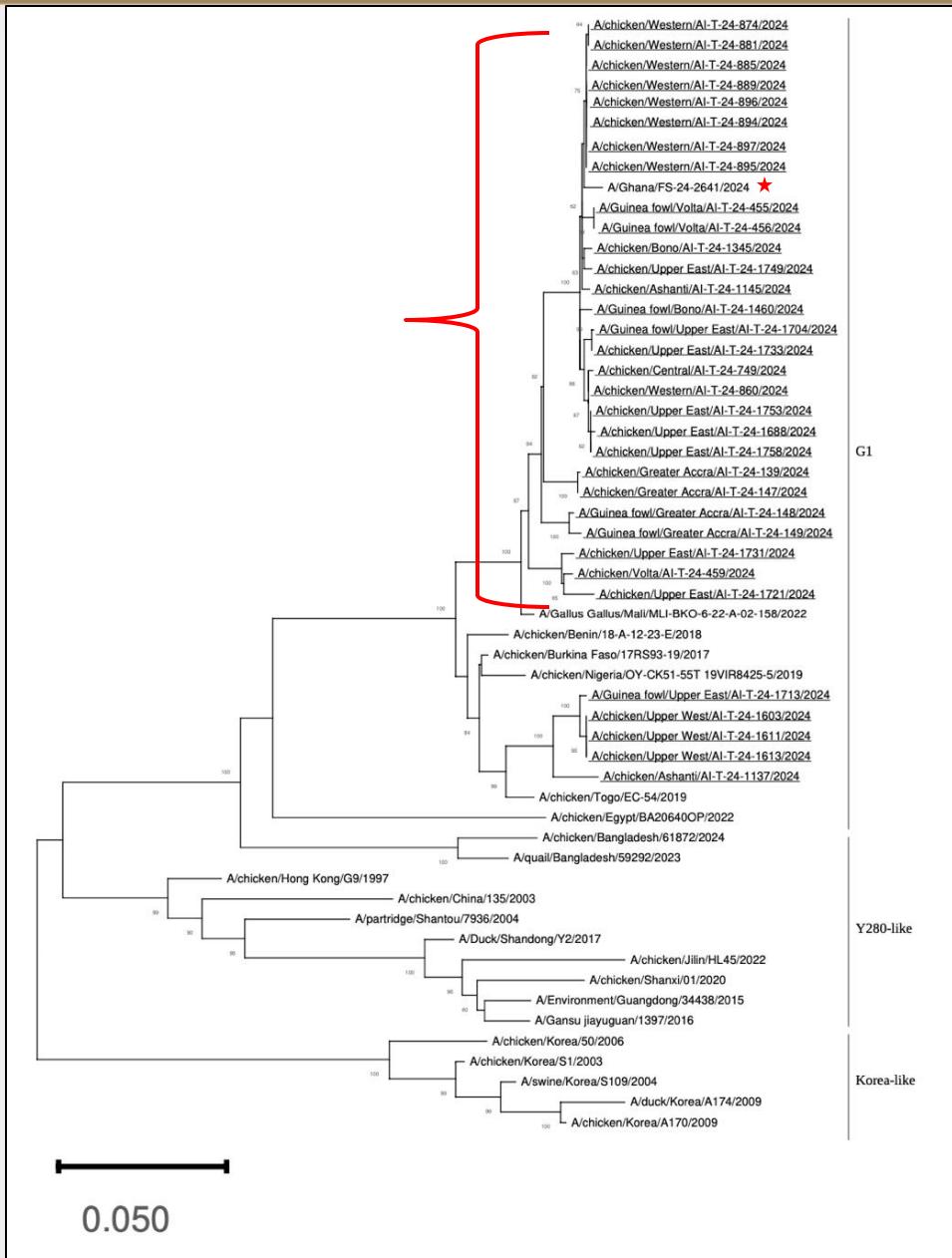


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# Phylogeny – Animals AH9



- ❖ H9N2 viruses clustered within the G1 lineage
- ❖ Human H9N2 case was also found in the G1 lineage
- ❖ Genetic similarity to strains from neighbouring countries supports active cross-border virus circulation along poultry

Magnusen et al., 2025 (In preparation)

# Genetic Analysis of AH9 isolates

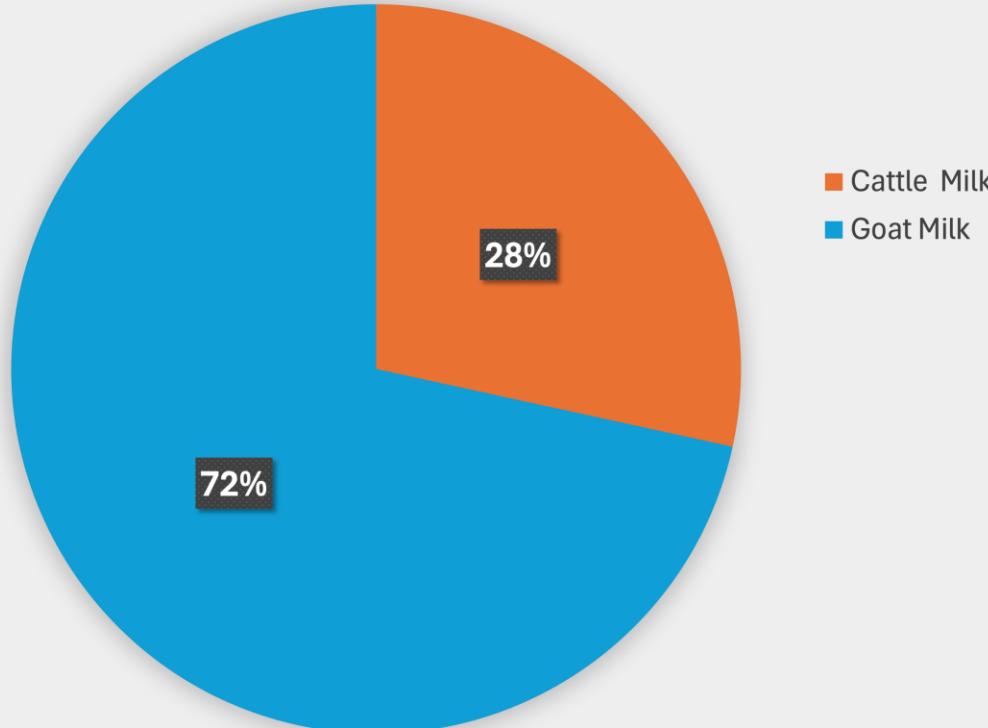
34

- ❖ RXXR cleavage motif – potential to evolve into HPAI strains.
- ❖ Mutations at positions 197T and 198A, which are linked to the virus's ability to bind avian-specific receptors, were found in all isolates.
- ❖ All isolates exhibited the 191H and 234L substitutions, which are associated with preferential binding to a cellular receptor present in various human respiratory epithelial cells – zoonotic potential.

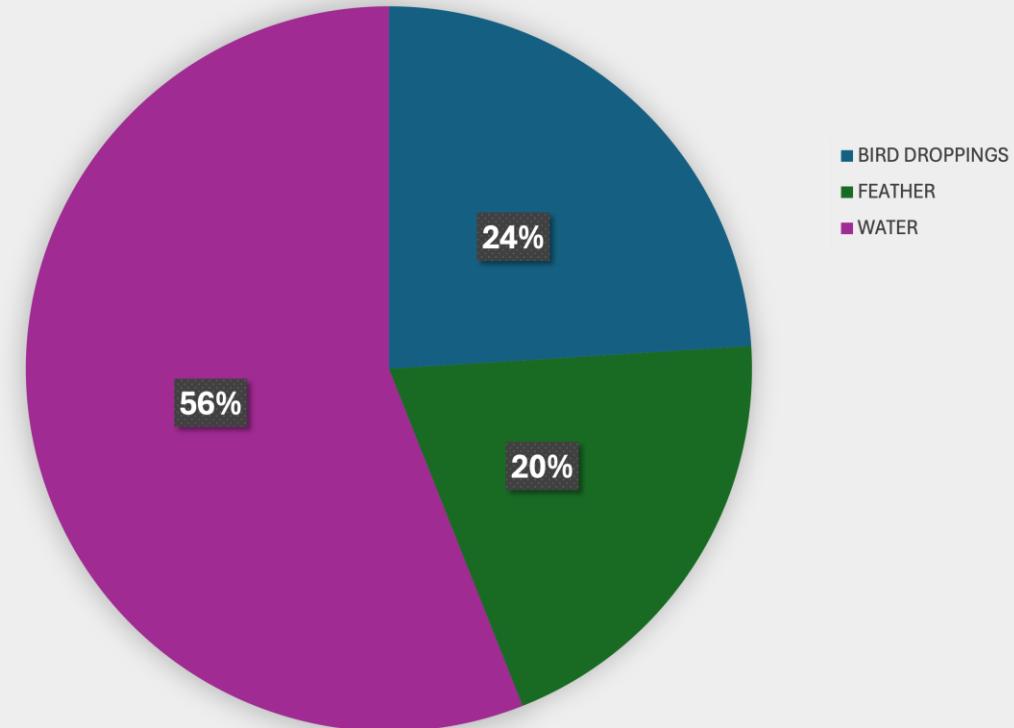
# Results – Milk & Environmental samples

35

Distribution of mammalian milk samples, 2024



Distribution of environmental samples, 2024



All milk samples tested negative for AIVs

All environmental samples tested negative for AIVs

## Summary - Farmers

- ❖ 457 farmers were sampled, with an influenza positivity rate of 2.0% (9/457) and a SARS-CoV-2 positivity rate of 0.4% (2/457).
  - All positive influenza samples were subtyped and they were influenza A(H3).
- ❖ Genetic analysis of Influenza A(H3) viruses from poultry farmers showed clustering within human seasonal clades, indicating likely human-to-human transmission, and were closely related to globally circulating strains.
- ❖ No positives diagnosed in the milk and environmental samples.

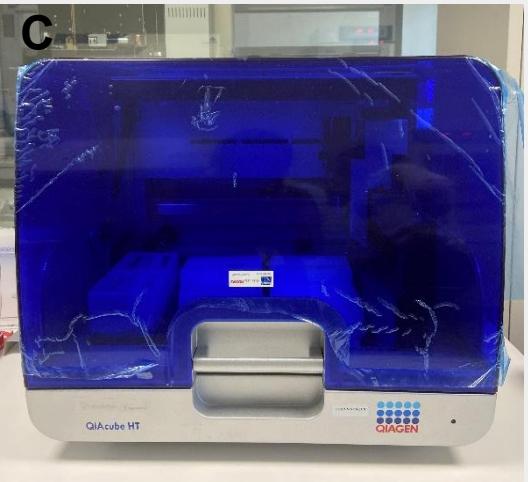
- ❖ H9N2 was prevalent in only avian samples (100%).
- ❖ Co-circulation of both H9N2 and H5N1 has been shown to increase the likelihood of morbidity and mortality in poultry (Ripa et al, 2021), therefore surveillance activities in Ghana are vital.
- ❖ Healthy animals showed higher AIV positivity (4.24%)
- ❖ Genetic analysis revealed mutations that could cause potential spill-overs, emphasizing the importance of continuous surveillance of AIVs.
- ❖ Pending work: microneutralization assays on farmers sera samples (training on MN assays)

# Progress:

- ❖ Expansion and regional reintegration. Newly formed regions: North East, Savannah, Bono East, Ahafo, Western North and Oti regions now have sentinel sites
- ❖ All sentinel sites enrolled onto SORMAS (Surveillance Outbreak Response Management and Analyses System)
- ❖ Respiratory pathogen surveillance guidelines for the country reviewed, printed and distributed to regions and districts
- ❖ Share viruses with WHO CC: London and US-CDC Atlanta as GISRS member (candidate vaccine analyses)
- ❖ 2021/2022 integration of SARS-CoV-2
- ❖ Annual Review meetings/annual animal sampling and zoonotic education activities
- ❖ Supportive supervision visits
- ❖ Training on denominator data collection (disease burden estimates) – Thursday 03.07.2025



# Genomic surveillance capacity



- A. Africa CDC sequencing lab
- B. Bioinformatics lab
- C. Automated nucleic acid isolation (Qiagen)
- D. Hamilton Microbe Star Liquid Handler
- E. Oxford Nanopore Tech. (ONT) MinION K1B
- F. ONT GridION
- G. Oxford Nanopore Tech. (ONT) MinION K1C
- H. ONT PromethION
- I. Illumina MiSeq (x2), NextSeq 1000 and 2000

Analytical platforms used:  
MIRA  
Bioedit  
MEGA

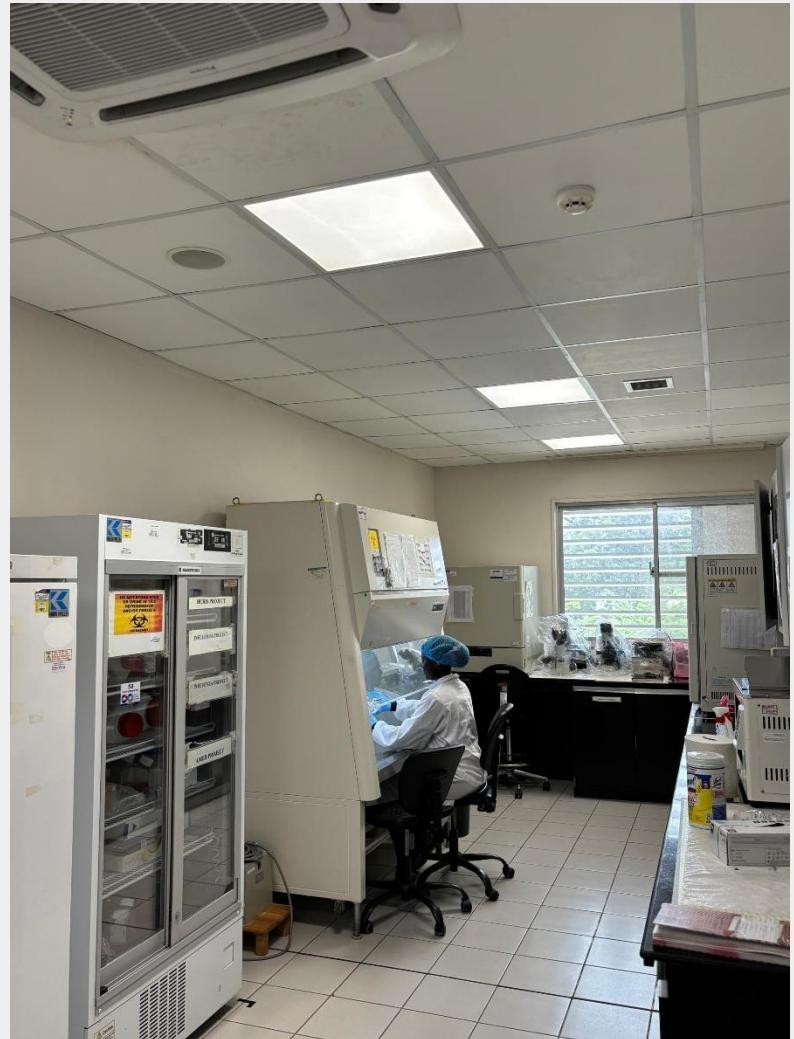


Extra storage capacity acquired (US CDC CoAg)

# Operational challenges/Going forward....

- ❖ Respiratory pathogen surveillance has contributed to providing data for circulating respiratory virus strains (influenza/SARS-CoV-2/RSV)
- ❖ Expansion of testing – across the country (logistics)
- ❖ Integration of other respiratory pathogens (RSV-2024/2025)
- ❖ Build capacity for advanced data analyses (disease burden, thresholds, modelling) towards introduction of influenza vaccines
- ❖ Build capacity for in-depth sequence analyses (identification of mutation patterns, tracing ancestry)
- ❖ Data storage capacity for sequences (limited)
- ❖ High throughput computing systems
- ❖ Sustainability

# The Noguchi Memorial Institute for Medical Research



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# Acknowledgements



World Health Organization



## Ghana Health Services

Dr Franklin Asiedu-Bekoe  
Dr Dennis O. Laryea  
Isaac Baffoe-Nyarko  
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## NAMRU#3

Dr. Naiki Attram  
Dr. Shirley Cameron-Paintsil  
Dr. Sanders Terrel

## GAF

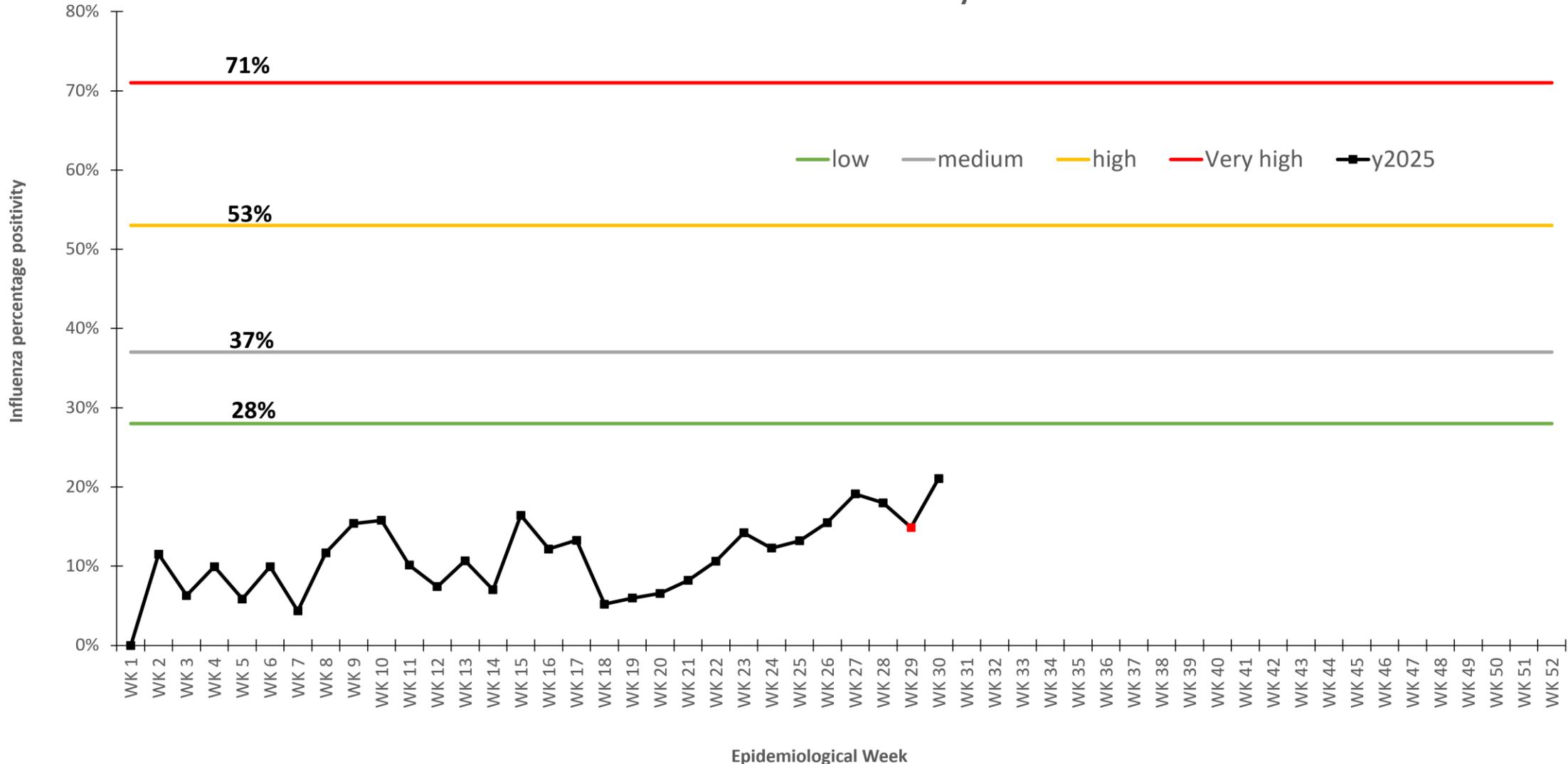
Daniel L. Mingle  
William Asiedu

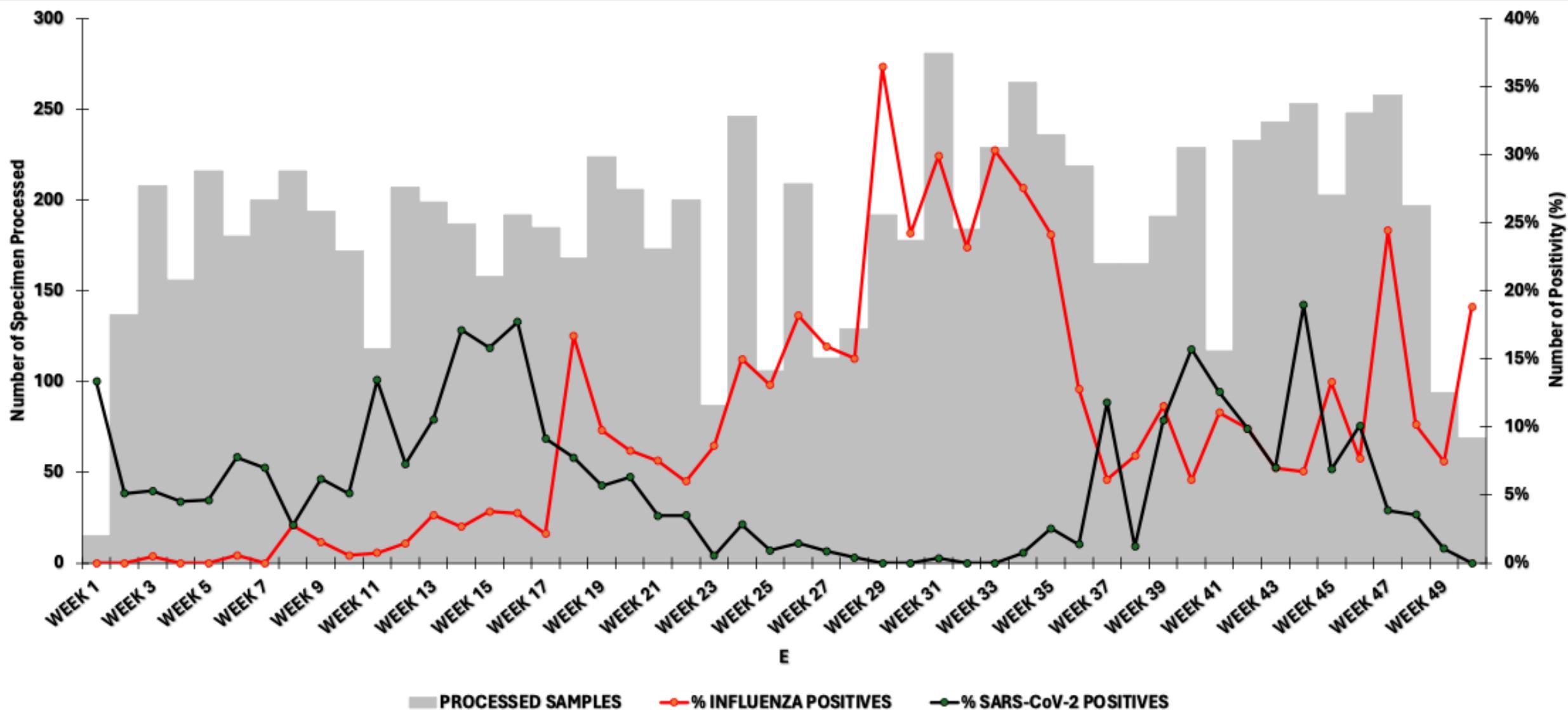
## VSD

Dr. Fenteng Danso  
Dr. Theophilus Odoom

United States Centers for Disease Control and Prevention, Influenza Division, Atlanta

## 2025 Influenza Activity





# Literature

## Troop education and avian influenza surveillance 2011

Research article | Open Access  
Volume 12, article number:

BMC Research Notes



BMC

► BMC Res Notes. 201

John Kofi Odoom, S  
Roland M L Sowa, Fe  
James Aboagye, Chr  
Oyofo & William KA

### Biosecurity management in Ghana

[Prince Godfred Agber](#)  
[Alhassan<sup>1</sup>, David Roc](#)  
[Aboagye<sup>2</sup>, Karl C Kro](#)

► Author information

PMCID: PMC4316646

## Veterinary Medicine and Science



ORIGINAL ARTICLE | [Open Access](#) |

### Phylogenetic and genetic characterization of influenza A H9N2 viruses isolated from backyard poultry in selected farms in Ghana

Erasmus Nikoi Kotey, Ivy Asantewaa Asante , Mildred Adusei-Poku, Augustina Arjarquah, Richard Ampadu, David Rodgers, Edward Owusu Nyarko, William Asiedu ... [See all authors](#) ▾

First published: 21 April 2022 | <https://doi.org/10.1002/vms3.809> | Citations: 1



# Background

RESEARCH ARTICLE

Open Access

## Troop education and avian influenza surveillance in military barracks in Ghana, 2011

John Kofi Odoom<sup>1</sup>, Samuel Bel-Nono<sup>2</sup>, David Rodgers<sup>2</sup>, Prince G Agbenohevi<sup>2</sup>, Courage K Dafeamekpor<sup>2</sup>, Roland M L Sowa<sup>2</sup>, Fentena Danso<sup>3</sup>, Reuben Tettev<sup>3</sup>, Richard Suu-Ire<sup>4</sup>, Joseph H K Bonney<sup>1</sup>, Ivy A Asante<sup>1</sup>.

SHORT REPORT

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## Biosecurity measures to reduce influenza infections in military barracks in Ghana

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### Abstract

**Background:** Military barracks in Ghana have backyard poultry populations but the methods used here involve low

2011 – 2012

Avian influenza surveillance in military barracks.  
(Odoom et. al., 2012; Odoom et. al., 2015).

Outbreaks of avian influenza in Ghana since 2007 led to yearly surveillance for avian influenza among poultry in Ghana since 2010.

ORIGINAL ARTICLE

WILEY

## Phylogenetic and genetic characterization of influenza A H9N2 viruses isolated from backyard poultry in selected farms in Ghana

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ORIGINAL ARTICLE



## Avian influenza H9N2 subtype in Ghana: virus characterization and evidence of co-infection

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### ABSTRACT

Between November 2017 and February 2018, Ghanaian poultry producers reported to animal health authorities a dramatic increase in mortality rate and a relevant drop in egg production

### ARTICLE HISTORY

Received 15 February 2019  
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2017 – 2019

LPAIV A(H9N2) among poultry  
(NIC-NAMRU-3, GAF)  
(Awuni et. al., 2019;  
Kotev et. al..2022).

2021 – 2022

Active avian influenza surveillance  
(NIC-NAMRU-3, GHS,  
GAF, VSD).

# Zoonoses education and animal sampling activities

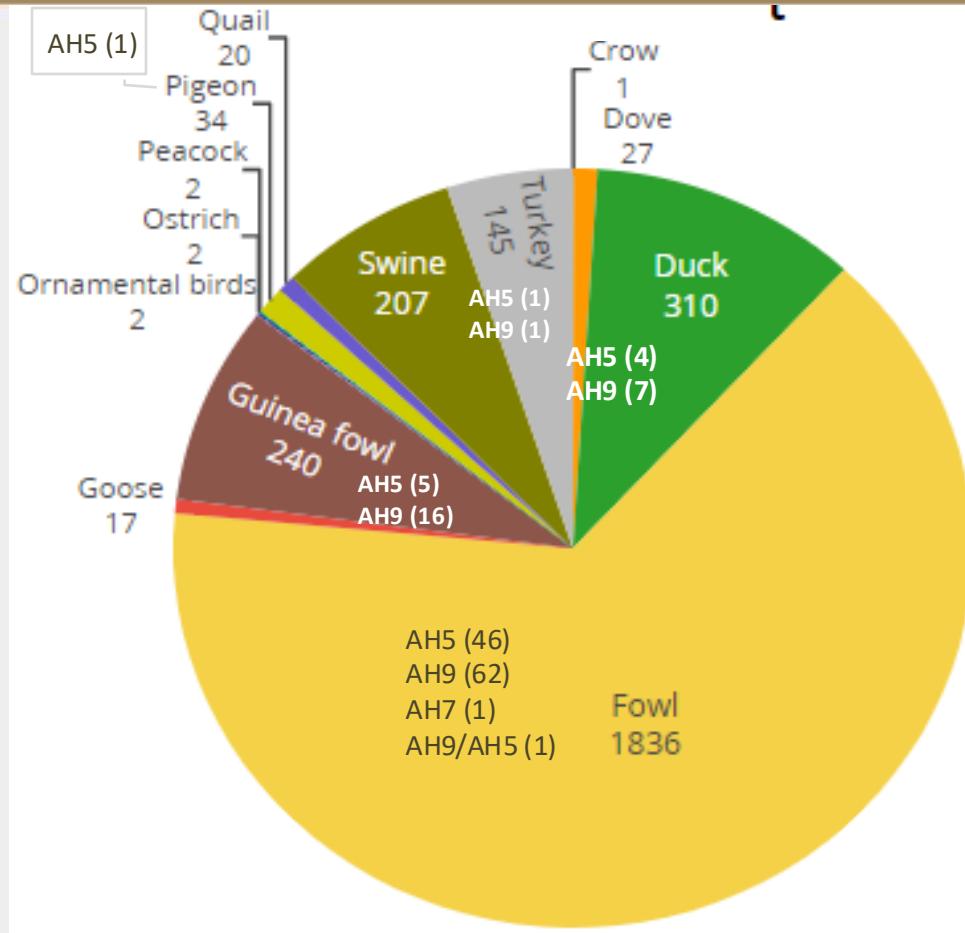


# Supporting VSD with avian influenza outbreak response (2021)



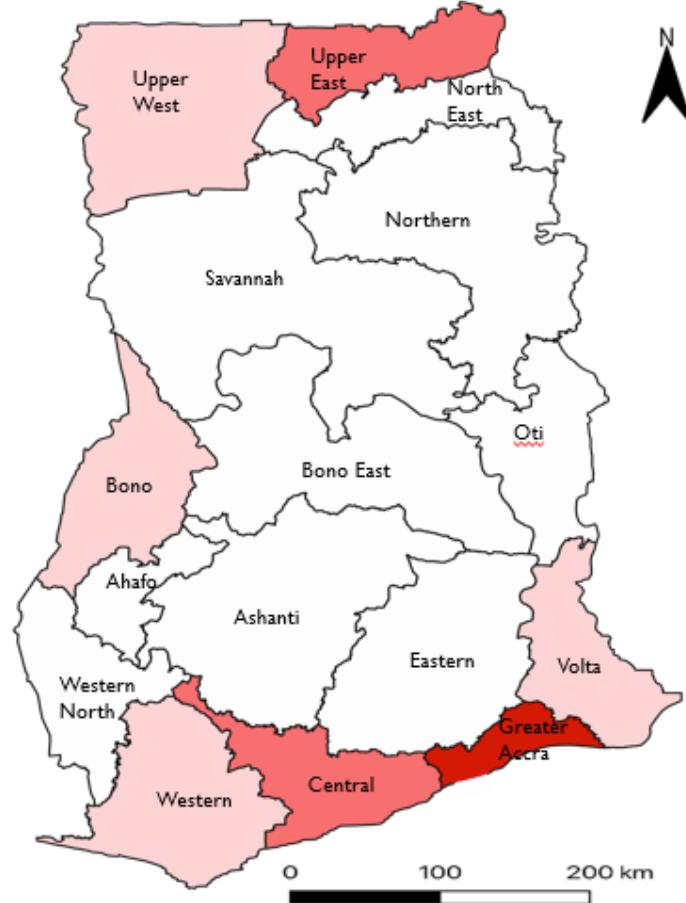
NIC-NMIMR supports with sample collection from farmers and contacts

# Results 2024



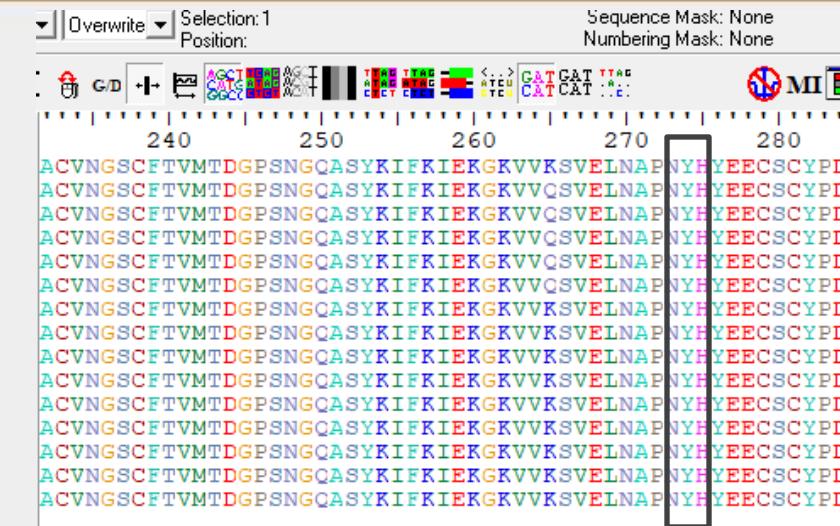
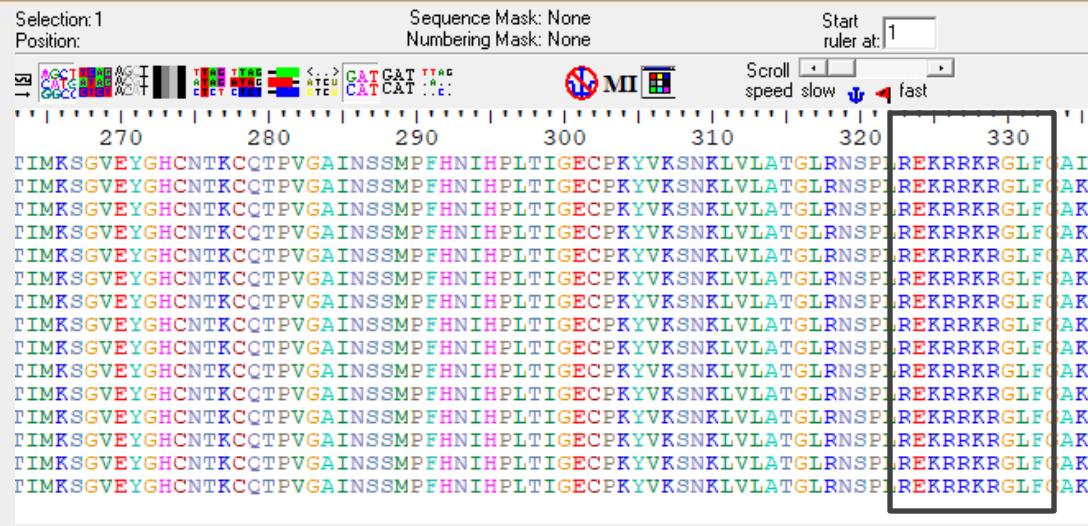
A total of 2,847 animal samples were taken. Positivity rate of 2.0% (57/2847) for AH5 viruses and 3.02% (86/2847) for AH9 viruses, AH7 (1 case), AH9/AH5 (1 case).

Currently, co-circulation of influenza AH9 and AH5 viruses among poultry in Ghana (2021-2022)

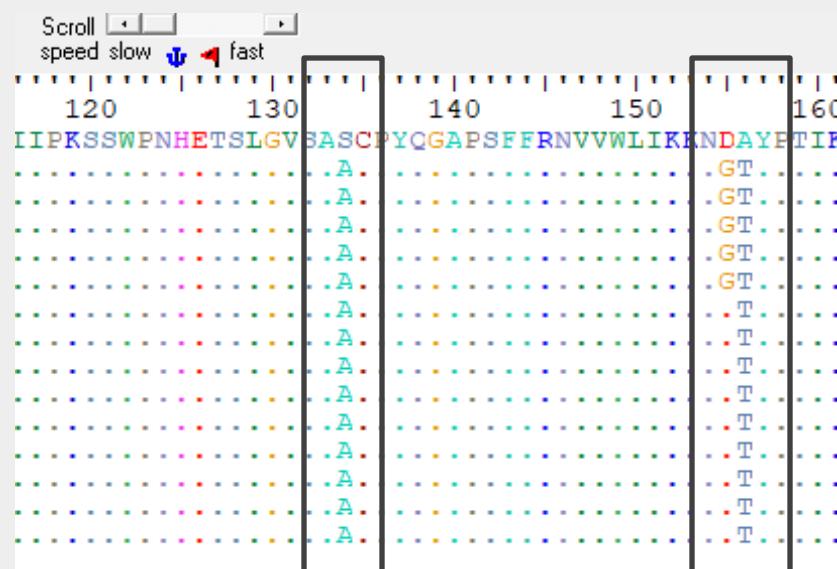


Greater Accra recorded the highest influenza (AH5) activity while Upper West, Bono, Western, and Volta regions recorded the least AI activity.

# Genetic Analyses: 2024



Position 323: REKRRKR\*GLF, polybasic cleavage site  
Indicative of high pathogenicity in infected birds.

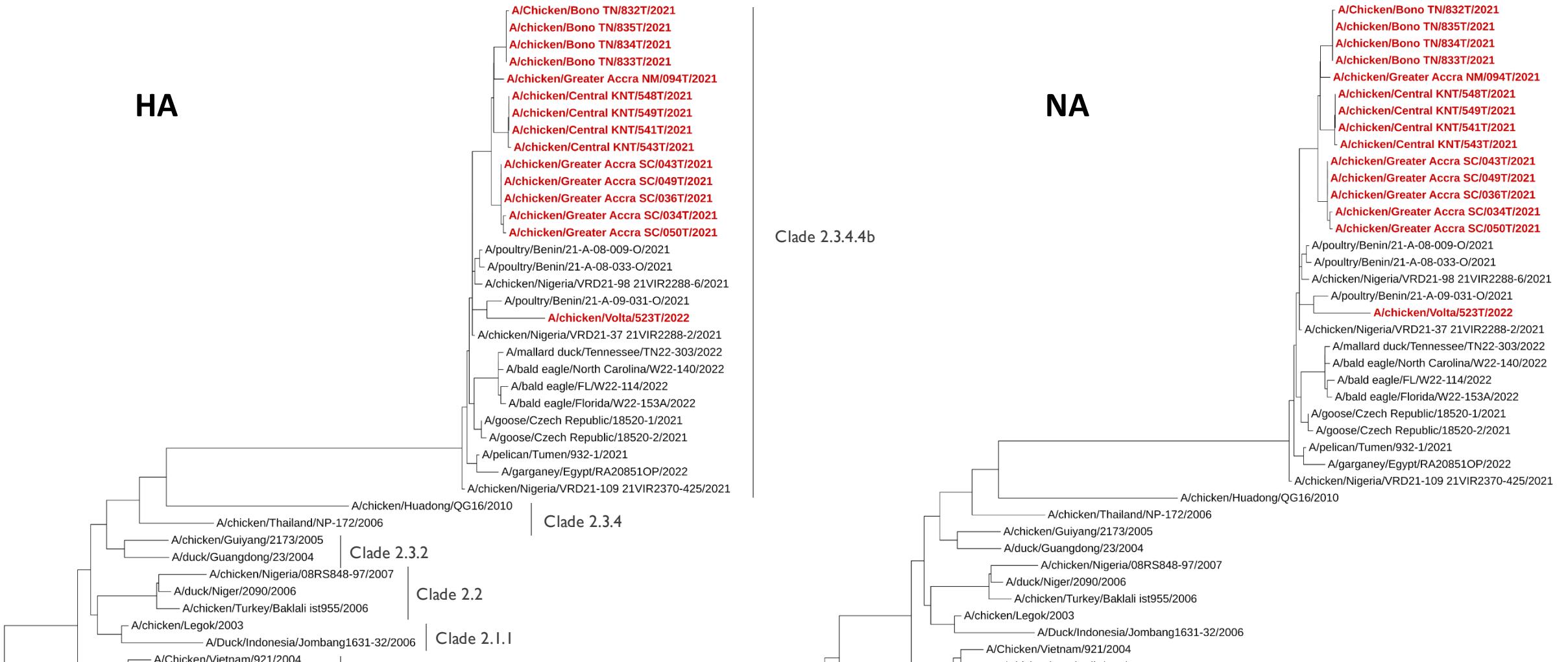


Neuraminidase  
H274Y mutation indicates susceptibility to antiviral (oseltamivir).

HA mammalian adaptive motifs : S134A, D155G, A156T

The HA mutations identified have been implicated in altering the virus's ability to bind to human host cells and evade immune responses.

# Phylogeny: 2024



Ghanaian HPAI A(H5N1) viruses isolated in 2021 to 2022 belonged to clade 2.3.4.4b and closely related to viruses from Nigeria and Benin.

# RESULTS - FARMERS

Influenza and SARS-CoV-2 positivity among Ghanaian farmers by site, 2024

Location / Site Visited	Region	No. Positive for Influenza	No. positive for SARS-CoV-2
4 INFANTRY BATTALION BARRACKS	ASHANTI	1	1
ADUGYAMA		1	0
EJISU ANIMAL MARKET		3	0
NUNGUA FARMS	GREATER ACCRA	1	0
BUNKPURUGU	NORTH EAST	1	0
AIR BORNE FORCE BARRACKS	NORTHERN	1	0
TUMU	UPPER WEST	1	0
NAVTRAC AGORTA	VOLTA	0	1
<b>Total</b>		<b>9</b>	<b>2</b>

Influenza AH3 and SARS-CoV-2 were prevalent in 9 and 2 farmers sampled