



# OFFLU AVIAN DATA PACKAGE FOR ZOOONOTIC INFLUENZA TC

February 2024 to September 2024

## SCOPE

In this document we present a summary of avian influenza A virus events reported from 1st February 2024 to 28th September 2024 and phylogenetic analysis of H5, H7, H9 and H10 viruses.

## Contents

---

Introduction, data sources, methods and acknowledgements .....	3
Summary .....	4
Global avian influenza events in animals.....	5
H5 Influenza A viruses .....	6
H5 Phylogenetic tree coloured by region .....	6
H5 Influenza A viruses- map .....	7
Activity table .....	8
Gs/Gd H5 2.3.4.4b phylogenetic tree.....	9
Gs/Gd H5 2.3.4.4b subsampled phylogenetic tree .....	10
Gs/Gd H5 2.3.4.4b Amino acid difference tables.....	11
Gs/Gd H5 2.3.4.4b Antigenic data .....	12
Gs/Gd H5 2.3.4.4b Antigenic data from previous report.....	13
Gs/Gd H5 2.3.2.1a phylogenetic tree.....	14
Gs/Gd H5 2.3.2.1a amino acid difference table .....	15
Gs/Gd H5 2.3.2.1a Antigenic data .....	16
LPAI H5 phylogenetic tree .....	17
H7 Influenza A viruses .....	18
H7 Eurasian lineage and american lineage amino acid difference tables .....	19
H9 Influenza A viruses .....	20
H9 Y280 (B4.7) phylogenetic tree.....	20
H9 Y280 (B4.7) amino acid difference table .....	21
H9 Y280 (B4.5) phylogenetic tree.....	22
H9 Y280 (B4.5) amino acid differences .....	23
H9 G1 (G5.7) phylogenetic tree .....	24
H9 G1 (G5.7) amino acid difference table .....	25
H9 G1 (G5.7) antigenic data .....	26
H9 G1 (G5.5) phylogenetic tree .....	27
H9 G1 (G5.5) amino acid difference table .....	28
H9 G1 (G5.5) Antigenic data.....	29
H10.....	30

## Introduction, data sources, methods and acknowledgements

The epidemiological summary was generated using data from the Food and Agriculture Organization of the United Nations (FAO) EMPRES Global Animal Disease Information System (EMPRES-i+) and the World Animal Health Information System (WAHIS) portal provided by the World Organisation for Animal Health (WOAH). Only data for confirmed reports in environmental samples, wild birds, captive wild birds, domestic birds and mammals were used; suspect cases were excluded where results were based solely on serology.

We thank the OFFLU avian group for their expertise and for sharing data. We acknowledge the following national laboratories, research institutes and surveillance programs and are very grateful for their collaboration: *Agence Nationale de Sécurité Sanitaire (France)*, *Animal and Plant Health Agency (UK)*, *Animal and Plant Quarantine Agency (Korea, Republic of)*, *Australian Centre for Disease Preparedness (Australia)*, *Bangladesh Livestock Research Institute (Bangladesh)*, *Canadian Food Inspection Agency (Canada)*, *Chittagong Veterinary and Animal Sciences University (Bangladesh)*, *Disease Investigation Centre Wates (Indonesia)*, *Friedrich-Loeffler-Institute (Germany)*, *Harbin Veterinary Research Institute (China)*, *Hokkaido University (Japan)*, *Institute Pasteur Cambodia (Cambodia)*, *Istituto Zooprofilattico Sperimentale delle Venezie (Italy)*, *Laboratório Federal de Defesa Agropecuária (Brazil)*, *National Centre for Foreign Animal Disease (Canada)*, *National Institute of High Security Animal Diseases (India)*, *Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria (Mexico)*, *The National Institute of Agricultural Technology (Argentina)*, *University of Chile (Chile)*, *Wageningen Bioveterinary Research (Netherlands)* for sharing unpublished data and virus isolates via the OFFLU network. We would also like to thank research programs and contributors who upload their data in a timely fashion to GISAID and Genbank and acknowledge the authors, originating and submitting laboratories of the sequences. Report contributions were made by Amelia Coggon, Lorcan Carnegie and Francesco Bonfante.

We acknowledge and thank the FAO and WOAH reference laboratory and diagnostic laboratory teams, WHO CCs: St Jude Children's Research Hospital, the Centers for Disease Control and prevention, Worldwide Influenza Centre and Hong Kong University, as well as United States Department of Agriculture-Agricultural Research Service National Animal Disease Centre and Royal Veterinary College and for sharing their expertise and data. Phylogenetic and sequence analyses were performed using the RVC and CEIRR pipeline. Avian influenza A virus haemagglutination inhibition (HI) assay data in this reporting period was generated using harmonised protocols by IZSve using ferret-origin reagents kindly provided by WHO CCs: CDC and WIC. We are also very grateful to a WHO-OFFLU initiative for the generation of additional ferret reagents at IZSve which have been shared between WHO CCs and the OFFLU network.

Analyses were conducted by subtype. Sequences collected between 1st February 2024 and 16th September 2024 were downloaded from GISAID and Genbank. These were added to data kindly provided through the OFFLU network and reference datasets. Sequences were analysed preliminarily using the Augur pipeline by Nextstrain (Hadfield et al., 2018). Sequences were aligned using MAFFT v7.475 (Kato and Standley, 2013) using default settings. Alignments were trimmed (HA1) from the start codon using H5 numbering to the start of the cleavage site. Incomplete, poor quality or duplicate sequences were removed from the dataset. Trees were run using IQ-TREE 2.1.3 (Nguyen et al., 2015) using an ALRT test (Guindon et al., 2010). Sequences were compared against the most similar CVV using the NADC IAV bioinformatic toolkit (<https://github.com/flu-crew>) for amino acid differences. Strains were selected for testing against reference ferret antisera in haemagglutination inhibition (HI) assays based on virus availability and *in-silico* analysis of changes in putative antigenic sites.

## Summary

Avian influenzas have caused outbreaks in poultry and/or in wild birds in every continent within the last reporting period. Low pathogenic H5 viruses continue to circulate in poultry in Central America and multiple clade H5 Gs/Gd lineage viruses can be found causing disease in poultry throughout the world. Clade 2.3.4.4b activity has once again predominated with continued circulation in wild birds and spillover into poultry. Despite continued predominance of the H5N1 subtype, some other subtypes have been detected in poultry and/or wild birds, including H5N2, H5N6 and H5N8. In Mexico H5N2 was detected which arose from reassortment of the Mexican lineage low pathogenic H5N2 with clade 2.3.4.4b H5N1 viruses. H5N5 viruses are restricted to wild birds in the Northern Hemisphere and have been circulating in an under surveilled host since 2021. H5N6 have been detected in wild birds in China and Japan with NA genes similar to the H5N6 enzootic in poultry in China and which has caused infections in humans. H5N6 has also been detected in Poland but no genetic data was available. In Germany an H5N8 was detected which arose from an H5N1 clade 2.3.4.4b reassorting with low pathogenic viruses.

Reports of H5 in poultry are at their lowest since the 2018-2019 season. Genomic evidence indicates that the virus is continually circulating within poultry in some countries and that disease outbreak reporting may not accurately reflect this. In well surveilled areas, less outbreaks are attributed to secondary spread. Reports of H5 in wild birds are also at their lowest since the 2019-2020 season, although it is clear that clade 2.3.4.4b viruses continue to circulate in local wild bird populations year round and surveillance does not fully capture the extent of this. Decreasing detections are potentially affected by immunity acquired by some wild bird species. With the autumn migration outbreaks are expected to increase and there have been detections in wild birds and poultry along the Central Asian flyway (China, India) and East-Asia East-Africa flyway in an eastward direction since May.

Spillover into mammalian species continue to be reported with an ever increasing number of abhorrent hosts listed, although the frequency of these reports (with the exception of dairy cattle) is decreasing. This is probably associated with the decrease in infected wild birds and decreased viral infection pressure in the environment. The breeding season for sea mammals in South America is just starting and so it will soon become apparent as to whether there are continued cases in these species however populations have been severely depleted after mass-mortality events associated with H5N1 infections in the previous breeding season.

Clade 2.3.2.1a viruses are geographically restricted to South Asia where they can be routinely found in live poultry markets or causing outbreaks on farm and co-circulate with clade 2.3.4.4b.

Clade 2.3.2.1c viruses are geographically restricted to the Mekong delta where they co circulate with clade 2.3.4.4b viruses.

Clade 2.3.2.1e viruses are restricted to the the Indonesian archipelago alongside clade 2.3.4.4b viruses although no sequence was gathered from these clades within this reporting period.

Many countries that have been vaccinating using G5 Gs/Gd lineage seed strains are considering updates to vaccines in response to clade 2.3.4.4b incursion and some countries which have relatively recently had incursions of clade 2.3.4.4b for the first time are considering vaccination.

Independent emergent events of high pathogenic H7 viruses in poultry have occurred in Germany (H7N5) and in 3 instances in Australia (H7N3, H7N8 and H7N9). Diverse lineage low pathogenicity H7 viruses continue to be detected in environmental samples, wild birds and occasionally poultry.

H9N2 viruses continue to be detected in healthy chickens and are often incidental findings when testing poultry for AIV.

# Global avian influenza events in animals

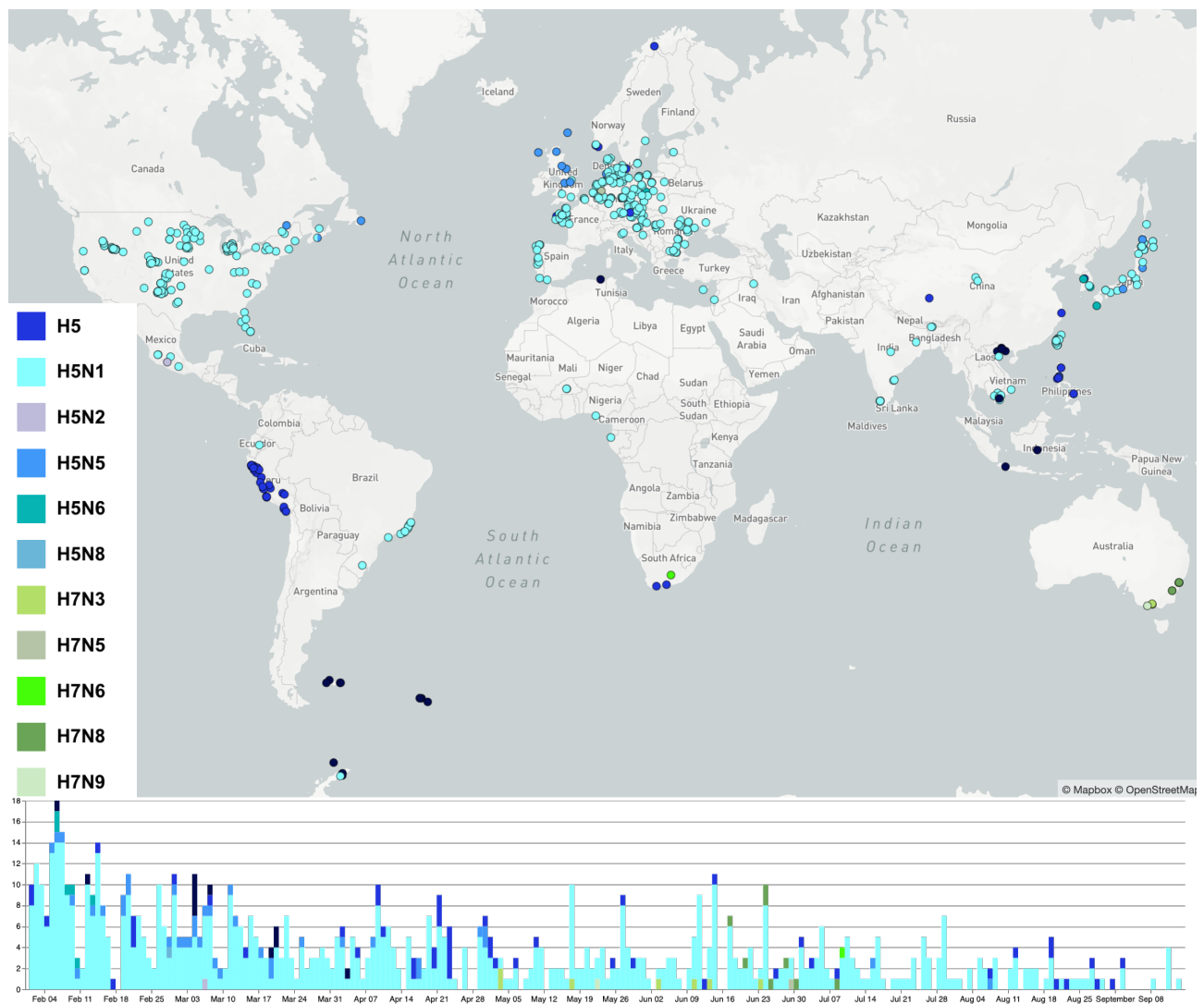


Figure 1: Geographical and temporal representation of outbreaks occurring between 1 February 2024 to 18th September 2024 reported to WOA or national authorities downloaded from EMPRESi+.

# H5 Influenza A viruses

H5 Phylogenetic tree coloured by region

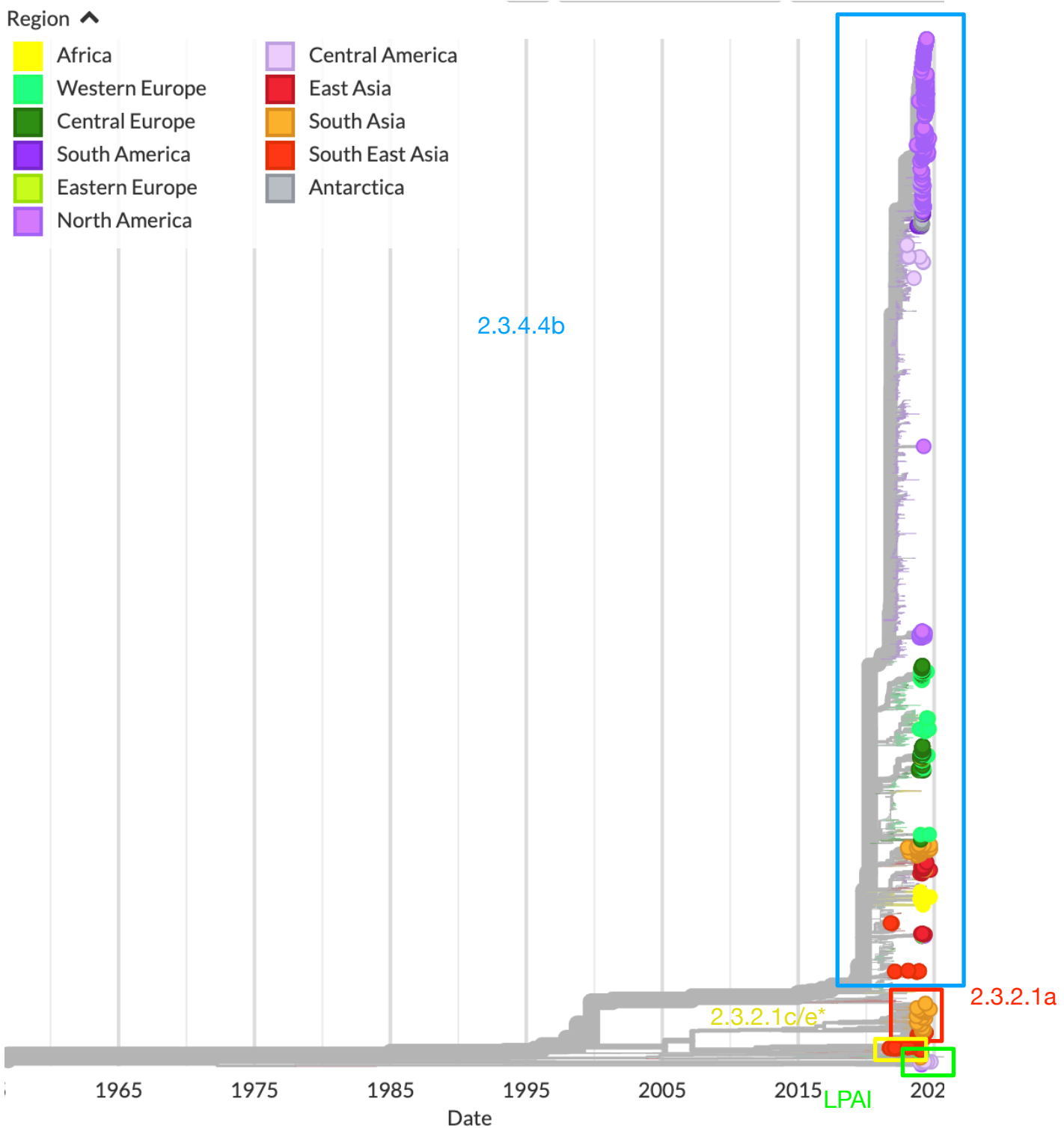


Figure 2: Avian H5 global summary time resolved phylogenetic tree. Analyses were conducted with reference sequences, sequences shared through the OFFLU network and data downloaded from GISAID (16th September 2024). Sequences from GISAID collected within the reporting period and **submitted** to OFFLU since February 2024 are coloured by region.

## H5 Influenza A viruses- map

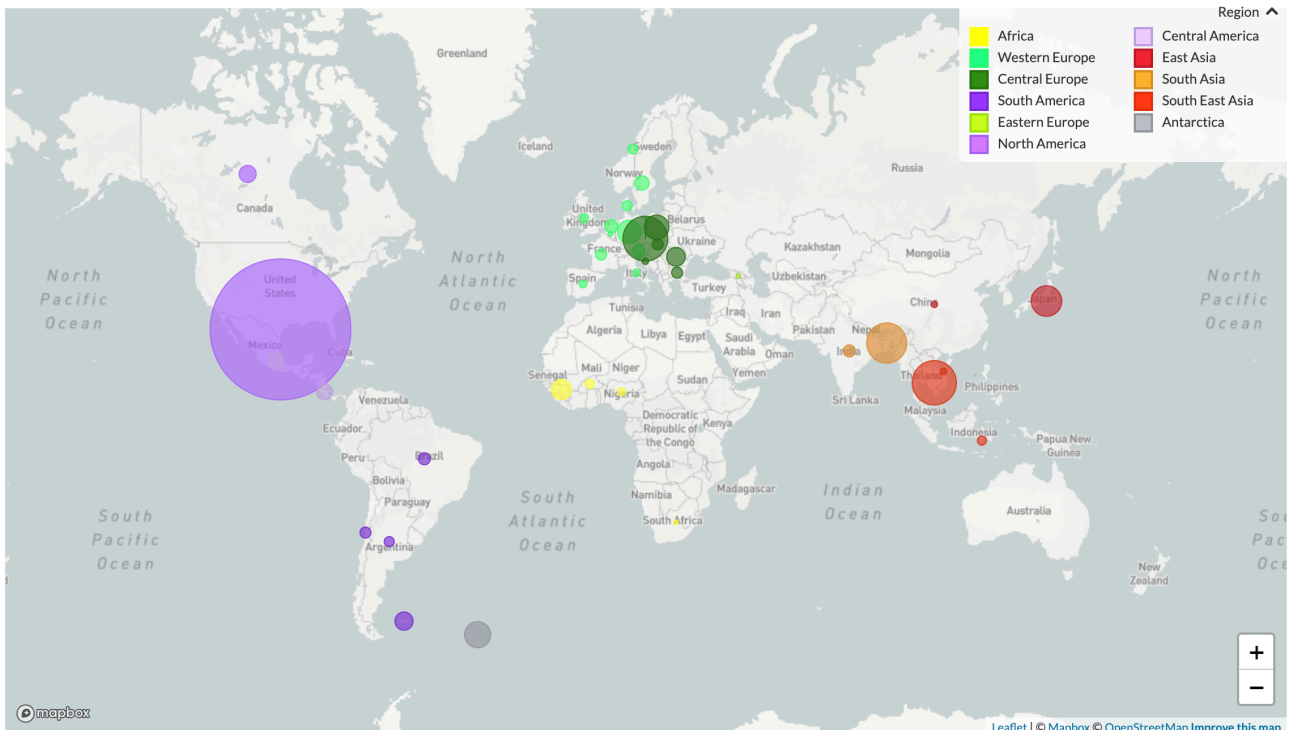


Figure 3: A map showing the geographic location of countries where the sequences from GISAID were collected within the reporting period and countries where sequences were **submitted** to OFFLU since February 2024. Points are coloured by region.

# Activity table

Table 1: Gs/Gd lineage activity since 20th February 2024 as collected by OFFLU in this report until 6th September

Algeria	poultry	(HPAI)
Antarctica	mammal (Southern elephant seal)	(H5N1)
Austria	wild birds	2.3.4.4b(H5N1)
Bangladesh	poultry	2.3.2.1a, 2.3.4.4b(H5N1)
Belgium	wild birds	2.3.4.4b(H5N1)
Bhutan	poultry	(H5N1)
Brazil	wild birds	2.3.4.4b(H5N1)
Bulgaria	poultry	2.3.4.4b(H5N1)
Burkina Faso	poultry	2.3.4.4b(H5N1)
Cambodia	poultry	2.3.2.1c(H5N1)
Canada	poultry	(H5N1)
	mammal (Skunk, Raccoon)	2.3.4.4b(H5N5)
China	wild birds	2.3.4.4b(H5N1)(H5N5)
	wild birds	2.3.4.4b (H5N1/6)
Croatia	wild birds	2.3.4.4b (H5N1)
Czech Republic	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Denmark	wild birds	(H5N1)
Ecuador	poultry	(H5N1)
Falkland Islands (Malvinas)	wild birds	(HPAI)
France	poultry	(H5Nx)
	wild birds	(H5N1)
Gabon	poultry	(H5N1)
	poultry	(H5N1)
Germany	wild birds	2.3.4.4b(H5N1)(H5N8)
	mammal (Red Fox)	2.3.4.4b (H5N1)
Hungary	poultry	(H5N1)
	wild birds	(H5N1)
India	poultry	2.3.2.1a, 2.3.4.4b(H5N1)
Indonesia	poultry	(HPAI)
Iraq	wild birds	(H5N1)
Israel	poultry	(H5N1)
Italy	poultry	2.3.4.4b (H5N1)
Japan	poultry	(H5N1)
	wild birds	2.3.4.4b (H5N1/5)
Latvia	wild birds	(H5N1)
Mexico	poultry	2.3.4.4b(H5N1/N2)
Moldova, Republic of	wild birds	(H5N1)
Netherlands	wild birds	2.3.4.4b (H5N1)
Nigeria	poultry	2.3.4.4b (H5N1)
Norway	wild birds	2.3.4.4b (H5N1)
	mammal (Red Fox)	2.3.4.4b (H5N5)
Pakistan	poultry	(H5N1)
Peru	poultry	(H5)
	wild birds	(H5)
Philippines	poultry	(H5N1)
Poland	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Portugal	wild birds	(H5N1)
Republic of Korea	poultry	(H5N1)
Romania	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Slovakia	poultry	2.3.4.4b (H5N1)
Slovenia	wild birds	(H5N1)
South Africa	wild birds	2.3.4.4b (H5N1)
South Georgia and the South Sandwich Islands	wild birds	(HPAI)
Spain	mammal (South America fur seal, Southern elephant seal)	
	wild birds	2.3.4.4b (H5N1)
Sweden	poultry	2.3.4.4b (H5N1)
	poultry	(H5N1)
Taiwan (Province of China)	wild birds	(H5N1)
	wild birds	2.3.4.4b (H5N1/N5)
Ukraine	wild birds	(H5N1)
United States of America	mammal (Alpaca, Bobcat, Cats, Cattle, Desert Cottontail, Goats, House mouse, Mink, Red Fox)	2.3.4.4b (H5N1)
	poultry	2.3.4.4b (H5N1)
Viet Nam	wild birds	2.3.4.4b (H5N1)
	poultry	(H5N1)



## Gs/Gd H5 2.3.4.4b phylogenetic tree

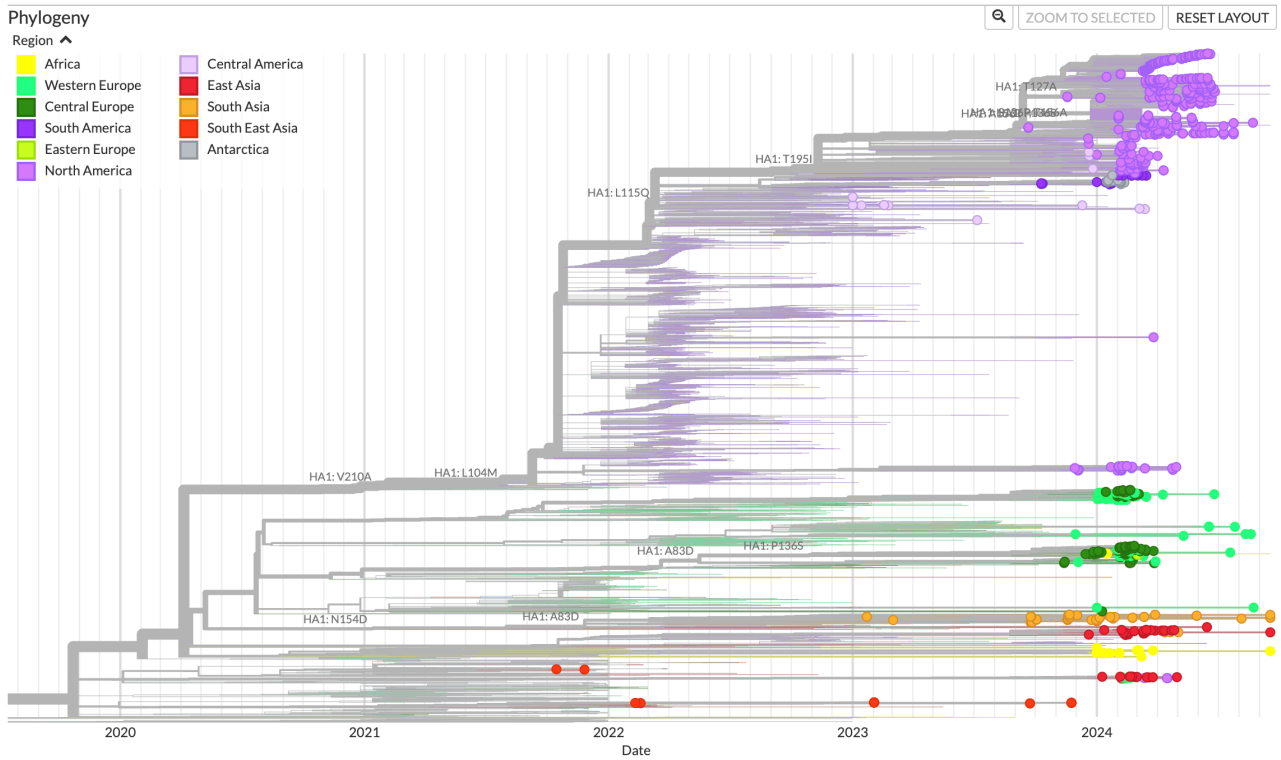


Figure 4: Gs/Gd lineage clade 2.3.4.4b time resolved phylogenetic tree. Sequences from GISAID collected within the reporting period and submitted to OFFLU since February 2024 are coloured by region. Amino acid annotations for major subclades are included along the branches.

# Gs/Gd H5 2.3.4.4b subsampled phylogenetic tree

Human  
CVV  
OFFLU HI

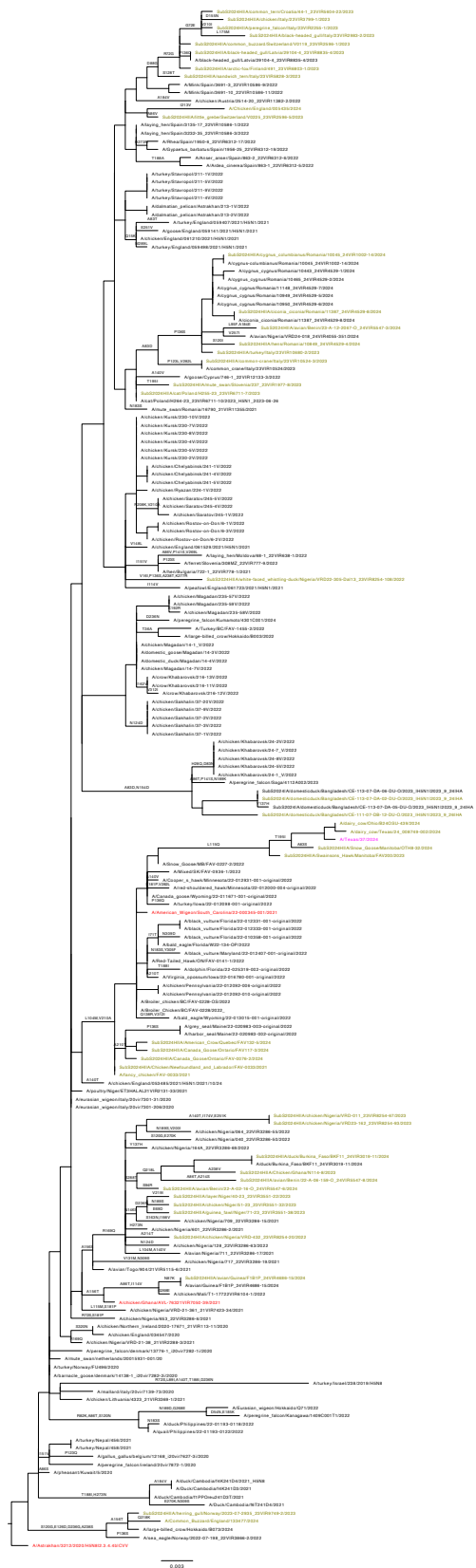


Figure 5: Gs/Gd lineage clade 2.3.4.4b phylogenetic tree, rooted by the astrakan CVV, with amino acid changes along the branches.

# Gs/Gd H5 2.3.4.4b Amino acid difference tables

site	Antigenic																
83	A		D	D		S							D	D			
86	A																
87	N																
94	S																
95	L																
104	L		M			M	M	M	M	M	M	M			M		
114	I																
115	L					Q	Q								Q		
120	S													G			
126	E													D	Antigenic		
136	P			S	S										Antigenic		
154	N												D	D	Antigenic		
156	A	T												T	Antigenic		
169	R																
184	A														Antigenic		
195	T						I								I		
210	V	A			A	A	T	T	T	A					A	Antigenic	
213	I													V			
214	A														Antigenic		
218	Q													K			
236	D													G			
238	A													S			
288	S																
	Aadiffs from CWV																
	Putative antigenic sites	2	2	2	2	2	3	5	2	2	2	2	2	2	6	1	4

A/Astrakhan/3212/2020/H5N8|2.3.4.4b|CWV  
 A/chicken/Ghana/AVL-76321VIR7050-39/2021  
 A/American\_Wigeon/South\_Carolina/22-000345-001/2021  
 SubS2024HI|A/cygnus\_columbianus/Romania/10045\_24VIR1002-14/2024  
 SubS2024HI|A/ciconia\_ciconia/Romania/11387\_24VIR4529-8/2024  
 SubS2024HI|A/Swainsons\_Hawk/Manitoba/FAV200/2023  
 SubS2024HI|A/Snow\_Goose/Manitoba/OTH8-32/2024  
 SubS2024HI|A/American\_Crow/Quebec/FAV132-5/2024  
 SubS2024HI|A/Canada\_Goose/Ontario/FAV117-3/2024  
 SubS2024HI|A/Canada\_Goose/Ontario/FAV-0076-2/2024  
 SubS2024HI|A/Chicken/Newfoundland\_and\_Labrador/FAV-0033/2021  
 SubS2024|HI|A/domestic\_duck/Bangladesh/CE-111-07-DB-12-DU-O/2023\_EP  
 SubS2024|HI|A/domestic\_duck/Bangladesh/CE-113-07-DA-06-DU-O/2023\_EP  
 SubS2024|HI|A/Common\_Buzzard/England/133477/2024\_EP1|H5N5|  
 SubS2024|HI|A/Chicken/England/005435/2024\_EP1|H5N1|  
 SubS2024|HI|A/Bovine/Ohio/B24OSU-439/2024\_EP2|H5N1|

# Gs/Gd H5 2.3.4.4b Antigenic data

Table 2: Avian H5 2.3.4.4b antigenic characterisation of viruses against CVV and reference post infection antisera. Fold changes are coloured.

		REFERENCE FERRET ANTISERA									
		Clade	Subtype	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b
		Ferret ID	ID	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b	2.3.4.4b
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>A/FUJIAN-SANYUAN/21099/2017 xA/PR/8/1934</span> <span>A/TURKEY/ITALY/17VIR576-11/2017</span> <span>A/Turkey/Israel/288/22VIR8411/2019</span> <span>A/ASTRAKHAN/3212/2020</span> <span>A/duck/Cambodia/11PPOreuz41D3T/2021</span> <span>A/poultry/Niger/ET3/HALAJ/21VIR2131-33/2021</span> <span>A/avian/Togo/904/21VIR5115-6/2021</span> <span>A/Hen/Bulgaria/722-1/22VIR778-1/2022</span> <span>A/chicken/Ghana/AVL-763/21VIR7050-39/2021</span> <span>A/American wigeon/South Carolina/22-000345-001/2021</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>2.3.4.4b H5N6</span> <span>2.3.4.4b H5N8</span> <span>2.3.4.4b H5N8</span> <span>2.3.4.4b H5N8</span> <span>2.3.4.4b H5N8</span> <span>2.3.4.4b H5N1</span> <span>2.3.4.4b H5N1</span> <span>2.3.4.4b H5N1</span> <span>2.3.4.4b H5N1</span> <span>2.3.4.4b H5N1</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>320</span> <span>640</span> <span>160</span> <span>640</span> <span>160</span> <span>1280</span> <span>2560</span> <span>320</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>320</span> <span>640</span> <span>80</span> <span>640</span> <span>160</span> <span>320</span> <span>640</span> <span>160</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>1280</span> <span>2560</span> <span>320</span> <span>1280</span> <span>320</span> <span>1280</span> <span>2560</span> <span>320</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>40</span> <span>640</span> <span>2560</span> <span>160</span> <span>1280</span> <span>160</span> <span>640</span> <span>1280</span> <span>160</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>160</span> <span>1280</span> <span>40</span> <span>640</span> <span>40</span> <span>320</span> <span>640</span> <span>80</span> <span>40</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>320</span> <span>640</span> <span>160</span> <span>640</span> <span>160</span> <span>80</span> <span>1280</span> <span>160</span> <span>40</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>80</span> <span>2560</span> <span>280</span> <span>1280</span> <span>80</span> <span>1280</span> <span>2560</span> <span>80</span> <span>160</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>16</span> <span>320</span> <span>640</span> <span>80</span> <span>1280</span> <span>320</span> <span>160</span> <span>2560</span> <span>160</span> <span>40</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>1280</span> <span>5120</span> <span>320</span> <span>1280</span> <span>640</span> <span>1280</span> <span>2560</span> <span>320</span> <span>160</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>80</span> <span>1280</span> <span>80</span> <span>640</span> <span>40</span> <span>640</span> <span>1280</span> <span>80</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>160</span> <span>5120</span> <span>40</span> <span>1280</span> <span>80</span> <span>2560</span> <span>5120</span> <span>160</span> <span>320</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>320</span> <span>2560</span> <span>80</span> <span>640</span> <span>40</span> <span>320</span> <span>1280</span> <span>160</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>80</span> <span>1280</span> <span>40</span> <span>320</span> <span>20</span> <span>320</span> <span>640</span> <span>40</span> <span>40</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>80</span> <span>1280</span> <span>40</span> <span>640</span> <span>20</span> <span>640</span> <span>640</span> <span>40</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>160</span> <span>1280</span> <span>40</span> <span>640</span> <span>20</span> <span>320</span> <span>1280</span> <span>80</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>160</span> <span>2560</span> <span>40</span> <span>640</span> <span>40</span> <span>320</span> <span>1280</span> <span>80</span> <span>80</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>160</span> <span>2560</span> <span>20</span> <span>640</span> <span>20</span> <span>320</span> <span>2560</span> <span>40</span> <span>160</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>2560</span> <span>2560</span> <span>640</span> <span>5120</span> <span>1280</span> <span>2560</span> <span>5120</span> <span>640</span> <span>320</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>160</span> <span>80</span> <span>640</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>160</span> <span>320</span> <span>320</span> <span>2560</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>160</span> <span>640</span> <span>2560</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>40</span> <span>160</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>40</span> <span>320</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>160</span> <span>80</span> <span>160</span> <span>5120</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>160</span> <span>320</span> <span>1280</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>320</span> <span>2560</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>80</span> <span>320</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>40</span> <span>160</span> <span>160</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>40</span> <span>80</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>40</span> <span>20</span> <span>40</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>40</span> <span>80</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>20</span> <span>40</span> <span>640</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>80</span> <span>80</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>80</span> <span>40</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>40</span> <span>20</span> <span>20</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>10</span> <span>20</span> <span>10</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>20</span> <span>40</span> <span>80</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>40</span> <span>160</span> <span>160</span> <span>1280</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>160</span> <span>160</span> <span>2560</span> </div>									
		<div style="display: flex; justify-content: space-around; font-size: 8px;"> <span>80</span> <span>160</span> <span>160</span> <span>1280</span> </div>									

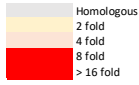
AA diffs compared to Astrakhan

A83D, P1365  
A83D, P1365  
A83D, S120I, P1365  
L104M, L115O, V210A  
A83S, L104M, L115O, T195I, V210A  
L104M, V210T  
L104M, V210T  
L104M, V210A

A83D, N154D  
A83D, N154D  
S120G, E126D, A156T, Q218K, D136G, A238A  
I213V  
L104M, L115O, T195I, V210A

# Gs/Gd H5 2.3.4.4b Antigenic data from previous report

Table 3: Avian H5 2.3.4.4b antigenic characterisation of viruses against CVV and reference post infection antisera from February 2023. Fold changes are coloured.



REFERENCE FERRET ANTISERA

Clade Subtype Ferret ID  
 2.3.4.4b H5N6 A/FUJIAN-SANYUAN/21099/2017 xA/PR/8/1934  
 2.3.4.4b H5N8 A/ASTRAKHAN/3212/2020  
 2.3.4.4b H5N8 A/TURKEY/ITALY/17VIR576-11/2017  
 2.3.4.4b H5N8 A/duck/Cambodia/11PP0reu241037/2021  
 2.3.4.4b H5N8 A/turkey/Israel/238/2019  
 2.3.4.4b H5N1 A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021  
 2.3.4.4b H5N1 A/chicken/Ghana/AVL-763/21VIR7050-39/2021  
 2.3.4.4b H5N1 A/hen/Bulgaria/722-1/22VIR778-1/2021  
 2.3.4.4b H5N1 A/avian/Togo/904/21VIR5115-6/2021  
 2.3.4.4b H5N1 A/american wigeon/South Carolina/22-000345-001/2021

Semester	Reference Antigen	Clade	Subtype	1	2	3	4	5	6	7	8
APHA Sep23- Feb24	A/FUJIAN-SANYUAN/21099/2017 xA/PR/8/1934	2.3.4.4b	H5N6	160	80	320	80	80	320	320	640
	A/ASTRAKHAN/3212/2020	2.3.4.4b	H5N8	10	160	320	160	320	20	320	20
	A/TURKEY/ITALY/17VIR576-11/2017	2.3.4.4b	H5N8	20	40	640	320	320	160	640	320
	A/duck/Cambodia/11PP0reu241037/2021	2.3.4.4b	H5N8	40	80	640	320	160	320	640	640
	A/turkey/Israel/238/2019	2.3.4.4b	H5N8	20	40	160	80	320	160	640	160
	A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021	2.3.4.4b	H5N1	10	20	160	40	40	640	320	320
	A/chicken/Ghana/AVL-763/21VIR7050-39/2021	2.3.4.4b	H5N1	0	20	320	320	160	320	640	640
	A/hen/Bulgaria/722-1/22VIR778-1/2021	2.3.4.4b	H5N1	10	80	40	40	40	1280	640	640
	A/avian/Togo/904/21VIR5115-6/2021	2.3.4.4b	H5N1	20	40	160	160	80	320	320	640
	<b>Test antigen</b>										
1 A/herring_gull/England/404234/2023	2.3.4.4b	H5N5	10	80	160	160	40	1280	320	640	
2 A/Duck/Bangladesh/CE-111-05-DA-05-DU-O/2022	2.3.4.4b	H5N1	20	80	160	80	80	640	640	1280	
3 A/Duck/Bangladesh/CE-111-05-DA-02-DU-O/2022	2.3.4.4b	H5N1	40	160	160	160	80	2560	1280	1280	
4 A/Kelp_Gull/Moltke_Harbour/133754/2023	2.3.4.4b	H5N1	0	0	40	10	10	320	320	1280	
5 A/Southern_fulmar/Falkland_Islands/133789/2023	2.3.4.4b	H5N1	10	20	40	10	20	640	320	640	
6 A/Kelp_Gull/Harpon_Bay/133943/2023	2.3.4.4b	H5N1	0	20	20	40	40	1280	640	1280	
7 A/Turkey/England/133330/2023	2.3.4.4b	H5N1	20	160	80	80	80	640	640	1280	
8 A/Duck/Bangladesh/AV-23-071766/2023	2.3.4.4b	H5N1	10	80	320	160	80	640	640	1280	

AA changes from 3212 putative antigenic sites

S120G, E126D, A156T, D236N, A238S  
 V210I, I299V  
 V210I, I299V  
 N84D, L104M, L115Q, Y137H, S163N, V210A  
 L104M, L115Q, V210A  
 L104M, L115Q, Y137H, V210A, I294V

A83D, N154D

Semester	Reference Antigen	Clade	Subtype	1	2	3	4	5	6	7	8
IZSVe Sep23- Feb24	A/FUJIAN-SANYUAN/21099/2017 xA/PR/8/1934	2.3.4.4b	H5N6	80	160	640	320	320	2560	1280	2560
	A/ASTRAKHAN/3212/2020	2.3.4.4b	H5N8	160	320	1280	640	320	5120	1280	2560
	A/TURKEY/ITALY/17VIR576-11/2017	2.3.4.4b	H5N8	20	80	320	160	160	640	640	1280
	A/duck/Cambodia/11PP0reu241037/2021	2.3.4.4b	H5N8	40	80	640	320	320	1280	1280	2560
	A/turkey/Israel/238/2019	2.3.4.4b	H5N8	20	40	320	160	320	640	1280	1280
	A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021	2.3.4.4b	H5N1	20	80	160	80	80	1280	640	1280
	A/chicken/Ghana/AVL-763/21VIR7050-39/2021	2.3.4.4b	H5N1	10	40	320	640	320	640	1280	5120
	A/hen/Bulgaria/722-1/22VIR778-1/2021	2.3.4.4b	H5N1	<10	40	160	80	80	2560	2560	2560
	A/avian/Togo/904/21VIR5115-6/2021	2.3.4.4b	H5N1	10	80	320	320	160	640	640	2560
	A/american wigeon/South Carolina/22-000345-001/2021	2.3.4.4b	H5N1	80	320	2560	1280	640	10240	2560	5120
<b>Test antigen</b>											
1 A/chicken/Nigeria/VRD-011_23VIR8254-67/2023	2.3.4.4b	H5N1	<10	40	80	80	40	160	320	320	
2 A/chicken/Nigeria/VRD23-162_23VIR8254-93/2023	2.3.4.4b	H5N1	<10	80	160	80	80	160	320	640	
3 A/chicken/Nigeria/VRD-432_23VIR8254-20/2022	2.3.4.4b	H5N1	10	80	640	320	640	1280	2560	40	
4 A/white-faced_whistling-duck/Nigeria/VRD22-305-Dal13_23VIR8254-10f	2.3.4.4b	H5N1	40	160	1280	640	320	5120	1280	5120	
5 A/black-headed_gull/Latvia/29104-4_23VIR8835-4/2023	2.3.4.4b	H5N1	40	80	640	160	320	1280	1280	2560	
6 A/common-crane/Italy/23VIR10524-3/2023	2.3.4.4b	H5N1	40	160	640	320	160	2560	1280	2560	
7 A/turkey/Italy/23VIR10680-2/2023	2.3.4.4b	H5N1	<10	80	80	<10	40	1280	1280	1280	
8 A/herring_gull/Norway/2023-07-2935_23VIR9749-2/2023	2.3.4.4b	H5N5	10	40	160	320	160	640	1280	1280	

A146S, I15V, A156S, R169Q, D236N,  
 A140T, A156S, R169Q, I174V, E251K  
 A156S, R169Q, A214T  
 V16I, P136S, A238T, K277R  
 R72G, D88G, P163Q  
 A83D, P123L, V282L  
 A83D, P123S  
 S120G, E126D, A156T, D236G, A238S

# Gs/Gd H5 2.3.2.1a phylogenetic tree

**Feb2024-Sept2024**  
**Sept2023-Feb2024**  
**Human**  
**CVV**  
**HI**

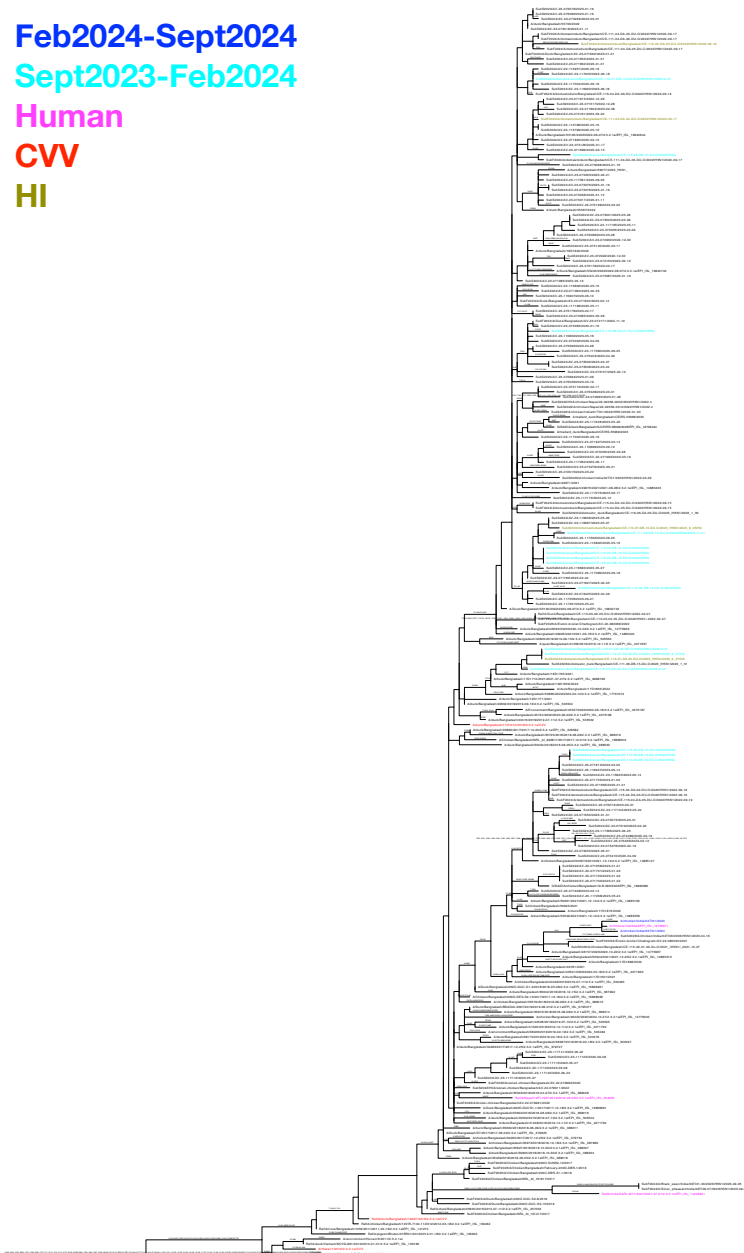


Figure 6: Gs/Gd lineage clade 2.3.2.1a phylogenetic tree, with amino acid changes along the branches.

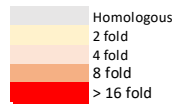
## Gs/Gd H5 2.3.2.1a amino acid difference table

Table 4: Amino acid comparison of the HA1 compared to within-clade CVVs. Putative antigenic sites are highlighted in grey.

H5 numbering site	A/duck/Bangladesh/17D1012/2018   2.3.2.1a   CW	Ref   A/duck/Bangladesh/19097/2013   2.3.2.1a   CW	A/chicken/India/03TI01/2024	A/chicken/India/04TI01/2024	SubS2024   A/domesticduck/Bangladesh/CE-116-07-DA-03-DU-O/2023   H5N1	SubF2024   A/domesticduck/Bangladesh/CE-113-04-DA-05-DU-O/2022   H5N1	SubF2024   A/domesticduck/Bangladesh/CE-111-04-DA-04-DU-O/2022   H5N1	SubS2024   A/domesticduck/Bangladesh/CE-115-07-DB-10-DU-O/2023   H5N1	A/Victoria/149/2024   EPI_ISL_19156871	SubS2024   A/Domestic-Duck/Bangladesh/CE-111-08-DB-13-DU-O/2023   H5N2	SubS2024   A/avian/Bangladesh/CE-113-08-DB-12-DU-O/2023   H5Nx	SubS2024   A/avian/Bangladesh/CE-113-08-DB-13-DU-O/2023   H5Nx	SubS2024   A/avian/Bangladesh/CE-113-09-DB-12-DU-O/2024   H5Nx	SubS2024   A/avian/Bangladesh/CE-116-08-DA-01-DU-O/2023   H5Nx	SubS2024   A/domestic-duck/Bangladesh/CE-113-07-DA-02-DU-C/2023   H5N1	Putative antigenic site
14	K	E	E					E								
20	M				V											
21	E				K											
22	K				R											
23	N				R											
24	V				I											
31	D					N										
36	T														A	
51	I	V	V					V								
115	R							Q	Q	Q						Putative antigenic site
124	D				N	N	N	N	N	N	N					Putative antigenic site
126	E	D	D					D								Putative antigenic site
129	L		R												M	Putative antigenic site
137	Y														H	
141	S	P	P					P								Putative antigenic site
154	N	D			D	X	D	D	D	D					D	Putative antigenic site
156	A	T	S	S				S								Putative antigenic site
163	S			N									N		N	Putative antigenic site
175	L														M	
185	A	T										T				Putative antigenic site
189	R	N	N					N				Q				Putative antigenic site
195	T	I	I					I				S				Putative antigenic site
210	V	I	I					I								Putative antigenic site
212	K	R	R					R						R		
273	N	H												D		Putative antigenic site
276	T			A											A	
285	I							V								
312	V											I				
AA diff	28	2	11	10	2	7	3	3	9	4	2	5	7	5	3	
Putative antigenic site	13	2	8	7	1	2	2	3	6	3	2	4	4	2	2	

## Gs/Gd H5 2.3.2.1a Antigenic data

Table 5: Avian Gs/Gd-lineage 2.3.2.1a antigenic characterisation of viruses against CVV and reference post infection antisera. Fold changes are coloured. Amino acid changes compared to the within-clade CVV are annotated.



REFERENCE FERRET ANTISERA			
Clade	2.3.2.1a	2.3.2.1a	2.3.2.1a
Subtype	H5N1	H5N1	H5N1
Ferret ID	F.2012-209	F.2014-26 (I)	2019-063
	A/HUBEI/1/2010	A/DUCK/BANGLADESH/19097/2013	A/DUCK/BANGLADESH/17D1012/2018

Semester	Reference Antigen	Clade	Subtype	AA changes compared to 2018 CVV		
	A/HUBEI/1/2010	2.3.2.1a	H5N1	2560	640	160
	A/DUCK/BANGLADESH/19097/2013	2.3.2.1a	H5N1	2560	320	160
	A/DUCK/BANGLADESH/17D1012/2018	2.3.2.1a	H5N1	640	160	640
<b>APHA Feb 24 - Sep 24</b>	<b>Test antigen</b>					
	A/domesticduck/Bangladesh/CE-116-07-DA-03-DU-O/2023	2.3.2.1a	H5N1	320	80	320
	A/domesticduck/Bangladesh/CE-115-07-DB-10-DU-O/2023	2.3.2.1a	H5N1	1280	160	80
	A/domesticduck/Bangladesh/CE-113-04-DA-05-DU-O/2022	2.3.2.1a	H5N1	320	160	80
	A/domesticduck/Bangladesh/CE-111-04-DA-04-DU-O/2022	2.3.2.1a	H5N1	640	80	80
	A/domesticduck/Bangladesh/CE-115-04-DA-02-DU-O/2022	2.3.2.1a	H5N1	160	10	320

AA changes compared to 2018 CVV

N154D, A156T

S163N, T276A 2018 CVV-like

R115Q, D124N, N154D 2013 CVV-like

D124N, N154D 2013 CVV-like

D31N, D124N, D154X

K40M, D124N, I200V



LPAI H5 phylogenetic tree

Feb2024-Sept2024  
 Sept2023-Feb2024  
 Human



Figure 7: Low pathogenicity H5 phylogenetic tree. Sequences were downloaded from GISAID and collected through OFFLU. Sequences from humans are pink.

# H7 Influenza A viruses

Feb2024-Sept2024  
 Sept2023-Feb2024  
 CVV

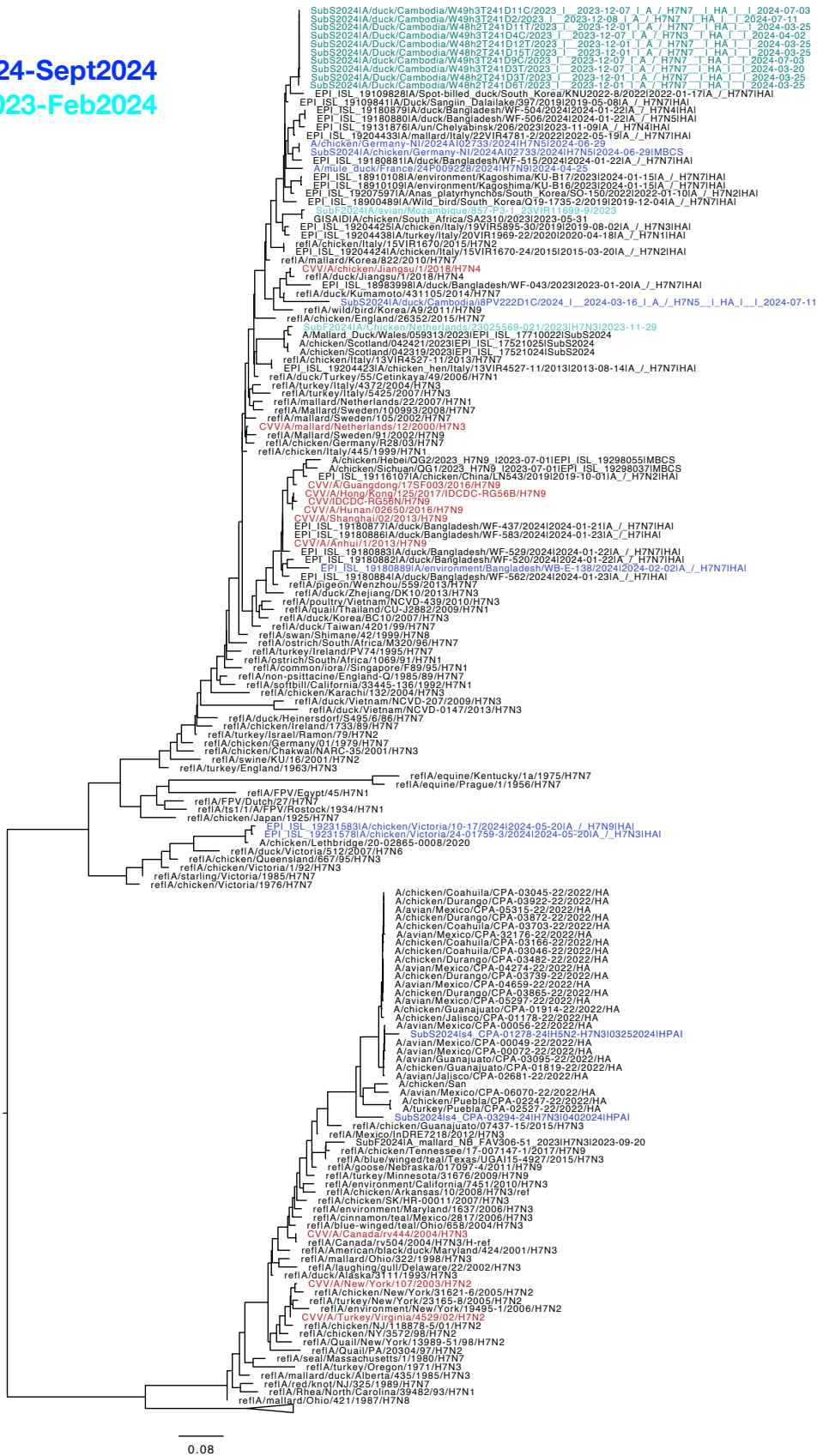


Figure 8: H7 maximum likelihood phylogenetic tree midpoint rooted. Analyses were conducted with reference sequences and data downloaded from GISAID, Genbank and kindly shared through the OFFLU network. Sequences are coloured according to collection date. CVVs are red

# H7 Eurasian lineage and american lineage amino acid difference tables

Table 7: Amino acid comparison of the HA1 compared to within-clade CVV. High path strains are highlighted in red.

site	CVV/A/mallard/Netherlands/12/2000/H7N3	SubS2024   A/chicken/Germany/NI/2024A02735/2024   H7N5   2024-06-29   MBC	A/chicken/Scotland/04/23/2023   EPI_ISL_17521024   SubS2024	SubF2024   A/avian/Mozambique/657-P3-1_23WR/11699-9/2023	GISMD   A/c_hicken/South_Africa/SA23110/2023   2023-05-31	A/chicken/Scotland/04/21/2023   EPI_ISL_17521025   SubS2024	A/Mallard_Duck/Wales/05/31/2023   EPI_ISL_17710022   SubS2024	SubS2024   A/Duck/Cambodia/W48h127241D117/2023   2023-12-01   A_/H7	SubS2024   A/Duck/Cambodia/W48h127241D127/2023   2023-12-01   A_/H7	SubS2024   A/Duck/Cambodia/W48h127241D157/2023   2023-12-01   A_/H7	SubS2024   A/Duck/Cambodia/W48h127241D167/2023   2023-12-01   A_/H7	SubS2024   A/Duck/Cambodia/W48h127241D17/2023   2023-12-01   A_/H7	SubS2024   A/Duck/Cambodia/W48h127241D18/2023   2023-12-07   A_/H7	SubS2024   A/duc k/Cambodia/W48h37241D4C/2023   2023-12-07   A_/H7	SubS2024   A/duc k/Cambodia/W48h37241D5/2023   2023-12-08   A_/H7N1	SubS2024   A/duc k/Cambodia/W48h37241D57/2023   2023-12-07   A_/H7N	SubS2024   A/duc k/Cambodia/W48h37241D5C/2023   2023-12-07   A_/H71	SubS2024   A/duc k/Cambodia/RPV2221C/2024   2024-03-16   A_/H7N5	
60		V	V																I
61																			L
68								R	R	R	R	R	R	R	R	R	R	R	L
78		V	V																
84		R	R																
95		D	D																
97																			S
109																N			
112		S	S																
118										N									Antigenic
127		N																	
130		T	T																K Antigenic
152		V	V	V	V														
164																			K
170		V	V	V	V														
171		V	V	V	V														V
180																			A Antigenic
181																			A
191		S		S	S														S
200		S																	K
228		M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
230																			D
238																			G
247		N																	
259		V		V	V														
262		E		E	E														E
265		I	I																
267																			T Antigenic
268		S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
270		D	D																
276		N	N	N	N	N	K	N	N	N	N	N	N	N	N	N	N	N	
291																			N
293		T				T	T	T	T	T	T	T	T	T	T	T	T	T	
294		I	I																I
296		R																	
304						G	G	G	G	G	G	G	G	G	G	G	G	G	K
307		M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
313																			
318		P	P																P
sites		9	9	14	14	9	9	7	7	7	8	7	7	7	7	7	8	7	21
		0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	3

site	CVV/Canada/rv444/2004/H7N3	SubS2024   A/cv/canada/444/2004/H7N3   2004-03-16   H7N3	SubS2024   A/cv/canada/444/2004/H7N3   2004-03-16   H7N3
22	R	K	
36	V	A	A
38	I	T	T
39	K		E
43	T	A	
44	Q	R	R
45	G	R	R
47	R	K	K
48	P		S
49	T	I	I
61	I	V	V
71	E		K
73	D	E	K
74	A		G
75	N	D	D
82	E		L
86	V	L	L
104	G	K	K
112	S		P
114	G	S	D
118	S	N	D
125	A	T	T
126	T	S	S
127	S	N	
130	R	K	K
132	S	I	L
133	G	K	N
134	X		S
135	X		P
139	A		T
147	N	T	
149	D		E
151	A	V	E
152	A	T	T
155	Q	N	N
157	T	N	
158	K	L	R
161	R	T	
164	R	K	
191	N	D	
202	Q	L	L
206	T	A	
208	S	I	I
211	A	P	P
214	Q	K	K
244	I		V
247	D		G
253	R	K	
257	L	I	I
259	V	I	I
267	S	L	
268	G	D	
276	S	N	N
304	T	K	
318	N	S	

# H9 Influenza A viruses

## H9 Y280 (B4.7) phylogenetic tree

Feb2024-Sept2024  
 Sept2023-Feb2024  
 CVV  
 Human



Figure 9: H9 phylogenetic tree. Analyses were conducted with reference sequences, data downloaded from GISAID, Genbank and shared from HKU, CDC and the OFFLU network. Sequences are coloured according to collection date. Sequences from humans are pink and CVVs are red. Branches of the B4.7 clade according to the Proposal for a Global Classification and Nomenclature System for A/H9 Influenza Viruses, are coloured purple.



# H9 Y280 (B4.5) phylogenetic tree

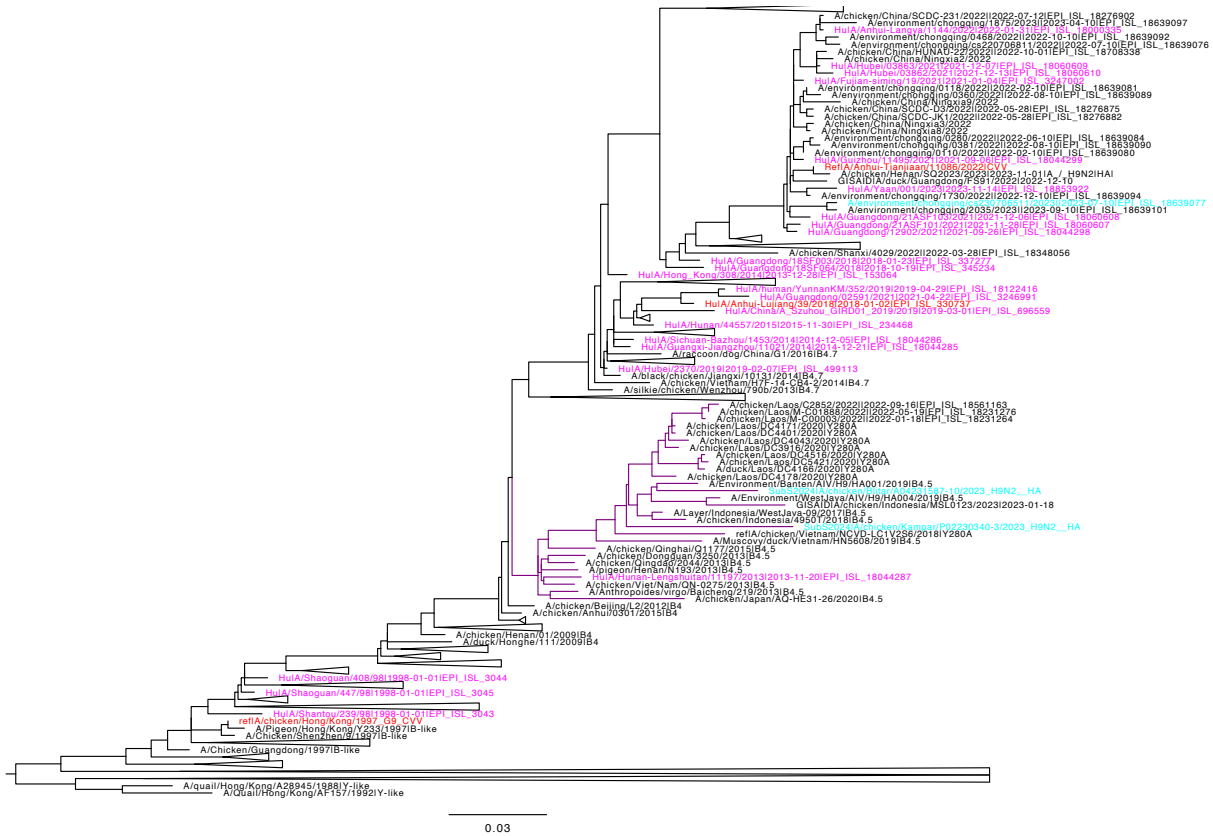


Figure 10: H9 phylogenetic tree. Analyses were conducted with reference sequences, data downloaded from GISAID, Genbank and shared from HKU, CDC and the OFFLU network. Sequences are coloured according to collection date. Sequences from humans are pink and CVVs are red. Branches of the B4.5 clade according to the Proposal for a Global Classification and Nomenclature System for A/H9 Influenza Viruses, are coloured purple.

## H9 Y280 (B4.5) amino acid differences

Table 9: Amino acid comparison of the HA1 of B4.5 lineage viruses compared to CVV.

site	A/Anhui-Lujiang/39/2018   CW	Ref   A/Anhui-Tianjiaan/11086/2022   CW	SubS2024   A/chicken/Kampar/P02230340-3/2023_H9N2_HA	SubS2024   A/quail/Solok/P02230452-1/2023(H9N2)_HA	SubS2024   A/chicken/Blitar/A04231587-10/2023_H9N2_HA
32	L	M	M		
34	H			Q	
37	H		X		
45	S	G	G		
48	Q	H	H	H	
51	I	V			
53	D	E			
57	V	I		I	
68	D	E			
69	L	P	P	P	Q
70	S	L	L	L	L
71	L	P			
73	G	E			
74	R	K			
79	I	V			
80	V	I	I		
87	N	D	D		
112	Q	R			
114	I	T	T		
115	Q	L	L	L	
125	S	T	T		
127	D	S	S	S	
131	T	N	K	K	K
132	A	T			
135	D	G			
140	S	N			
145	T	N			
146	R	Q	Q	Q	
148	D	N	N	N	N
149	G	N	N	N	N
150	N	A	A	A	A
153	T	I			
163	G			E	
165	N	S			
178	D	E			
179	D	T	T	T	
180	T	V	A	A	A
182	R	T	T	T	
183	N	T			
202	I	T	T	T	
238	D	N	N	N	
248	H	Y			
260	K	R			
279	L	F	F		
298	K	R	R		
302	I	T	T		
309	V	I	I		
320	X		R		

48 25 25 27 18

H9 G1 (G5.7) phylogenetic tree

Feb2024-  
Sept2024  
Sept2023-  
Feb2024  
Human  
HI strain  
CVV

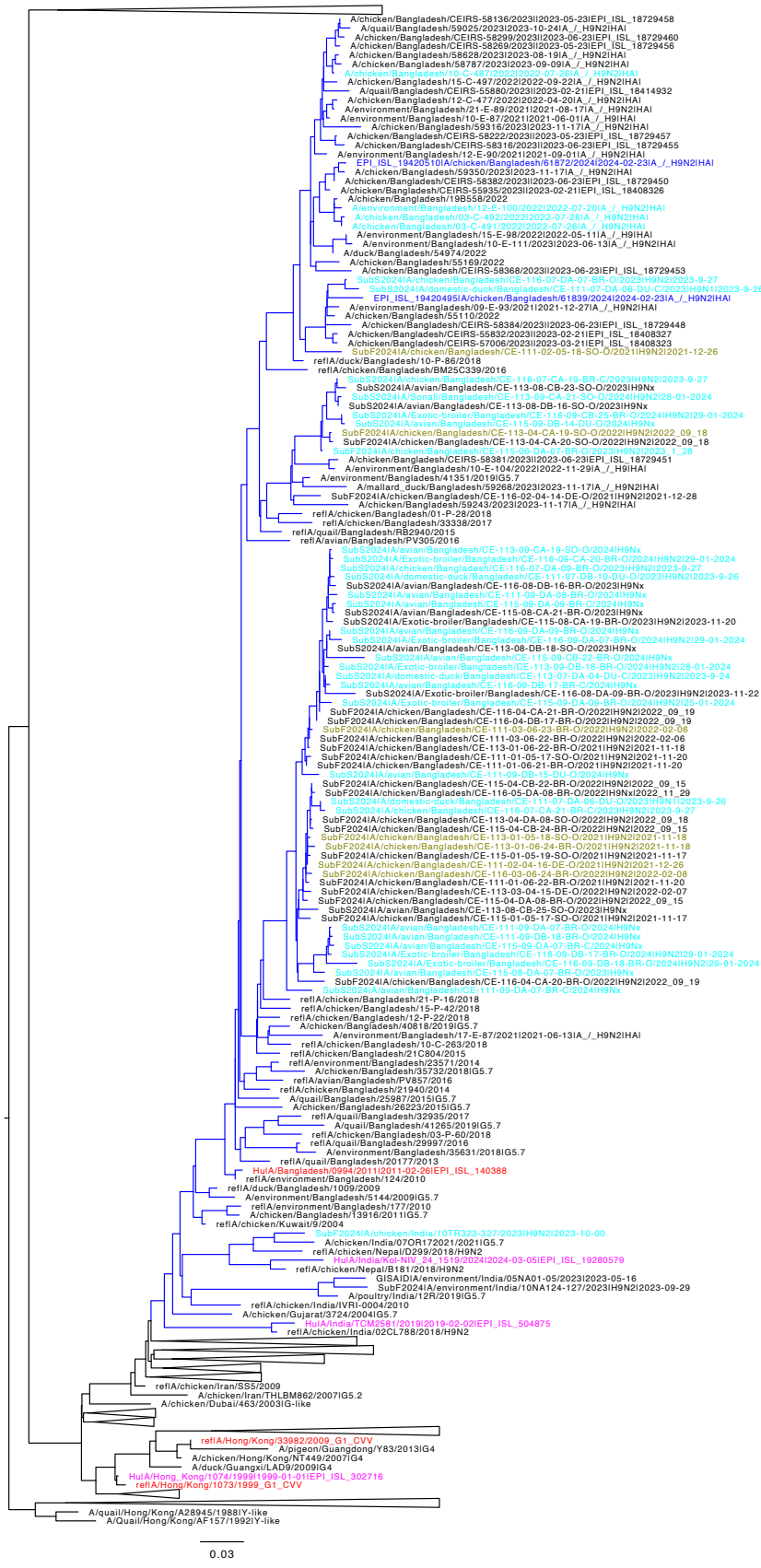


Figure 11: H9 phylogenetic tree. Analyses were conducted with reference sequences, data downloaded from GISAID, Genbank and shared from HKU, CDC and the OFFLU network. Sequences are coloured according to collection date. Sequences from humans are pink and CVVs are red. Branches of the G4.7 clade according to the Proposal for a Global Classification and Nomenclature System for A/H9 Influenza Viruses, are coloured blue.





## H9 G1 (G5.7) antigenic data

Table 10: Avian H9 G5.7 antigenic characterisation of viruses against CVV and reference post infection antisera from February 2023. Fold changes are coloured.

Semester		Reference Antigen		Clade	REFERENCE FERRET ANTISERA		
					A/Oman/2747/2019	A/Bangladesh/0994/2011	
					G1	G1	
					H9N2	H9N2	
				Ferret ID			
				Subtype			
		A/Oman/2747/2019		G1	H9N2	640	40
		A/Bangladesh/0994/2011		G1	H9N2	320	1280
<b>APHA Sep23-</b>		<b>Test antigen</b>					
<b>Feb24</b>	<b>1</b>	A/chicken/Bangladesh/CE-111-02-04-16-DE-O/2021		G1	H9N2	320	40
	<b>2</b>	A/chicken/Bangladesh/CE-113-04-CA-19-SO-O/2022		G1	H9N2	160	20
	<b>3</b>	A/chicken/Bangladesh/CE-111-06-DB-16-BR-O/2023		G1	H9N2	160	80
	<b>4</b>	A/chicken/Bangladesh/CE-116-03-06-24-BR-O/2022		G1	H9N2	320	40

# H9 G1 (G5.5) phylogenetic tree



Figure 12: H9 phylogenetic tree. Analyses were conducted with reference sequences, data downloaded from GISAID, Genbank and shared from HKU, CDC and the OFFLU network. Sequences are coloured according to collection date. Sequences from humans are pink and CVVs are red. Branches of the G4.5 clade according to the Proposal for a Global Classification and Nomenclature System for A/H9 Influenza Viruses, are coloured green.

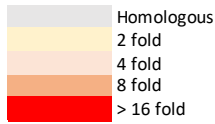
# H9 G1 (G5.5) amino acid difference table

Table 11: Amino acid comparison of the HA1 compared to within-clade CVVs. Putative antigenic sites are highlighted in grey.

site	A/Oman/2747/2019 CW	HuJ/A/Ghana/FS-24-2641/2024 2024-05-15 EPI_ISL_19266347	A/viam/Guinear/F1B2EC.1_24VIR4686-18/2024 H9N2_SubS2024	A/viam/Nigeria/VRD24-07B_24VIR4055-348/2024 H9N2_SubS2024	A/viam/Nigeria/VRD24-07C_24VIR4055-349/2024 H9N2_SubS2024	A/viam/Nigeria/VRD23-216E_24MR4055-345/2023 H9N2_SubS2024	A/viam/Nigeria/VRD23-216F_24MR4055-346/2023 H9N2_SubS2024	EPI_ISL_19390439 A/chicken/Jordan/24-12/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390373 A/chicken/Jordan/24-06/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390370 A/chicken/Jordan/24-05/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390433 A/chicken/Jordan/24-10/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19420485 A/chicken/Bangladesh/61839/2024 2024-02-23 A_/H9N2	EPI_ISL_19390445 A/chicken/Jordan/24-13/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390317 A/chicken/Jordan/24-01/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390380 A/chicken/Jordan/24-07/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390359 A/chicken/Jordan/24-03/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390452 A/chicken/Jordan/24-14/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390323 A/chicken/Jordan/24-02/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19420510 A/chicken/Bangladesh/61872/2024 2024-02-23 A_/H9N2	EPI_ISL_19390384 A/chicken/Jordan/24-08/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390428 A/chicken/Jordan/24-09/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390364 A/chicken/Jordan/24-04/2024 2024-05-12 A_/H9N2 HA	EPI_ISL_19390458 A/chicken/Jordan/24-15/2024 2024-05-12 A_/H9N2 HA	
5	I		V	V																				
28	Q							H											H					
36	E							N											D					Antigenic
40	M							K	K	K			K	K					K	K	K			Antigenic
45	N		K	K	K	K																		
48	R	H						H																Antigenic
54	T							K											K					
56	T							N											N					
57	I																		V					
69	M								I	S				I	I				S			I		
72	G							E																
77	S	A	A	A	A	A	A																	
86	V					A	E																	
98	V					I	I																	
103	T	A																						Antigenic
104	L	F	F	F	F																			
112	Q							K																
114	V	I	I					I											I					
116	L							I											I					Antigenic
120	S							T											T					
121	I					X																		Antigenic
127	T		S	S																				Antigenic
135	D							G																Antigenic
148	N		S																					Antigenic
149	G									S									S					Antigenic
150	G	N	N	N	N	N	N			L									L					Antigenic
153	I									V									V					Antigenic
158	Y									F									F					Antigenic
161	N		K																					Antigenic
180	A		T	T																		V		Antigenic
188	T	I																						Antigenic
198	T						A	D											E					
214	N			K	K																			
219	R			X																				Antigenic
226	V								I										I					
238	N										T											T		
246	F								Y										Y					
249	V			I	I																			
254	S			X																				
260	R									K														
262	D			N	N	N	N																	
264	S	K	K							N														Antigenic
265	S	N		I	I	X																		
266	G						S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	Antigenic
283	M									L									L					
288	I																		V					
295	T	I					N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	
298	K			X																				
305	L			X																				
311	L						M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	
315	H									P									P					
316	A		T																					
317	R		K	K						K									K					
319	S									K									K					
Aadiffs from CW	8	11	9	8	14	10	4	6	4	4	25	4	4	5	4	4	4	3	24	4	4	5	5	
Putative antigenic sites	4	6	3	2	2	2	2	3	1	2	8	2	2	1	1	2	1	7	2	2	1	3		

# H9 G1 (G5.5) Antigenic data

Table 11: H9 G5.5 antigenic characterisation of viruses against CVV and reference post infection antisera. Fold changes are coloured.



REFERENCE FERRET ANTISERA

	A/BANGLADESH/0994/2011	A/Oman/2747/2019
Clade	G1	G1
Subtype	H9N2	H9N2

Semester		Clade	Subtype	Ferret ID	
	Reference Antigen				
	A/BANGLADESH/0994/2011	G1	H9N2	320	40
	A/Oman/2747/2019	G1	H9N2	320	320
<u>IZS</u> <u>Ve</u> <u>Sep</u>	Test antigen				
<u>23 - Feb 24</u>					
<u>1</u>	A/avian/Nigeria/VRD23-216B_24VIR4055-342/2023	G1	H9N2	80	640
<u>2</u>	A/avian/Nigeria/VRD23-216D_24VIR4055-344/2023	G1	H9N2	80	640
<u>3</u>	A/avian/Guinea/F1B2P_24VIR4686-16/2024	G1	H9N2	20	160

# H10

Feb2024-Sept2024  
Sept2023-Feb2024  
Human  
CVV

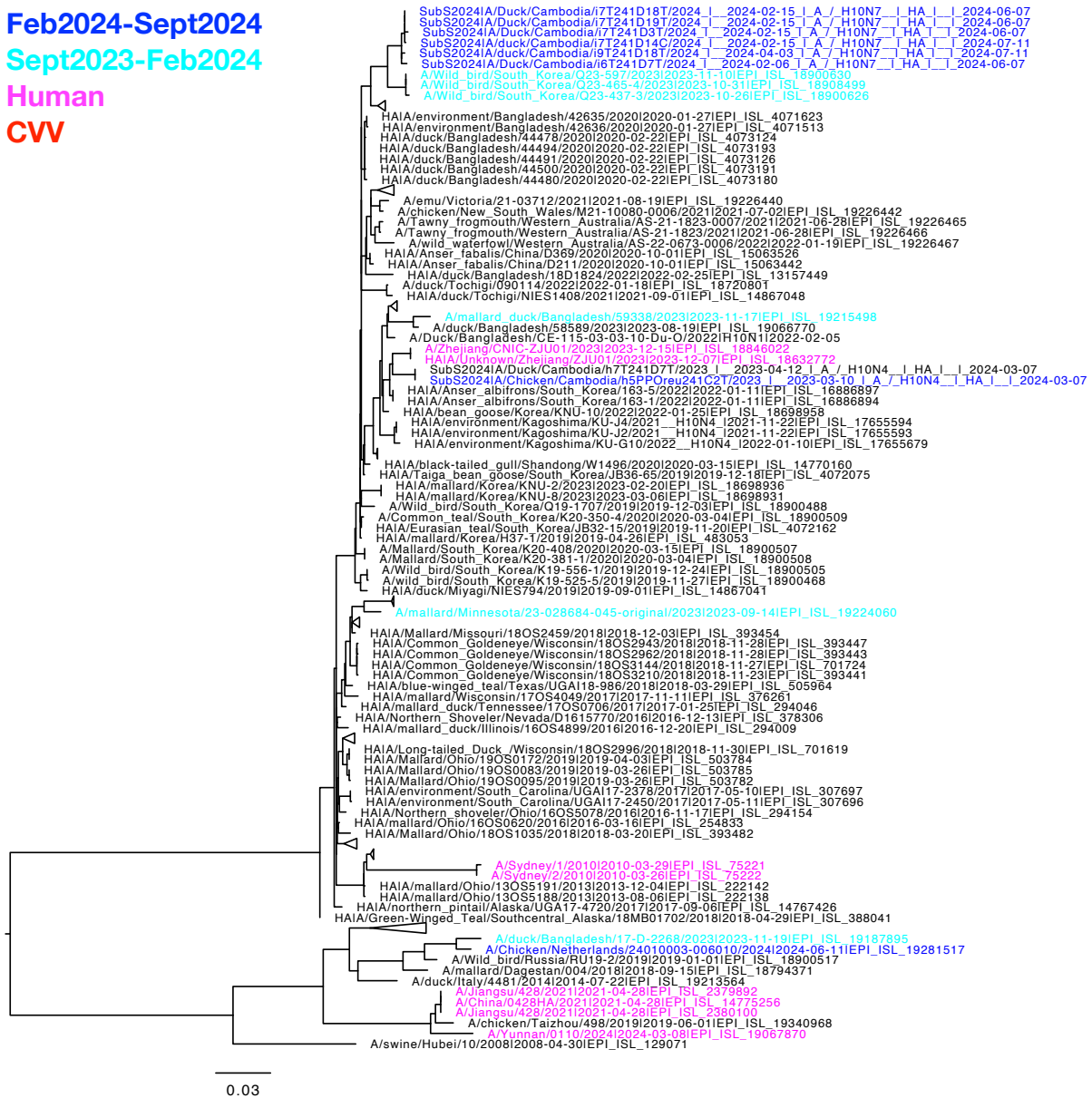
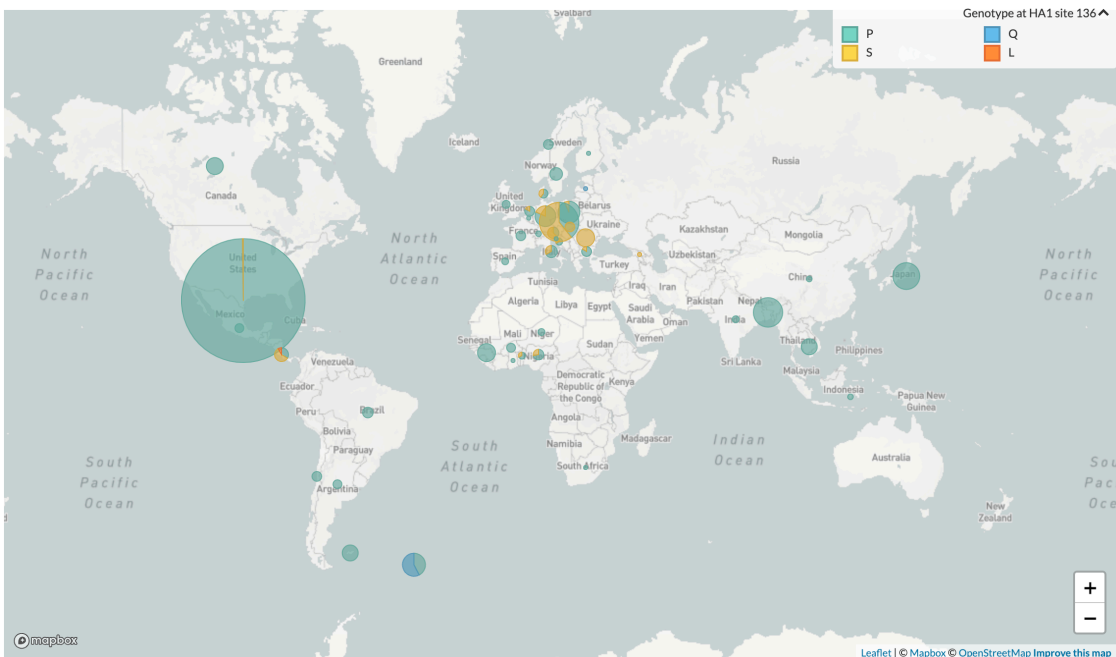
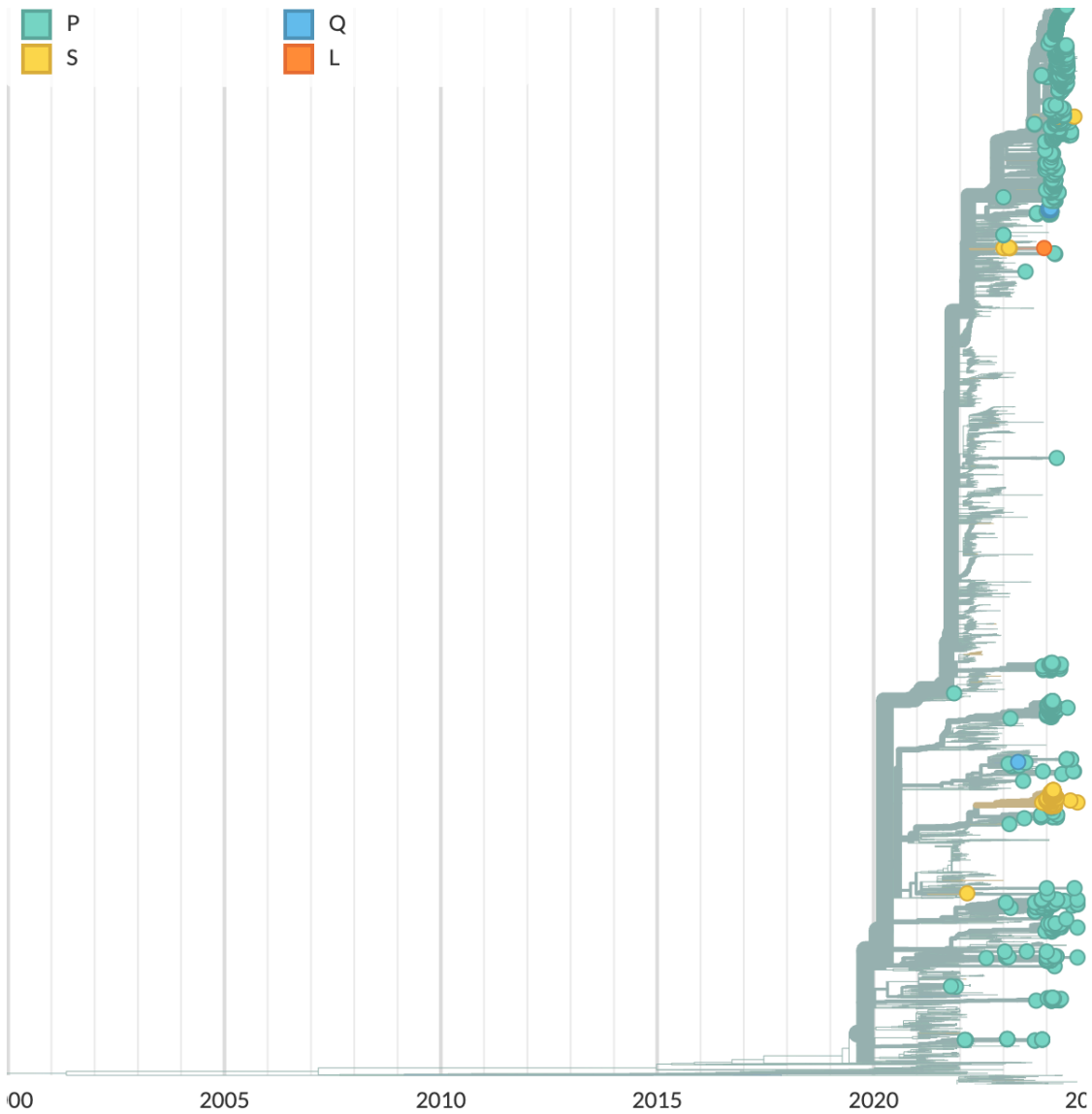


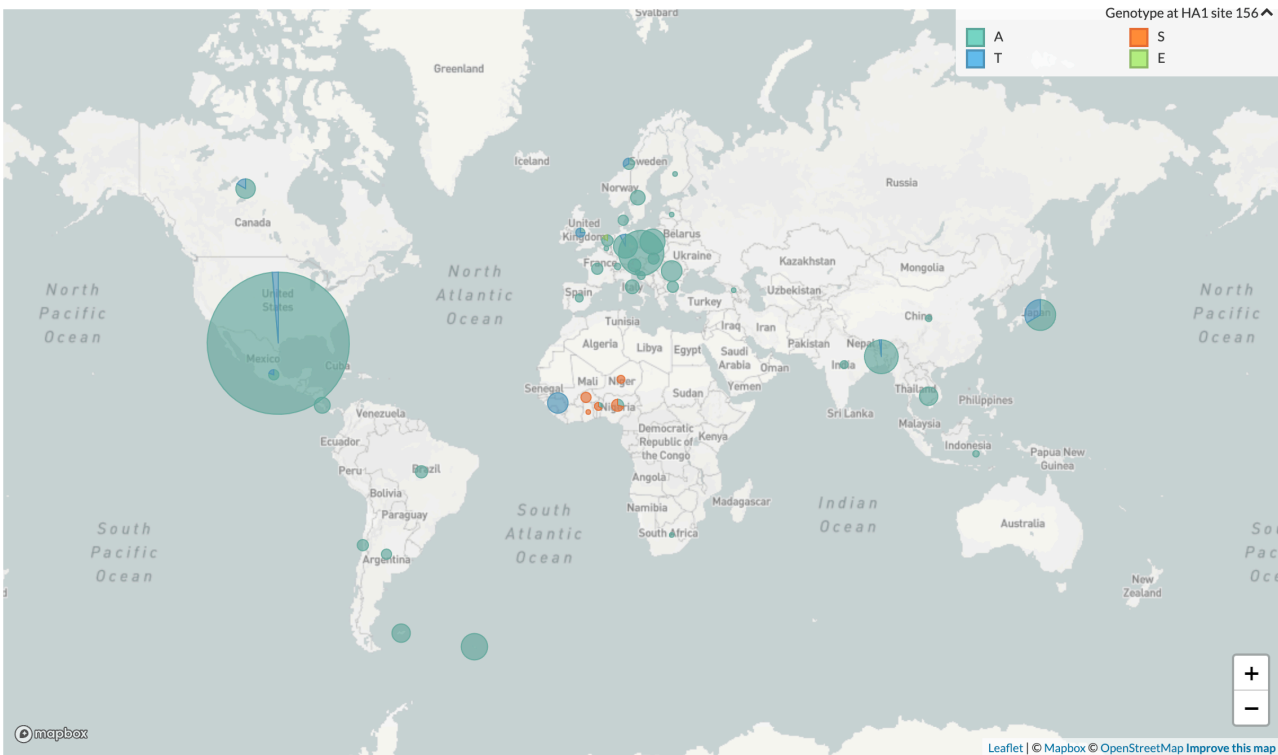
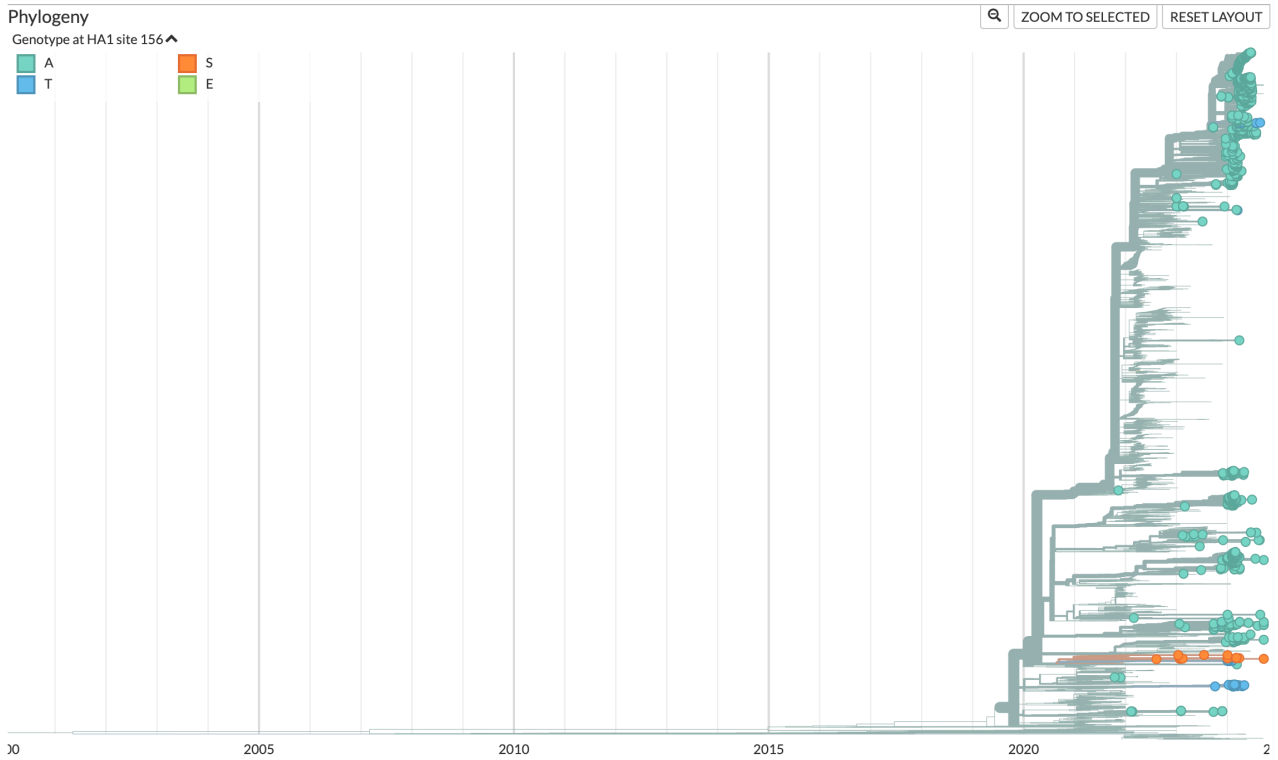
Figure 13: Avian H10 maximum likelihood phylogenetic tree midpoint rooted. Analyses were conducted with sequences and data downloaded from GISAID and shared with OFFLU. Sequences are coloured according to collection date. Sequences from humans are pink and CVVs are red.

Annex

2.3.4.4b: HA1 site 136 - sequences from this reporting period and submitted to OFFLU

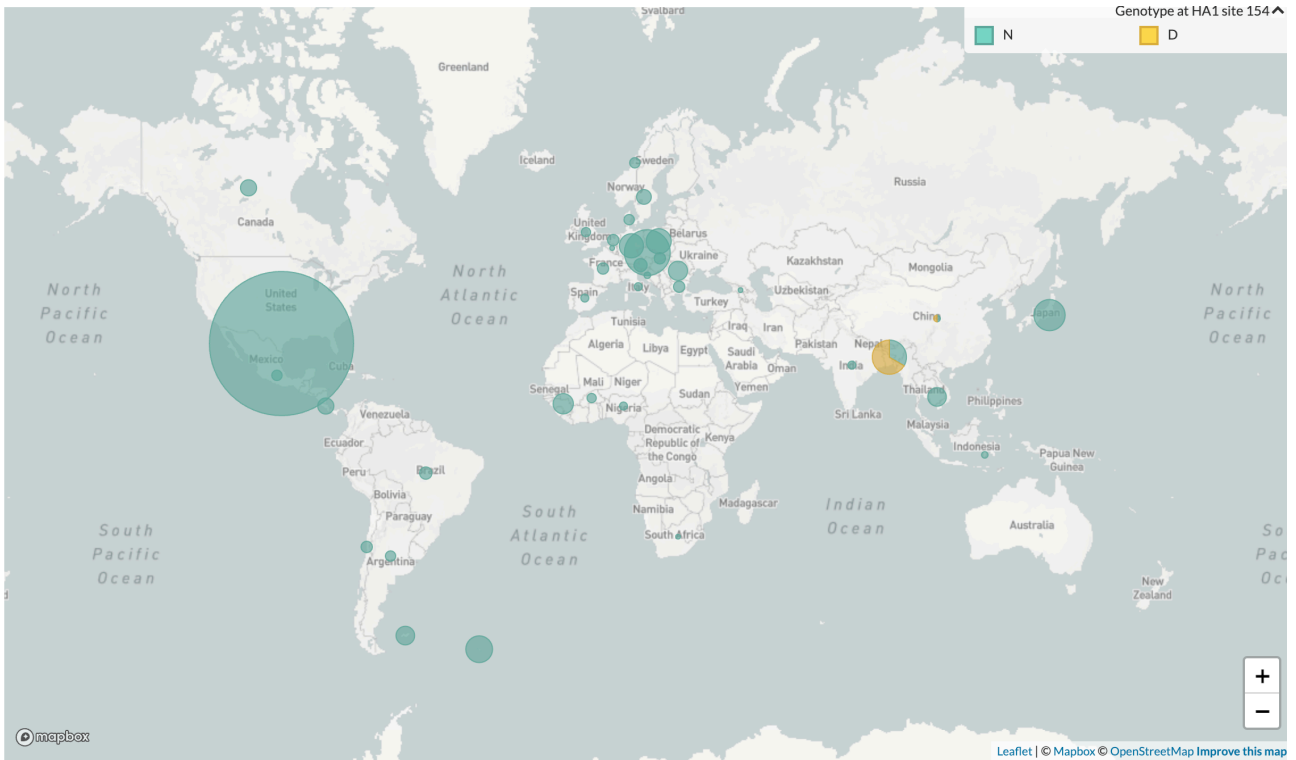


2.3.4.4b: HA1 site 156 - sequences from this reporting period and submitted to OFFLU

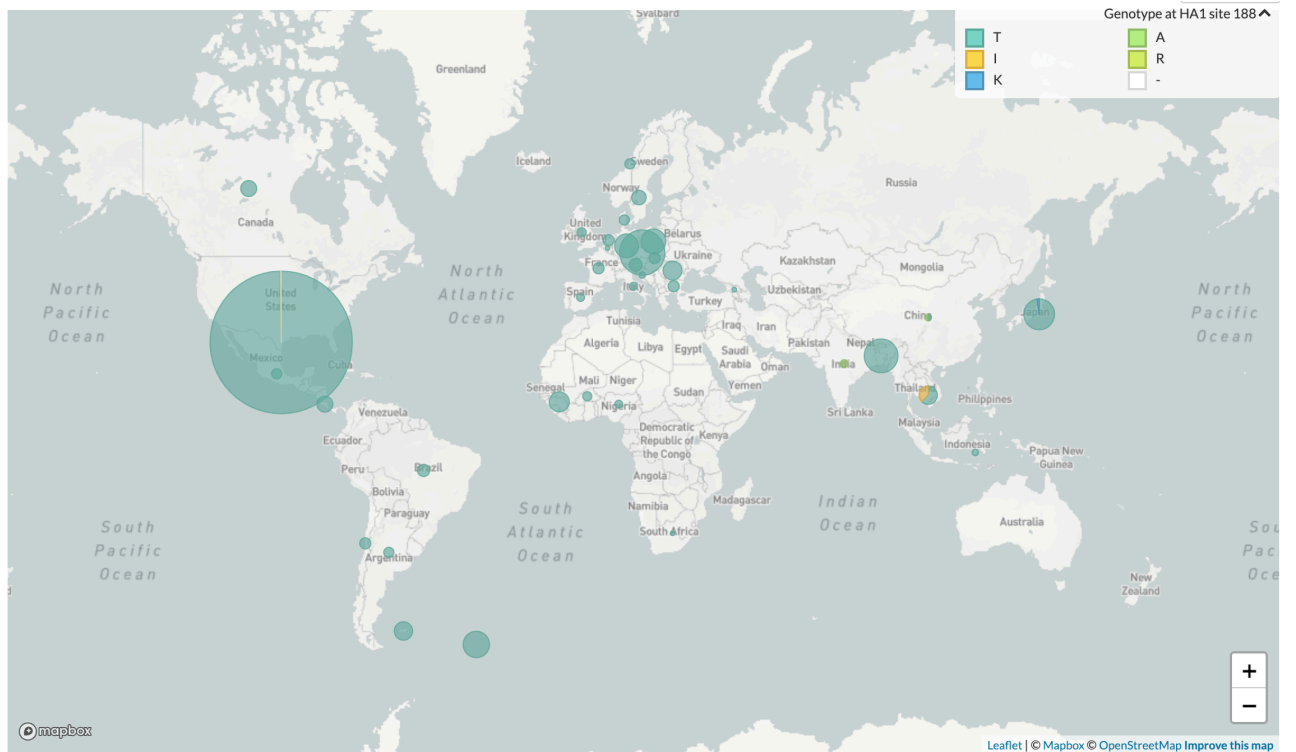




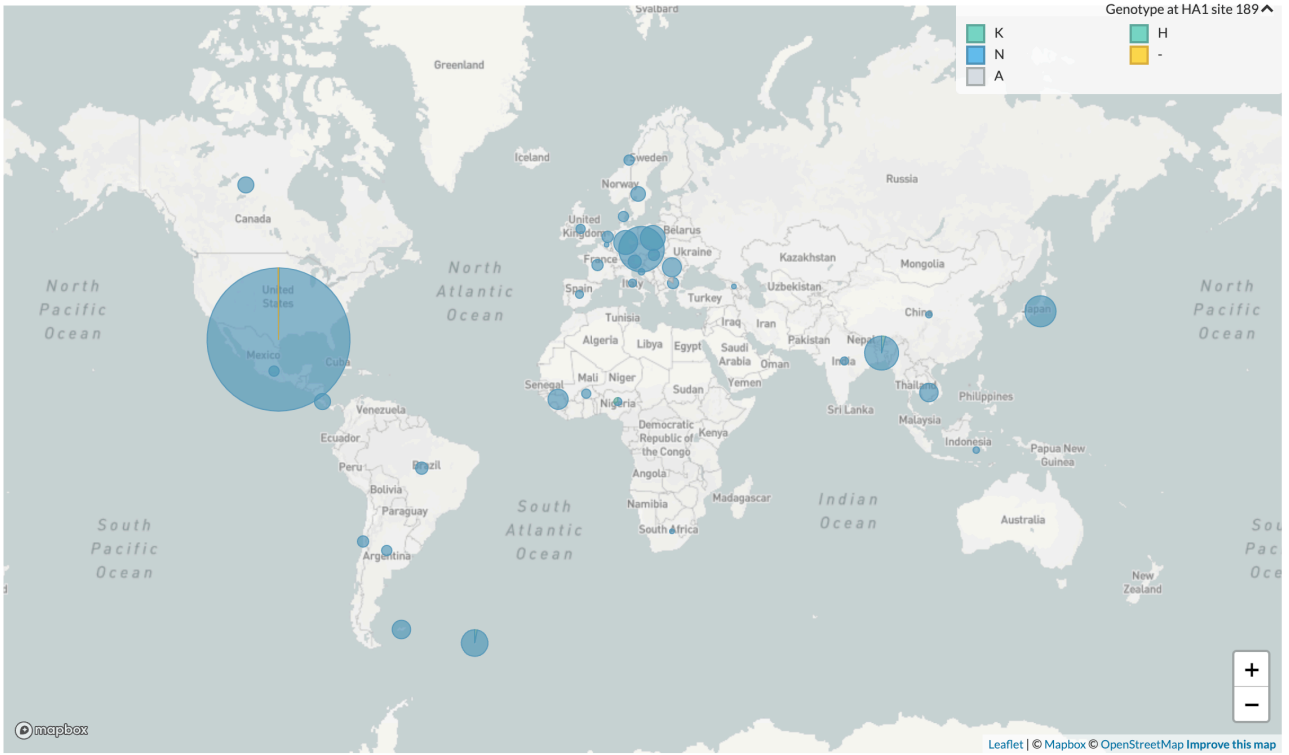
2.3.4.4b: HA1 site 154 - sequences from this reporting period and submitted to OFFLU



2.3.4.4b: HA1 site 188 - sequences from this reporting period and submitted to OFFLU



2.3.4.4b: HA1 site 189 - sequences from this reporting period and submitted to OFFLU



2.3.4.4b: HA1 site 189 - sequences since 2020

