OFFLU avian data package for Zoonotic influenza VCM

September 2024 to February 2025

SCOPE

In this document we present a summary of avian influenza A virus events reported from 1st September 2024 to 17th February 2025 and phylogenetic analysis of H5, H7, H9, H10 viruses.

Table of Contents

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.

Analyses were conducted by subtype. Sequences collected or released between 1st September 2024 and 17th February 2025 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 (Katoh 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. H9 sequence clades were assigned using the A/H9 influenza virus lineage and clade assignment tool (https://nmdc.cn/influvar/tools/H9aiv) (Fusaro et al., 2024).

Note: There has been a recent update to this nomenclature to reflect the genetic diversification of the A(H5) viruses, particularly clade 2.3.2.1c, to add 2.3.2.1d, e, f, and g (Ort et al., 2025). Where relevant, updated clade nomenclatures have been adopted in this report.

Summary

Avian influenza outbreaks have been reported in poultry and wild birds across all continents during the latest reporting period. The global spread of Gs/Gd H5 remains primarily driven by the clade 2.3.4.4b H5N1 subtype, though other subtypes have been detected, including H5N8 in Egyptian poultry, H5N3 in the Republic of Korea, H5N2 in poultry in Canada and in the Philippines, and H5N5 in wild birds and poultry across North America and Europe, where its range is expanding into lower latitudes. In South Asia, clade 2.3.2.1a remains a concern and is believed to co-circulate with clade 2.3.4.4b in some countries, including India, while clade 2.3.2.1e‡ (formerly classified as clade 2.3.2.1c) remains restricted to the Mekong Delta and clade 2.3.2.1g‡ (formerly classified as clade 2.3.2.1c), continues to circulate in Indonesia.

In North America, clade 2.3.4.4b activity remains high, with multiple genotypes co-circulating and new virus incursions from the Pacific Flyway. The United States has reported infections of B3.13 genotype viruses in dairy cows across several states, including California, alongside continued detections in poultry and wild birds. Human cases have increased, mostly linked to cattle and poultry exposure. Recently, two separate primary introductions of H5N1 D1.1 genotype viruses in cattle have been reported in Nevada and Arizona, one of which is associated with a human case. Additionally, the first detection of H5N5 in wild birds in the U.S. has been confirmed. Canada has recorded multiple H5N1 poultry outbreaks and ongoing detections of H5N5 in wild birds and wild mammals. In South America, H5N1 has been detected this season, with poultry outbreaks reported in Colombia, Peru, and Argentina. Outbreaks in wild birds in Peru have raised concerns over potential wildlife die-offs. However, overall activity remains lower than in previous years, when significant outbreaks and die-offs were observed further south. In Africa, H5N1 and H5N8 remain active in Egypt, with continued HPAI detections in Nigeria and Niger. South Africa has reported no recent H5 activity. Clade 2.3.4.4b has not been detected in Oceania, but Australia and New Zealand maintain active surveillance, particularly during migratory bird seasons, to monitor for potential incursions. The detection of clade 2.3.4.4b H5N1 in Antarctic and sub-Antarctic islands after the austral winter is a serious ecological concern, suggesting either novel introductions or overwintering of the virus.

Europe continues to experience widespread outbreaks in domestic poultry, alongside significant wild bird mortality, particularly among waterfowl. While the number of circulating genotypes has declined, H5N1 virus activity remains high, primarily driven by a single genotype that emerged in late 2023 in Eastern Europe. In Western Europe, limited outbreaks of a gull-adapted H5N1 genotype have been reported, with notable impacts on coastal bird populations. Since September 2024, Northern Europe has seen a rapid increase in H5N5 outbreaks in wild birds of the Laridae family, along with recent mammal infections, including grey seals in the UK and cats in Iceland.

In Asia, Japan is experiencing its largest H5 clade 2.3.4.4b outbreak since 2020. Vietnam has reported sporadic outbreaks in poultry and wild birds. The Republic of Korea has detected H5N3 clade 2.3.4.4b in wild birds and H5N1 clade 2.3.4.4b in poultry, with a large number of H5N1 outbreaks affecting various poultry production systems between December 2024 and February 2025. Indonesia saw increased H5N1 activity at the end of 2024, while the Philippines reported a stable situation with few detections of H5N1 and H5N2 in poultry.

Additionally, several H7 viruses have been detected in poultry, including separate incursions of HPAI viruses in poultry in New Zealand and Australia. H9N2 continues to be detected in chickens and other galliformes poultry species, with human cases repeatedly reported in China. These viruses remain endemic in poultry across Central Asia, South and Southeast Asia, North and West Africa, and the Middle East, particularly in live bird markets. H10 subtype viruses adapted to galliformes continue to circulate in poultry in China and other countries in South and Southeast Asia.

Finally, avian influenza vaccination efforts are expanding in regions with endemic H5 clades or ongoing outbreaks, including parts of Europe, Asia, Africa, and South America. North America and Europe are conducting field trials on vaccine candidates for H5 clade 2.3.4.4b, targeting dairy cows and poultry. The United States and Canada have lifted restrictions on certain French poultry imports, which were initially imposed due to H5N1 vaccination in French ducks. Additionally, the USDA has granted conditional approval for an avian influenza poultry vaccine.

Global avian influenza events in animals
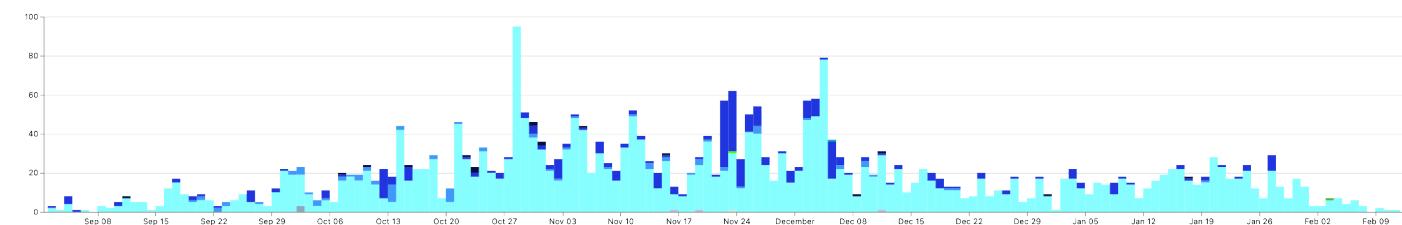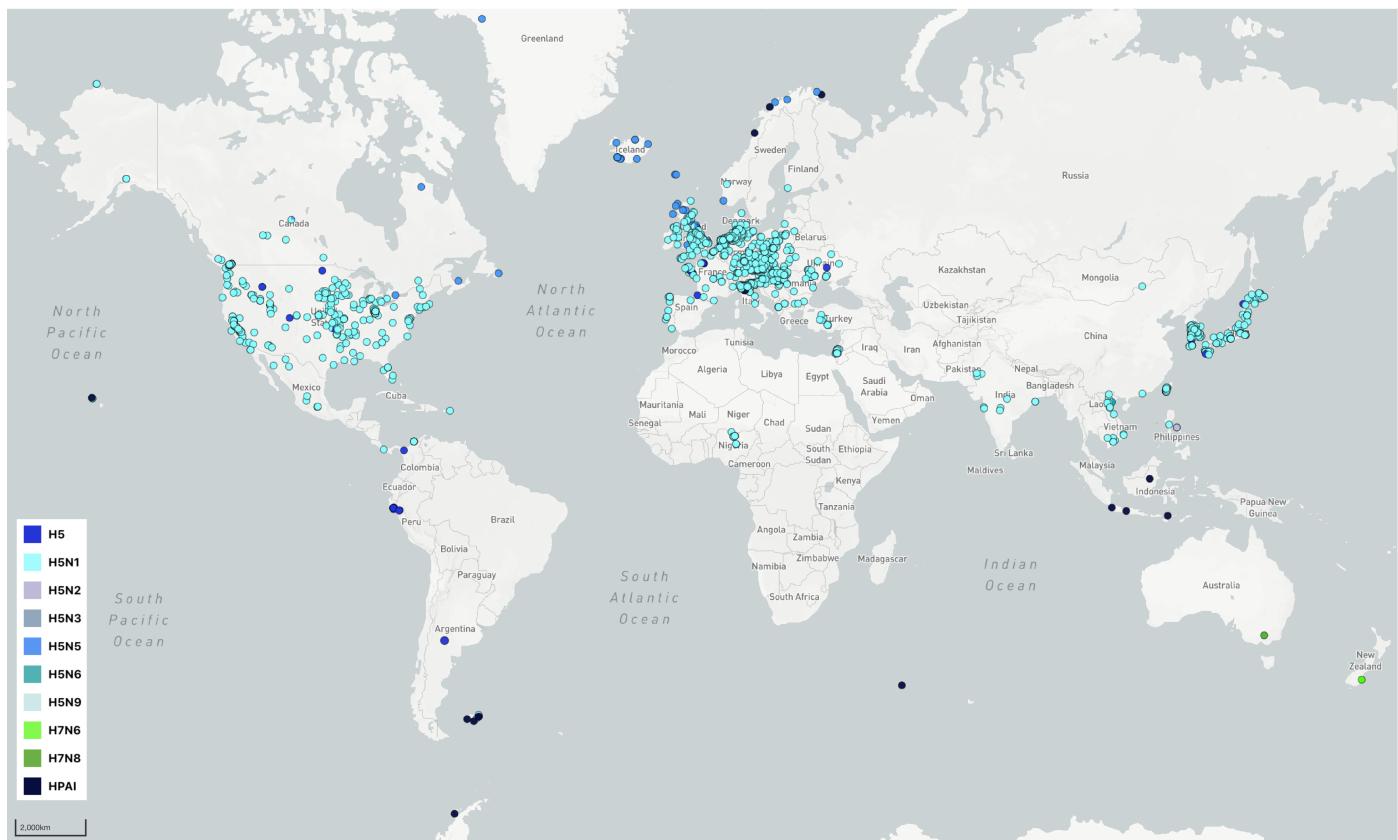
Figure 1. Microreact map showing the geographical and temporal distribution of confirmed Gs/Gd H5 and HPAI H7 highly pathogenic avian influenza outbreaks (excluding human cases) reported **to WOAH via the WAHIS platform and to national authorities gathered through FAO EMPRES-i.** Data shown falls within the reporting period of 1st September 2024 to present (last updated **17th February 2025**). Points are coloured by subtype and the outbreak date is represented along the bottom timeline.

Figure 2. Timeline of the number of confirmed Gs/Gd H5 and HPAI H7 highly pathogenic avian influenza outbreaks (excluding human cases) from September 2021 to present (last updated **14th February 2025**) coloured by type. Includes only outbreaks **reported to WOAH via the WAHIS platform and to national authorities gathered by FAO EMPRES-i.**
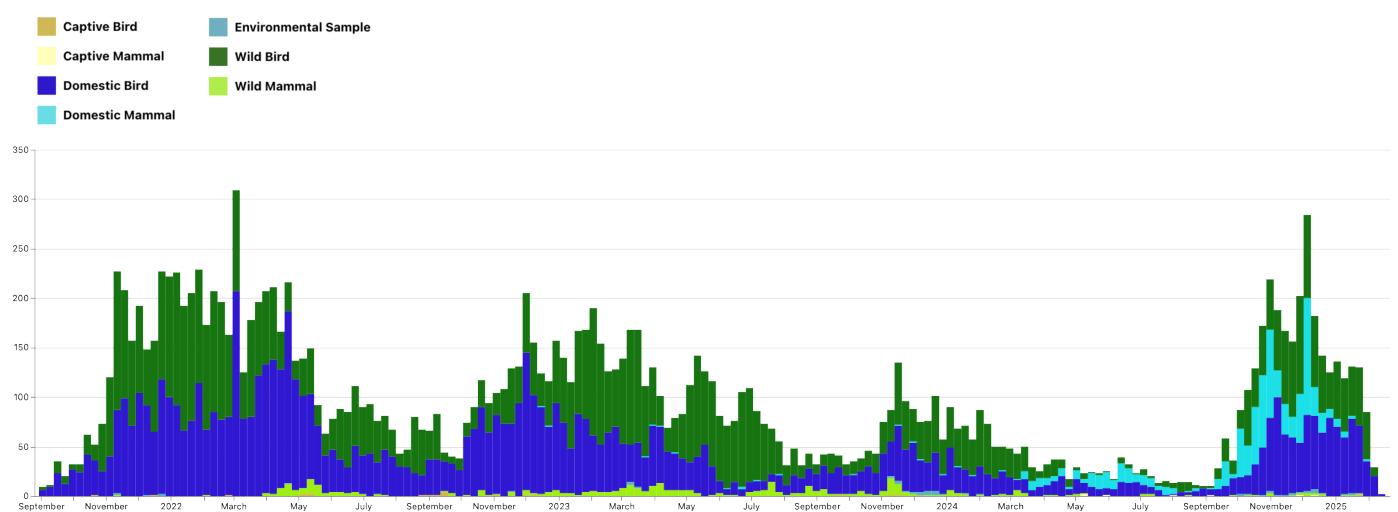
H5 Influenza A viruses

Activity table (H5)

Table 1. Gs/Gd lineage activity since **24th September 2024** as collected by OFFLU in this report until **17th February 2025**.

Country, area or territory	Host	Genetic clade
Antarctica (including both the Antarctic Peninsula and subantarctic islands)	Wild birds	unknown (H5), clade 2.3.4.4b (H5N1)
	Mammal (southern elephant seal, elephant seal, crab eater seal)	unknown (H5)
Albania	Poultry	2.3.4.4b (H5N1)
Austria	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Argentina	Poultry	unknown (H5)
Bangladesh	Poultry	2.3.2.1a (H5N1)
Belgium	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N5); 2.3.4.4b (H5N1)
Bosnia and Herzegovina	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Bulgaria	Poultry	2.3.4.4b (H5N1)
Canada	Human	2.3.4.4b (H5N1)
	Poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N2)
	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	Mammal (striped skunk, red fox, ringed seal, ringed seal)	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
Cambodia	Human	2.3.2.1e‡ (H5N1)
	Poultry	2.3.2.1e‡ (H5N1)
	Wild birds	2.3.2.1e‡ (H5N1)
China	Poultry	2.3.4.4b (H5N1), 2.3.4.4b (H5N6), 2.3.4.4h (H5N1), 2.3.4.4h (H5N6)
	Wild birds	unknown (H5)
Taiwan, China	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Colombia	Poultry	unknown (H5N1); unknown (H5)
Croatia	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Czech Republic	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Denmark	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Egypt	Poultry	unknown (H5N1); 2.3.4.4b (H5); unknown (H5N8)
Falkland Islands	Wild birds	2.3.4.4b (H5N1); unknown (H5)
	Mammal (South American sea lion)	unknown (H5)
Faroe Islands	Wild birds	unknown (H5N5)
Finland	Wild birds	unknown (H5N1)
France	Poultry	2.3.4.4b (H5); 2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Crozet and Kerguelen Islands (French Southern and Antarctic Lands)	Wild birds	2.3.4.4b (H5N1)
	Mammal (southern elephant seal)	2.3.4.4b (H5N1)
Germany	Poultry	2.3.4.4b (H5); 2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Greenland	Wild birds	unknown (H5N5)
Greece	Wild birds	unknown (H5N1)
Hungary	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Iceland	Poultry	2.3.4.4b (H5N5), unknown (H5N1)
	Wild birds	2.3.4.4b (H5N5)
	Mammal (cats, mink)	2.3.4.4b (H5N5)
India	Poultry	2.3.4.4b, 2.3.2.1a (H5N1)
	Wild Birds	unknown (H5)
	Mammal (cats)	unknown (H5N1)
	Captive mammals (tigers)	2.3.2.1a (H5N1)
Indonesia	Poultry	unknown (H5)
Ireland, Republic of	Wild birds	2.3.4.4b (H5N1)
Israel	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Italy	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
	Mammal (cats, red fox)	2.3.4.4b (H5N1)
Japan	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Lao People's Democratic Republic	Poultry	2.3.4.4b (H5N1), 2.3.2.1e‡ (H5N1)

Lithuania	Poultry	unknown (H5)
	Wild birds	unknown (H5)
Mexico	Wild birds	unknown (H5N1)
Moldova, Republic of	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Netherlands (the Kingdom of)	Poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	Wild birds	2.3.4.4b (H5N5); 2.3.4.4b (H5N1)
	Mammals (unspecified)	2.3.4.4b (H5N1)
Nepal	Poultry	unknown (H5N1)
Niger	Poultry	unknown (H5N1)
Nigeria	Poultry	unknown (H5N1)
North Macedonia	Poultry	unknown (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Norway	Wild birds	2.3.4.4b (H5N5); unknown (H5)
	Mammal (otter, Eurasian lynx)	2.3.4.4b (H5N5)
Peru	Poultry	unknown (H5)
	Wild birds	unknown (H5)
	Mammal (unspecified)	unknown (H5)
Panama	Poultry	unknown (H5N1)
Philippines	Poultry	unknown (H5N1); unknown (H5N2)
Poland	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Portugal	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Puerto Rico	Poultry	unknown (H5N1)
Korea, Republic of	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N3)
Romania	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Russian Federation	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Serbia	Wild birds	unknown (H5N1)
Slovakia	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Slovenia	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
	Mammal (red fox)	2.3.4.4b (H5N1)
Spain	Wild birds	2.3.4.4b (H5N1)
Switzerland	Wild birds	unknown (H5N1)
Türkiye	Poultry	unknown (H5N1)
United Kingdom of Great Britain and Northern Ireland (the)	Human	2.3.4.4b (H5N1), unknown (H5)
	Poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	Wild birds	2.3.4.4b (H5N5); 2.3.4.4b (H5N5)
	Mammal (grey seals)	2.3.4.4b (H5N5)
Ukraine	Poultry	unknown (H5); unknown (H5N1)
	Wild birds	unknown (H5N1)
United States of America (the)	Human	2.3.4.4b (H5N1), 2.3.4.4b (H5)
	Poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N9)
	Mammals (cats, cattle, swine, cougar, polar bear, red fox, mountain lion, bottlenose dolphin, eastern gray squirrel, harbor seal, house mouse, deer mouse, bobcat, mountain lion, raccoon, coyote, black rats)	2.3.4.4b (H5N1)
	Captive mammals (cheater, mountain lion, cougar, geoffroy's cat, canada lynx, serval, eurasian lynx, tiger, bobcat)	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N2); 2.3.4.4b (H5N5)
	Captive birds (swamp hen, kookaburra, indian goose)	2.3.4.4b (H5N1)
Viet Nam	Human	unknown (H5)
	Poultry	2.3.2.1e[‡] (H5N1); 2.3.4.4b (H5N1); unknown (H5N6);
	Captive mammals (tigers, leopard, lions)	2.3.2.1e[‡] (H5N1)

[‡]Formerly classified as H5 clade 2.3.2.1c.

H5 phylogenetic tree coloured by region
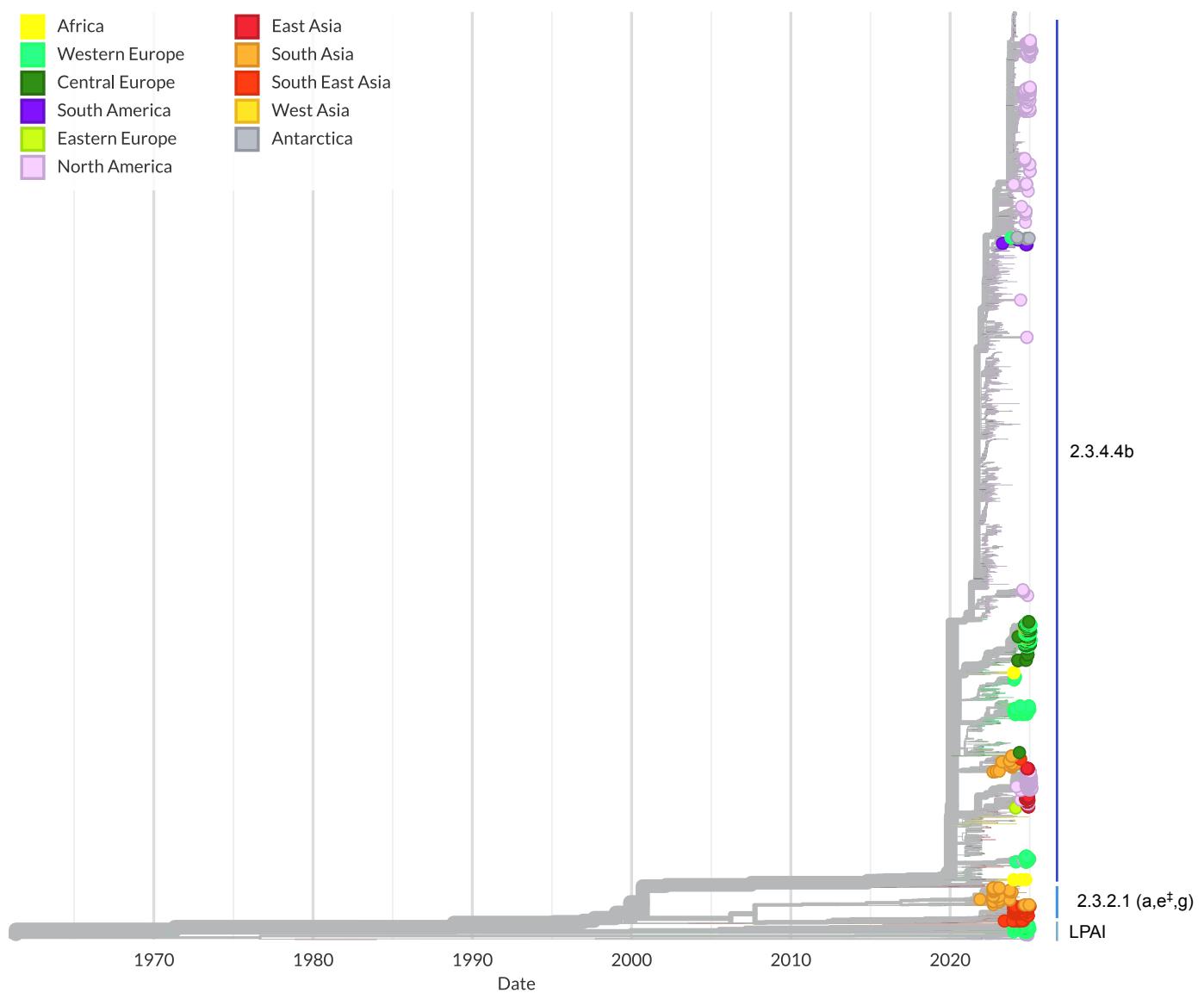
Figure 3. Avian H5 global summary time resolved phylogenetic tree. Analyses were conducted with reference sequences, sequences shared through the OFFLU network and data downloaded from GISAID (**17ᵗʰ February 2025**). Sequences from GISAID released within the reporting period or submitted to OFFLU since September 2024 are coloured by region.

H5 Influenza A viruses - map
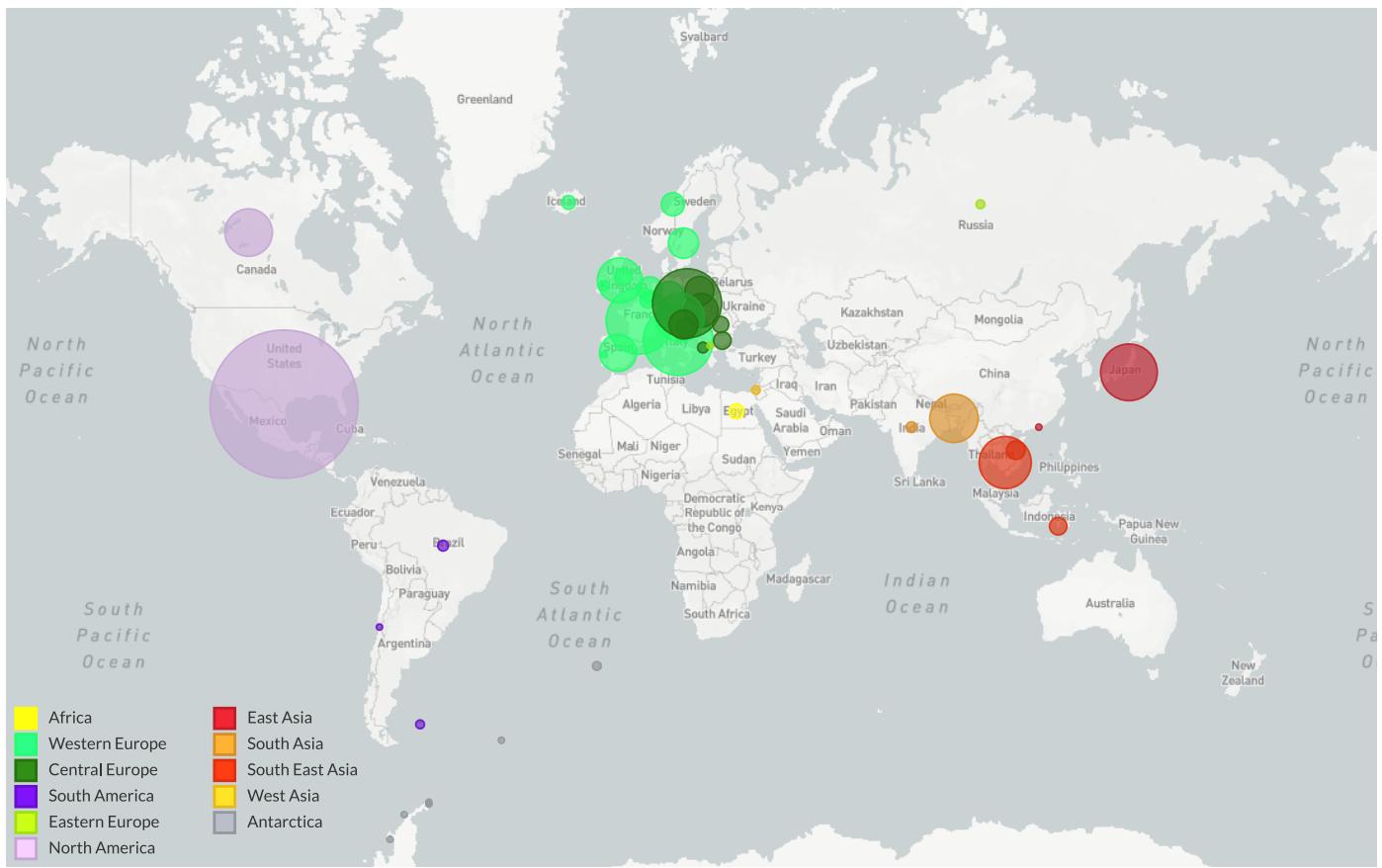
Figure 4. A map showing the geographic origins of viruses released on GISAID (as of **17th February 2025**) or submitted to OFFLU during the reporting period. Points are colour-coded by region.

Gs/Gd H5 2.3.4.4b phylogenetic tree
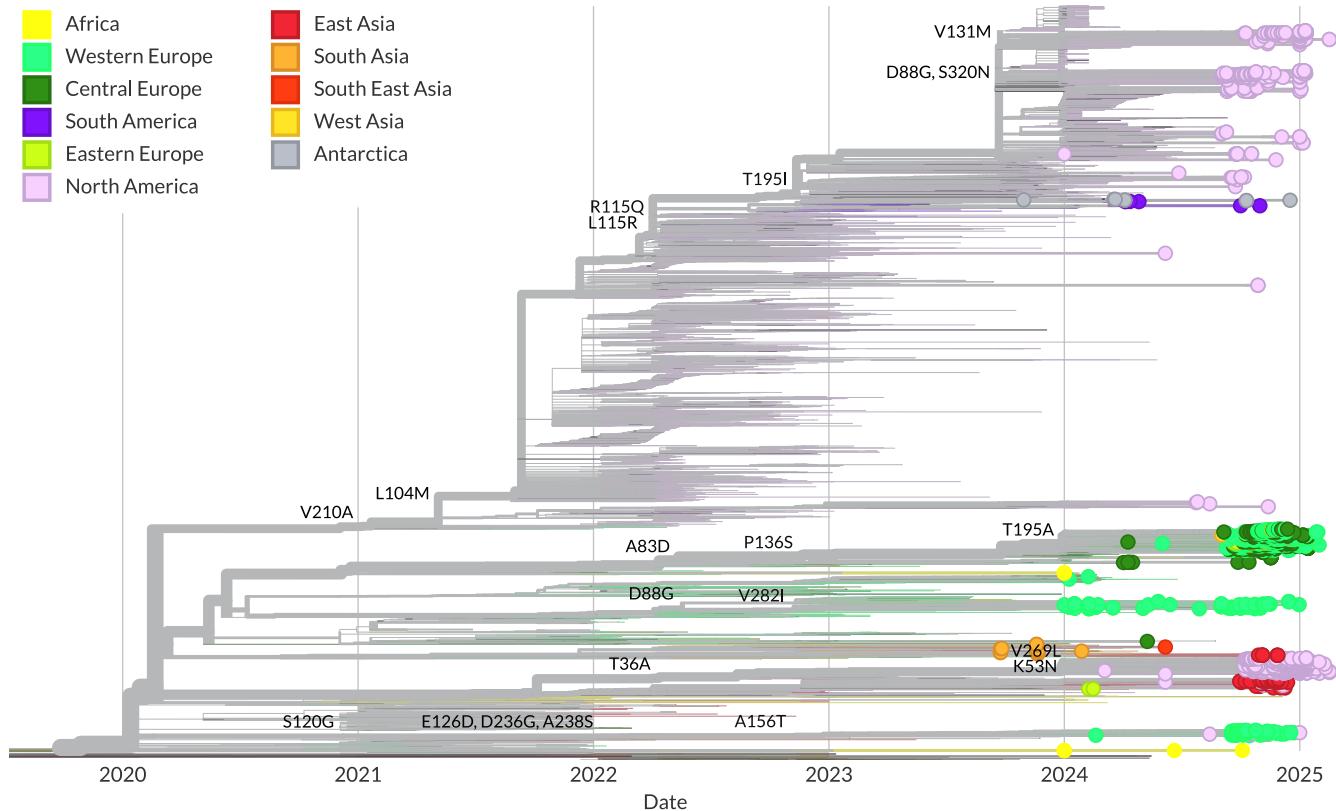
Figure 5. Gs/Gd lineage clade 2.3.44b time resolved phylogenetic tree. Sequences from GISAID (**17th February 2025**) released within the reporting period or submitted to OFFLU since **September 1st 2024** are coloured by region. Amino acid annotations are included along the branches.

Gs/Gd H5 2.3.4.4b subsampled phylogenetic tree
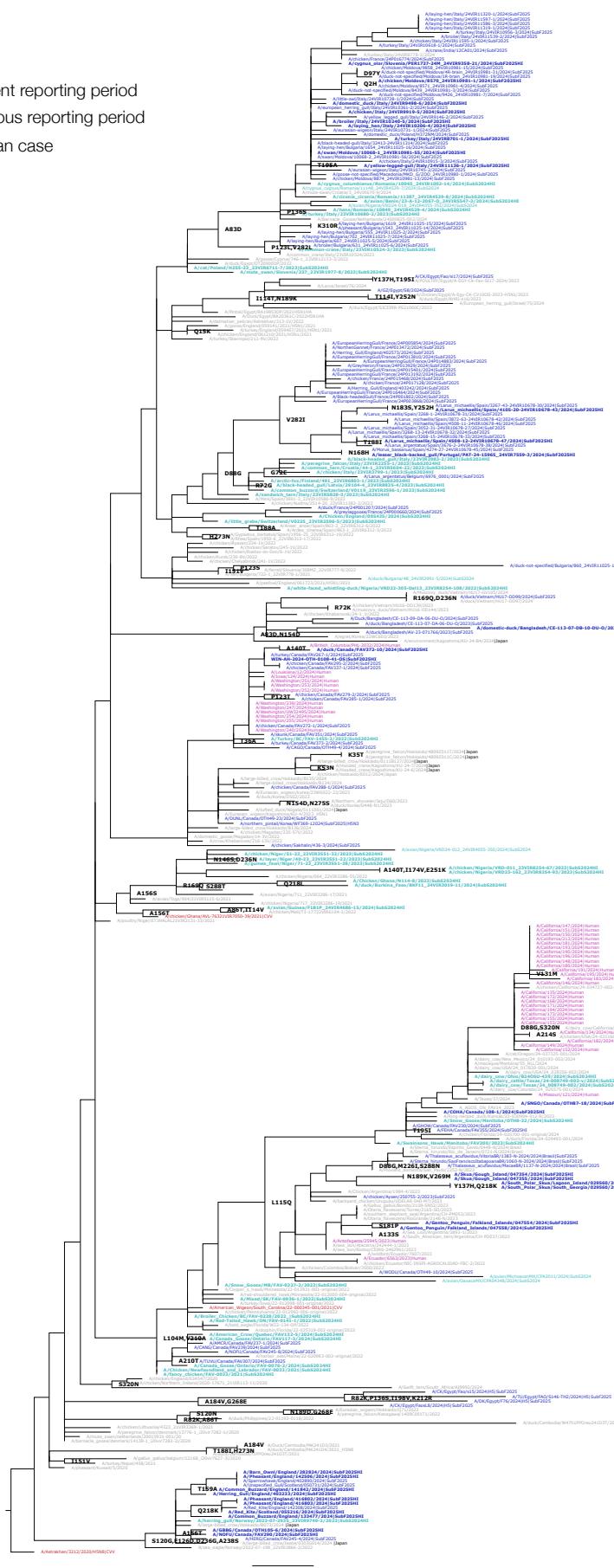
Figure 6. Phylogenetic tree of the Gs/Gd lineage clade 2.3.4.4b, rooted by the Astrakhan CWV, with amino acid changes annotated along the branches. The tree was subsampled using PARNAS, retaining sequences submitted to OFFLU since September 1st 2024, all CWVs, and recently antigenically characterised viruses. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterised strains, CWVs are marked in red, and human cases are shown in pink.

Gs/Gd H5 2.3.4.4b amino acid difference tables

Table 2. Avian H5 2.3.4.4b clade sequence comparison to the within clade CWs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CWs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.
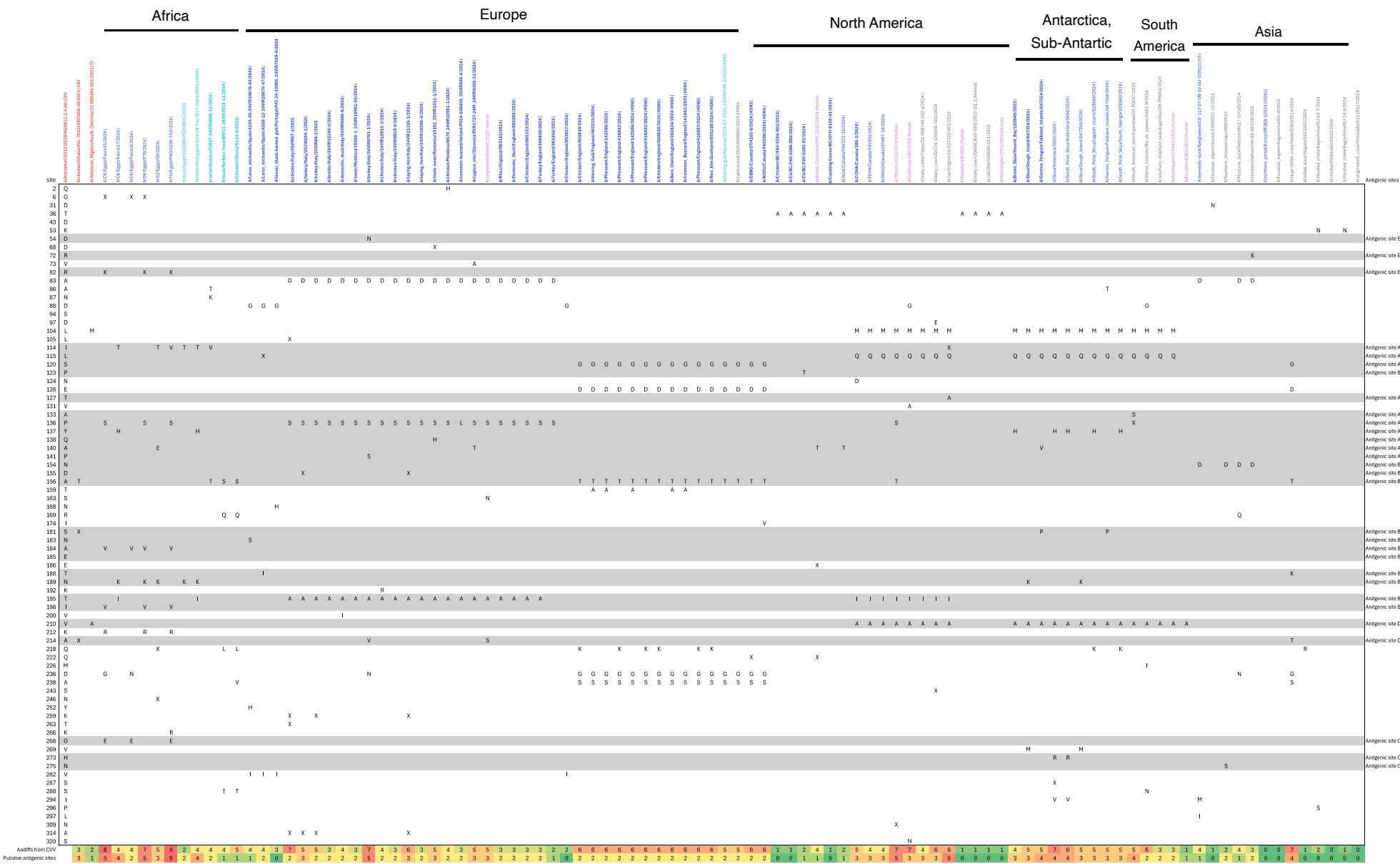
Gs/Gd H5 2.3.4.4b antigenic data

Table 3. Avian H5 2.3.4.4b antigenic characterisation of a subsection of viruses submitted to OFFLU (this reporting period) against CW and reference post infection antisera. Fold changes are coloured. Amino acid changes compared to the within-clade CW are annotated.

Legend:
- Homologous
- 2 fold
- 4 fold
- 8 fold
- > 16 fold

REFERENCE FERRET ANTISERA

Semester	Test antigen	Clade	Subtype	A/turkey/Israel/238/2019 (2.3.4.4b H5N8)	A/Astrakhan/3212/2021 (2.3.4.4b H5N8)	A/American wigeon/South Carolina/22-000345-001/2021 (2.3.4.4b H5N1)	A/chicken/Ghana/AVL-763/21VIR7050-39/2021 (2.3.4.4b H5N1)	A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021 (2.3.4.4b H5N1)	AA diffs compared to Astrakhan
	Reference Antigen								
	A/turkey/Israel/238/2019	2.3.4.4b	H5N8	**320**	160	40	1280	320	
	A/ASTRAKHAN/3212/2020	2.3.4.4b	H5N8	640	**640**	20	640	160	
	A/American wigeon/South Carolina/22-000345-001/2021	2.3.4.4b	H5N1	80	320	**160**	1280	1280	
	A/chicken/Ghana/AVL-763/21VIR7050-39/2021	2.3.4.4b	H5N1	160	80	40	**640**	640	
	A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021	2.3.4.4b	H5N1	80	40	40	320	**2560**	
	Test antigen								
APHA Sep 24 - Feb 25	A/Gentoo_Penguin/Falkland_Islands/047554/2024	2.3.4.4b	H5N1	320	1280	160	1280	5120	**L115Q, A140V, S181P, V210A**
	A/Skua/Gough_Island/047354/2024	2.3.4.4b	H5N1	10	0	40	40	320	L104M, **L115Q, N189K, V210A,** V269M
	A/Pheasant/England/416802/2024	2.3.4.4b	H5N5	160	80	80	1280	320	**S120G, E126D, A156T,** Q218K, D236G, A238S,
	A/Pheasant/England/142506/2024	2.3.4.4b	H5N5	320	160	80	1280	640	**S120G, E126D, A156T,** T159A, D236G, A238S
	A/Brown_Skua/Hound_Bay/133949/2023	2.3.4.4b	H5N1	80	20	160	1280	1280	L104M, **L115Q, Y137H, V210A**
	A/Chicken/England/050610/2024	2.3.4.4b	H5N5	320	320	160	2560	640	**S120G, E126D, A156T,** Q218K, D236G, A238S
	A/Chicken/England/053917/2024	2.3.4.4b	H5N1	160	80	80	640	2560	D88G, V282I
	A/Turkey/England/058848/2024	2.3.4.4b	H5N1	160	160	80	1280	2560	A83D, **P136S, T195A**
	A/Domestic_Duck/England/060280/2024	2.3.4.4b	H5N1	80	160	160	1280	2560	A83D, **P136S, T195A**
	A/Turkey/England/061858/2024	2.3.4.4b	H5N1	80	160	160	1280	2560	A83D, **P136S**
	A/Rhea/England/063182/2024	2.3.4.4b	H5N1	80	160	160	1280	2560	A83D, **P136S, T195A**
	A/Chicken/England/065333/2024	2.3.4.4b	H5N1	40	80	40	640	1280	A83D, **P136S, T195A**

Legend:
- Homologous
- 2 fold
- 4 fold
- 8 fold
- > 16 fold

REFERENCE FERRET ANTISERA

Semester	Test antigen	Clade	Subtype	A/Astrakhan/3212/2021 (2.3.4.4b H5N8)	A/American wigeon/South Carolina/22-000345-001/2021 (2.3.4.4b H5N1)	A/chicken/Ghana/AVL-763/21VIR7050-39/2021 (2.3.4.4b H5N1)	A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021 (2.3.4.4b H5N1)	AA diffs compared to Astrakhan
	Reference Antigen							
	A/ASTRAKHAN/3212/2020	2.3.4.4b	H5N8	**320**	320	640	1280	
	A/american wigeon/South Carolina/22-000345-001/2021	2.3.4.4b	H5N1	640	**320**	1280	5120	
	A/Chicken/Ghana/AVL-763/21VIR7050-39/2021	2.3.4.4b	H5N1	80	40	**640**	320	
	A/Poultry/Niger/HALAL/21VIR2131-33/2021	2.3.4.4b	H5N1	80	40	320	**640**	
	Test antigen							
IZSVe Sep 24 - Feb 25	A/chicken/Moldova/8570_24VIR10981-1/2024	2.3.4.4b	H5N1	10	160	1280	5120	Q2H, A83D, **P136S, T195A**
	A/swan/Moldova/10068-1_24VIR10981-55/2024	2.3.4.4b	H5N1	20	80	640	1280	A83D, **P136S, T195A**
	A/cygnus_olor/Slovenia/PER1737-24M_24VIR9358-21/2024	2.3.4.4b	H5N1	<10	80	320	1280	V73A, A83D, **P136S, A140T, T195A**
	A/Larus_michaellis/Spain/4105-20-24VIR10678-43/2024	2.3.4.4b	H5N1	80	40	320	640	D88G, **N183S,** Y252H, V282I
	A/Larus_michaellis/Spain/4508-12-24VIR10678-47/2024	2.3.4.4b	H5N1	80	40	320	640	D88G, **L115R/L, T188I,** V282I
	A/lesser_black-backed_gull/Portugal/PAT-24-15965_24VIR7559-4/2024	2.3.4.4b	H5N1	160	160	640	1280	D88G, N168H, V282I
	A/turkey/Italy/24VIR8701-1/2024	2.3.4.4b	H5N1	<10	40	640	640	**D54N,** A83D, **P136S, P141S, T195A, A214V,** D236N
	A/chicken/Italy/24VIR9919-5/2024	2.3.4.4b	H5N1	<10	80	640	1280	A83D, **P136S, T195A**
	A/laying_hen/Italy/24VIR10206-4/2024	2.3.4.4b	H5N1	80	160	1280	2560	A83D, **P136S, T195A**
	A/broiler/Italy/24VIR10240-5/2024	2.3.4.4b	H5N1	20	80	320	1280	A83D, **P136S, T195A**
	A/domestic_duck/Italy/24VIR9498-6/2024	2.3.4.4b	H5N1	<10	80	640	1280	A83D, **P136S, T195A**
	A/chicken/Italy/24VIR10915-3/2024	2.3.4.4b	H5N1	80	80	640	1280	A83D, **P136S,** K192R, **T195A**
	A/laying-hen/Italy/24VIR11319-1/2024	2.3.4.4b	H5N1	20	160	1280	5120	A83D, **P136S, D155N/D, T195A**
	A/chicken/Italy/25VIR67-1/2024	2.3.4.4b	H5N1	20	80	640	1280	A83D, **P136S, T195A**
	A/turkey/Italy/25VIR69-2/2025	2.3.4.4b	H5N1	40	160	640	2560	A83D, **P136S, T195A**
	A/turkey/Italy/25VIR294-2/2025	2.3.4.4b	H5N1	80	80	1280	2560	A83D, **P136S, D155N/D, T195A**
	A/common-buzzard/Ireland/PV24-036458_25VIR806-4/2024	2.3.4.4b	H5N1	40	160	1280	2560	V16I, A83D, **P136L, T195A**
	A/mute-swan/Romania/15102_25VIR1011-1/2024	2.3.4.4b	H5N1	40	160	640	2560	D68E/D, **P136S,** Q138H, **T195A**
	A/ Cooper's Hawk/BC/OTH-0108-001/2024	2.3.4.4b	H5N1	40	80	640	640	L104M, **L115Q,** N124D, **T195I, V210A**
	A/GBBG/NL/OTH105-6/2024	2.3.4.4b	H5N5	80	40	640	320	**S120G, E126D, A156T,** Q222X, D236G, A238S
	A/NOFU/Canada/FAV290/2024	2.3.4.4b	H5N5	40	40	640	320	**S120G, E126D, A156T,** I174V, D236G, A238S
	A/Cackling Goose/BC/OTH-0108-41/2024	2.3.4.4b	H5N1	10	80	640	2560	T36A
	A/Ck/BC/FAV-0284-001/2024	2.3.4.4b	H5N1	40	80	640	1280	T36A
	A/Ck/BC/FAV-0266-002/2024	2.3.4.4b	H5N1	<10	80	320	1280	T36A
	A/Ck/BC/FAV-0285-02/2024	2.3.4.4b	H5N2	40	40	640	320	T36A, **P123T**

Antivirals

Table 4. Avian H5 2.3.4.4b clade viruses of different geographical origin were assessed for their susceptibility to neuraminidase inhibitors (Oseltamivir and Zanamivir) by means of a fluorescence assay based on the enzymatic cleavage of the substrate 20-(4-methylumbelliferyl)-a-D-N-acetylneuraminic acid (MUNANA). The presence of a ***indicates presence of NA truncation. Substitution known (bold) or suspected (light) to affect antiviral susceptibility. Dash lines refers to absence of substitution of interest/concern.

Region	Strain	Subtype	Genetic markers	Oseltamivir	Zanamivir
Europe	A/cygnus_olor/Slovenia/PER1737-24M_24VIR9358-21/2024	H5N1	-	2,0	0,5
	A/chicken/Moldova/8570_24VIR10981-1/2024	H5N1	-	1,9	0,2
	A/laying_hen/Italy/24VIR10206-4/2024	H5N1	-	1,8	0,4
	A/Larus_michaellis/Spain/4508-12_24VIR10678-47/2024	H5N1	-	2,1	0,5
	A/lesser_black-backed_gull/Portugal/PAT-24-15965_24VIR7559-4/2024	H5N1	Q136H	6,5	5,2
	A/red-fox/Italy/25VIR819-1/2024	H5N1	-	2,2	0,4
	A/mallard_duck/Italy/24VIR10241-1/2024	H5N1	-		
	A/mute-swan/Slovenia/PER1992TA-24_25VIR818-5/2024	H5N1	V149I	1,7	0,4
	A/mute-swan/Slovenia/PER2235MA-24_25VIR818-12/2024	H5N1	**S110F**	1,9	0,6
North America	A/COHA/Canada/108-1/2024	H5N1	-	3,6	0,4
	A/Chicken/BC/FAV-0284-001/2024	H5N1	**H275Y**	726,6	1,0
	A/Cackling_Goose/BC/OTH-0108-41/2024	H5N1	-	3,1	0,9
	A/GBBG/NL/OTH105-6/2024***	H5N5	-	1,2	1,2
	A/NOFU/Canada/FAV290/2024***	H5N5	-	0,9	1,9
Africa	A/avian/Guinea/F1B1P_24VIR4686-15/2024***	H5N1	-	2,2	0,5
	A/duck/Burkina_Faso/BKF11_24VIR3019-11/2024***	H5N1	-	2,6	0,6
	A/chicken/Nigeria/164A_22VIR3286-69/2022***	H5N1	S247N	12,8	2,2
	A/avian/Nigeria/711_22VIR3286-17/2021***	H5N1	V149F	1,3	0,9
Control Virus	A/California/4/2009	H1N1	-	1,0	0,9

Gs/Gd H5 2.3.2.1a subsampled phylogenetic tree
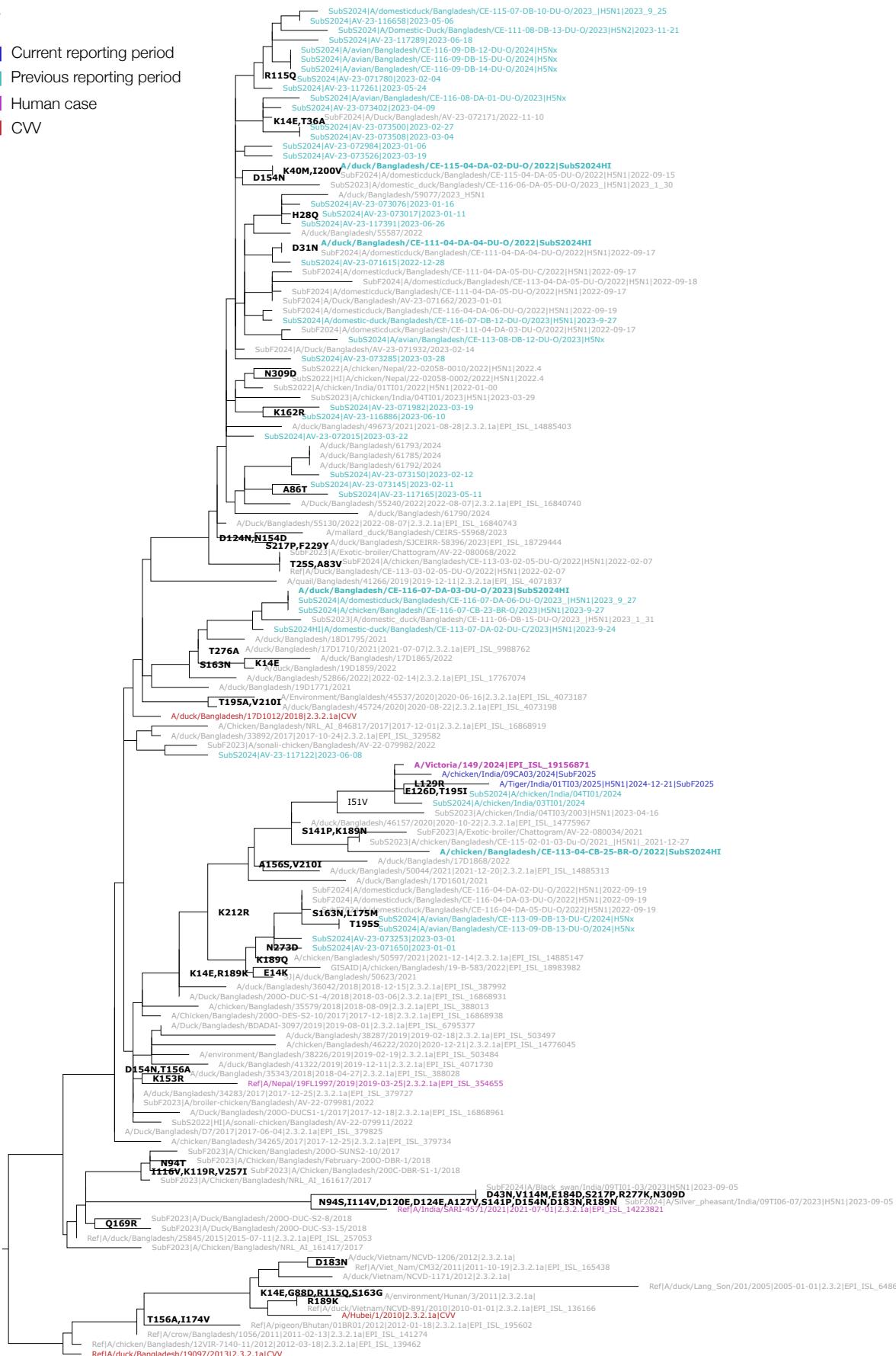
Figure 7. Gs/Gd lineage clade 2.3.2.1a phylogenetic tree, with amino acid changes along the branches. The tree was downsized using PARNAS. Sequences submitted to OFFLU since September 2024 are retained, along with all CVVs and strains which have been antigenically characterised. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink.

Gs/Gd H5 2.3.2.1a amino acid difference table

Table 5. Avian H5 2.3.2.1a clade sequence comparison to the within clade CWs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CWs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.

Column key (left → right):

- C1 = A/duck/Bangladesh/17D1012/2018 | CW
- C2 = A/duck/Bangladesh/19097/2013 | CW
- C3 = A/Victoria/149/2024 | Human
- C4 = SubF2025 | A/chicken/India/09CA03/2024 (India)
- C5 = SubF2025 | A/Tiger/India/01TI03/2025 (India)
- C6 = SubS2024 | A/chicken/India/03TI01/2024 (India)
- C7 = SubS2024 | A/chicken/India/04TI01/2024 (India)
- C8 = SubS2023 | A/chicken/India/04TI03/2003 | H5N1 | 2023-04-16 (India)
- C9 = **SubS2024HI | A/chicken/Bangladesh/CE-113-04-CB-25-BR-O/2022** (Bangladesh)
- C10 = **SubS2024HI | A/duck/Bangladesh/CE-116-07-DA-03-DU-O/2023** (Bangladesh)
- C11 = **SubS2024HI | A/domesticduck/Bangladesh/CE-115-07-DB-10-DU-O/2023** (Bangladesh)
- C12 = **SubS2024HI | A/domestic-duck/Bangladesh/CE-113-07-DA-02-DU-C/2023** (Bangladesh)
- C13 = SubS2024 | A/Domestic-Duck/Bangladesh/CE-111-08-DB-13-DU-O/2023 (Bangladesh)
- C14 = SubS2024 | A/avian/Bangladesh/CE-113-09-DB-12-DU-O/2024 (Bangladesh)
- C15 = SubS2024 | A/avian/Bangladesh/CE-116-08-DA-01-DU-O/2023 (Bangladesh)

site	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	Antigenic site
1	D								A							
2	H								S							
3	I								F							
11	N								X							
12	S								X							
13	T								P							
14	K			E	E	E	E	E						E	E	
34	E								X							
36	T				K				K						A	
51	I			V	V	V	V	V								
71	I								T							
88	G								D							
115	R										Q		Q			
123	S								P							
124	D												N	N	N	
126	E			D	D	D	D	D								Antigenic site A
129	L					R		R				M				Antigenic site A
137	Y														H	
140	N								K							Antigenic site A
141	S			P	P	P	P	P	P							Antigenic site A
154	N	D									D		D		D	Antigenic site B
156	A	T		S	S	S	S	S	S							Antigenic site B
163	S										N		N		N	Antigenic site D
175	L												M			
185	A						T									Antigenic site B
189	R			N	N	N	N	N	N					Q		Antigenic site B
195	T			I	I	I	I	I						S		Antigenic site B
210	V			I	I	I	I	I	I							Antigenic site D
212	K			R	R	R	R	R	R					R		
226	I					V										
273	N						H							D		Antigenic site C
276	T										A		A			
285	I													V		
Aadiffs from CW		2	9	10	11	11	10	11	13	2	3	3	4	7	5	
Putative antigenic sites		2	6	6	7	8	7	5	4	1	1	2	1	4	1	

Gs/Gd H5 2.3.2.1e‡ subsampled phylogenetic tree
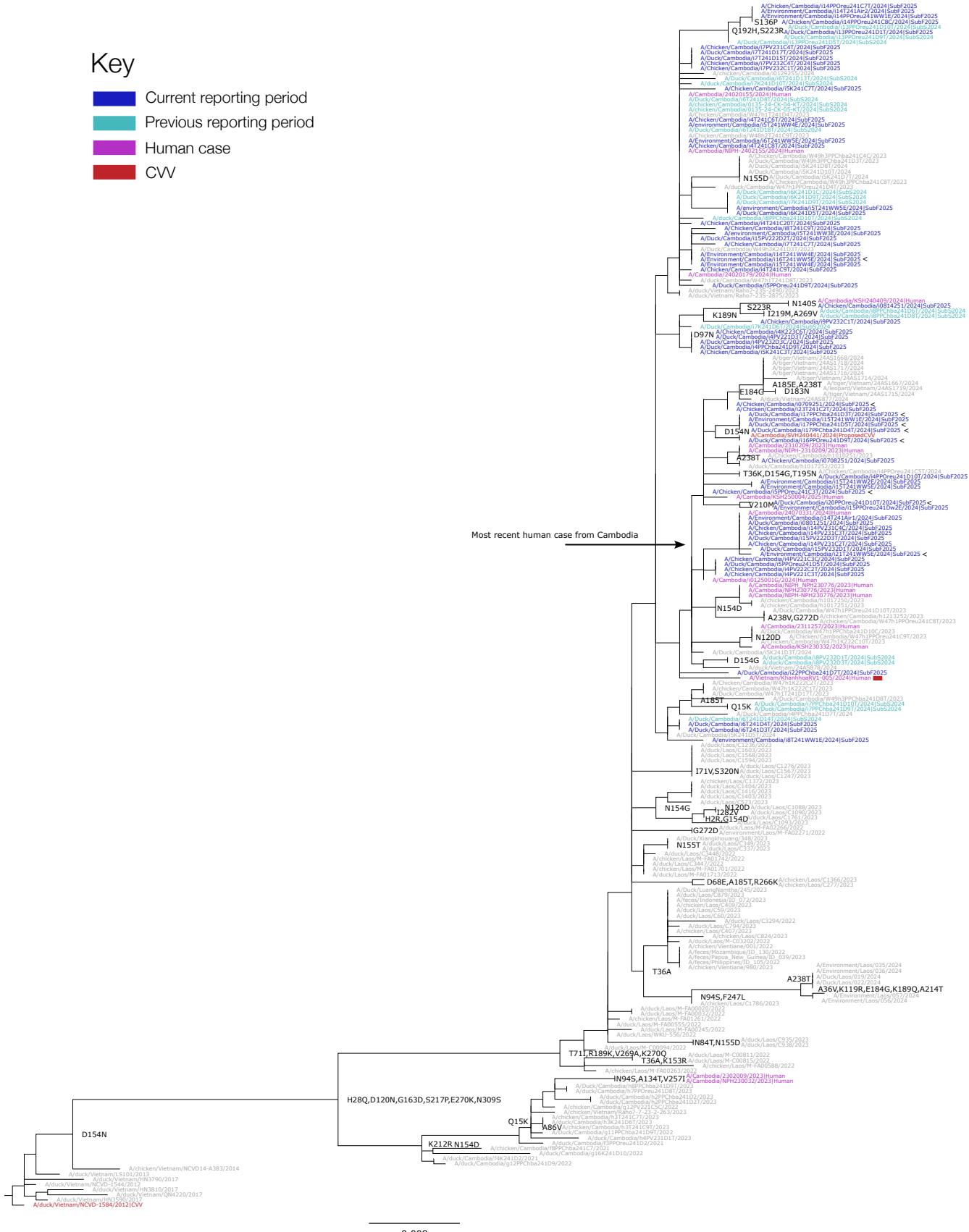
Figure 8. H5 clade 2.3.2.1e‡ (formerly classified as clade 2.3.2.1c) subsampled phylogenetic tree. The tree was downsized using PARNAS. Sequences submitted to OFFLU since September 2024 are retained, along with all CVVs and strains which have been antigenically characterised. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink. Red box indicates possible Vietnam virus replacement for proposed Cambodia virus CVV.

Gs/Gd H5 2.3.2.1e‡ amino acid difference table

Table 6. Avian H5 clade 2.3.2.1e‡ (formerly classified as clade 2.3.2.1c) sequence comparison to the within clade CVVs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.

Country groupings: **Cambodia** (A/Environment/Cambodia/i16T… through A/duck/Cambodia/i8PV232D1T/2024), **Vietnam** (A/leopard/Vietnam/24AS1719/2024 – A/tiger/Vietnam/24AS1714/2024), **Laos** (A/Environment/Laos/057/2024 – A/Duck/Laos/019/2024).

site	A/Cambodia/SVH240441/2024|ProposedCVV	A/duck/Vietnam/NCVD-1584/2012|CVV	A/Vietnam/KhanhhoaRV1-005/2024|Human	A/Cambodia/KSH250004/2025|Human	A/Environment/Cambodia/i16T241WW5E/2024|SubF202	A/Duck/Cambodia/i16PPOreu241D9T/2024|SubF2025	A/Duck/Cambodia/i17PPChba241D3T/2024|SubF2025	A/Duck/Cambodia/i17PPChba241D4T/2024|SubF2025	A/Duck/Cambodia/i17PPChba241D5T/2024|SubF2025	A/Duck/Cambodia/i20PPOreu241D10T/2024|SubF2025	A/Environment/Cambodia/i21T241WW5E/2024|SubF202	A/Duck/Cambodia/i22PPChba241D7T/2024|SubF2025	A/Chicken/Cambodia/i23T241C2T/2024|SubF2025	A/Duck/Cambodia/i13PPOreu241D10T/2024|SubS2024	A/Duck/Cambodia/i6K241D9T/2024|SubS2024	A/Duck/Cambodia/i7PPChba241D9T/2024|SubS2024	A/chicken/Cambodia/0135-24-CK-04-KT/2024|SubS2024	A/duck/Cambodia/i7K241D10T/2024|SubS2024	A/duck/Cambodia/i8PPChba241D10T/2024|SubS2024	A/duck/Cambodia/i8PV232D1T/2024|SubS2024	A/leopard/Vietnam/24AS1719/2024	A/tiger/Vietnam/24AS1667/2024	A/tiger/Vietnam/24AS1714/2024	A/Environment/Laos/057/2024	A/Duck/Laos/022/2024	A/Duck/Laos/019/2024	Antigenic site
15	Q												K														
28	Q	H																									
36	T																							V	V	V	
49	P										L																
50	L										Q																
71	I	T																									
94	N																							S	S	S	
119	K																							R	R	R	Antigenic site A
120	N	D																									Antigenic site A
133	A																					X					Antigenic site A
134	A																					X					Antigenic site A
136	S												P														Antigenic site A
154	N								D	D		D								G	D	D	D				Antigenic site B
156	A								T																		Antigenic site B
163	D	G																									
165	N																						H				
183	D																				N						Antigenic site B
184	E																		G		G	G	G	G	G	G	Antigenic site B
185	A														T			S			E	E	E				Antigenic site B
189	K	R																						Q	Q	Q	Antigenic site B
192	Q										H				H												
195	T	S																									Antigenic site B
198	I																							V			Antigenic site B
210	V									M																	Antigenic site D
214	A																							T	T	T	Antigenic site D
217	P	S																									
223	S												R														Antigenic site D
238	A																				T	T	T		T	T	
247	F																							L	L	L	
269	A	V																									
270	Q	E																									
309	S	N																									
Aadiffs from CVV	10	1	2	0	0	0	0	0	2	2	3	1	3	0	2	0	0	1	1	1	5	6	5	8	8	8	
Putative antigenic sites	3	1	2	0	0	0	0	0	2	2	0	1	2	0	1	0	0	1	1	1	4	4	3	5	4	4	

Gs/Gd H5 2.3.2.1g‡ subsampled phylogenetic tree
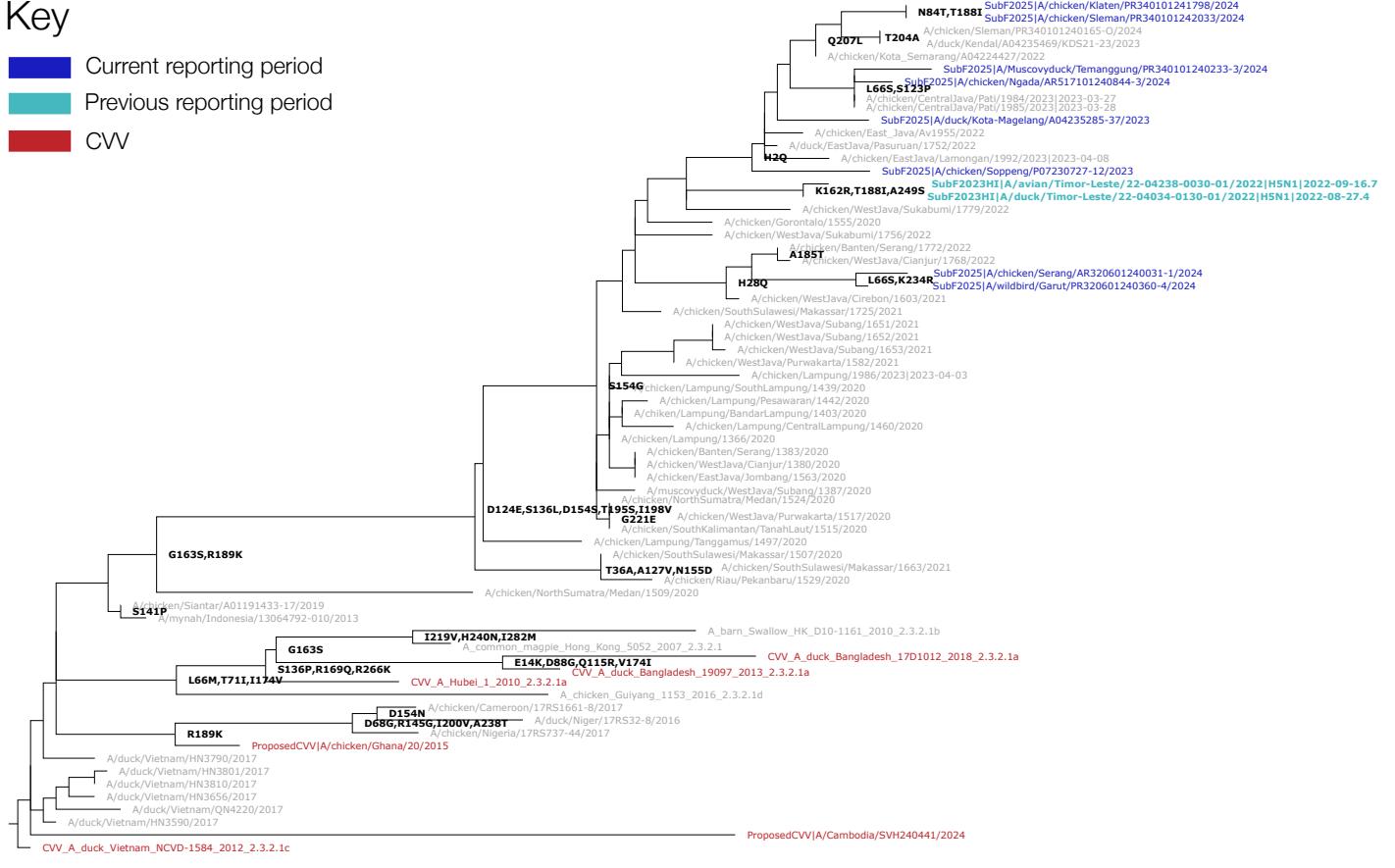
Figure 9. Gs/Gd lineage clade 2.3.2.1g‡ (formerly classified as clade 2.3.2.1c) subsampled phylogenetic tree. The tree was downsized using PARNAS. Sequences submitted to OFFLU since September 2024 are retained, along with all CVVs and strains which have been antigenically characterised. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red.

LPAI H5 subsampled phylogenetic tree: Eurasian lineage

Key

■ Current reporting period
■ Previous reporting period
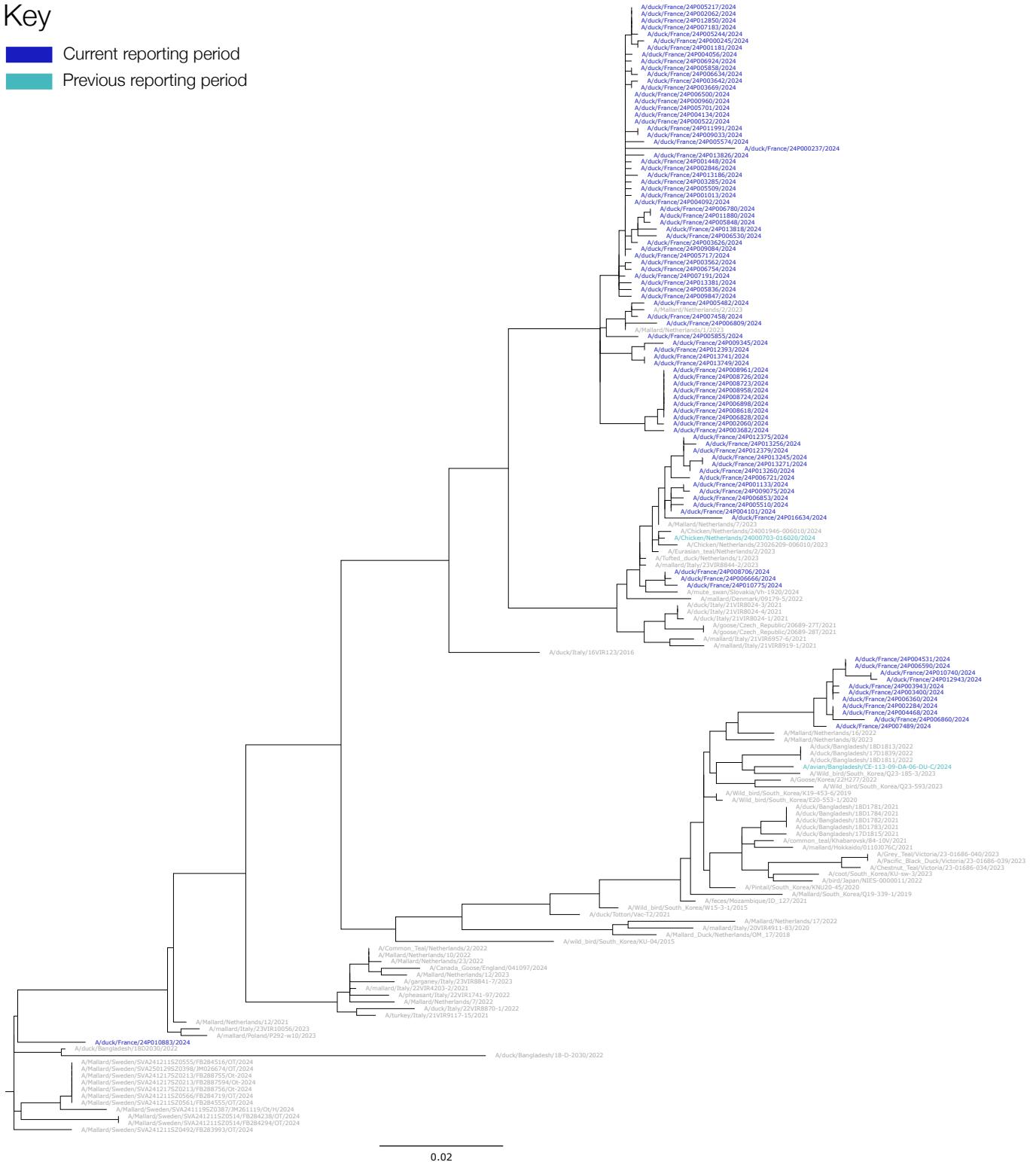
Figure 10. LPAI H5 phylogenetic tree: Eurasian lineage. Sequences were downloaded from GISAID and collected through OFFLU. Sequences are coloured according to collection date. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period.

LPAI H5 subsampled phylogenetic tree: American lineage

Key

- ■ Current reporting period
- ■ Previous reporting period
- ■ Human case
- ■ CVV
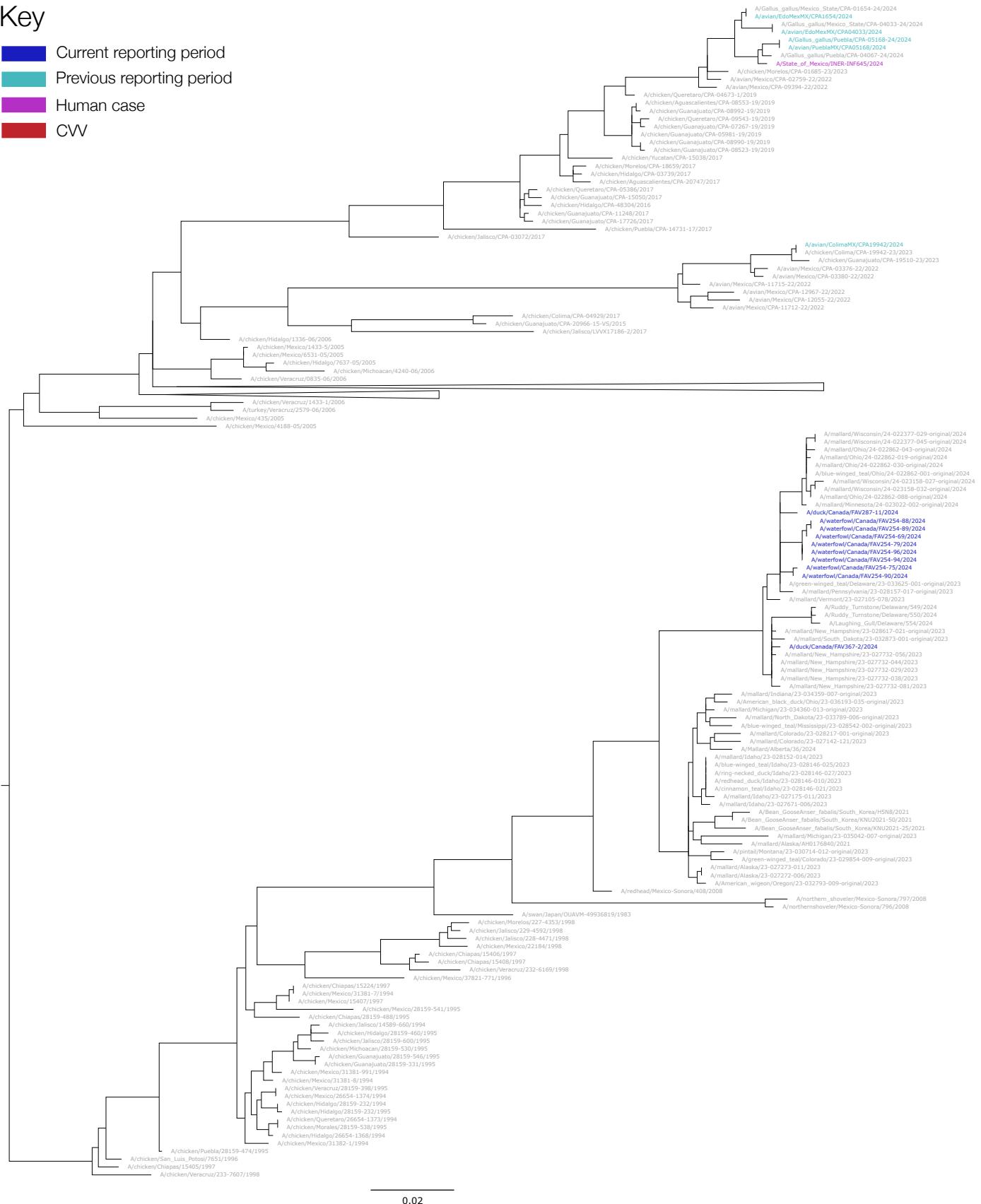
Figure 11. LPAI H5 phylogenetic tree: American lineage. Sequences were downloaded from GISAID and collected through OFFLU. Sequences are coloured according to collection date. Sequences from humans are pink. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, and human cases are marked in pink.

H7 Influenza A viruses

H7 subsampled phylogenetic tree
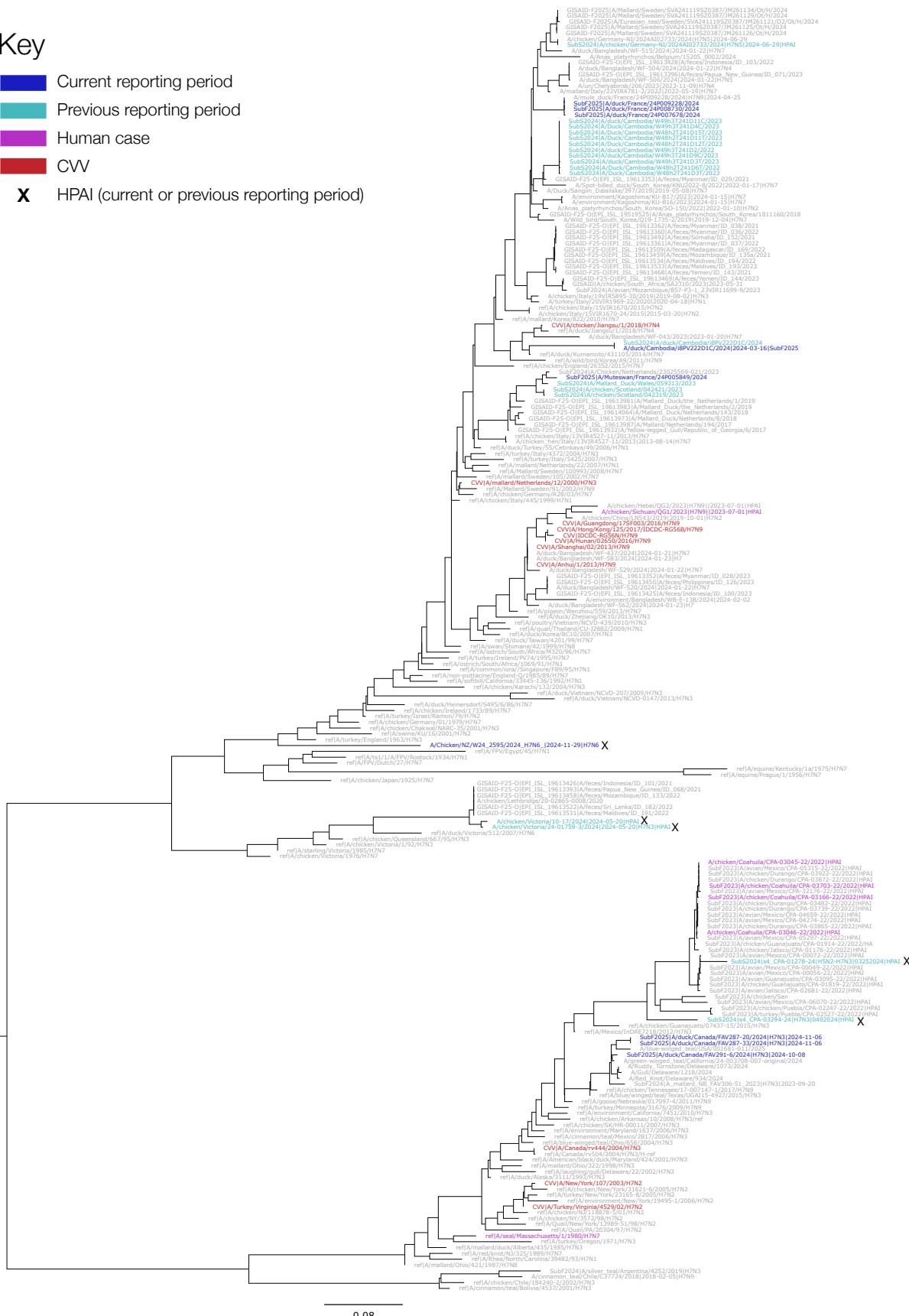
Figure 12. H7 subsampled phylogenetic tree. The tree was downsized using PARNAS. Sequences submitted to OFFLU since September 2024 are retained, along with all CVVs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, CVVs are indicated in red, and human cases are marked in pink.

H7 amino acid difference tables

Table 7. Avian H7 clade sequence comparison to the within clade CVVs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, and CVVs are indicated in red. Changes in putative antigenic sites are highlighted grey.

New Zealand / France table

Column headers (left to right):
- CVV|A/mallard/Netherlands/12/2000/H7N3
- CVV|A/chicken/Jiangsu/1/2018/H7N4
- SubF2025|A/duck/France/24P007678/2024
- SubF2025|A/duck/France/24P008730/2024
- SubF2025|A/duck/France/24P009228/2024
- SubF2025|A/Muteswan/France/24P005849/2024
- GISAID-F2025|A/Chicken/NZ/W24_2595/2024
- GISAID-F2025|A/Mallard/Sweden/SVA241119SZ0387/JM261134/0t/H/2024
- GISAID-F2025|A/Eurasian_teal/Sweden/SVA241119SZ0387/JM261121/D2/0t/H/202
- GISAID-F2025|A/Mallard/Sweden/SVA241119SZ0387/JM261125/0t/H/2024
- GISAID-F2025|A/Mallard/Sweden/SVA241119SZ0387/JM261126/0t/H/2024
- GISAID-F2025|A/Mallard/Sweden/SVA241119SZ0387/JM261129/0t/H/2024
- SubF2024|A/chicken/Victoria/10-17/2024/2024-05-20
- SubF2024|A/chicken/Victoria/24-01759-5/2024
- SubF2024|A/chicken/Germany-NI/2024A02733/2024
- SubF2024|A/Chicken/Netherlands/23025569-021/2023
- SubS2024|A/Mallard_Duck/Wales/059313/2023
- SubS2024|A/chicken/Scotland/042421/2023
- SubS2024|A/chicken/Scotland/042319/2023
- SubS2024|A/Duck/Cambodia/W49h3T241D4C/2023
- SubS2024|A/Duck/Cambodia/W48h2T241D15T/2023
- Antigenic Sites

site	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	Antigenic Sites
5	L												I	I								
10	V						I															
11	S						P															
15	K							R	R	R	R	R										
16	V							I	I			I										
22	R						K															
23	G						E															
35	R												Q	Q								
36	T												M	M								
38	V						T						I	I								
43	S												T	T								Antigenic site C
48	T			I									A	A								
49	V												I	I								
59	T												I	I								
60	I												V	V								
61	T						I															
68	Q						R										R			R	R	
73	S												A	A								
82	E						X															Antigenic site E
84	S	N	N	N		N							D	D								
95	E	D																				
101	I				V																	
109	D												N	N								
113	M												T	T								
125	A												V	V								RBD
127	S							N	N	N	N	N					N					
130	R						Q															Antigenic site A
138	A				V																	
145	L				V																	
147	N				T																	
148	T				S																	
152	A				V											V	V	V	V			
155	Q				S																	
161	K				R																	
163	T												I	I								Antigenic site D
165	K	R											N	N								
166	D												K	K								
170	I			V												V	V	V	V			
171	I	V		V	V								V	V		V	V	V	V			
178	G				A																	
181	T	A											A	A								
191	N	S			S												S	S	S	S		
200	N	K										R				S						
210	G										R											
214	Q					L																
219	S					P																
225	H	Q					Q															
228	I		M	M	M	M		M	M	M	M	M				M	M	M	M	M	M	
230	N	D			D			D	S	S	S	S	S									
238	S	T																				
247	D															N						
249	A												V	V								
252	L				M								F	F								
253	R				K								Q	Q								
257	M												I	I								
259	I			V												V	V	V	V			
262	G			E	D											E	E	E	E			
264	Q												P	P								
265	V		I	I	I																	
267	A												V	V								Antigenic site C
268	N			D	S	S		S	S	S		S								S	S	
272	D												E	E								
274	Y												H	H								
276	S	N	N	N	N		N	N	N	N	N				K	N	N	N	N			
281	I												A	A								
291	S	X																				
293	A						T	T	T	T	T				T				T	T		
296	K			R									R	R								
302	K				R																	
304	E	K											K	K						G	G	
307	L	M	M	M	M		M	M	M	M		M				M	M	M	M	M	M	
318	I	L					G															

| Aadiffs from CVV | 11 | 7 | 5 | 5 | 13 | 26 | 9 | 11 | 8 | 8 | 9 | 28 | 29 | 9 | 11 | 9 | 9 | 9 | 9 | 7 | 7 |
| Putative antigenic sites | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Canada table

Column headers (left to right):
- CVV|A/Canada/rv444/2004/H7N3
- SubF2025|A/duck/Canada/FAV287-20/2024|H7N3|2024-11-06_HA
- SubF2025|A/duck/Canada/FAV287-33/2024|H7N3|2024-11-06_HA
- SubF2025|A/duck/Canada/FAV291-6/2024|H7N3|2024-10-08_HA
- SubS2024_s4_CPA-01278-24|H5N2-H7N3|03252024|HPAI
- SubS2024_s4_CPA-03294-24|H7N3|04202024|HPAI
- Antigenic Sites

site	CVV	FAV287-20	FAV287-33	FAV291-6	CPA-01278	CPA-03294	Antigenic Sites
22	R					K	
36	V	A	A	A	A	A	
38	I				T	T	
39	K					E	
43	T				A		Antigenic site C
44	Q					R	
45	G				R	R	
47	R				K	K	Antigenic site E
48	P					S	
49	T	I	I		I	I	
61	I				V	V	
71	E					K	
73	D	G	G		E	K	
74	A					G	
75	N	D	D	D	D	D	Antigenic site E
82	E				L		Antigenic site E
86	V				L	L	
91	K	R	R				
104	G				K	K	
108	I	V	V	V			
112	S					P	
114	G				S	D	
118	S				N	D	Antigenic site B
125	A				T	T	RBD
126	T				S	S	
127	S				N		
130	R				K	K	Antigenic site A
132	S				I	L	
133	G				K	N	
134	X					S	
135	X					P	
139	A				T		
147	N				T		
149	D					E	Antigenic site B
151	A				V	E	Antigenic site B
152	A				T	T	
155	Q				N	N	
157	T				N		
158	K				L	R	
161	R				T		
164	R				K		
165	N	S	S	S			
181	T	A	A	A			
191	N	D	D		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	I	I	I	
262	D	G	G				
267	S				L		Antigenic site C
268	G	S	S	S	D		
270	E	K	K	K			
276	S	N	N	N	N	N	
304	T				K		
318	N				S		

| Aadiffs from CVV | 14 | 14 | 9 | 42 | 41 |
| Putative antigenic sites | 0 | 0 | 0 | 7 | 7 |

H9 Influenza A viruses

H9 phylogenetic tree

Figure 13. H9 subsampled phylogenetic tree providing overview of clade diversity. Analyses were conducted with reference sequences and data downloaded from GISAID, Genbank and kindly shared through the OFFLU network. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink. H9 sequence clades were assigned using the A/H9 influenza virus lineage and clade assignment tool (https://nmdc.cn/influvar/tools/H9aiv) (Fusaro et al., 2024).

H9 G1 (G5.5, G5.6, G5.7) subsampled phylogenetic tree

Key

- ■ Current reporting period
- ■ Previous reporting period
- ■ Human case
- ■ CVV
- ■ Geographical outlier
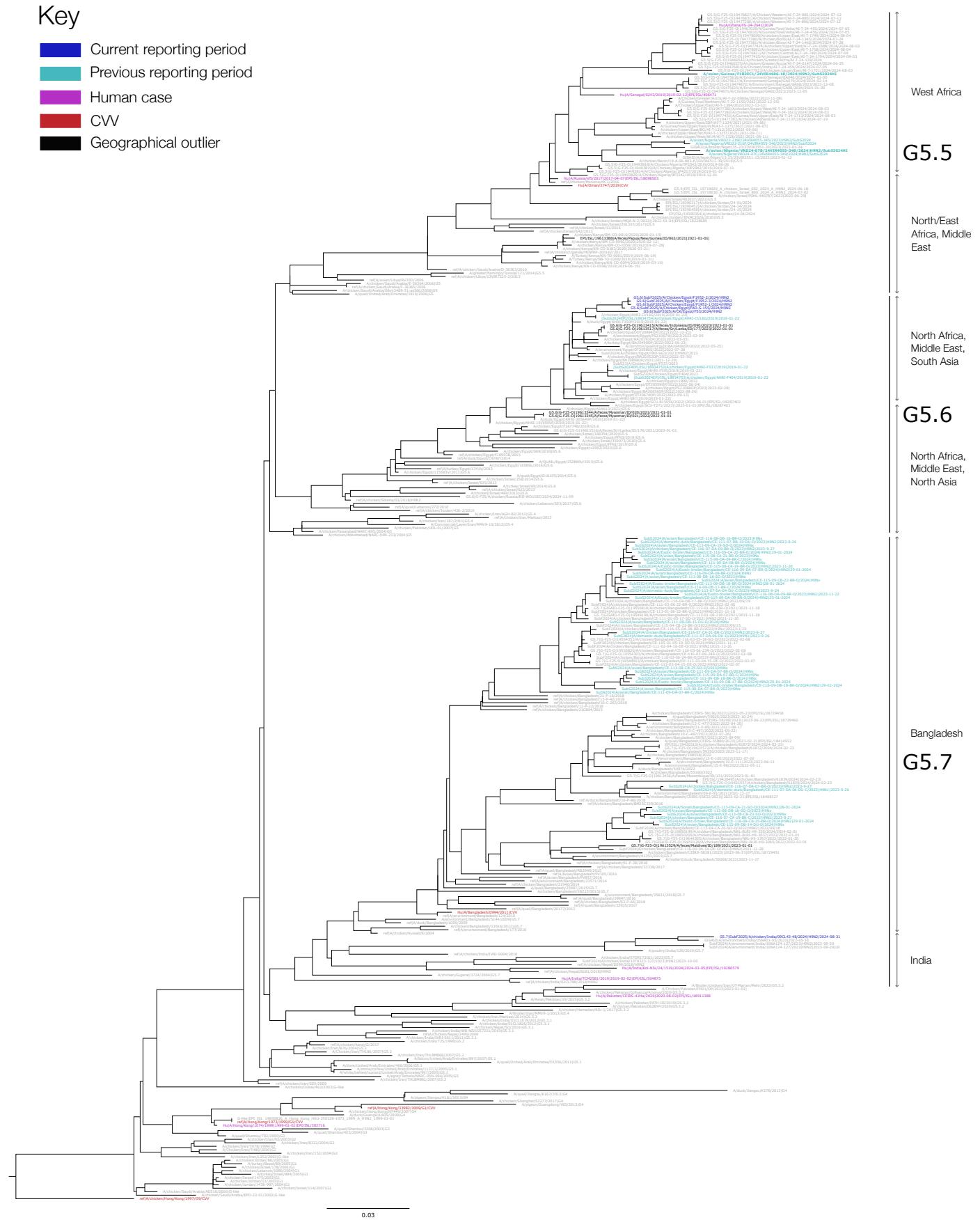
Figure 14. H9 G1 lineage subsampled phylogenetic tree. Analyses were conducted with reference sequences and data downloaded from GISAID, Genbank and kindly shared through the OFFLU network. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink. H9 sequence clades were assigned using the A/H9 influenza virus lineage and clade assignment tool (https://nmdc.cn/influvar/tools/H9aiv) (Fusaro et al., 2024).

H9 G1 amino acid difference tables

Table 8. Avian H9 G1-like sequence comparison to the within clade CVVs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVVs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.

Egypt

India

Column strains (left to right):

- A/Oman/2747/2019 | CVV
- A/Bangladesh/0994/2011 | CVV
- A/Chicken/Hong Kong/1997/G9 | CVV
- Hu| A/Ghan A/FS-24-2641/2024
- SubS2024HI| A/avian/Guine A/F182EC1/24VIR.4686-18/2024|H9N2
- SubS2024HI| A/avian/Niger| A/VRD24-078/24VIR.4055-348/2024|H9
- SubF2025| A/CK/Egypt/F53/2024/H9N2
- SubF2025| A/Chicken/Egypt/F1952-1/2024/H9N2
- SubF2025| A/Chicken/Egypt/F1952-2/2024/H9N2
- SubF2025| A/Chicken/Egypt/F1952-3/2024/H9N2
- SubF2025| A/Chicken/Egypt/FAO-S-155/2024/H9N2
- SubF2024| A/chicken/Egypt/FAO-SG3/2023|H9N2| 2023
- SubS2023| A/Chicken/Egypt/F404/2023
- SubS2023| A/Chicken/Egypt/F537/2023
- SubF2024| A/chicken/Indi A/10TR323-327/2023|H9N2|2023.10-00
- A/feces/Myanmar/ID/020/2021/2021-01-01
- A/feces/Myanmar/ID/021/2022/2022-01-01
- A/feces/Papu A/New/Guine A/ID/063/2021|2021-01-01|
- A/feces/Indonesi A/ID/090/2023/2023-01-01
- A/feces/Sri/Lank A/ID/176/2021/2022-01-01
- A/feces/Sri/Lank A/ID/177/2023
- SubF2025| A/Chicken/Indi A/09CL43-48/2024/H9N2
- A/chicken/Bangladesh/61839/2024
- A/chicken/Bangladesh/NRL-BLRI-H9-330/2024
- A/chicken/Bangladesh/NRL-H9-1767/2022/2022-01-20

site	ref	Antigenic site
1	D	
5	I	
7	H	
17	D	
22	T	
23	N	
28	Q	
30	K	
36	E	Antigenic site C
40	M	Antigenic site C
43	A	Antigenic site C
45	N	
48	R	
53	D	
54	T	
56	T	
57	I	
60	L	
69	M	
72	G	
74	R	
75	E	
77	S	
89	T	
95	V	
102	R	
103	T	Antigenic site E
104	L	
108	S	
109	S	
112	Q	
114	V	
115	Q	Antigenic site A
116	L	Antigenic site A
120	S	
125	T	Antigenic site A
127	T	Antigenic site A
132	T	Antigenic site A
135	D	Antigenic site A
140	N	Antigenic site A
148	N	Antigenic site B
149	G	Antigenic site B
150	G	Antigenic site B
152	P	
153	I	Antigenic site B
156	A	
158	Y	Antigenic site A
159	T	
161	N	Antigenic site D
162	R	Antigenic site D
163	G	Antigenic site D
164	K	
165	D	
169	V	
173	H	
176	P	Antigenic site B
177	T	Antigenic site B
179	T	Antigenic site B
180	A	Antigenic site B
187	X	Antigenic site B
188	T	Antigenic site B
194	V	
195	T	
198	T	
199	L	
200	D	
204	K	Antigenic site D
206	L	
216	L	Antigenic site D
217	I	Antigenic site D
221	N	
226	V	
228	K	
242	I	
246	F	
249	V	
260	R	
262	D	
264	S	Antigenic site C
265	S	
267	N	Antigenic site C
269	V	Antigenic site C
276	K	
281	S	
283	M	
285	F	
288	I	
295	T	
300	I	
309	I	
315	H	
316	A	
317	R	
318	S	
319	S	

	Aadiffs from CVV	Putative antigenic sites
A/Ghan A/FS-24-2641/2024	22	7
SubS2024HI Guine	42	12
SubS2024HI Niger	9	4
A/CK/Egypt/F53	12	7
F1952-1	10	4
F1952-2	21	9
F1952-3	23	9
FAO-S-155	23	9
FAO-SG3	23	9
F404	24	9
F537	24	9
Indi 10TR323	27	12
Myanmar 020	26	12
Myanmar 021	25	10
Papu New Guine	26	11
Indonesi 090	26	11
Sri Lank 176	12	2
Sri Lank 177	24	10
Indi 09CL43-48	26	9
Bangladesh 61839	24	10
NRL-BLRI-H9-330	32	11
NRL-H9-1767	26	8
	32	13
	34	14

H9 Y280 (B4.5, B4.6, B4.7) subsampled phylogenetic tree

Key

- **Current reporting period** (dark blue)
- **Previous reporting period** (teal)
- **Human case** (magenta)
- **CVV** (red)

South Asia

B4.7

China,
South Asia

B4.6
Republic of
Korea

B4.5
South Asia

0.02

Figure 15. H9 Y280 lineage maximum likelihood phylogenetic tree. Analyses were conducted with reference sequences and data downloaded from GISAID, Genbank and kindly shared through the OFFLU network. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CWs are indicated in red, and human cases are marked in pink. H9 sequence clades were assigned using the A/H9 influenza virus lineage and clade assignment tool (https://nmdc.cn/influvar/tools/H9aiv) (Fusaro et al., 2024).

H9 Y280 amino acid difference tables

Table 9. Avian H9 Y280-like sequence comparison to the within clade CVs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CVs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.

Indonesia / Cambodia

Column strains:
- A/Anhui-Lujiang/39/2018 | CW
- A/Anhui-Tianjiaan/11086/2022 | CW
- Hu | A/HCM/VP16/2024 | 2024-03-21 | Vietnam | EPI_ISL_19290539
- Hu | A/Hong_Kong/VN24002346/2024 | 2024-02-16 | EPI_ISL_18926219
- Hu | A/Yaan/001/2023 | 2023-11-14 | EPI_ISL_18853922
- SubF2025 | A/Chicken/Humbahas/AR1275023/2024 | 2024-02-01
- SubF2025 | A/Chicken/Mimika/AR94/7101240051-24-28/2024 | 2024-05-20
- SubF2025 | A/Chicken/Polewali Mandar/A07230266-147/2023 | 2023-10-16
- SubF2025 | A/enw/Bandung/A1223178-1/2023 | 2023-01-13
- SubF2025 | A/Chicken/Cambodia/16K223C10T/2024/2024-09-05
- SubF2025 | A/Chicken/Cambodia/16K223C1T/2024/2024-09-05
- SubF2025 | A/Chicken/Cambodia/16K223C4T/2024/2024-09-05
- SubF2025 | A_Chicken_Cambodia_16K223C6T_2024_2024-09-05
- SubF2025 | A/Chicken/Cambodia/16K223C7T/2024/2024-09-05
- SubF2025 | A/Chicken/Cambodia/17K223C1T/2024/2024-09-23
- SubF2025 | A/Chicken/Cambodia/17PPOreu241C7T/2024/2024-09-22
- SubF2025 | A/Chicken/Cambodia/18K223C1T/2024/2024-10-03
- SubF2025 | A/Chicken/Cambodia/18PPOreu241C5T/2024/2024-09-27
- SubF2025 | A/Chicken/Cambodia/19PPOreu241C5T/2024/2024-10-10/19528868
- SubF2025 | A/Duck/Cambodia/119T241D2C/2024/2024-10-10

site																							Antigenic Sites
2	K			R																			
32	L		M		M																		
33	L								I														
34	H			Q	Q		Q																Antigenic site C
36	E														G					G	G		Antigenic site C
48	Q			H	H	H	H																
51	I	V		V												E		V					
53	D	E		E													E						
57	V	I	I	I	I		I	I	I	I	I	I	I	I	I	I	I	I	I				
60	L						I						V					V	V				
68	D	E													G								
69	L	P	P	P	P	P	P	S	P	P	P	P	P	P	P	P	P	P	P	P	P		
70	S	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	M	L	L			
71	L	P	P		P					P	P	P	P	P	P	P	P	P	P	P			
72	E		D						G	D	D	D	D	D	D	D	D		D	D			
73	G	E	E	E	E		E			E	E	E	E	E	E	E	E	E	E	E			
74	R	K			K														K				
79	I	V			V		V											V					
86	V		I	A						T	T	T	T	T	I	I	I	T		I	I		
87	N		D			D				D	D	D	D	D				D					
94	N			S																			
98	L				I																		
104	L		V															R					
109	R		K																				
112	Q	R		R	R													R					
114	I			V	T																		
115	Q			L	L	L	L																Antigenic site A
121	I																			V			
125	S		T																				Antigenic site A
127	D		N		S	S	S	S									N						Antigenic site A
131	T	N	N	N	N	K	K	K	K	N	N	N	N	N	N	N	K	N	N	N			Antigenic site A
132	A	T	T	T	T					T	T	T	T	T		T	T	T					Antigenic site A
135	D	G	G	G	S					G	G	G	G	G	G	G	G	G	G	G			Antigenic site A
140	S	N	N	N	N					N	N	N	N	N	N	N	N	N	N	N			Antigenic site A
145	T	N		Y	N													N					Antigenic site B
146	R		Q		Q	Q	Q	Q						Q				Q	Q				Antigenic site B
148	D	N		N	N	N	N										N						Antigenic site B
149	G	N		N	N	N	N	N						S			N	S	S				Antigenic site B
150	N			A	A	A	A																Antigenic site B
153	T	I		I	I	I	I										I						Antigenic site B
162	Q						H																Antigenic site D
163	G			E	E	E																	Antigenic site D
165	N	S		S	S												S						
174	H		N							N	N	N	N	N	N	N	N		N	N			Antigenic site B
177	T			S																			Antigenic site B
178	D	E		E	E												E						Antigenic site B
179	D				T	T	T	T															Antigenic site B
180	T	V	V		V	V	A	A	V	V	V	V	V	V			V	V					Antigenic site B
182	R				T	T	T	T															Antigenic site B
183	N	T			T													T					Antigenic site B
187	R		K																				Antigenic site B
190	T																S						
199	I		M	M					M	M	M	M	M	M	M	M		M	M				
202	I		V		T	T	T	T															
214	N		S														H						
221	N															S							
228	K													R				R	R				
238	D				N	N	N																
242	I		V						V	V	V	V	V	V		V		V	V				
246	Y			H																			
248	H	Y	Y	Y	Y					Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y			
249	I																V						
251	S		L							L	L	L	L	L	L	L	L		L	L			
260	K	R	R	R	R					R	R	R	R	R	R	R	R	R	R	R			
264	K		T																				Antigenic site C
265	R		K					T								K			K	K			
267	S				D																		Antigenic site C
281	T					A																	
300	I			V													V						
302	I		V		L	M									V			V	V				
303	K																R						
Aadiffs from CW		25	19	32	26	24	23	19	22	19	19	19	19	19	23	18	21	29	23	24			
Putative antigenic sites		11	6	14	11	14	13	12	12	6	6	6	6	6	7	5	7	11	7	7			

H10 Influenza A viruses

H10 subsampled phylogenetic tree

Figure 16. H10 maximum likelihood phylogenetic tree. Analyses were conducted with reference sequences and data downloaded from GISAID, Genbank and kindly shared through the OFFLU network. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, and human cases are marked in pink.

H10 amino acid difference table

Table 10. Avian H10 sequence comparison to the within clade CWs. Dark blue indicates sequences from the current reporting period, light blue represents the previous reporting period, bold labels highlight antigenically characterized strains for these reporting periods, CWs are indicated in red, and human cases are marked in pink. Changes in putative antigenic sites are highlighted grey.

Column groups: **China** — A/Unknown/Zhejiang/ZJU01/2023|Human, A/Yunnan/0110/2024|Human, A/Zhejiang/CNIC-ZJU01/2023|Human. **Cambodia** — A/Duck/Cambodia/7T241D16T/2024|SubF2025, A/Duck/Cambodia/7T241D4T/2024|SubF2025, A/Duck/Cambodia/7T241D8T/2024|SubF2025, A/Chicken/Cambodia/h5PPOreu241C2T/2023|SubS2024, A/Duck/Cambodia/h7T241D7T/2023|SubS2024, A/Duck/Cambodia/6T241D7T/2024|SubS2024.

site	A/Jiangsu/428/2021|CW	A/Unknown/Zhejiang/ZJU01/2023|Human	A/Yunnan/0110/2024|Human	A/Zhejiang/CNIC-ZJU01/2023|Human	A/Duck/Cambodia/7T241D16T/2024|SubF2025	A/Duck/Cambodia/7T241D4T/2024|SubF2025	A/Duck/Cambodia/7T241D8T/2024|SubF2025	A/Chicken/Cambodia/h5PPOreu241C2T/2023|SubS2024	A/Duck/Cambodia/h7T241D7T/2023|SubS2024	A/Duck/Cambodia/6T241D7T/2024|SubS2024	A/Chicken/Netherlands/24010003-006010/2024|SubS2024	A/duck/Bangladesh/17-D-2268/2023	A/Mallard/Sweden/SVA241211SZ05514/FB284289/OT/2024	A/mallard/USA/001569-001/2025	A/mallard/Michigan/24-023416-025-original/2024	A/northern_shoveler/Mississippi/24-004130-008-original/2024	A/green-winged_teal/Idaho/24-022469-005-original/2024	A/Ruddy_Turnstone/Delaware/116/2024	A/Mallard/Alberta/99/2024
12	A	S			S	S	S	S	S	S	S				S	S	S	S	S
22	S	N	N	N	N	N	N	N	N	N	N		N	N	N	N	N	N	N
23	E												X						
24	Q	K		K	K	K	K	K	K	K					K	K	K	K	K
36	S			I															
37	K											T	T	T					
38	G	S		S	S	S	S	S	S	S		S	S	S	S	S	S	S	S
40	N	D		D	D	D	D	D	D	D					D	D	D	D	D
41	K											R	R	R					
44	M				L	L	L			L									
46	G														S	S	S	S	S
48	N																	K	
49	H	Y		Y	Y	Y	Y	Y	Y	Y					Y	Y	Y	Y	Y
54	N											S	S	S					
60	M							V	V										
61	L	I		I	I	I	I	I	I	I					I	I	I	I	I
64	T				A														
73	G												X						
74	T												I				K		
77	T							I	I										
82	E														D	D	D	D	D
84	A	S		S	S	S	S	S	S	S					S	S	S	S	S
85	I		T		V	V	V			V			T						
92	A							T	T		V								
94	I	V		V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
109	I									V								V	
110	S	D		D	D	D	D	D	D	D					D	D	D	D	M
112	I											R							
113	S															T			
115	G												D						
129	K	R		R				R	R		R							R	
130	A																		S
132	M																R		
136	E	G		G	G	G	G	G	G	G		R	G	G	G	G	G	G	G
143	L		F																
150	N	S		S	S	S	S	S	S	S	T	T	T	S	S	S	S	S	S
163	R														K				
167	T	S		S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
168	A		D								V		V						
172	I	V		V	V	V	V	V	V	V									
173	M	I		I	I	I	I	I	I	I					I	I	I	I	I
176	I																	V	
182	T										A	A	A						
204	Y	Q	H	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
205	S	N		N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
206	N		S									S							
216	R	Q		Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
220	Q		L																
222	S	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
223	X	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
230	L	V		V	M	M	M	V	V	M					M	M	I	M	M
231	V							I	I										
232	Q	K		K				K	K						R	R	R	R	R
243	G												X						
249	S		N																
255	I	K		K	K	K	K	K	K	K					K	K	K	K	K
257	R																		K
263	S	T		T				T	T										
264	D	G		G	G	G	G	G	G	G	N	N	N		G	G	G	G	G
266	P	T		T	S	S	S	A	A	S					S	S	S	S	S
267	I	V		V	V	V	V	V	V	V					V	V	V	V	V
270	N	G	S	G	G	G	G	G	G	G					D	D	D	D	D
278	R	K		K	K	K	K	K	K	K					K	K	K	K	K
279	E	G		G	G	G	G	G	G	G		G	G		G	G	G	G	G
285	R	K		K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K
298	Q										K								
305	K				R	R	R			R									
306	K	R		R				R	R						R				
309	M	L		L	L	L	L	L	L	L				L	L	L	L	L	L
320	I	V		V				V	V			L	L	L	V	V	V	V	V
321	I	V		V	V	V	V	V	V	V	M	M	M		V	V	V	V	V
322	Q																		K

## Gs/Gd H5 2.3.4.4b mutations of concern - geographical distribution
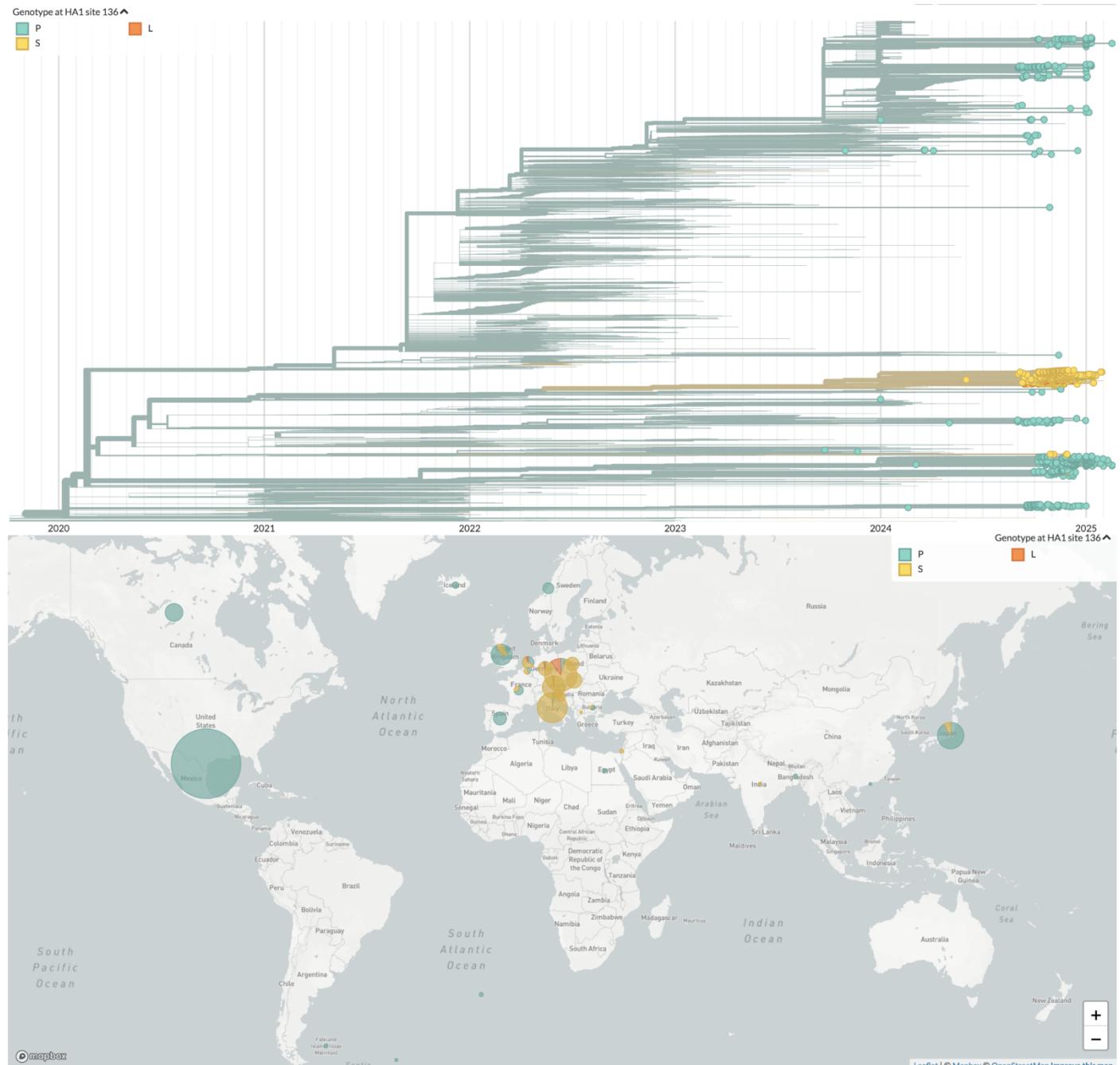
Figure A.1. Clade 2.3.4.4b HA1 **site 136** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
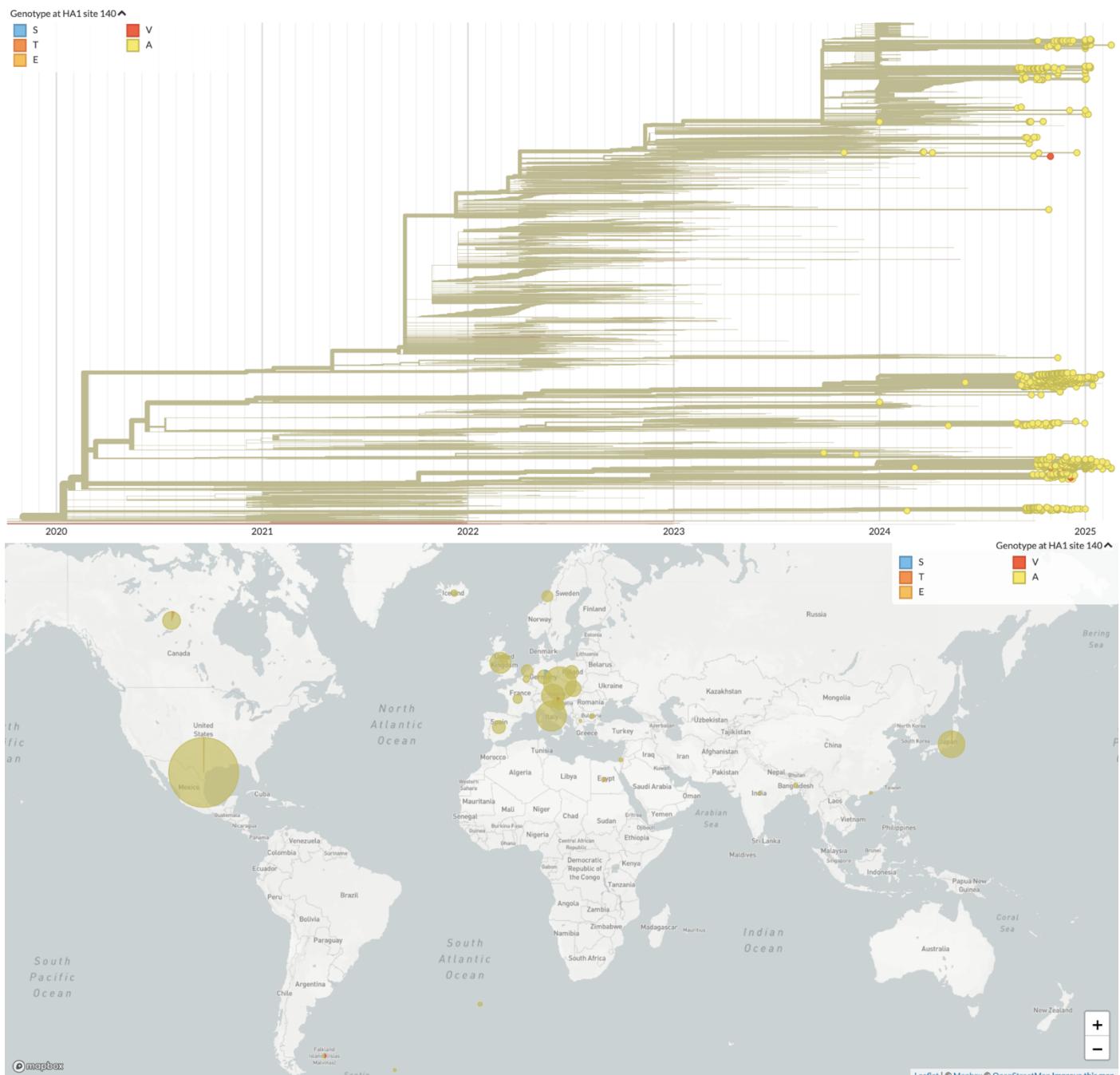
Figure A.2. Clade 2.3.4.4b HA1 **site 140** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
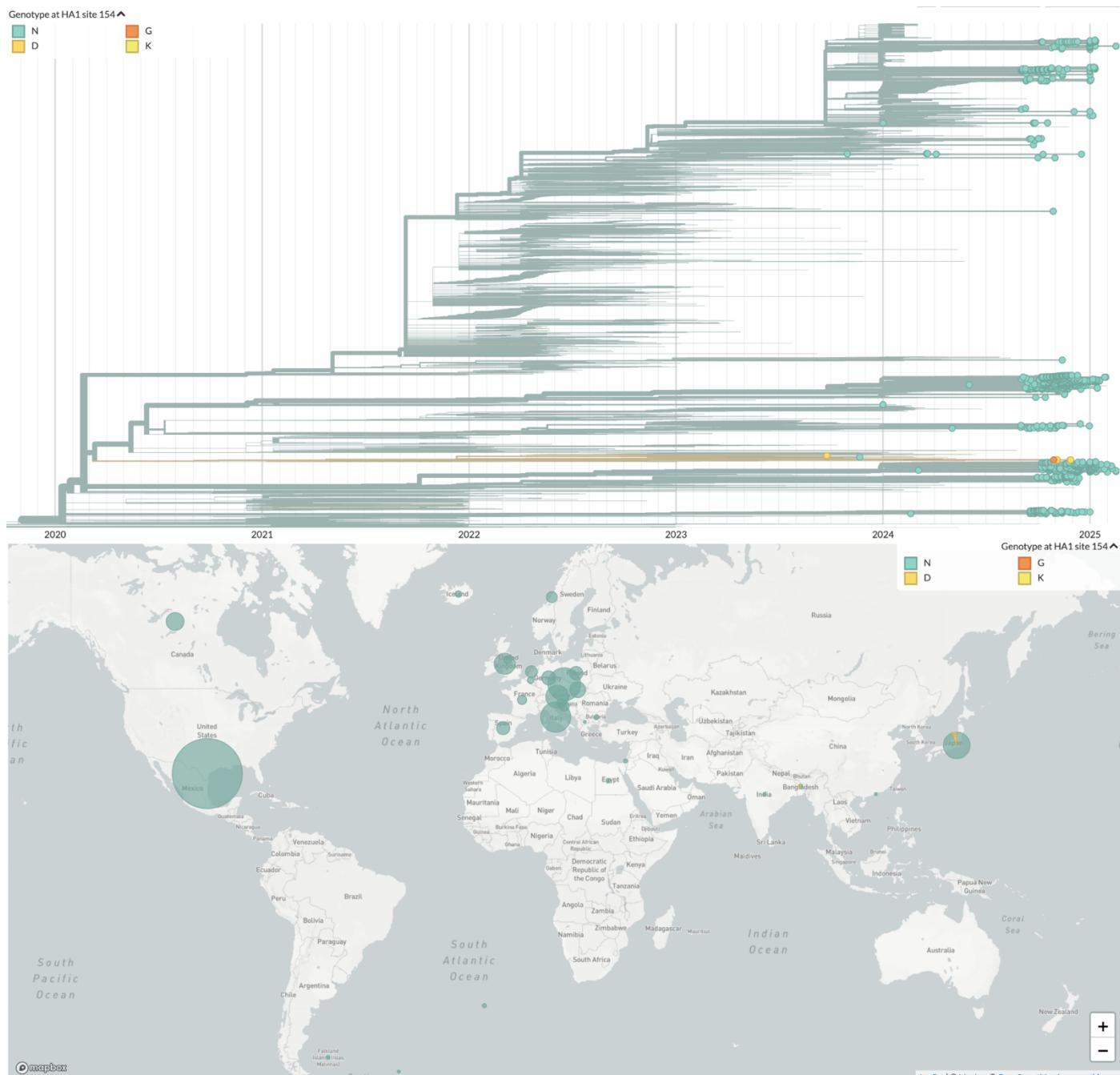
Figure A.3. Clade 2.3.4.4b HA1 **site 154** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
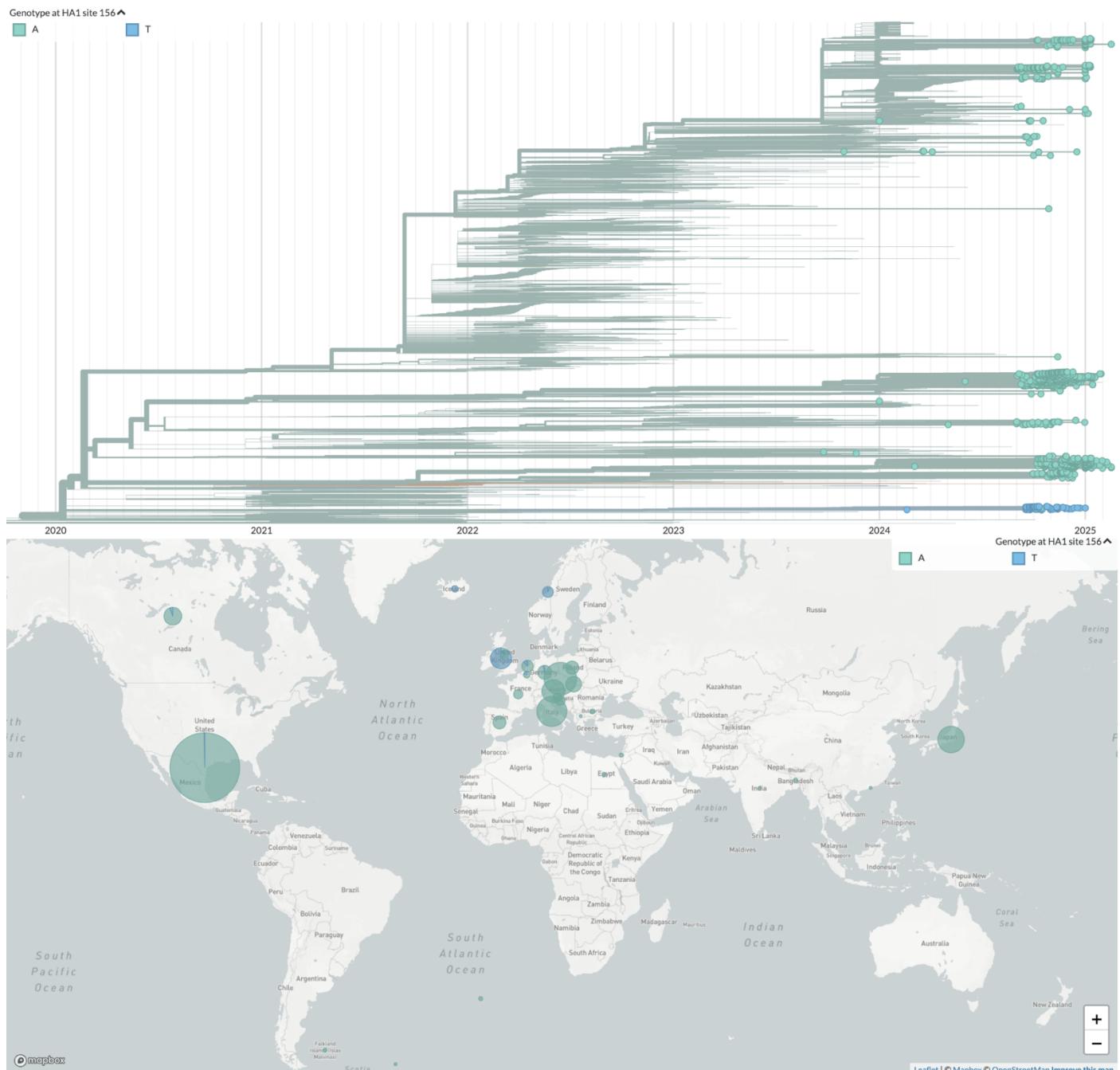
Figure A.4. Clade 2.3.4.4b HA1 **site 156** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
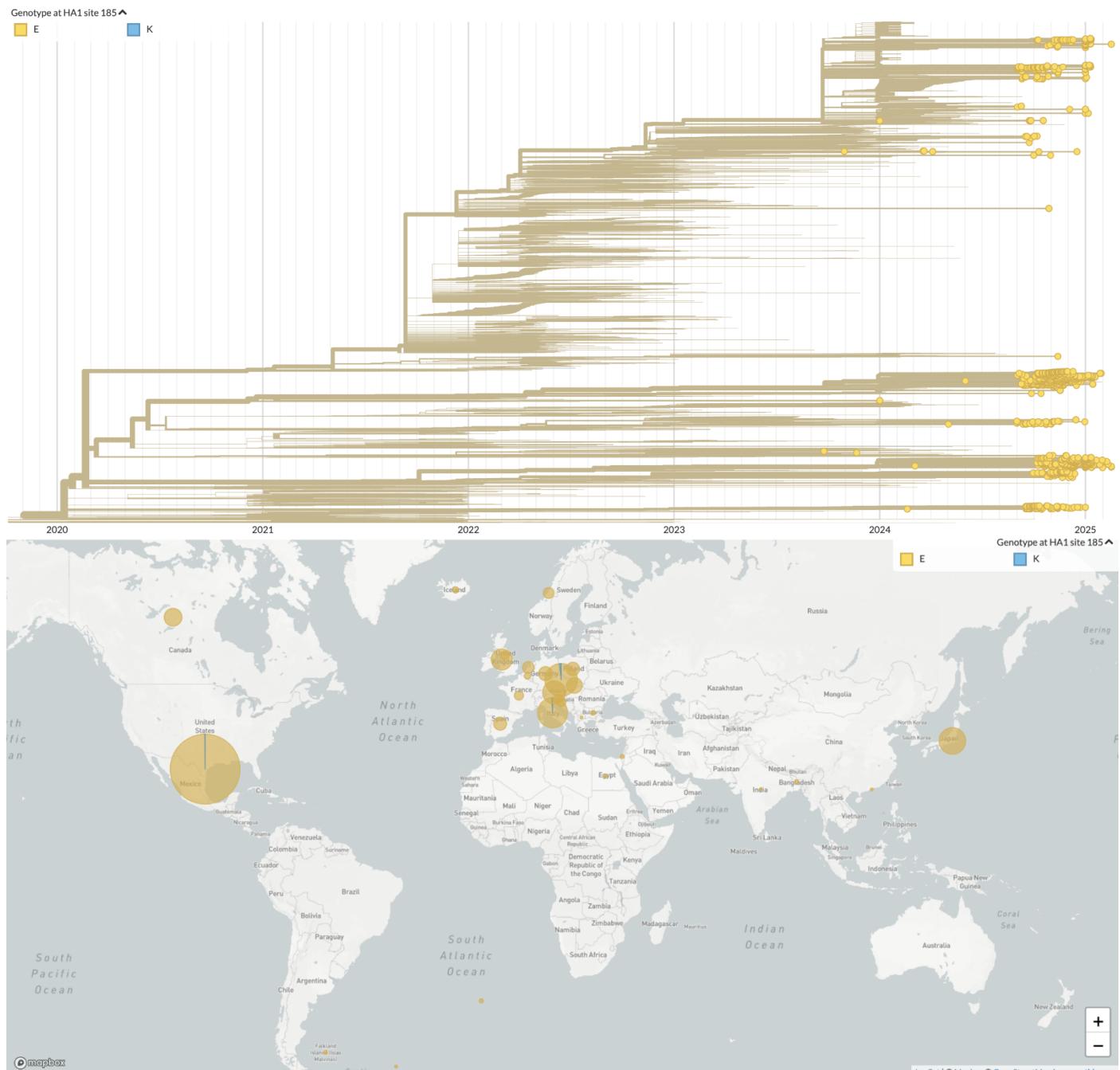
Figure A.5. Clade 2.3.4.4b HA1 **site 185** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
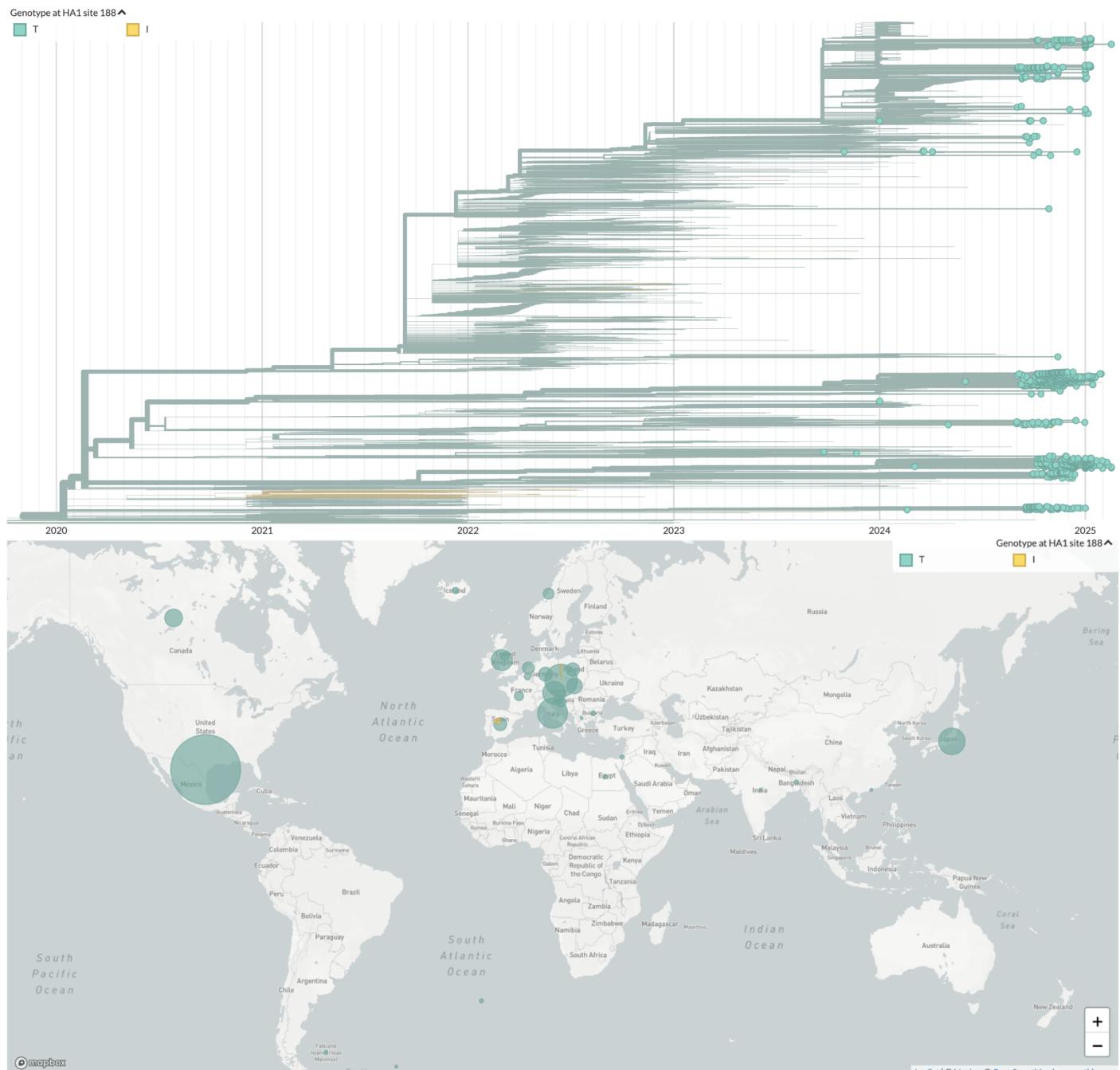
Figure A.6. Clade 2.3.4.4b HA1 **site 188** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
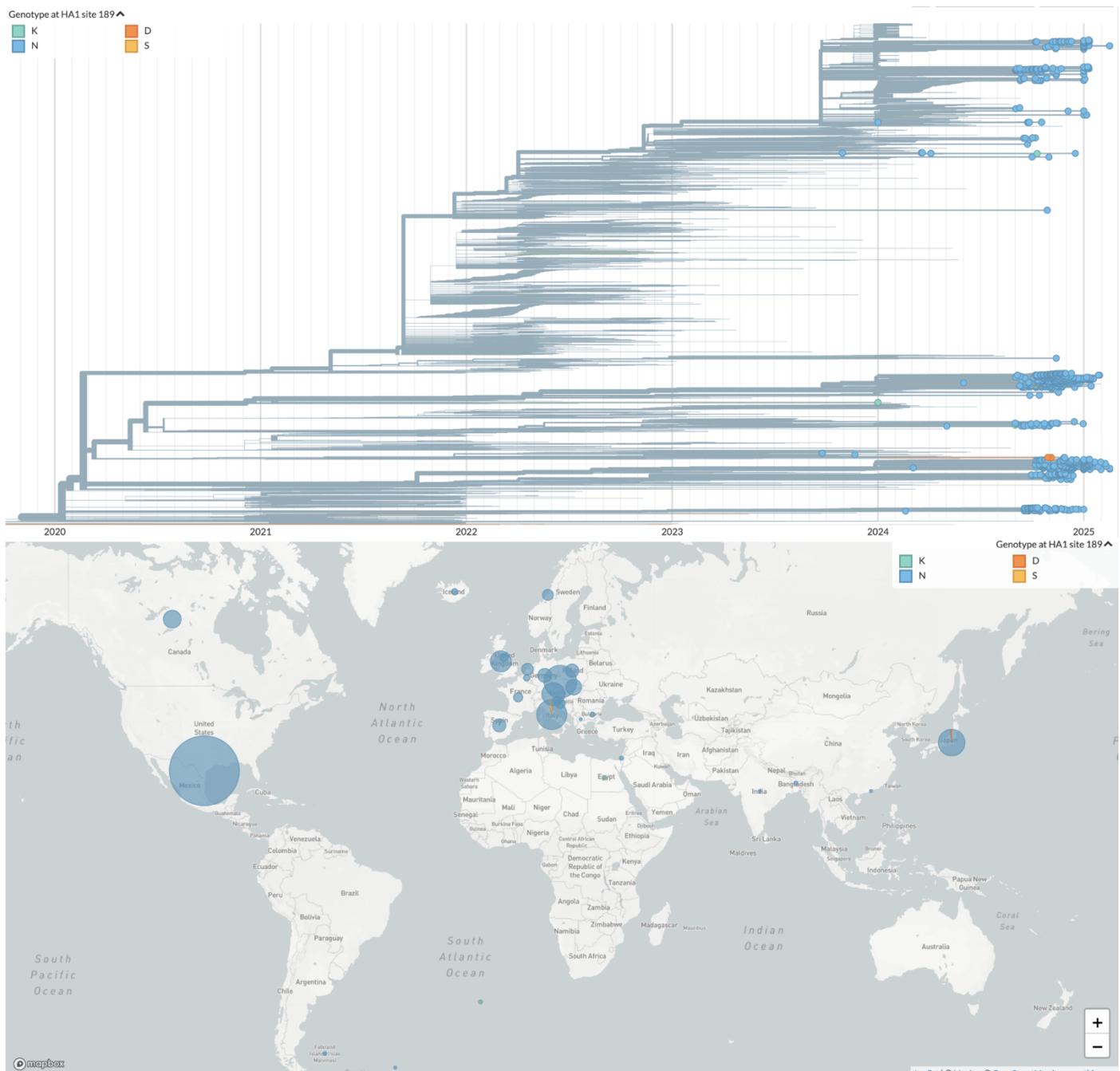
Figure A.7. Clade 2.3.4.4b HA1 **site 189** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
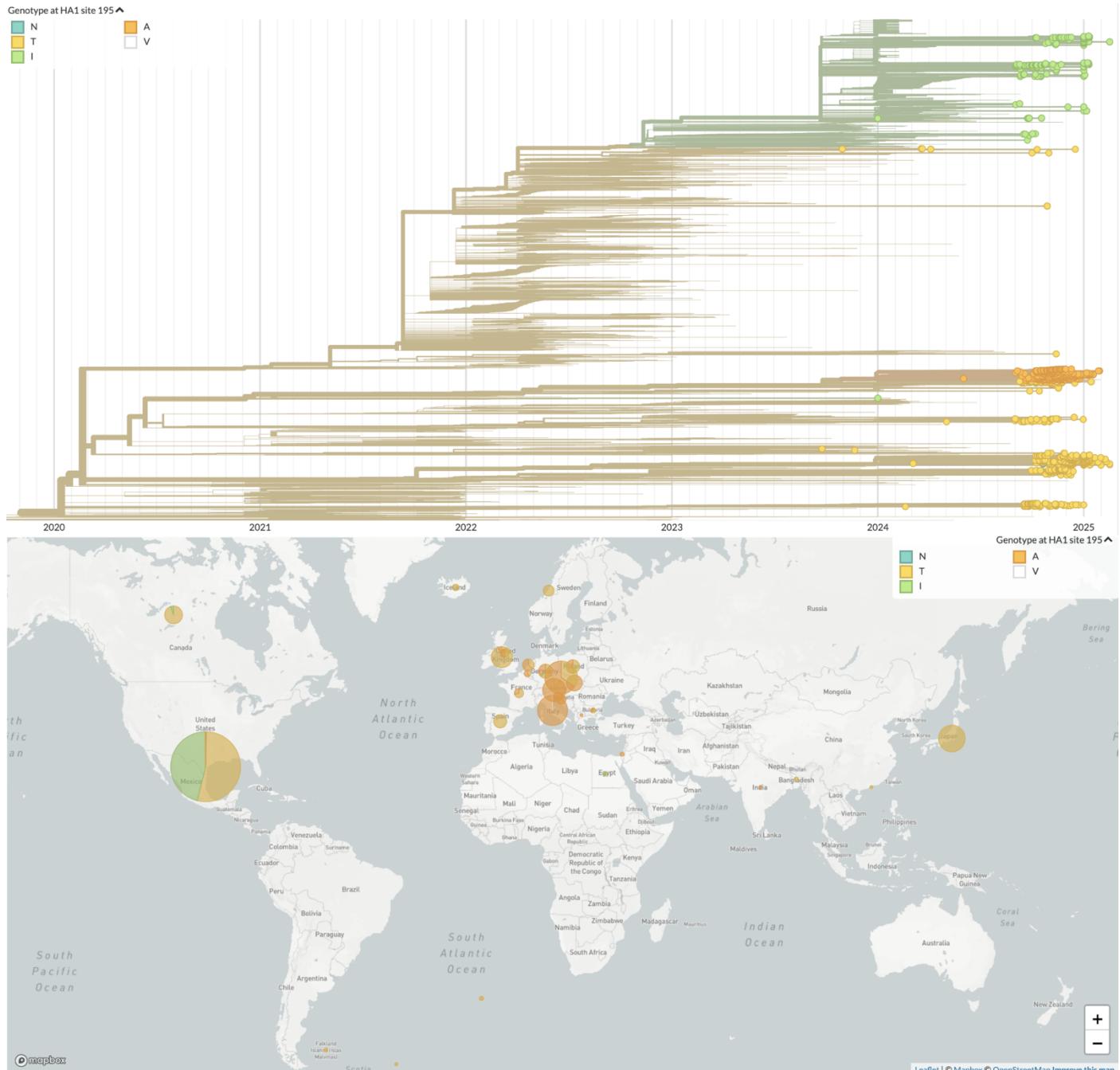
Figure A.8. Clade 2.3.4.4b HA1 **site 195** sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.
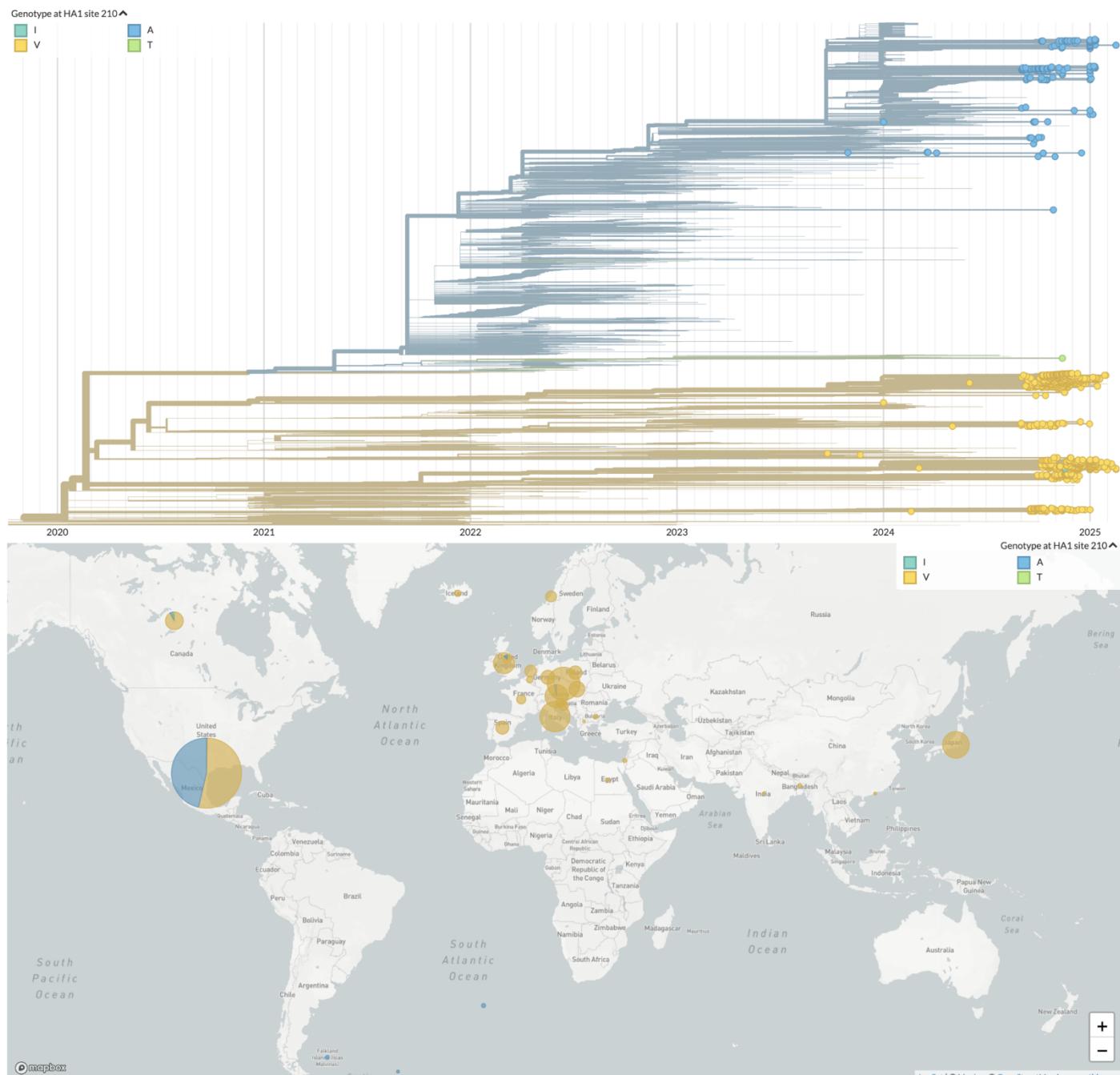
Figure A.9. Clade 2.3.4.4b HA1 site 210 sequences either submitted to OFFLU during this reporting period, antigenically characterised during this reporting period, or obtained from GISAID and corresponding to this reporting period.