Coverage of emerging strains of influenza A(H5N1) by available candidate vaccine viruses

What research is important to prepare and respond to H5N1 influenza outbreaks?

19 March 2025

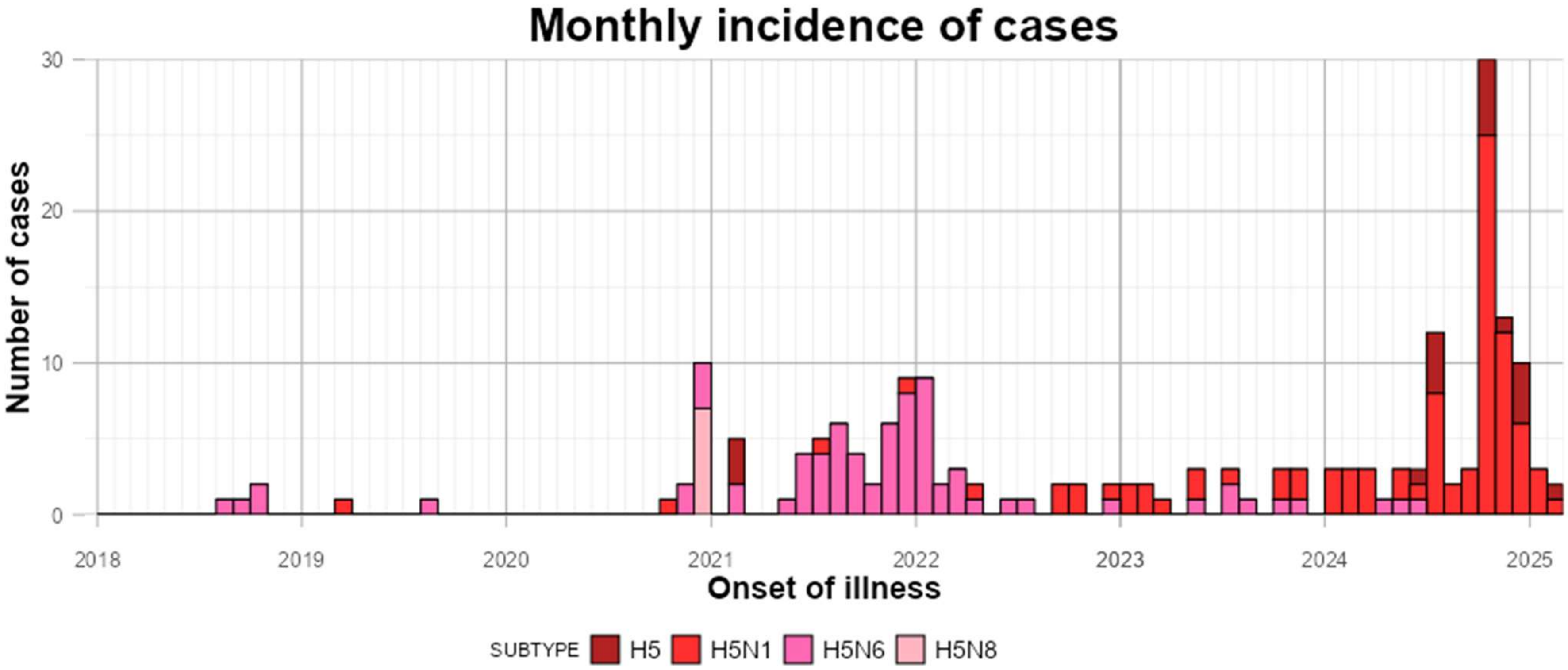
GLOBAL INFLUENZA STRATEGY 2019 – 2030
Prevent. Control. Prepare.

GISRS
GLOBAL INFLUENZA SURVEILLANCE & RESPONSE SYSTEM

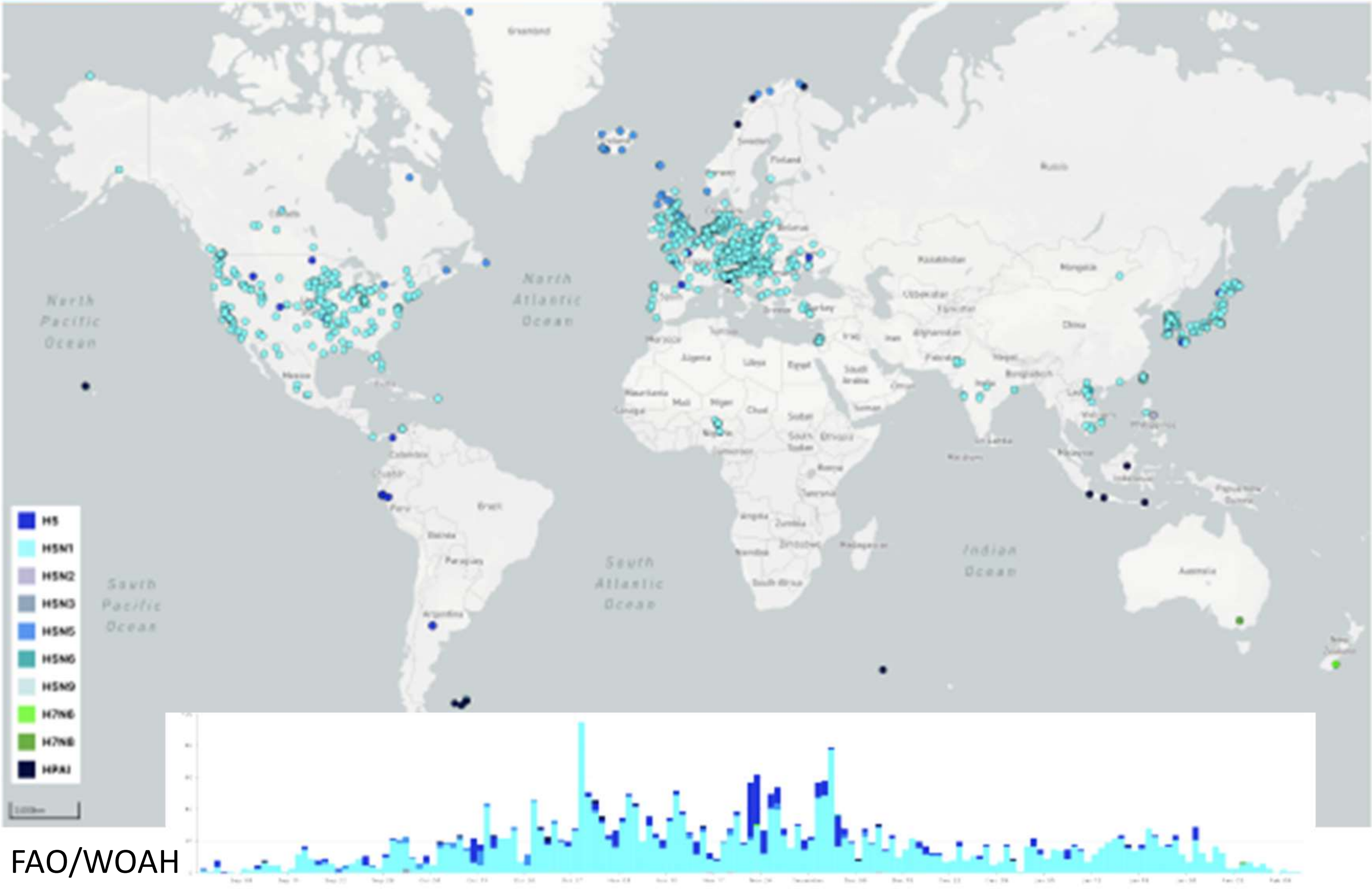
WHO Influenza vaccine meeting – zoonotic influenza

- Surveillance data
- Genetic characterization
- Antigenic characterization
- Availability of CVVs

Gs/Gd-lineage H5 zoonotic infections



H5/H7 activity in animals



FAO/WOAH

🟦 **H5**
🟦 **H5N1**
🟪 **H5N2**
🟦 **H5N5**
🟩 **H5N6**
🟦 **H5N8**
🟩 **H7N3**
🟩 **H7N5**
🟩 **H7N6**
🟩 **H7N8**
🟩 **H7N9**
⬛ **HPAI**

Zoonotic influenza highlights A(H5)

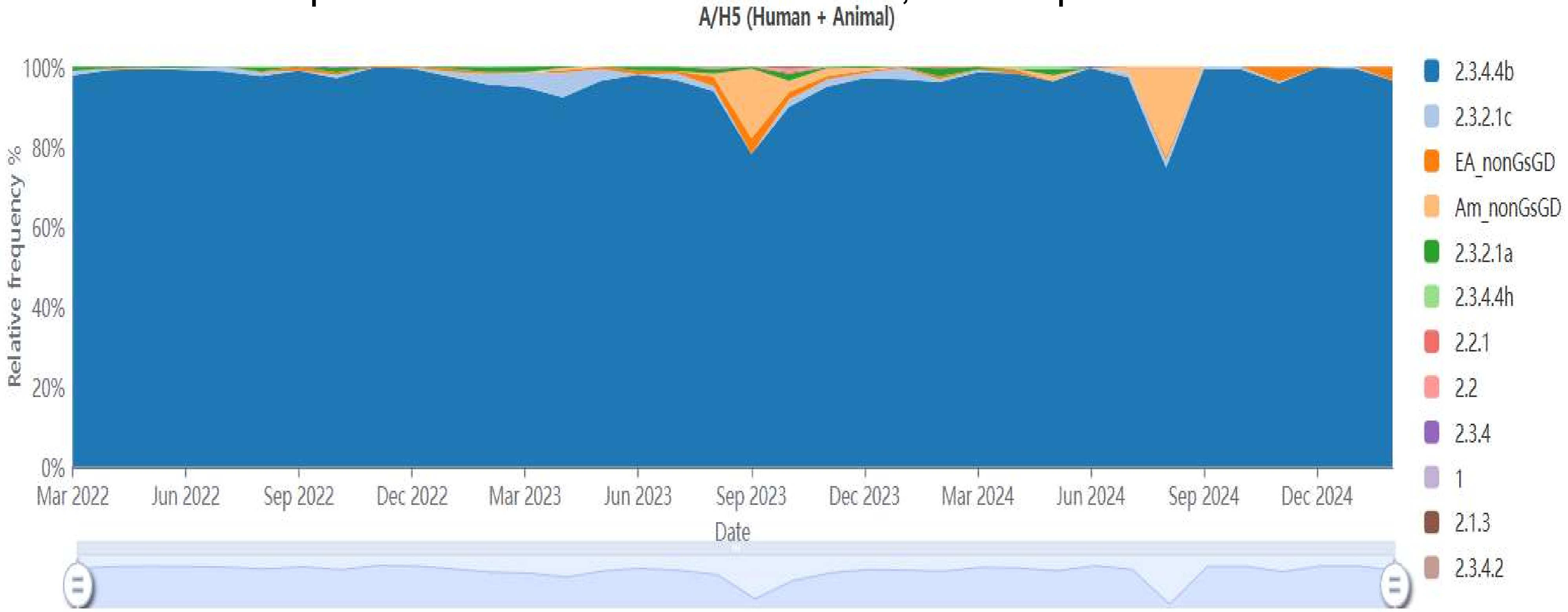
Human cases in since September 2024

Country	Subtype (clade)	Cases	Clinical severity	Exposure	Age
Cambodia	H5N1 (2.3.2.1e/previously 2.3.2.1c)	2	Fatal	Poultry	28 and 2
Canada	H5N1 (2.3.4.4b)	1	Severe	Unknown	<18
United Kingdom	H5N1 (2.3.4.4b/unknown)	2	Asymptomatic/ mild	Poultry	adults
United States of America	H5N1 (2.3.4.4b)	59	Mild to fatal	Bovine/poultry/ unknown	range
Viet Nam	H5	1	Severe	Poultry	18

Cumulative totals: eighteen A(H5), seven A(H5N8), 93 A(H5N6) and 956 A(H5N1)

Currently circulating H5 clades

- Available sequences from human and animal, since April 2024



Source: GISAID

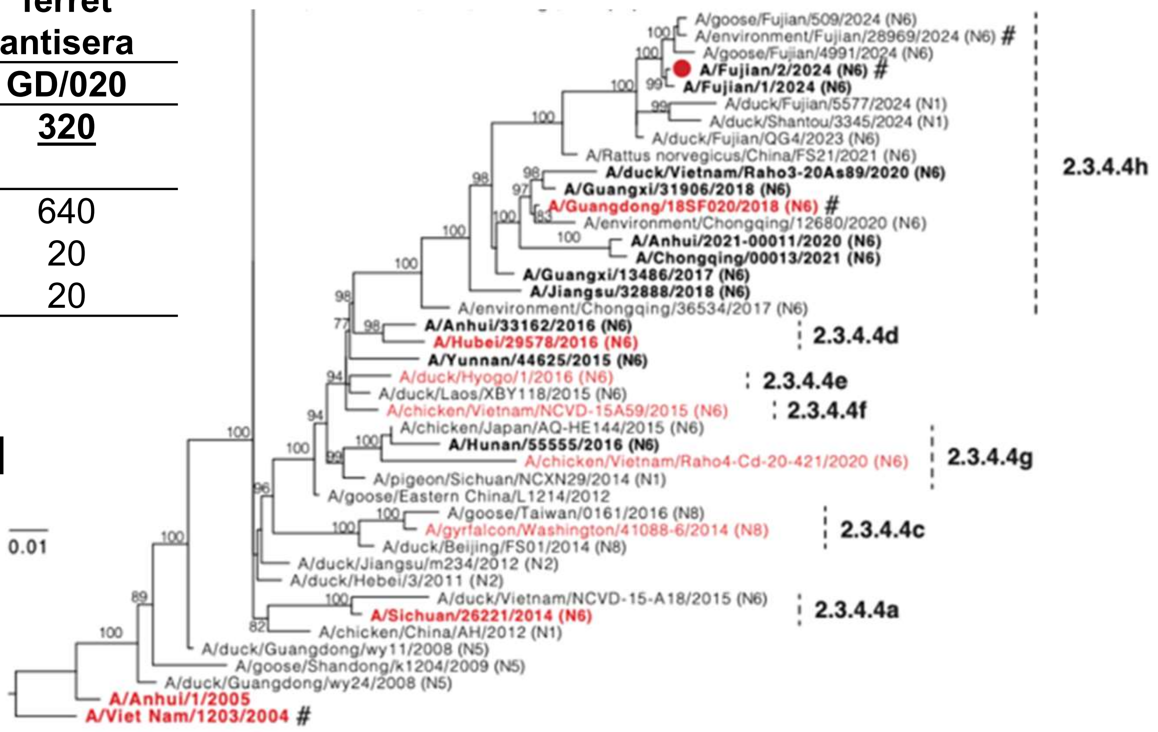
H5 clade 2.3.4.4b – antigenic characterization

Reference antigens	**Subtype**	**Clade**	**Genotype**	**IDCDC-RG71A**	**IDCDC-RG78A**	**IDCDC-RG80A**	**Ezo red fox**
IDCDC-RG71A (A/Astrakhan/3212/2020-like)	H5N8	2.3.4.4b		**160**	80	640	40
IDCDC-RG78A (A/American Wigeon/South Carolina/22-000345-001/2021)	H5N1	2.3.4.4b	A1	160	**160**	1280	80
IDCDC-RG80A (A/chicken/Ghana/AVL-763_21VIR7050-39/2021)*	H5N1	2.3.4.4b		40	40	**1280**	160
NIID-002 (A/Ezo red fox/Hokkaido/1/2022)	H5N1	2.3.4.4b	A3	160	160	1280	**80**
Test antigens							
A/Washington/239/2024	H5N1	2.3.4.4b	D1.1	160	320	1280	80
A/Washington/240/2024	H5N1	2.3.4.4b	D1.1	160	160	1280	80
A/Washington/255/2024	H5N1	2.3.4.4b	D1.1	160	160	1280	80
A/British Columbia/PHL-2032/2024	H5N1	2.3.4.4b	D1.1	160	320	1280	80
A/Iowa/124/2025	H5N1	2.3.4.4b	D1.1	40	160	1280	80
A/Nevada/10/2025	H5N1	2.3.4.4b	D1.1	80	80	1280	80
A/Canada goose/Kansas/W24-962/2024	H5N1	2.3.4.4b	D1.1	20	40	1280	40
A/snow goose/Kentucky/W24-1021B/2024	H5N1	2.3.4.4b	D1.1	80	40	640	40
A/turkey/Ohio/B2500277/2025	H5N1	2.3.4.4b	D1.3	160	20	640	40
A/Canada goose/Kentucky/W25-036/2025	H5N1	2.3.4.4b	D1.1	80	80	640	40
A/red fox/Missouri/W24-1081/2024	H5N1	2.3.4.4b	D1.1	320	80	1280	80
A/California/151/2024	H5N1	2.3.4.4b	B3.13	80	320	1280	80
A/California/152/2024	H5N1	2.3.4.4b	B3.13	80	160	640	40
A/California/153/2024	H5N1	2.3.4.4b	B3.13	40	160	1280	40
A/bovine/California/CL001/2024	H5N1	2.3.4.4b	B3.13	10	160	1280	40

2.3.4.4h

		Post-infection ferret antisera
Reference antigens		**GD/020**
A/Guangdong/18SF020/2018 RG	H5N1	**320**
Test antigens		
A/Fujian/1/2024	H5N6	640
A/Fujian/2/2024	H5N6	20
A/Environment/Fujian/28969/2024	H5N6	20

A/Fujian/2/2024-like CVV proposed



H5 *Gs/Gd* lineage updated nomenclature

Source: HKU

- ☐ To reflect the genetic diversification of the A(H5) viruses, particularly clade 2.3.2.1c
- ☐ New nomenclature was proposed for this clade: addition of c-g subclades
- ☐ Previous 2.3.2.1c are now in clade **2.3.2.1e**

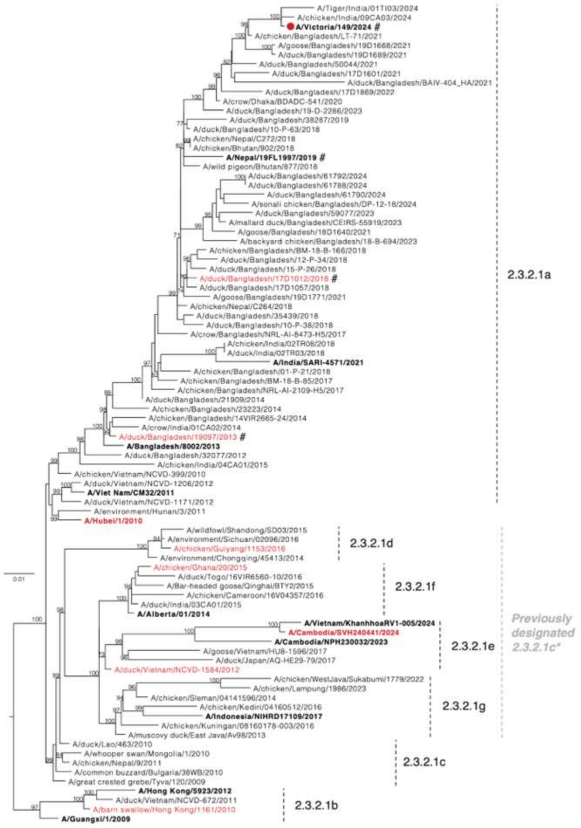


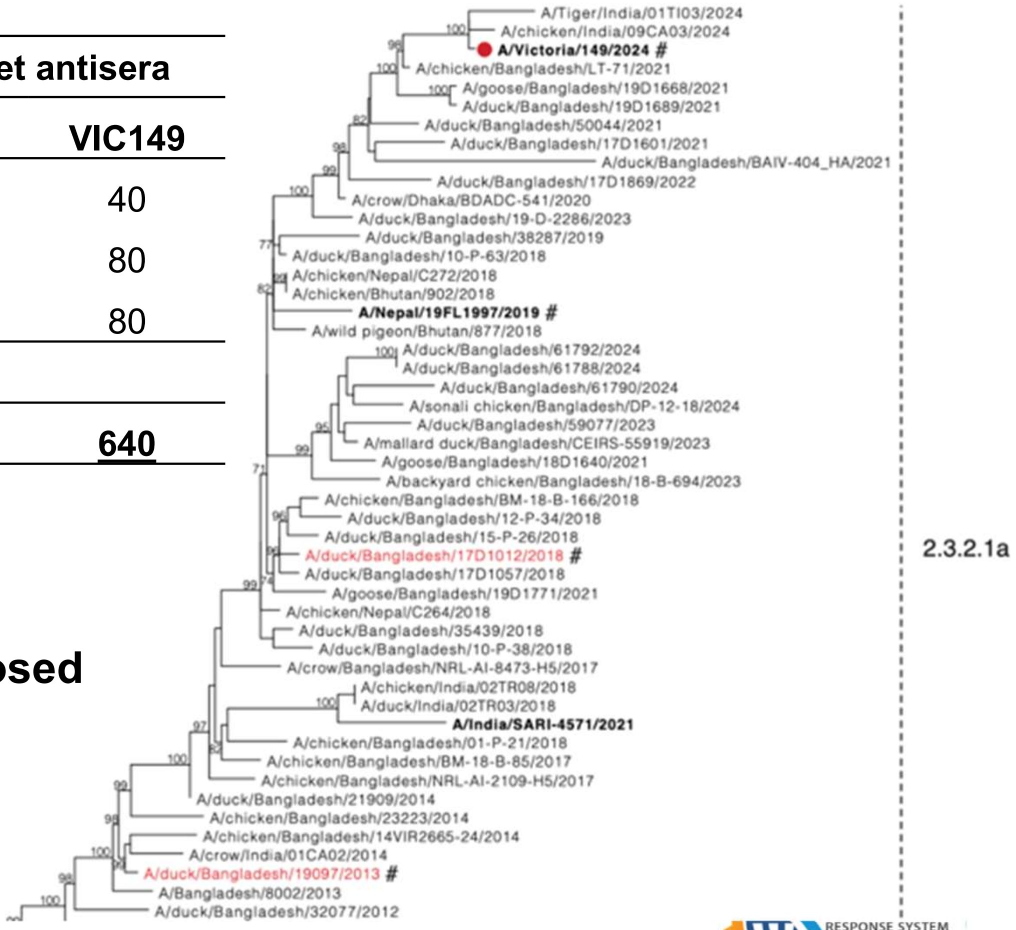
Figure 2. Phylogenetic relationships of A(H5) clade 2.3.2.1 HA genes. CVVs that are available or in preparation are in red. The proposed CVV is indicated by a red dot (●). Human viruses are in bold font. The tree was built from the nucleotide sequences coding for the mature HA1 protein. The viruses tested in hemagglutination inhibition assay are indicated by hashes (#). The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes. * The previous designated clade 2.3.2.1c was updated by assigning its divergent sub-lineages of viruses to new 2.3.2.1d/e/f/g clades.

[Development of avian influenza A(H5) virus datasets for Nextclade enables rapid and accurate clade assignment - PubMed]()

2.3.2.1a

Reference antigens	Post-infection ferret antisera SJ007	 Dk/17D	 VIC149
SJ007 (A/duck/Bangladesh/19097/2013	**1280**	1280	40
A/duck/Bangladesh/17D1012/2018	160	**640**	80
A/Nepal/19FL1997/2019	320	2560	80
Test antigens			
A/Victoria/149/2024	40	80	**640**

A/Victoria/149/2024-like (clade 2.3.2.1a) CVV proposed



2.3.2.1e

- Clade 2.3.2.1e viruses were detected in poultry in Cambodia, Lao People's Democratic Republic, and Viet Nam and in captive tigers and a captive leopard in Viet Nam

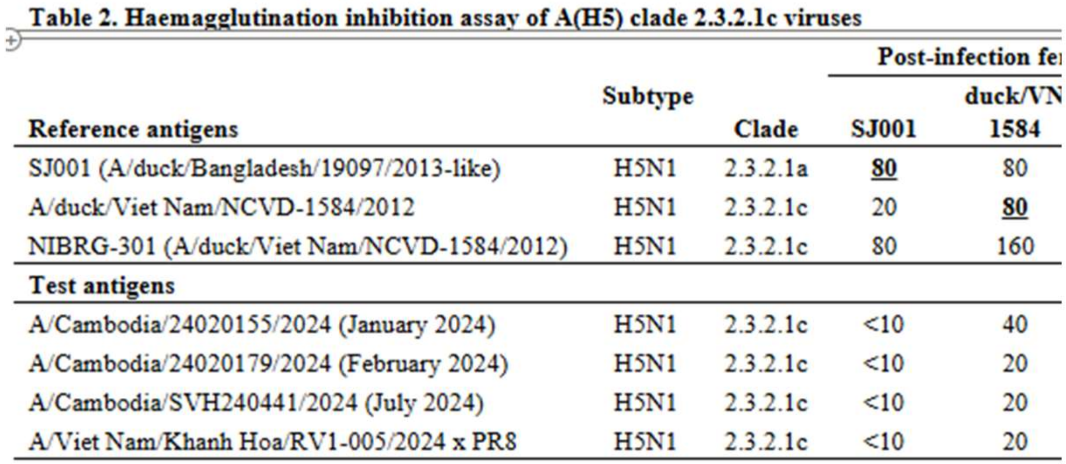
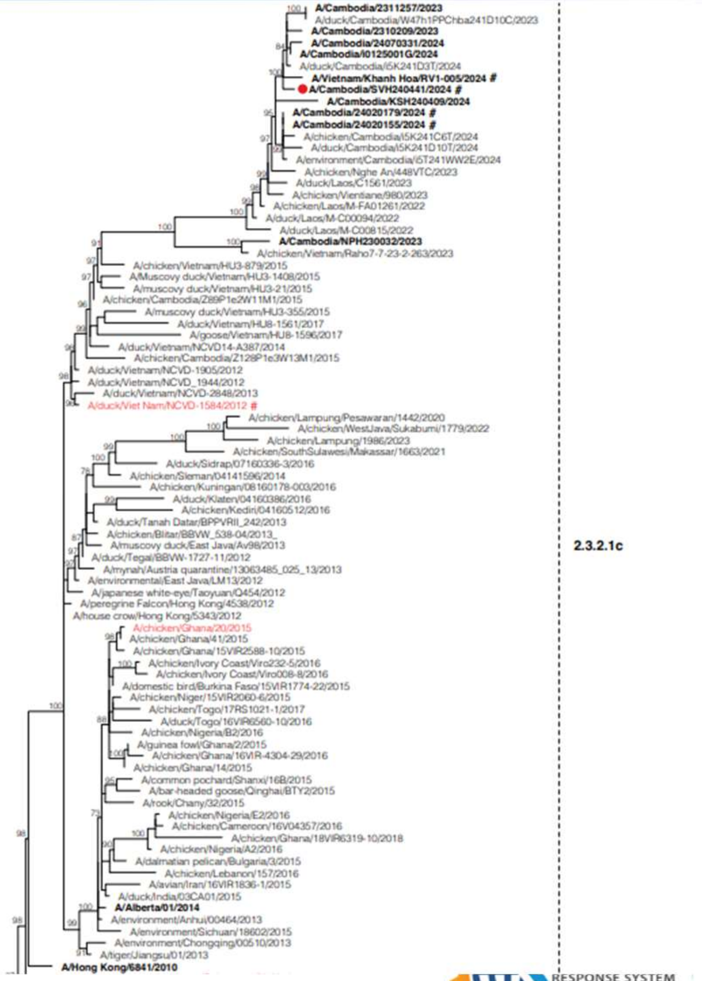


Table 2. Haemagglutination inhibition assay of A(H5) clade 2.3.2.1c viruses

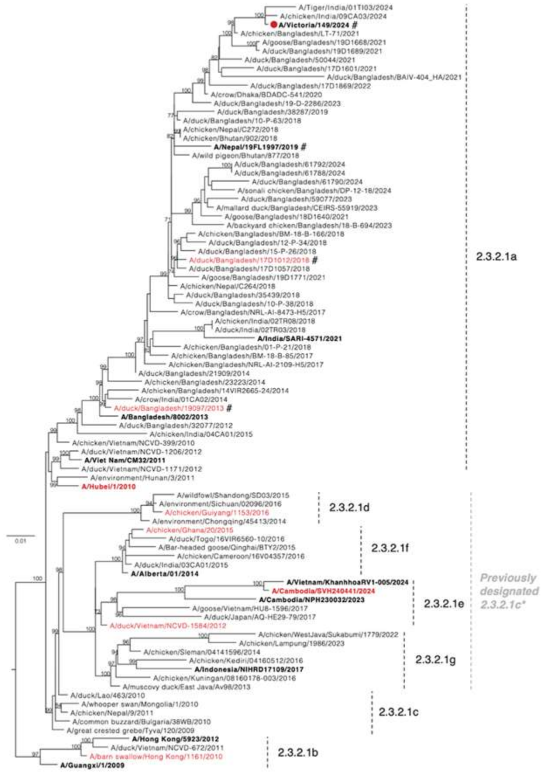
Reference antigens	Subtype	Clade	Post-infection fe SJ001	 duck/VN 1584
SJ001 (A/duck/Bangladesh/19097/2013-like)	H5N1	2.3.2.1a	**80**	80
A/duck/Viet Nam/NCVD-1584/2012	H5N1	2.3.2.1c	20	**80**
NIBRG-301 (A/duck/Viet Nam/NCVD-1584/2012)	H5N1	2.3.2.1c	80	160
Test antigens				
A/Cambodia/24020155/2024 (January 2024)	H5N1	2.3.2.1c	<10	40
A/Cambodia/24020179/2024 (February 2024)	H5N1	2.3.2.1c	<10	20
A/Cambodia/SVH240441/2024 (July 2024)	H5N1	2.3.2.1c	<10	20
A/Viet Nam/Khanh Hoa/RV1-005/2024 x PR8	H5N1	2.3.2.1c	<10	20

A/Viet Nam/KhanhhoaRV1-005/2024 (clade 2.3.2.1e) CVV under development



H5 clade 2.3.2.1g – antigenic characterization

- ❑ *Clade 2.3.2.1g* HA sequences from viruses circulating in multiple islands of the Republic of Indonesia in the previous reporting period were analysed.
- ❑ Currently, there is no CVV proposed for this clade.
- ❑ These viruses accumulated many amino acid substitutions when compared to the sequences of CVVs of closely related clades previously classified as clade 2.3.2.1c.
- ❑ No antigenic data were available from recently detected viruses and will require further monitoring



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Source: HKU

Acknowledgement

- WHO Global Influenza Surveillance and Response System (GISRS) member institutions and other national influenza reference laboratories.
- WHO Regional Offices and Country Offices
- OFFLU, WOAH and FAO

Resources

- ☐ Summary of zoonotic influenza characterization and candidate vaccine viruses for avian and swine influenza including A(H5N1)
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/zoonotic-influenza-viruses-and-candidate-vaccine-viruses

- ☐ WHO zoonotic CVVs webpage:
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/zoonotic-influenza-viruses-and-candidate-vaccine-viruses

Thank you