Genetic and antigenic characteristics of zoonotic influenza A viruses and development of candidate vaccine viruses for pandemic preparedness

September 2025

The development of influenza candidate vaccine viruses (CVVs), coordinated by the World Health Organization (WHO), remains an essential component of the overall global strategy for influenza pandemic preparedness.

Selection and development of CVVs are the first steps towards timely vaccine production and do not imply a recommendation for initiating manufacture. National authorities may consider the use of one or more of these CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need.

Zoonotic influenza viruses continue to be identified and evolve both antigenically and genetically, leading to the need for additional CVVs for pandemic preparedness purposes. Changes in the antigenic and genetic characteristics of these viruses relative to existing CVVs and their potential risks to public health justify the need to develop new CVVs.

This document summarizes the antigenic and genetic characteristics of recent zoonotic influenza viruses and related viruses circulating in animals[1] that are relevant to CVV updates. Institutions interested in receiving these CVVs should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website[2].

Influenza A(H5)

Since their emergence in 1997, high pathogenicity avian influenza (HPAI) A(H5) viruses of the A/goose/Guangdong/1/96 haemagglutinin (HA) lineage have become enzootic in many countries, have infected wild birds and continue to cause outbreaks in poultry and sporadic human and other mammalian infections across a wide geographic area. A(H5) HA gene segments have paired with a variety of neuraminidase (NA) subtypes (N1, N2, N3, N4, N5, N6, N8 or N9). These viruses have diversified genetically and antigenically, leading to the need for multiple CVVs. This summary provides updates on the characterization of A/goose/Guangdong/1/96-lineage A(H5) viruses and the status of the development of influenza A(H5) CVVs.

Influenza A(H5) activity from 25 February to 22 September 2025

Since 2003, 17 A(H5), seven A(H5N8), 93 A(H5N6) and 979 A(H5N1) human infections or detections have been reported. Since 25 February 2025, 24 human infections with A/goose/Guangdong/1/96-lineage viruses have been reported to WHO. A/goose/Guangdong/1/96-lineage A(H5) viruses have been detected in both domestic and wild birds with spillover to mammals in many countries (Table 1).

Table 1. H5 activity reported to international agencies from 25 February to 22 September 2025

Country, area or territory	Host	Genetic clade
Albania	poultry	2.3.4.4b (H5N1)
Antarctica	wild birds	2.3.4.4b (H5N1)
Argentina	poultry	2.3.4.4b (H5N1)
Austria	wild birds	2.3.4.4b (H5N1)
Bangladesh	human (4)*	2.3.2.1a (H5N1), unknown (H5)
	poultry	2.3.2.1a (H5N1)
	captive mammals (serval)	unknown (H5N1)
	wild birds	2.3.2.1a (H5N1)
Belgium	poultry	2.3.4.4b (H5N1)

[1]For information relevant to other notifiable influenza virus infections in animals refer to https://wahis.woah.org/#/home
[2]https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/zoonotic-influenza-viruses-and-candidate-vaccine-viruses

	wild birds	2.3.4.4b (H5N1)
	domestic mammals (cat)	2.3.4.4b (H5N1)
Bhutan	poultry	unknown (H5N1)
Bolivia	poultry	2.3.4.4b (H5N1)
Botswana	poultry	unknown (H5N1)
Brazil	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Bulgaria	poultry	2.3.4.4b (H5N1)
Cambodia	human (15)*	2.3.2.1e‡ (H5N1), unknown (H5N1)
	poultry	2.3.2.1e‡ (H5N1)
Canada	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	domestic mammals (cat)	2.3.4.4b (H5N5)
	wild mammals (mink, red fox, raccoon, skunk, striped skunk)	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
China	human (1)*	2.3.4.4b (H5N1)
	poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N6); 2.3.4.4h (H5N1)
Hong Kong, China SAR	poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N6); 2.3.4.4h (H5N1)
Taiwan, China	poultry	unknown (H5N1)
	wild birds	unknown (H5N1)
	captive birds	unknown (H5N1)
Czech Republic	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Croatia	poultry	unknown (H5)
	wild birds	2.3.4.4b (H5N1)
Denmark	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Egypt	poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N8)
Estonia	wild birds	2.3.4.4b (H5N1)
Falklands Islands	wild birds	2.3.4.4b (H5N1)
Finland	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	wild mammals (otter, red fox)	2.3.4.4b (H5N1)
France	wild birds	2.3.4.4b (H5N1)
Germany	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
	wild mammals (red fox)	2.3.4.4b (H5N1)
Ghana	poultry	unknown (HPAIV)
Greece	wild birds	unknown (H5N1)
Hungary	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Iceland	wild birds	2.3.4.4b (H5N5)
India	human (2)*	2.3.2.1a (H5N1)
	poultry	2.3.2.1a (H5N1)
	wild birds	2.3.2.1a (H5N1)
	domestic mammals (cat)	2.3.2.1a (H5N1)
	captive mammals (tiger)	unknown (HPAIV)
Indonesia	poultry	2.3.2.1g (H5N1)
Ireland, Republic of	wild birds	2.3.4.4b (H5N1)
Italy	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Israel	wild birds	unknown (H5N8)
Japan	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N2)
	wild mammals (harbor seal, sea otter)	2.3.4.4b (H5N1)
Korea, Republic of	poultry	unknown (H5N1)
	wild birds	unknown (H5N1)
	wild mammals (cat)	unknown (H5N1)
Latvia	poultry	2.3.4.4b (H5N1)
Lithuania	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Mexico	human (1)*	2.3.4.4b (H5N1)

	wild birds	2.3.4.4b (H5N1)
Moldova, Republic of	poultry	unknown (H5N1)
Netherlands (Kingdom of the)	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
	wild mammals (red fox)	2.3.4.4b (H5N1)
Nigeria	poultry	2.3.4.4b (H5N1)
Norway	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	wild mammals (red fox)	2.3.4.4b (H5N5)
Peru	poultry	unknown (H5)
	wild birds	unknown (H5)
Philippines	poultry	unknown (H5N1); unknown (H5N9)
	wild birds	unknown (H5N1)
Poland	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Portugal	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Romania	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Russian Federation	wild birds	2.3.4.4b (H5N1)
	poultry	2.3.4.4b (H5N1)
South Africa	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Spain	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1)
Svalbard and Jan Mayen Islands	wild mammals (red fox)	unknown (H5N5)
Sweden	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
Togo	poultry	2.3.4.4b (H5N1)
Türkiye	poultry	unknown (H5N1)
United Kingdom of Great Britain and Northern Ireland (the)	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	domestic mammals (sheep)	2.3.4.4b (H5N1)
	wild mammals (otter, seal)	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
Ukraine	poultry	unknown (H5)
United States of America (the)	poultry	2.3.4.4b (H5N1)
	wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	captive birds	2.3.4.4b (H5N1)
	domestic mammals (dairy cattle, cats)	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	wild mammals (black bear, black rat, bobcat, fox, gray fox, harbor seal, house mouse, mink, mountain lion, raccoon, red fox, skunk, striped skunk)	2.3.4.4b (H5N1)
	captive mammals (American black bear, mountain lion)	2.3.4.4b (H5N1)
Viet Nam	human (1)*	2.3.2.1e‡ (H5N1)
	poultry	unknown (H5N1)

†unknown: denotes instances where specific lineage designations were not available
*Number of cases and/or detections
‡Formerly classified as A(H5) clade 2.3.2.1c.

Genetic and antigenic characteristics of influenza A(H5) viruses

Twenty-four new human infections or detections with A/goose/Guangdong/1/96-lineage viruses were reported. Most infected individuals had recent exposure to birds. The human cases included four A(H5N1) clade 2.3.2.1a infections, two in Bangladesh and two fatal infections in India. Bangladesh reported additional single A(H5) and A(H5N1) cases where clade designations could not be determined due to lack of sequence data. The HA of the 2.3.2.1a viruses from Bangladesh and India had up to one and seven amino acid substitutions relative to the A/Victoria/149/2024 CVV, respectively. Antigenic analyses of the viruses from the human cases are pending, but a genetically related virus from poultry in Bangladesh reacted well to post-infection ferret antisera raised against the A/Victoria/149/2024 CVV. Two human cases of A(H5N1) clade 2.3.4.4b virus infection were detected; one in China in an individual with recent travel history to Viet Nam, and one fatal case in Mexico. The A(H5N1) clade 2.3.4.4b virus from China had an HA with four amino acid substitutions relative to the

A/Jiangsu/NJ210/2023 CVV. The virus from the human case in Mexico had an HA with three amino acid substitutions relative to the A/Astrakhan/3212/2020 and A/Ezo red fox/Hokkaido/1/2022 CVVs, however, one of the substitutions added a putative glycosylation site in antigenic site B. Antigenic analyses are pending.

Cambodia reported fifteen human cases of A(H5N1) of which six were fatal. Viruses from twelve cases were confirmed as belonging to A(H5N1) clade 2.3.2.1e; clade designations could not be determined for the other three due to lack of sequence data. One human infection with an A(H5N1) clade 2.3.2.1e virus was identified in Viet Nam. The HAs of the human viruses from Cambodia and Viet Nam had, at most, four amino acid differences relative to the A/Cambodia/SVH240441/2024 CVV. Ferret antisera raised against A/Cambodia/SVH240441/2024 and the A/Cambodia/SVH240441/2024 CVV reacted well with virus isolated from the human case detected in Viet Nam but less well with a virus from a Cambodian human case. Ferret antisera raised against A/duck/Vietnam/NCVD-1584/2012 and the clade 2.3.2.1f A/chicken/Ghana/20/2015 CVV reacted well with the Cambodian virus. Antigenic characterisation of other viruses isolated from human cases in Cambodia is pending.

A(H5) viruses from birds and non-human mammals belonged to the following clades

Clade 2.3.2.1a viruses were detected in poultry and wild birds in Bangladesh and in poultry, wild birds, captive tigers and leopards, and domestic cats in India. Circulation of viruses with clade 2.3.2.1a HAs in these countries has continued despite the introduction of clade 2.3.4.4b viruses. The HA of viruses detected in poultry in Bangladesh and India had up to one and five amino acid substitutions relative to the A/Victoria/149/2024 CVV, respectively. No antigenic data are available for these viruses. Viruses collected in the previous reporting period had HAs genetically similar to either the A/Victoria/149/2024 or A/duck/Bangladesh/17D1012/2018 CVVs and reacted well to post-infection ferret antisera raised against at least one of the available clade 2.3.2.1a CVVs.

Clade 2.3.4.4b viruses were detected in birds in Africa, North and South America, Antarctica, Asia and Europe. A(H5N1) viruses circulated in birds in most regions; A(H5N6) viruses were detected in poultry in China; A(H5N5) viruses were detected in Europe and North America; A(H5N8) viruses continued to circulate in Egypt; and A(H5N2) viruses were detected in wild birds in Japan. Infections in wild and captive mammals have been reported in many countries and the outbreak in dairy cattle continued in the USA. The HAs of A(H5N1) clade 2.3.4.4b viruses detected in birds in Argentina, Bolivia and Brazil were similar to viruses circulating in the region during previous reporting periods with up to six amino acid substitutions relative to the A/American wigeon/South Carolina/22-000345-001/2021 CVV. No antigenic data were available. Although some heterogeneity was observed, A(H5N1) viruses from birds and mammals in Bangladesh, Japan and the USA and multiple countries in Africa and Europe generally reacted well with post-infection ferret antisera raised against at least one of the available clade 2.3.4.4b CVVs; a virus from Crozet Islands and an increasing number of viruses from Egypt reacted less well. The A(H5N6) and A(H5N1) viruses identified in China had 2 to 14 HA amino acid substitutions relative to clade 2.3.4.4b CVVs and most reacted well with post-infection ferret antisera raised against CVV-like viruses. The HAs of A(H5N5) viruses detected in Europe and North America were genetically related to viruses detected in previous reporting periods and reacted well to ferret antisera raised against at least one of the available clade 2.3.4.4b CVVs.

Clade 2.3.2.1e viruses were detected in poultry in Cambodia, Lao People's Democratic Republic and Viet Nam. The HAs of these viruses were similar to viruses detected in previous periods in the region, with one to nine amino acid substitutions relative to the recommended clade 2.3.2.1e A/Cambodia/SVH240441/2024 CVV. Antigenic analyses are pending.

Clade 2.3.2.1g viruses were detected in poultry in multiple islands of the Republic of Indonesia. These viruses had HAs genetically similar to those of viruses circulating in the previous reporting period (Figure 1). 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. Antigenic analyses showed these viruses reacted poorly with post-infection ferret antisera raised against the clade 2.3.2.1e A/duck/Vietnam/NCVD-1584/2012 and the clade 2.3.2.1a A/duck/Bangladesh/17D1012/2018 CVVs. Some of the recent Indonesian viruses reacted well to post-infection ferret antiserum raised against the clade 2.3.2.1f A/chicken/Ghana/20/2015 CVV.

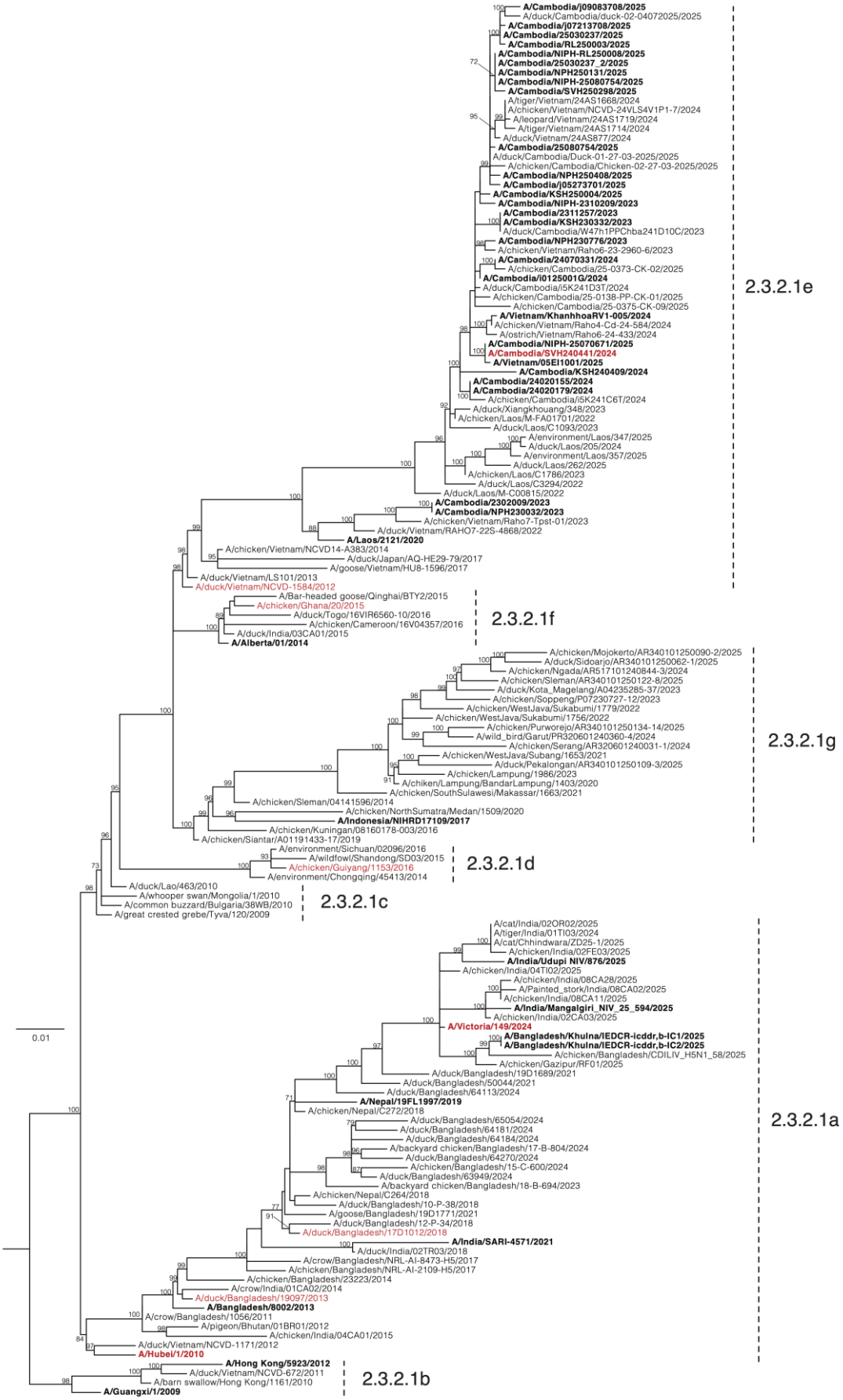

Figure 1. Phylogenetic relationships of A(H5) clade 2.3.2.1 HA genes. CVVs that are available or in preparation are in red. Human viruses are in bold font. The tree was built from the nucleotide sequences coding for the mature HA1 protein. The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes.

Influenza A(H5) candidate vaccine viruses

Based on current genetic, antigenic and epidemiologic data, no new CVVs are proposed. The available and pending A(H5) CVVs are listed in Table 2.

Table 2. Status of influenza A(H5) candidate vaccine virus development[*]

Candidate vaccine viruses (like virus)[†]	Clade	Institution[‡]	Available
CDC-RG (A/Viet Nam/1203/2004)	1	CDC	Yes
SJRG-161052 (A/Viet Nam/1203/2004)	1	SJCRH	Yes
NIBRG-14 (A/Viet Nam/1194/2004)	1	MHRA	Yes
NIBRG-88 (A/Cambodia/R0405050/2007)	1.1	MHRA	Yes
IDCDC-RG34B (A/Cambodia/X0810301/2013)	1.1.2	CDC	Yes
SJRG-166614 (A/duck/Hunan/795/2002)	2.1.1	SJCRH/HKU	Yes
CDC-RG2 (A/Indonesia/5/2005)	2.1.3.2	CDC	Yes
NIIDRG-9 (A/Indonesia/NIHRD11771/2011)	2.1.3.2a	NIID	Yes
SJRG-163222 (A/bar-headed goose/Qinghai/1A/2005)	2.2	SJCRH/HKU	Yes
IBCDC-RG7 (A/chicken/India/NIV33487/2006)	2.2	CDC/NIV	Yes
SJRG-163243 (A/whooper swan/Mongolia/244/2005)	2.2	SJCRH	Yes
IDCDC-RG11 (A/Egypt/2321-NAMRU3/2007)	2.2.1	CDC	Yes
NIBRG-23 (A/turkey/Turkey/1/2005)	2.2.1	MHRA	Yes
IDCDC-RG29 (A/Egypt/N03072/2010)	2.2.1	CDC	Yes
IDCDC-RG13 (A/Egypt/3300-NAMRU3/2008)	2.2.1.1	CDC	Yes
NIBRG-306 (A/Egypt/N04915/2014)	2.2.1.2	MHRA	Yes
SJRG-166615 (A/common magpie/Hong Kong/5052/2007)	2.3.2.1	SJCRH/HKU	Yes
IDCDC-RG30 (A/Hubei/1/2010)	2.3.2.1a	CDC	Yes
SJ007 (A/duck/Bangladesh/19097/2013)	2.3.2.1a	SJCRH	Yes
IDCDC-RG63A (A/duck/Bangladesh/17D1012/2018)	2.3.2.1a	CDC	Yes
SJ003 (A/barn swallow/Hong Kong/D10-1161/2010)	2.3.2.1b	SJCRH/HKU	Yes
NIBRG-301 (A/duck/Viet Nam/NCVD-1584/2012)	2.3.2.1e	MHRA	Yes
SJ009 (A/chicken/Guiyang/1153/2016)	2.3.2.1d	SJCRH/HKU	Yes
SJ002 (A/chicken/Hong Kong/AP156/2008)	2.3.4	SJCRH/HKU	Yes
IBCDC-RG6 (A/Anhui/1/2005)	2.3.4	CDC	Yes
CBER-RG1 (A/duck/Laos/3295/2006)	2.3.4	FDA	Yes
SJRG-164281 (A/Japanese white eye/Hong Kong/1038/2006)	2.3.4	SJCRH/HKU	Yes
IDCDC-RG36 (A/chicken/Bangladesh/11rs1984-30/2011)	2.3.4.2	CDC	Yes
IDCDC-RG35 (A/Guizhou/1/2013)	2.3.4.2	CDC/CCDC	Yes
IDCDC-RG42A (A/Sichuan/26221/2014) (H5N6)	2.3.4.4a	CDC/CCDC	Yes
IDCDC-RG71A (A/Astrakhan/3212/2020) (H5N8)	2.3.4.4b	CDC	Yes
CBER-RG8A (A/Astrakhan/3212/2020) (H5N8)	2.3.4.4b	FDA	Yes
IDCDC-RG78A (A/Am. Wigeon/South Carolina/22-000345-001/2021)	2.3.4.4b	CDC	Yes
NIID-002 (A/Ezo red fox/Hokkaido/1/2022)	2.3.4.4b	NIID	Yes
CNIC-JSNJ210 (A/Jiangsu/NJ210/2023)	2.3.4.4b	CCDC	Yes
IDCDC-RG43A (A/gyrfalcon/Washington/41088-6/2014) (H5N8)	2.3.4.4c	CDC	Yes
NIID-001 (A/duck/Hyogo/1/2016) (H5N6)	2.3.4.4e	NIID	Yes
IDCDC-RG65A (A/Guangdong/18SF020/2018) (H5N6)	2.3.4.4h	CDC	Yes
IDCDC-RG69A (A/ck/Vietnam/RAHO4-CD-20-421/2020-like)(H5N6)	2.3.4.4g	CDC	Yes
SJRG-165396 (A/goose/Guiyang/337/2006)	4	SJCRH/HKU	Yes
IDCDC-RG12 (A/chicken/Vietnam/NCVD-016/2008)	7.1	CDC	Yes
IDCDC-RG25A (A/chicken/Vietnam/NCVD-03/2008)	7.1	CDC	Yes
Candidate vaccine viruses in preparation	**Clade**	**Institution**	**Availability**
A/Victoria/149/2024-like	2.3.2.1a	Pending	Pending
A/Cambodia/SVH240441/2024-like	2.3.2.1e	CDC	Pending
IDCDC-RG75A (A/chicken/Ghana/20/2015-like)	2.3.2.1f	CDC	Pending
CNIC-FJ21099 (A/Fujian-Sanyuan/21099/2017-like) (H5N6)	2.3.4.4b	CCDC	Pending
A/chicken/Ghana/AVL-76321VIR7050-39/2021-like	2.3.4.4b	CDC	Pending
CNIC-HB29578 (A/Hubei/29578/2016-like) (H5N6)	2.3.4.4d	CCDC	Pending
SJ010 (A/chicken/Vietnam/NCVD-15A59/2015) (H5N6)	2.3.4.4f	SJCRH	Pending
A/Guangdong/18SF020/2018-like (H5N6)	2.3.4.4h	CCDC	Pending
A/Fujian/2/2024-like (H5N6)	2.3.4.4h	CCDC	Pending

[*]All listed CVVs have been produced using reverse genetics.

[†]Where not indicated, the virus subtype is H5N1.

[‡]Institutions developing and/or distributing the candidate vaccine viruses:
CDC – Centers for Disease Control and Prevention, USA
NIV – National Institute of Virology, India

CCDC – Chinese Center for Disease Control and Prevention, China
FDA – Food and Drug Administration, USA
HKU – The University of Hong Kong, Hong Kong Special Administrative Region (SAR), China
MHRA – Medicines and Healthcare products Regulatory Agency (previously known as NIBSC), United Kingdom of Great Britain and Northern Ireland
NIID – National Institute of Infectious Diseases, Japan
SJCRH – St. Jude Children's Research Hospital, USA

Influenza A(H9N2)

Influenza A(H9N2) viruses are enzootic in poultry in many parts of Africa, Asia and the Middle East, with the majority of viruses belonging to either the B or G HA lineage[3]. Since the late 1990s, when the first human infection was identified, sporadic detections of A(H9N2) viruses in humans and pigs have been reported, with associated mild disease in most human cases and no evidence for sustained human-to-human transmission.

Influenza A(H9N2) activity from 25 February to 22 September 2025

Twenty-four human infections with A(H9N2) viruses have been identified in China, four with disease onset dates in the previous reporting period. A(H9N2) viruses were detected in poultry in multiple countries in Africa, Asia and the Middle East and in an illegally imported poultry product in Japan.

Genetic and antigenic characteristics of influenza A(H9N2) viruses

The HAs of the 15 sequenced human viruses belonged to clade B4.7. Fourteen of these viruses belonged to clade B4.7.2 and had up to 25 amino acid substitutions relative to the A/Anhui-Tianjiaan/11086/2022 CVV. The other human virus had a clade B4.7.4 HA with 14 amino acid substitutions relative to the A/Anhui-Lujiang/39/2018 CVV. The majority of human viruses tested antigenically reacted well to post-infection ferret antisera raised against the A/Anhui-Tianjiaan/11086/2022 or the A/Anhui-Lujiang/39/2018 CVV.

A(H9N2) viruses from birds belonged to the following clades:

A *Clade B4.6* virus was detected in an imported poultry product in Japan. The HA of this virus was genetically similar to viruses previously reported in China, Lao PDR, and Singapore. There is currently no CVV for clade B4.6, but the virus reacted well to post-infection ferret antisera raised against both the clade G5.5 A/Oman/2747/2019 and clade B-like A/chicken/Hong Kong/G9/97 CVVs.

Clade B4.7 viruses were detected in poultry in Cambodia and Viet Nam. The HAs of these viruses continued to diversify genetically and accumulated up to 21 amino acid substitutions relative to the A/Anhui-Tianjiaan/11086/2022 CVV. No antigenic data were available from these viruses.

Clade G5.5 viruses were detected in poultry in Israel, Nigeria and Togo. Moreover, viruses belonging to clade G5.5 were identified in poultry in Mauritania and Senegal, although from samples collected in the previous reporting period. The HAs of the viruses from Israel had accumulated eight amino acid substitutions relative to the A/Oman/2747/2019 CVV. The HAs of viruses from Nigeria, Mauritania, Senegal and Togo were genetically related to viruses circulating in West Africa in the previous period and had up to 12 amino acid substitutions relative to the A/Oman/2747/2019 CVV. Ferret antiserum raised against the A/Oman/2747/2019 CVV reacted well with a virus from Togo. No antigenic data were available for the other G5.5 viruses.

Clade G5.6 viruses were detected in poultry in Egypt. These viruses had up to 35 amino acid substitutions relative to the A/Oman/2747/2019 CVV. Ferret antisera raised against either the A/Hong Kong/G9/97 or A/Oman/2747/2019 CVVs, however, reacted well with the majority of the viruses tested.

Clade G5.7 viruses were detected in poultry in Bangladesh and India, although from samples collected during the previous reporting period. The HAs of viruses identified in India were genetically related to those circulating during previous reporting periods and had accumulated up to 28 amino acid substitutions relative to the A/Bangladesh/0994/2011 CVV with eight amino acid substitutions occurring in putative antigenic sites. Ferret antiserum raised against the A/Bangladesh/0994/2011 CVV reacted well with the majority of Bangladesh viruses tested, however, some viruses with mutations in putative antigenic sites reacted less well.

[3] https://wwwnc.cdc.gov/eid/article/30/8/23-1176_article

Clade Y8 viruses were detected in poultry in France and Madagascar, and in wild birds in Europe and North America. The HA sequences of viruses detected in Madagascar were similar to previously reported viruses in the country. The HA sequence of the virus from France was genetically similar to viruses previously reported in Europe. No antigenic data were available for these viruses and there is currently no CVV for this clade.

Influenza A(H9N2) candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, no new CVVs are proposed. The available and pending A(H9N2) CVVs are listed in Table 3.

Table 3. Status of influenza A(H9N2) candidate vaccine virus development

Candidate vaccine viruses (like virus)	Clade†	Type	Institution*	Available
A/Hong Kong/1073/99	G-like	Wild type	MHRA	Yes
NIBRG-91 (A/chicken/Hong Kong/G9/97)	B-like	Reverse genetics	MHRA	Yes
IBCDC-2 (A/chicken/Hong Kong/G9/97)	B-like	Conventional	CDC	Yes
IDCDC-RG26 (A/Hong Kong/33982/2009)	G4	Reverse genetics	CDC	Yes
IDCDC-RG31 (A/Bangladesh/994/2011)	G5.7	Reverse genetics	CDC	Yes
SJ008 (A/Hong Kong/308/2014)	B4.7	Reverse genetics	SJCRH	Yes
IDCDC-RG61A (A/Anhui-Lujiang/39/2018)	B4.7.4	Reverse genetics	CDC/CCDC	Yes
IDCDC-RG66A (A/Oman/2747/2019)	G5.5	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation	**Clade**	**Type**	**Institution**	**Availability**
A/Anhui-Lujiang/39/2018-like	B4.7.4	Conventional	MHRA	Pending
A/Anhui-Tianjiaan/11086/2022-like	B4.7.2	Reverse genetics	CDC	Pending

*Institutions distributing the candidate vaccine viruses:
CCDC – Chinese Center for Disease Control and Prevention, China
CDC – Centers for Disease Control and Prevention, USA
MHRA – Medicines and Healthcare products Regulatory Agency (previously known as NIBSC), United Kingdom of Great Britain and Northern Ireland
SJCRH – St. Jude Children's Research Hospital, USA
† Note on nomenclature https://wwwnc.cdc.gov/eid/article/30/8/23-1176_article

Influenza A(H10)

A(H10) viruses are frequently detected in poultry in many regions of the world and are considered endemic in poultry in China, with rare human infections reported. Prior to this reporting period, four A(H10N3), one A(H10N5) and three A(H10N8) human infections were detected in China and A(H10N7) viruses were detected in individuals with conjunctivitis or mild upper respiratory tract symptoms in Australia (n=2) and Egypt (n=2).

Influenza A(H10) activity from 25 February to 22 September 2025

Two human A(H10N3) virus infections were identified in China.

Antigenic and genetic characteristics of influenza A(H10N3) viruses

One of the human A(H10N3) viruses was sequenced and had an HA that was genetically similar to human A(H10N3) viruses from 2024, maintaining avian virus signatures at key receptor binding sites. As with previous viruses, the recent A(H10N3) virus had some gene segments derived from A(H9N2) viruses. No virus was recovered from the clinical material.

A(H10N3), A(H10N4) and an A(H10N8) virus were detected in ducks and chickens in Fujian and Jiangxi Provinces of China, some with collection dates during the previous reporting period. The HAs of these viruses formed subtype-specific phylogenetic clades with those of the A(H10N3) viruses being genetically similar to the human A(H10N3) viruses. A(H10N7) viruses, genetically similar to those detected in previous periods, were detected in ducks in Cambodia.

Influenza A(H10N3) candidate vaccine viruses

Based on the available genetic and epidemiologic data, no new CVVs are proposed. The pending A(H10N3) CVV is listed in Table 4.

Table 4. Status of influenza A(H10N3) candidate vaccine virus development

Candidate vaccine viruses (like virus)	Lineage	Type	Institution*	Available
A/Jiangsu/428/2021	Eurasian	Reverse genetics	CDC/CCDC	Pending

*Institution distributing the candidate vaccine viruses:
CDC – Centers for Disease Control and Prevention, USA
CCDC – Chinese Center for Disease Control and Prevention, China

Influenza A(H1)v[4]

Influenza A(H1) viruses are enzootic in swine populations in most regions of the world. The genetic and antigenic characteristics of the viruses circulating in different regions are diverse. Viruses isolated from human infections with swine influenza A(H1) viruses are designated as A(H1) variant ((H1)v) viruses and have been previously detected in the Americas, Asia and Europe.

Influenza A(H1)v activity from 25 February to 22 September 2025

One case of infection with an A(H1N1)v virus was detected in Germany. Multiple clades of A(H1) viruses were detected in swine populations globally (Table 5).

Antigenic and genetic characteristics of influenza A(H1N1)v viruses

The A(H1N1)v virus case from Germany was sequenced and had an HA belonging to clade 1C.2.2 similar to other 1C.2.2 viruses detected in swine in the region. The HA had 27 amino acid substitutions compared to the clade 1C.2.2 CVV, A/Hessen/47/2020. No antigenic data were available.

Table 5. Recent swine and A(H1)v activity shared with international agencies and/or collected from sequence repositories.

Country, area or territory	Host	Genetic clade
Austria	Swine	1A.3.3.2; 1B.1.2.1
Belgium	Swine	1A.3.3.2; 1B.1.2.1; 1C.2.2
Canada	Swine	1A.1.1.3; 1A.2; 1A.3.3.2
Finland	Swine	1C.2.4.2
France	Swine	1A.3.3.2; 1C.2.1; 1C.2.4.2; 1C.2.7
Germany	Swine	1A.3.3.2; 1C.2.2
	Human (1)*	1C.2.2
Italy	Swine	1A.3.3.2; 1C.2.2; 1C.2.4.1; 1C.2.4.2; 1C.2.4.3
Portugal	Swine	1A.3.3.2; 1C.2.1
Russian Federation	Swine	1A.3.3.2; 1C.2.1; 1C.2.4.1
Sweden	Swine	1A.3.3.2; 1C.2.4.1; 1C.2.5
United Kingdom of Great Britain and Northern Ireland (the)	Swine	1B.1.1.1; 1C.2.2
United States of America (the)	Swine	1A.1.1.3; 1A.3.3.2; 1A.3.3.3-c1; 1A.3.3.3-c3; 1B.2.1; 1B.2.2.2

*Number of cases and/or detections

Influenza A(H1)v candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, no new A(H1)v CVVs are proposed. The available and pending A(H1)v CVVs are listed in Table 6.

Table 6. Status of influenza A(H1)v candidate vaccine virus development

Candidate vaccine viruses (like viruses)	Clade	Type	Institution*	Available
CNIC-1601 (A/Hunan/42443/2015) (H1N1)v	1C.2.3	Conventional	CCDC	Yes
IDCDC-RG48A (A/Ohio/9/2015) (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Yes
IDCDC-RG58A (A/Michigan/383/2018) (H1N2)v	1B.2.1	Reverse genetics	CDC	Yes
IDCDC-RG59 (A/Ohio/24/2017) (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Yes

[4] Standardization of terminology for the influenza virus variants infecting humans: Update https://cdn.who.int/media/docs/default-source/influenza/global-influenza-surveillance-and-response-system/nomenclature/standardization_of_terminology_influenza_virus_variants_update.pdf?sfvrsn=d201f1d5_6

IDCDC-RG90A (A/California/71/2021) (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Yes
NIB-124C (A/Hessen/47/2020) (H1N1)v	1C.2.2	Conventional	MHRA	Yes
NIB-131C (A/Bretagne/24241/2021) (H1N2)v	1C.2.4	Conventional	MHRA	Yes
Candidate vaccine viruses in preparation	**Clade**	**Type**	**Institution**	**Availability**
A/Catalonia/NSAV198289092/2023-like (H1N1)v	1A.3.3.2	Reverse genetics	MHRA	Pending
A/England/234600203/2023-like (H1N2)v	1B.1.1.1	Reverse genetics	MHRA	Pending
A/Iowa/32/2016-like (H1N2)v	1B.2.2.1	Reverse genetics	CDC	Pending
A/Ohio/35/2017-like (H1N2)v	1B.2.1	Reverse genetics	MHRA	Pending
A/Netherlands/10370-1b/2020 (H1N1)v	1C.2.1	Reverse genetics	MHRA	Pending
A/Bretagne/24241/2021 (H1N2)v	1C.2.4	Reverse genetics	SJCRH	Pending
A/Wisconsin/03/2021 (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Pending
A/Pennsylvania/27/2024 (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Pending
		Conventional	MHRA	Pending

*Institution distributing the candidate vaccine viruses:
CDC – Centers for Disease Control and Prevention, USA
CCDC – Chinese Center for Disease Control and Prevention, China
MHRA – Medicines and Healthcare products Regulatory Agency (previously known as NIBSC), United Kingdom of Great Britain and Northern Ireland
SJCRH – St. Jude Children's Research Hospital, USA

Influenza A(H3N2)v

Influenza A(H3N2) viruses with diverse genetic and antigenic characteristics are enzootic in swine populations in most regions of the world. Human infections with influenza A(H3N2)v viruses originating from swine have been previously documented in the Americas, Asia, Australia and Europe.

Influenza A(H3N2)v activity from 25 February to 22 September 2025

No cases of infection with A(H3N2)v viruses were detected in this reporting period. A(H3N2) viruses were detected in swine in Canada, France, Italy, Portugal, Russian Federation and the USA (Table 7).

Table 7. Recent swine and A(H3)v activity shared with international agencies and/or collected from sequence repositories.

Country, area or territory	Host	Genetic clade
Canada	Swine	1990.4.b2; 1990.4.c; 2010.1
France	Swine	Other-Human-2020
Italy	Swine	2010.3
Portugal	Swine	2000.3
Russian Federation	Swine	Other-Human-2020
United States of America (the)	Swine	1990.4; 1990.4.a; 1990.4.b1; 1990.4.i; 2010.1; 2010.2; Other-Human-2020

Influenza A(H3N2)v candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, no new CVVs are proposed. The available A(H3N2)v CVVs are listed in Table 8.

Table 8. Status of influenza A(H3N2)v candidate vaccine virus development

Candidate vaccine viruses (like viruses)	Lineage	Type	Institution*	Available
NYMC X-203 (A/Minnesota/11/2010)	3.1990.4.A	Conventional	CDC	Yes
NYMC X-213 (A/Indiana/10/2011)	3.1990.4.A	Conventional	CDC	Yes
IDCDC-RG55C (A/Ohio/28/2016)	3.2010.1	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation		**Type**	**Institution**	**Availability**
A/Ohio/13/2017-like	3.2010.1	Reverse genetics	CDC	Pending
A/swine/Iowa/23TOSU0850/2023	3.1990.4A	Reverse genetics	CDC	Pending

*Institution distributing the candidate vaccine viruses:
CDC – Centers for Disease Control and Prevention, USA

Acknowledgements

Acknowledgement goes to the WHO Global Influenza Surveillance and Response System (GISRS) which provides the mechanism for detection and monitoring of zoonotic influenza viruses. We thank the National Influenza Centres (NICs) of GISRS who contributed information, clinical specimens and viruses, and associated data; WHO collaborating centres of GISRS for their in-depth characterisation and analysis of viruses and preparation of CVVs; WHO Essential Regulatory Laboratories of GISRS; and WHO H5 Reference Laboratories for their complementary analyses and preparation of CVVs. We acknowledge the WOAH/FAO Network of Expertise on Animal Influenza (OFFLU) laboratories for their in-depth characterization and comprehensive analysis of viruses and other national public and veterinary health institutions for contributing information and viruses. We also acknowledge the GISAID Global Data Science Initiative for the EpiFlu™ database, and other sequence databases which were used to share gene sequences and associated information.