

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

February 2026

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<sup>1</sup> that are relevant to CVV updates. Institutions interested in receiving these CVVs should contact WHO at [girs@who.int](mailto:girs@who.int) or the institutions listed in announcements published on the WHO website<sup>2</sup>.

### 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 23 September 2025 to 23 February 2026

Since 2003, 17 A(H5), one A(H5N2), one A(H5N5), seven A(H5N8), 93 A(H5N6) and 983 A(H5N1) human infections or detections have been reported. Since 23 September 2025, six 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). Antibodies specific for A(H5N1) viruses were detected in one dairy cow on a farm in the Netherlands where A(H5N1) virus was detected in a cat. All cattle were PCR negative for influenza virus indicating no evidence of active infection in the herd at the time of sampling.

**Table 1.** A(H5) activity reported to international agencies from 23 September 2025 to 23 February 2026.

Country, area or territory	Host	Genetic clade
Antarctica (including Sub-Antarctic Islands)	Wild birds	2.3.4.4b (H5N1)
Argentina	Poultry	unknown <sup>†</sup> (H5)
Austria	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)

<sup>1</sup>For information relevant to other notifiable influenza virus infections in animals refer to <https://wahis.woah.org/#/home>

<sup>2</sup><https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/zoonotic-influenza-viruses-and-candidate-vaccine-viruses>

Bosnia and Herzegovina	Wild birds	unknown (H5N1)
Bangladesh	Human (1)*	2.3.2.1a (H5N1)
	Poultry	2.3.2.1a (H5N1); 2.3.4.4b (H5N1)
Belgium	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Brazil	Poultry	2.3.4.4b (H5N1)
	Wild birds	unknown (H5N1)
Bulgaria	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Bhutan	Poultry	unknown (H5N1)
Cambodia	Poultry	2.3.2.1e <sup>±</sup> (H5N1)
	Human (3)*	2.3.2.1e <sup>±</sup> (H5N1)
Canada	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Cayman Islands	Poultry	2.3.4.4b (H5N1)
China	Poultry	2.3.4.4b (H5N1); 2.3.4.4b (H5N6)
	Wild birds	unknown (H5)
Hong Kong SAR, China	Wild birds	unknown (H5N1)
Taiwan, China	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Colombia	Poultry	unknown (H5N1)
Czechia	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Denmark	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
Egypt	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Estonia	Poultry	2.3.4.4b (H5N1)
	Wild birds	unknown (H5N1)
	Wild mammals (red fox)	2.3.4.4b (H5N1)
Falkland Islands	Wild birds	unknown (HPAI)
Finland	Wild birds	unknown (H5); 2.3.4.4b (H5N1)
France	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Germany	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Georgia	Wild birds	2.3.4.4b (H5N1)
Guatemala	Poultry	2.3.4.4b (H5N1)
Hungary	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Heard Island and McDonald Islands	Wild mammals (southern elephant seal)	2.3.4.4b (H5N1)
Iceland	Wild birds	unknown (H5); unknown (H5N5)
	Wild mammals (polar fox)	unknown (H5); unknown (H5N5)
India	Poultry	2.3.4.4b (H5N1); unknown (H5N1)
	Wild birds	unknown (H5N1)
Indonesia	Poultry	unknown (HPAI)

Iran (Islamic Republic of)	Poultry	unknown (H5N1)
Iraq	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Ireland	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Isle of Man	Wild birds	2.3.4.4b (H5N1)
Israel	Wild birds	unknown (H5N1)
Italy	Poultry	2.3.4.4b (H5N1)
	Wild birds	unknown (H5); 2.3.4.4b (H5N1)
	Wild mammals (red fox)	2.3.4.4b (H5N1)
Japan	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	Wild mammals (marten, racoon, racoon dog)	2.3.4.4b (H5N1)
Kazakhstan	Wild birds	2.3.4.4b (H5N1)
Lao People's Democratic Republic	Poultry	2.3.4.4b (H5N1), 2.3.2.1e (H5N1)
Latvia	Poultry	unknown (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Lithuania	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Luxembourg	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Mongolia	Wild birds	2.3.4.4b (H5N1)
Mexico	Human (1)*	2.3.4.4b (H5N2)
	Poultry	2.3.4.4b (H5N2)
Namibia	Wild birds	unknown (H5N1)
Netherlands (Kingdom of the)	Poultry	unknown (H5); 2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
	Wild mammals (red fox, harbour seal, domestic cat)	2.3.4.4b (H5N1)
Nigeria	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
North Macedonia	Wild birds	unknown (H5N1)
Norway	Wild birds	unknown (H5); 2.3.4.4b (H5N1)
Philippines	Poultry	unknown (H5); unknown (H5N1), unknown (H5N8)
Poland	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Portugal	Poultry	unknown (H5); 2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)
Republic of Korea	Poultry	2.3.4.4b (H5N1); unknown (H5N9)
	Wild birds	unknown (H5N1); unknown (H5N6); unknown (H5N9)
Republic of Moldova	Wild birds	unknown (H5N1)
Romania	Poultry	2.3.4.4b (H5N1)
	Wild birds	unknown (H5N1)
Russian Federation (the)	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1)

Serbia	Wild birds	unknown (H5N1)
Slovakia	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)
Slovenia	Wild birds	unknown (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	unknown (H5); 2.3.4.4b (H5N1)
	Wild mammals (fox)	2.3.4.4b (H5N1)
Svalbard and Jan Mayen	Wild birds	2.3.4.4b (H5N5)
Sweden	Poultry	2.3.4.4b (H5N1)
	Wild birds	2.3.4.4b (H5N1; H5N2)
Switzerland	Wild birds	unknown (H5N1)
Türkiye	Poultry	unknown (H5N1)
Ukraine	Poultry	2.3.4.4b (H5N1)
	Wild birds	unknown (H5N1)
	Human (1)*	2.3.4.4b (H5N5)
	Poultry	2.3.4.4b (H5N1)
	Domestic mammals (dairy cow, domestic cat)	2.3.4.4b (H5N1)
United States of America (the)	Wild birds	2.3.4.4b (H5N1); 2.3.4.4b (H5N5)
	Wild mammals (black bear, bobcat, domestic cat, house mouse, raccoon, skunk, striped skunk, Virginia opossum, mountain lion)	unknown (H5); 2.3.4.4b (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)
Viet Nam	Poultry	unknown (H5N1)
	Wild birds	unknown (H5N1)

<sup>†</sup>unknown: denotes instances where specific lineage designations were not available

\*Number of cases and/or detections

<sup>‡</sup>Formerly classified as A(H5) clade 2.3.2.1c.

### Genetic and antigenic characteristics of influenza A(H5) viruses

Six new human infections or detections with A/goose/Guangdong/1/96-lineage viruses were reported. Most infected individuals had recent exposure to birds. The A(H5N1) human cases included one fatal infection in Bangladesh with a clade 2.3.2.1a virus and three infections in Cambodia with clade 2.3.2.1e viruses, two of which were severe the other fatal. Two infections with subtypes of A/goose/Guangdong/1/96-lineage viruses not previously reported in humans were detected; a severe A(H5N2) clade 2.3.4.4b virus infection in Mexico and a fatal infection with an A(H5N5) clade 2.3.4.4b virus in the United States of America. Both cases occurred following likely exposure to infected birds or contaminated environments.

The HA1 of the human clade 2.3.2.1a virus from Bangladesh had one amino acid substitution relative to the A/Victoria/149/2024 CVV. Antigenic analysis of the virus from the human case was not available, but a genetically related virus from poultry in Bangladesh reacted well to post-infection ferret antisera raised against the A/Victoria/149/2024 CVV. The HA1 of the A(H5N2) virus reported by Mexico had seven amino acid substitutions relative to the A/Astrakhan/3212/2020 CVV. Antigenic analyses are pending. The HA1 of the A(H5N5) virus from the human case in the United States of America had five amino acid substitutions relative to the A/Astrakhan/3212/2020 CVV, including a gain of a potential glycosylation site. Post-infection ferret antisera raised against clade 2.3.4.4b A/American Wigeon/South Carolina/22-000345-001/2021, A/Ezo red fox/Hokkaido/1/2022 and A/Astrakhan/3212/2020 CVVs showed reduced reactivity to the A(H5N5) virus. Viruses from the three cases reported by Cambodia belonged to clade 2.3.2.1e. The HA1s of the two

human viruses for which complete sequences were available had two amino acid substitutions relative to the A/Cambodia/SVH240441/2024 CVV; antigenic characterization of the viruses 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 in Bangladesh, despite the introduction of clade 2.3.4.4b viruses. The HA of the clade 2.3.2.1a viruses were genetically similar to either the A/Victoria/149/2024 or A/duck/Bangladesh/17D1012/2018 CVVs. Post-infection ferret antisera raised against at least one of the available clade 2.3.2.1a CVVs recognised these viruses well.

*Clade 2.3.4.4b* viruses were detected in birds in Africa, Antarctica, Asia, Europe and North and South America. A(H5N1) viruses circulated in birds in most regions; A(H5N6) viruses were detected in poultry in China and in wild birds in the Republic of Korea; A(H5N5) viruses were detected in Europe, Japan and North America; A(H5N2) viruses were detected in poultry in Mexico and in wild birds in Sweden; and A(H5N9) viruses were detected in wild birds and poultry in the Republic of Korea.

Although some heterogeneity was observed, A(H5N1) viruses from wild birds and poultry in Japan, the United States of America 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. The HA1 sequences of A(H5N1) viruses circulating in wildlife in subantarctic islands were similar to viruses circulating in the region during previous reporting periods and reacted well with post-infection ferret antisera raised against at least one of the available clade 2.3.4.4b CVVs. A(H5N1) viruses identified in poultry in Bangladesh and Viet Nam had no more than six HA1 amino acid substitutions compared to the A/Ezo red fox/Hokkaido/1/2022 CVV, and post-infection ferret antisera raised against at least one of the available clade 2.3.4.4b CVVs reacted well with these viruses, albeit with some showing reduced reactivity. A(H5N1) viruses from poultry in Egypt and Lao People's Democratic Republic had up to 10 HA1 amino acid substitutions relative to the A/Ezo red fox/Hokkaido/1/2022 CVV with antigenic data pending. The HA sequences of A(H5N1) clade 2.3.4.4b viruses detected in poultry in Brazil were similar to viruses circulating in the region during previous reporting periods with up to six HA1 amino acid substitutions relative to the A/American wigeon/South Carolina/22-000345-001/2021 CVV. No antigenic data were available for the viruses from Brazil. The A(H5N6) and A(H5N1) viruses identified in poultry in China had from seven to 12 HA amino acid substitutions relative to clade 2.3.4.4b CVVs, and post-infection ferret antisera raised against related CVVs reacted well with most viruses. The HAs of A(H5N5) viruses detected in wild birds in Europe, Japan and North America were genetically related to viruses detected in previous reporting periods. Ferret antisera raised against at least one of the available clade 2.3.4.4b CVVs reacted well with the A(H5N5) viruses isolated from wild birds in Europe. Infections in wild and captive mammals have been reported in many countries. The outbreak in dairy cattle continued in the United States of America and one additional spillover of A(H5N1) virus into dairy cattle was reported.

*Clade 2.3.2.1e* viruses were detected in poultry in Cambodia, Lao People's Democratic Republic and Viet Nam. The HAs of viruses circulating in Cambodia and Viet Nam were genetically similar to viruses detected in previous periods, with two to five HA1 amino acid substitutions relative to the clade 2.3.2.1e A/Cambodia/SVH240441/2024 CVV. These viruses reacted well to ferret antisera raised against either the A/duck/Vietnam/NCVD-1584/2012, A/chicken/Ghana/20/2015 or the A/Cambodia/SVH240441/2024-like CVV. Viruses identified in Lao People's Democratic Republic had four to 11 HA1 amino acid substitutions relative to the A/Cambodia/SVH240441/2024 CVV with antigenic analyses pending.

*Clade 2.3.2.1g* viruses were detected in poultry in multiple islands of the Republic of Indonesia, although from samples collected in the previous reporting period. These viruses had HAs genetically similar to those of viruses circulating in previous reporting periods. Currently, there is no CVV for this clade.

### **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\***

<b>Candidate vaccine viruses (like virus)<sup>†</sup></b>	<b>Clade</b>	<b>Institution<sup>‡</sup></b>	<b>Available</b>
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
NIID-003 A/Victoria/149/2024-like	2.3.2.1a	NIID	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
IDCDC-RG88A (A/Cambodia/SVH240441/2024-like)	2.3.2.1e	CDC	Yes
SJ009 (A/chicken/Guiyang/1153/2016)	2.3.2.1d	SJCRH/HKU	Yes
SJ002 (A/chicken/Hong Kong/API56/2008)	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
SJ010 (A/chicken/Vietnam/NCVD-15A59/2015) (H5N6)	2.3.4.4f	SJCRH	Yes
IDCDC-RG65A (A/Guangdong/18SF020/2018) (H5N6)	2.3.4.4h	CDC	Yes
CNIC- FJ02 (A/Fujian/2/2024) (H5N6)	2.3.4.4h	CCDC	Yes
IDCDC-RG69A (A/chicken/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
<b>Candidate vaccine viruses in preparation</b>	<b>Clade</b>	<b>Institution</b>	<b>Availability</b>
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
A/Guangdong/18SF020/2018-like (H5N6)	2.3.4.4h	CCDC	Pending
A/Washington/2148/2025 (H5N5) (A/chicken/Ghana/AVL-76321VIR7050-39/2021-like)	2.3.4.4b	CDC	Pending

\*All listed CVVs have been produced using reverse genetics.

<sup>†</sup>Where not indicated, the virus subtype is H5N1.<sup>‡</sup>Institutions developing and/or distributing the candidate vaccine viruses:

CDC – Centers for Disease Control and Prevention, United States of America

NIV – National Institute of Virology, India

CCDC – Chinese Center for Disease Control and Prevention, China

FDA – Food and Drug Administration, United States of America

## Influenza A(H7)

Influenza A(H7) viruses are maintained in waterfowl and occasionally spill over to poultry populations with the associated disease ranging from mild to severe. A total of 1 568 laboratory-confirmed human infections with avian influenza A(H7N9) virus of the A/Anhui/1/2013-lineage, including 616 fatal cases (CFR: 39%), have been reported to WHO since early 2013. The last case of human infection with avian influenza A(H7N9) reported to WHO was in 2019.

### Influenza A(H7) activity from 23 September 2025 to 23 February 2026

No A(H7N9) human infections were reported in this period. An HPAI A/Anhui/1/2013-lineage A(H7N9) virus was detected in an environmental sample from China. HPAI A(H7N3) viruses are considered endemic in poultry in Mexico and continue to evolve. These viruses do not belong to the A/Anhui/1/2013-lineage.

### Genetic and antigenic characteristics of influenza A(H7) viruses

The HA of the A/Anhui/1/2013-lineage A(H7N9) virus was most similar to those of viruses detected in 2022-2023 and had 20 HA1 amino acid substitutions relative to the A/Gansu/23277/2019 CVV. No antigenic data were available.

HPAI A(H7N3), A(H7N8) and A(H7N9) viruses detected during previous reporting periods in poultry in Australia were antigenically characterized and reacted well to a post-infection ferret antiserum raised against the A(H7N3) A/mallard/Netherlands/12/2000 CVV. No genetic or antigenic data were available for A(H7N3) viruses known to circulate in Mexico.

### Influenza A(H7) candidate vaccine viruses

Based on the current epidemiologic and virologic data, no new A(H7) CVVs are proposed. Available A(H7) CVVs are shown in Table 3.

**Table 3. Status of influenza A(H7) candidate vaccine virus development**

Candidate vaccine virus (like virus)	Lineage (subtype)	Type	Institution*	Available
IDCDC-RG33A (A/Anhui/1/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
NIBRG-268 (A/Anhui/1/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	MHRA	Yes
NIIDRG-10.1 (A/Anhui/1/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	NIID	Yes
SJ005 (A/Anhui/1/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	SJCRH	Yes
NIBRG-267 (A/Shanghai/2/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	MHRA	Yes
CBER-RG4A (A/Shanghai/2/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	FDA	Yes
IDCDC-RG32A (A/Shanghai/2/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
IDCDC-RG32A.3 (A/Shanghai/2/2013)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
IDCDC-RG56B (A/Hong Kong/125/2017)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
IDCDC-RG56N (A/Guangdong/17SF003/2016)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
NIBRG-375 (A/Guangdong/17SF003/2016)	A/Anhui/1/2013 (H7N9)	Reverse genetics	MHRA	Yes
CBER-RG7C (A/Guangdong/17SF003/2016)	A/Anhui/1/2013 (H7N9)	Reverse genetics	FDA	Yes
CBER-RG7D (A/Guangdong/17SF003/2016)	A/Anhui/1/2013 (H7N9)	Reverse genetics	FDA	Yes
IDCDC-RG64A (A/Gansu/23277/2019)	A/Anhui/1/2013 (H7N9)	Reverse genetics	CDC	Yes
IBCDC-5 (A/turkey/Virginia/4529/2002)	American (H7N2)	Conventional	CDC	Yes
SJRG-161984-B (A/Canada/rv444/2004)	American (H7N3)	Reverse genetics	SJCRH	Yes
NIBRG-109 (A/New York/107/2003)	American (H7N2)	Conventional	MHRA	Yes
IBCDC-1 (A/mallard/Netherlands/12/2000)	Eurasian (H7N7)	Conventional	CDC	Yes
NIBRG-60 (A/mallard/Netherlands/12/2000)	Eurasian (H7N3)	Reverse genetics	MHRA	Yes
NIBRG-63 (A/mallard/Netherlands/12/2000)	Eurasian (H7N1)	Reverse genetics	MHRA	Yes
Candidate vaccine virus in preparation	Lineage (subtype)	Type	Institution*	Available
A/chicken/Jiangsu/1/2018-like	Eurasian (H7N4)	Reverse genetics	CCDC	Pending
A/Hunan/02650/2016-like	A/Anhui/1/2013 (H7N9)	Reverse genetics	CCDC	Pending

\*Institutions developing and/or distributing the candidate vaccine viruses:

CDC – Centers for Disease Control and Prevention, United States of America  
 CCDC – Chinese Center for Disease Control and Prevention  
 FDA – Food and Drug Administration, United States of America  
 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

## 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 lineages<sup>1</sup>. 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 23 September 2025 to 23 February 2026

Fourteen human infections with A(H9N2) viruses were identified in China. A(H9N2) viruses were detected in poultry in multiple countries in Africa and Asia.

### Genetic and antigenic characteristics of influenza A(H9N2) viruses

The HAs of the 10 sequenced human viruses belonged to clade B4.7 (Figure 1). Eight of these HAs belonged to clade B4.7.2 and had up to 29 HA1 amino acid substitutions relative to the A/Anhui-Tianjiaan/11086/2022 CVV. A subset of these viruses, as represented by A/Hunan/40087/2025, had HAs that formed a separate cluster within the B4.7.2 clade that also contained human viruses and viruses detected in environmental samples from China in 2024 and 2025 (Figure 1). Viruses from this cluster reacted less well with post infection ferret antiserum raised against A/Anhui-Tianjiaan/11086/2022 (Table 4). The HAs of the other two human viruses belonged to clade B4.7.3 and had 10 and 11 HA1 amino acid substitutions relative to the A/Anhui-Lujiang/39/2018 CVV; these viruses were not tested antigenically.

**Table 4. Hemagglutination inhibition assays of recent B4.7 A(H9N2) viruses**

	Clade	HK-G9	HK308	AHLJ39	AHTJ11086
<b>Reference antigen</b>					
A/chicken/HK/G9/1997	B-like	<b>1280</b>	<20	40	<20
A/HK/308/2014	B4.7.4	40	<b>5120</b>	2560	160
A/Anhui-Lujiang/39/2018	B4.7.4	<20	80	<b>5120</b>	80
A/Anhui-Tianjiaan/11086/2022	B4.7.2	<20	40	320	<b>640</b>
<b>Test antigens</b>					
A/Hunan/40087/2025	B4.7.2	<20	<20	160	80
A/environment/Guangxi/39889/2025	B4.7.2	<20	<20	320	80
A/environment/Guangxi/40835/2025	B4.7.2	40	<20	320	80
A/environment/Fujian/41008/2025	B4.7.2	80	80	320	640
A/Guangxi-Jinchengjiang/11839/2025	B4.7.2	<20	80	640	640

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

*Clade B4.7* viruses were detected in poultry in Cambodia, China, Lao People’s Democratic Republic and Viet Nam. The HAs of these viruses continued to diversify genetically, accumulating amino acid substitutions relative to the A/Anhui-Tianjiaan/11086/2022 and A/Anhui-Lujiang/39/2018 CVVs. Despite this diversification, and with the exception of viruses with HAs belonging to the B4.7.2 subcluster detailed above, the majority of tested viruses reacted well with post-infection ferret antisera raised against available CVVs.

*Clade G5.6* viruses were detected in poultry in Egypt. These viruses were genetically similar to viruses detected in Egypt in previous periods that reacted well with post-infection antiserum raised against the A/Oman/2747/2019 CVV, despite the accumulation of many HA amino acid substitutions.

*Clade G5.7* viruses were detected in poultry in Bangladesh. The HAs of these viruses had accumulated up to 22 HA1 amino acid substitutions relative to the A/Bangladesh/0994/2011 CVV. 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.

## Influenza A(H9N2) candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, a new A/Hunan/40087/2025-like CVV is proposed. The available and pending A(H9N2) CVVs are listed in Table 5.

**Table 5. Status of influenza A(H9N2) candidate vaccine virus development**

Candidate vaccine viruses (like virus)	Clade <sup>†</sup>	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
A/Hunan/40087/2025-like	B4.7.2	Reverse genetics	CCDC	Pending

\*Institutions distributing the candidate vaccine viruses:

CCDC – Chinese Center for Disease Control and Prevention, China

CDC – Centers for Disease Control and Prevention, United States of America

MHRA – Medicines and Healthcare products Regulatory Agency, United Kingdom of Great Britain and Northern Ireland

SJCRH – St. Jude Children’s Research Hospital, United States of America

<sup>†</sup> Note on nomenclature [https://wwwnc.cdc.gov/eid/article/30/8/23-1176\\_article](https://wwwnc.cdc.gov/eid/article/30/8/23-1176_article)



**Figure 1.** Phylogenetic relationships of A(H9) B lineage HA genes. CVVs that are available or in preparation are in red. Human viruses are in bold font. The proposed CVV is indicated by a red dot (●). The tree was built from the nucleotide sequences coding for the mature HA1 protein. The viruses tested in haemagglutination 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.

## Influenza A(H10)

A(H10) viruses are detected in poultry in some regions of the world with rare human infections reported. Prior to this reporting period, six 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 23 September 2025 to 23 February 2026

A human A(H10N3) virus infection was identified in China. Two A(H10N4) viruses were detected in a wild bird and a chicken in China.

### Antigenic and genetic characteristics of influenza A(H10N3) viruses

The human A(H10N3) virus had an HA that was genetically similar to human A(H10N3) viruses from 2024-2025 and contained a mix of avian and mammalian signatures at position 228 of the receptor binding site. The virus had 12 HA1 amino acid substitutions relative to the A/Jiangsu/428/2021 CVV and it reacted with a post-infection ferret antiserum raised against this CVV albeit with a four-fold reduction in haemagglutination inhibition titre. As with previous viruses, the recent A(H10N3) virus had some gene segments derived from A(H9N2) viruses.

The HAs of the A(H10N4) viruses from birds in China were phylogenetically distinct from each other and from the human A(H10N3) virus. Despite this divergence in HA sequence, the two A(H10N4) viruses were antigenically similar, but they reacted less well to a post-infection ferret antiserum raised to a human A(H10N3) virus from 2024. A(H10N7) viruses were identified in domestic ducks in Cambodia from samples collected during the previous reporting period. The HA sequences of these viruses were genetically related to viruses circulating in previous reporting periods and had accumulated up to 37 amino acid substitutions in the HA1 relative to the A/Jiangsu/428/2021 CVV.

### 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 6.

**Table 6. 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, United States of America

CCDC – Chinese Center for Disease Control and Prevention, China

## Influenza A(H1)v<sup>1</sup>

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 23 September 2025 to 23 February 2026

One case of A(H1N1)v in China and single cases of A(H1N2)v in China and the United States of America were detected during this reporting period. Multiple clades of A(H1) viruses were detected in swine populations globally (Table 7).

**Table 7. Recent swine and A(H1)v activity shared with international agencies and/or collected from sequence repositories.**

Country, area or territory	Host	Genetic clade
Belgium	Swine	1A.3.3.2; 1B.1.2.1; 1C.2.2
Canada	Swine	1A.1.1.3; 1A.3.3.2
Chile	Swine	1A.3.3.2
China	Human (2)*	1C.2.3
France	Swine	1A.3.3.2; 1B.1.2.1; 1C.2.1; 1C.2.2; 1C.2.4.2
Italy	Swine	1A.3.3.2; 1C.2.2; 1C.2.4.1; 1C.2.4.2; 1C.2.4.3
Japan	Swine	1A.5.3

Mexico	Swine	1A.3.1; 1A.3.3.2; 1B.2.9; 1C.2.x
Portugal	Swine	1A.3.3.2; 1B.1.2
United Kingdom of Great Britain and Northern Ireland (the)	Swine	1B.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
	Human (1)	1A.1.1.3

\*Number of cases and/or detections

### Antigenic and genetic characteristics of influenza A(H1)v viruses

The A(H1N1)v and A(H1N2)v cases from China had HAs belonging to clade 1C.2.3 that were similar to viruses detected in swine in the region. The HA1s of the A(H1N1)v and A(H1N2)v viruses had 20 and 12 amino acid substitutions compared to the A/Hunan/42443/2015 clade 1C.2.3 CVV, respectively. Antigenic analyses showed that the A(H1N2)v virus reacted well to post-infection ferret antisera raised against the A/Hunan/42443/2015 CVV. No antigenic data were available for the A(H1N1)v virus.

The virus from the A(H1N2)v case from the United States of America had an HA belonging to clade 1A.1.1.3 that was similar to viruses detected in swine in the region. The HA1 had seven amino acid substitutions compared to the clade 1A.1.1.3 A/Pennsylvania/27/2024 CVV, and virus reacted well to post-infection ferret antisera raised against wild type A/Pennsylvania/27/2024.

### 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 8.

**Table 8. 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
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/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, United States of America;

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, United States of America

### Influenza A(H3N2)v

Influenza A(H3N2)v 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 23 September 2025 to 23 February 2026

One case of A(H3N2)v was detected in Brazil during this reporting period. A(H3N2)v viruses were detected in swine in Canada, Chile, Italy, Mexico, Portugal and the United States of America (Table 9).

### Antigenic and genetic characteristics of influenza A(H3)v viruses

The virus from the A(H3N2)v case from Brazil had an HA belonging to clade 2010.4 that was similar to other viruses detected in swine in the region. Currently, there is no CVV for this clade. No antigenic data were available for the A(H3N2)v virus.

**Table 9. Recent swine and A(H3)v activity shared with international agencies and/or collected from sequence repositories.**

Country, area or territory	Host	Genetic clade
Brazil	Human (1)*	2010.4
Canada	Swine	1990.4.b2; 1990.4.c; 1990.4.i; 2010.1
Italy	Swine	2010.3
Mexico	Swine	1990.4.x4; Other-Human-2020
Portugal	Swine	2000.3
Russian Federation (the)	Swine	Other-Human-2020
United States of America (the)	Swine	1990.4.a; 1990.4.b1; 1990.4.i; 2010.1; 2010.2; Other-Human-2020

\*Number of cases and/or detections

### 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 10.

**Table 10. 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
IDCDC-RG92A(A/swine/23TOSU0850/2023)	3.1990.4A	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation	Lineage	Type	Institution	Availability
A/Ohio/13/2017-like	3.2010.1	Reverse genetics	CDC	Pending

\*Institution distributing the candidate vaccine viruses:

CDC – Centers for Disease Control and Prevention, United States of America

### 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 characterization 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 World Organization for Animal Health (WOAH) and the Food and Agriculture Organization of the United Nations (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.