Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness

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

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

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.

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

Influenza A(H5)

Since their re-emergence in 2003, highly pathogenic avian influenza (HPAI) A(H5N1) viruses of the A/goose/Guangdong/1/96 haemagglutinin (HA) lineage have become enzootic in some countries, have infected wild birds and continue to cause outbreaks in poultry and sporadic human infections. These A(H5N1) viruses have diversified genetically and antigenically leading to the need for multiple CVVs. Viruses have been recently detected with N2, N3, N6 or N8 genes substituted for the N1 gene. This summary provides updates on the characterization of A/goose/Guangdong/1/96-lineage A(H5) viruses and the current status of the development of influenza A(H5) CVVs.

Influenza A(H5) activity from 24 September 2014 to 23 February 2015

A(H5) viruses have been detected in birds in Africa, Asia, Europe, the Middle East and North America. A(H5) human infections have been reported to WHO by China (3 cases) and Egypt (109 cases), countries in which infections have been detected in birds (Table 1). Two of the human infections in China were caused by A(H5N6) viruses. One human case in China and those in Egypt were caused by A(H5N1) viruses. A(H5) viruses were detected in birds in Bangladesh, Bulgaria, Canada, China, Egypt, Germany, India, Indonesia, Israel, Italy, Japan, Netherlands, Nigeria, Republic of Korea, Russian Federation, United Kingdom of Great Britain and Northern Ireland (United Kingdom), United States of America (USA), Viet Nam and West Bank and Gaza Strip.

[1] http://www.who.int/influenza/vaccines/virus/en/

Table 1. Recent influenza A(H5) activity reported to international agencies

Reporting country, area or territory	Host/source	Genetic clade*
Bangladesh	Poultry	2.3.2.1a
Bulgaria	Wild birds	2.3.2.1c
Canada	Poultry/wild birds	2.3.4.4 (H5N1/N2/N8)
China	Poultry/environmental	2.3.2.1, 2.3.2.1c, 2.3.4.4 (H5N1/N2/N3/N6/N8)
	Human (3)#	2.3.4.4 (H5N6), unknown (H5N1)
Egypt	Poultry	2.2.1
	Human (109)	2.2.1
Germany	Poultry/wild birds	2.3.4.4 (H5N8)
India	Poultry	2.3.2.1c
Indonesia	Poultry	unknown
Israel	Poultry	2.2.1
Italy	Poultry	2.3.4.4 (H5N8)
Japan	Poultry/wild birds	2.3.4.4 (H5N8)
Netherlands	Poultry/wild birds	2.3.4.4 (H5N8)
Nigeria	Poultry	2.3.2.1c
Republic of Korea	Poultry/wild birds	2.3.4.4 (H5N8)
Russian Federation	Wild birds	2.3.4.4 (H5N8)
United Kingdom of Great Britain and Northern Ireland	Poultry	2.3.4.4 (H5N8)
United States of America	Poultry/wild birds	2.3.4.4 (H5N1/N2/N8)
Viet Nam	Poultry	2.3.2.1c, 2.3.4.4 (H5N6)
West Bank and Gaza Strip	Poultry	2.2.1

* based on available sequences
# denotes number of human cases reported to WHO within reporting period

Antigenic and genetic characteristics of influenza A(H5) viruses

The nomenclature for phylogenetic relationships among the Haemagglutinin (HA) genes of A/goose/Guangdong/1/96-lineage A(H5) viruses is defined in consultation with representatives of WHO, the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE) and academic institutions[2].

Viruses circulating and characterized from 24 September 2014 to 23 February 2015 belonged to the following clades.

Clade 2.2.1 viruses were detected in poultry in Israel and West Bank and Gaza Strip, and in poultry and humans in Egypt. A sharp increase in the number of human cases has been reported in Egypt. As compared to the CVV produced from A/Egypt/N03072/2010, the HA proteins of clade 2.2.1 viruses isolated in recent years have continued to evolve (Figure 1) and accumulated a number of amino acid substitutions. Although some cross-reactivity was observed, ferret antiserum raised against this CVV had reduced titres to recent human viruses (Table 2). A CVV derived from an A/Egypt/N04915/2014-like virus is proposed.

Clade 2.3.2.1 viruses were detected in environmental samples in China. The HA genes of these viruses were similar to those of viruses detected previously. Antigenic data are not yet available.

Clade 2.3.2.1a viruses were detected in birds in Bangladesh. The HA genes of these viruses were similar to those of viruses detected previously. The majority of viruses reacted well with ferret antiserum raised against A/duck/Bangladesh/19097/2013 for which a CVV is available. A smaller number of viruses showed reduced reactivity with this antiserum, a pattern consistent with previous reports.

[2] WHO/OIE/FAO H5N1 Evolution Working Group. Revised and updated nomenclature for highly pathogenic avian influenza A(H5N1) viruses. John Wiley & Sons Ltd. 2014 (http://onlinelibrary.wiley.com/doi/10.1111/irv.12230/full#irv12230)

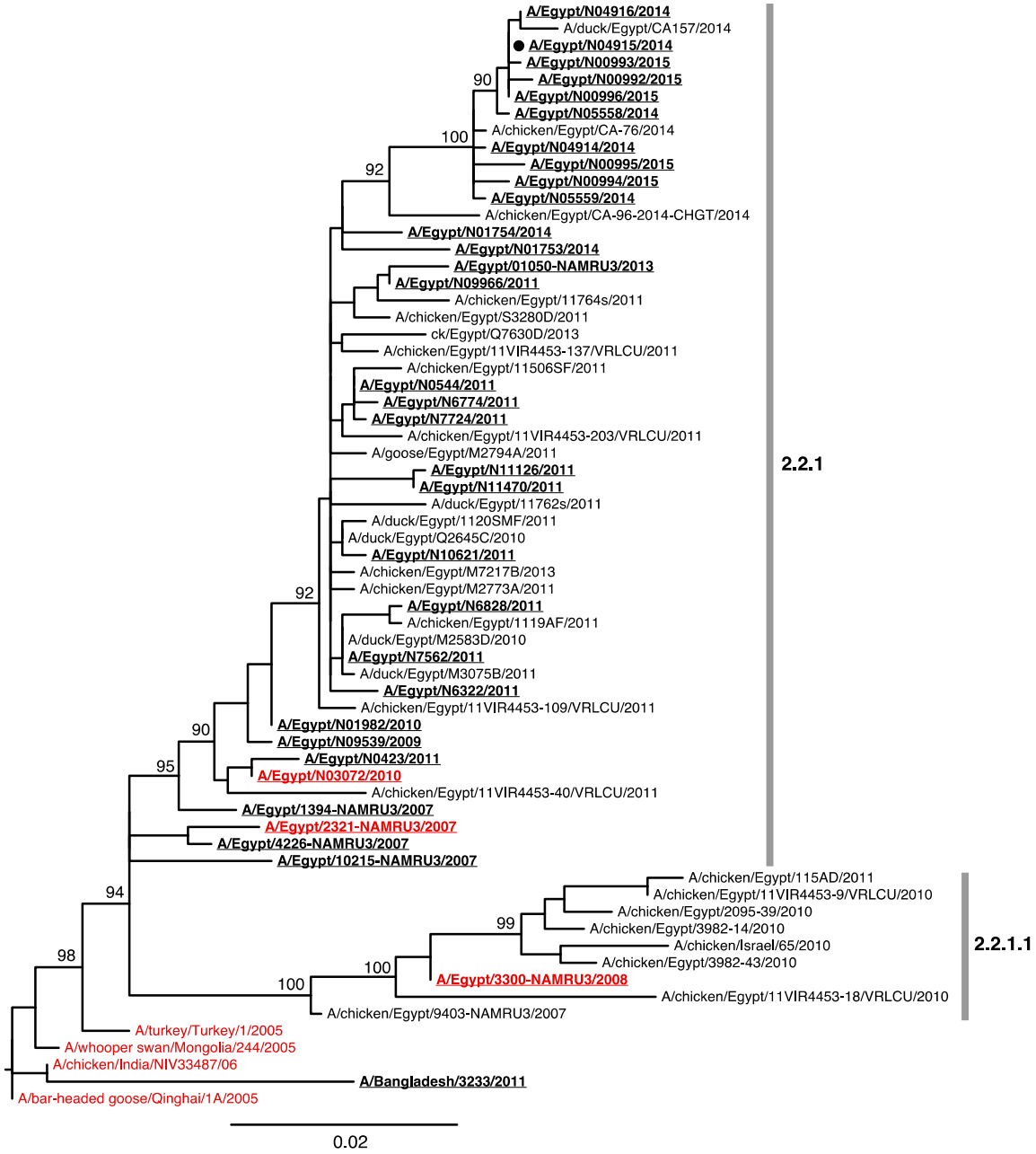

Figure 1. Phylogenetic relationships of A(H5N1) clade 2.2.1 HA genes. The available CVVs are in red. The proposed CVV is indicated by a circle. Human viruses are underlined and in bold font. The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes.

Table 2. Haemagglutination inhibition reactions of influenza A(H5N1) clade 2.2.1 viruses.

		EG/N03072			
REFERENCE ANTIGENS	**EG/N03072**	**RG29**	**EG/00994**	**EG/01050**	**chicken/EG**
A/Egypt/N03072/2010	**1280**	640	640	1280	160
A/Egypt/N03072/2010 IDCDC RG29	1280	**1280**	320	2560	80
A/Egypt/N00994/2011	160	160	**160**	1280	160
A/Egypt/01050-NAMRU3/2013	640	640	640	**1280**	640
A/chicken/Egypt/Q7630D/2013	40	80	10	640	**160**
TEST ANTIGENS					
A/Egypt/N04915/2014	80	80	80	640	160
A/Egypt/N00992/2015	640	640	640	640	640
A/Egypt/N00996/2015	160	160	320	1280	320
A/Egypt/N00993/2015	160	160	320	1280	320
A/Egypt/N00994/2015	80	160	320	1280	320

Clade 2.3.2.1c viruses were detected in birds in Bulgaria, India, Nigeria and Viet Nam and in birds and environmental samples in China. The HA genes of these viruses were similar to those of viruses detected previously. No antigenic information is available.

Clade 2.3.4.4[3] viruses were detected in birds in Canada, Germany, Italy, Japan, Netherlands, Republic of Korea, Russian Federation, United Kingdom, USA and Viet Nam, and in birds, environmental samples and two humans in China. There was considerable diversity in the HA genes of these clade 2.3.4.4 viruses and in the subtype of neuraminidase (NA) with which they were paired (Figure 2). The A(H5N6/N8) viruses isolated in China, the A(H5N6) viruses from Viet Nam and previously characterized A(H5N6) viruses from Lao People's Democratic Republic were antigenically diverse although ferret antisera raised against viruses similar to A/Sichuan/26221/2014 (H5N6), from which a CVV is in development, reacted with most viruses across this group (Table 3). The HA gene sequences of viruses isolated in Canada, Germany, Italy, Japan, Netherlands, Republic of Korea, Russian Federation, United Kingdom, USA and some of the viruses from China clustered together, although there was considerable diversity in the sequences of the other viral genes. This diversity was highlighted by the introduction of the A(H5N8) virus into North America and by subsequent reassortment with North American lineage avian viruses generating novel A(H5N1) and A(H5N2) viruses. The antiserum raised against an A/Sichuan/26221/2014-like virus did not react well with A(H5N2/N8) viruses isolated in the USA (Table 4). Conversely, ferret antisera raised against A/gyrfalcon/Washington/41088-6/2014 (H5N8) and A/chicken/Kumamoto/1-7/2014 (H5N8) did not react well with the A/Sichuan/26221/2014 (H5N6)-like virus. A new CVV based on an A/gyrfalcon/Washington/41088-6/2014-like virus is proposed.

Table 3. Haemagglutination inhibition reactions of influenza A(H5) clade 2.3.4.4 viruses.

REFERENCE ANTIGENS	Clade	bs/HK	gs/GZ
A/barn swallow/HK/D10-1161/2010	2.3.2.1b	**80**	<10
A/goose/Guizhou/3375/2014 (H5N6) *	2.3.4.4	<10	**80**
TEST ANTIGENS			
A/chicken/Guangdong/2400/2013 (H5N6) *	2.3.4.4	<10	80
A/silkie chicken/Guangdong/2809/2013 (H5N6)	2.3.4.4	<10	320
A/chicken/Guangdong/1061/2013 (H5N6)	2.3.4.4	<10	80

* A/Sichuan/26221/2014 (H5N6)-like viruses

Table 4. Haemagglutination inhibition reactions of influenza A(H5) clade 2.3.4.4 viruses.

REFERENCE ANTIGENS	Clade	Anh/1	ck/BA RG36	Guiz/1 RG35	gf/WA	ck/VN	ck/Ku#
A/Anhui/1/2005	2.3.4	**1280**	80	40	<10	10	<10
A/ck/Bangladesh/11RS-1984-30/2011 IDCDC RG36	2.3.4.2	40	**320**	40	<10	20	<10
A/Guizhou/1/2013 IDCDC RG35	2.3.4.2	80	160	**160**	<10	20	<10
A/gyrfalcon/Washington/41088-6/2014 (H5N8)	2.3.4.4	80	80	40	**80**	10	320
A/chicken/Vietnam/NCVD-14-A324/2014 (H5N6)*	2.3.4.4	<10	40	<10	<10	**640**	40
TEST ANTIGENS							
A/Northern pintail/Washington/40964/2014 (H5N2)	2.3.4.4	40	20	40	40	20	320
A/chicken/Laos/206/2014 (H5N6)	2.3.4.4	20	80	10	20	160	1280

homologous antigen for A/chicken/Kumamoto/1-7/2014 antiserum was not available

*an A/Sichuan/26221/2014 (H5N6)-like virus

[3] http://www.promedmail.org/direct.php?id=3090250

Figure 2. Phylogenetic relationships of A(H5) clade 2.3.4 HA genes. The available CVVs are in red. The proposed CVV is indicated by a circle. Human viruses are underlined and in bold font. The scale bar represents the number of substitutions per site. NA subtypes other than N1 are specified. Bootstrap supports of topology are shown above selected nodes. Novel A(H5N1) and A(H5N2) viruses that acquired North American lineage NA genes are indicated with an asterisk.

Influenza A(H5) candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, A/Egypt/N04915/2014-like (clade 2.2.1) and A/gyrfalcon/Washington/41088-6/2014-like (clade 2.3.4.4) CVVs are proposed. The available and pending A(H5) CVVs are listed in Table 5. National authorities may consider the use of one or more of these A(H5) CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need. As the viruses continue to evolve, new A(H5) CVVs may be developed.

Table 5. Status of influenza A(H5) candidate vaccine virus development

Candidate vaccine viruses	Clade	Institution*	Available
A/Viet Nam/1203/2004 (CDC-RG; SJRG-161052)	1	CDC and SJCRH	Yes
A/Viet Nam/1194/2004 (NIBRG-14)	1	NIBSC	Yes
A/Cambodia/R0405050/2007 (NIBRG-88)	1.1	NIBSC	Yes
A/Cambodia/X0810301/2013 (IDCDC-RG34B)	1.1.2	CDC	Yes
A/duck/Hunan/795/2002 (SJRG-166614)	2.1.1	SJCRH/HKU	Yes
A/Indonesia/5/2005 (CDC-RG2)	2.1.3.2	CDC	Yes
A/Indonesia/NIHRD11771/2011 (NIIDRG-9)	2.1.3.2a	NIID	Yes
A/bar-headed goose/Qinghai/1A/2005 (SJRG-163222)	2.2	SJCRH/HKU	Yes
A/chicken/India/NIV33487/2006 (IBCDC-RG7)	2.2	CDC/NIV	Yes
A/whooper swan/Mongolia/244/2005 (SJRG-163243)	2.2	SJCRH	Yes
A/Egypt/2321-NAMRU3/2007 (IDCDC-RG11)	2.2.1	CDC	Yes
A/turkey/Turkey/1/2005 (NIBRG-23)	2.2.1	NIBSC	Yes
A/Egypt/N03072/2010 (IDCDC-RG29)	2.2.1	CDC	Yes
A/Egypt/3300-NAMRU3/2008 (IDCDC-RG13)	2.2.1.1	CDC	Yes
A/common magpie/Hong Kong/5052/2007 (SJRG-166615)	2.3.2.1	SJCRH/HKU	Yes
A/Hubei/1/2010 (IDCDC-RG30)	2.3.2.1a	CDC	Yes
A/duck/Bangladesh/19097/2013 (SJ007)	2.3.2.1a	SJCRH	Yes
A/barn swallow/Hong Kong/D10-1161/2010 (SJ-003)	2.3.2.1b	SJCRH/HKU	Yes
A/chicken/Hong Kong/AP156/2008 (SJ002)	2.3.4	SJCRH/HKU	Yes
A/Anhui/1/2005 (IBCDC-RG6)	2.3.4	CDC	Yes
A/duck/Laos/3295/2006 (CBER-RG1)	2.3.4	FDA	Yes
A/Japanese white eye/Hong Kong/1038/2006 (SJRG-164281)	2.3.4	SJCRH/HKU	Yes
A/chicken/Bangladesh/11rs1984-30/2011 (IDCDC-RG36)	2.3.4.2	CDC	Yes
A/Guizhou/1/2013 (IDCDC-RG35)	2.3.4.2	CDC/CCDC	Yes
A/goose/Guiyang/337/2006 (SJRG-165396)	4	SJCRH/HKU	Yes
A/chicken/Viet Nam/NCVD-016/2008 (IDCDC-RG12)	7.1	CDC	Yes
A/chicken/Viet Nam/NCDV-03/2008 (IDCDC-RG25A)	7.1	CDC	Yes
Candidate vaccine viruses in preparation	**Clade**	**Institution**	**Availability**
A/duck/Viet Nam/NCVD-1584/2012-like	2.3.2.1c	NIBSC	Pending
A/environment/Hubei/950/2013-like	7.2	CDC/CCDC	Pending
A/Sichuan/26221/2014-like	2.3.4.4	CDC/CCDC	Pending
A/Egypt/N04915/2014-like	2.2.1	NIBSC	Pending
A/gyrfalcon/Washington/41088-6/2014-like	2.3.4.4	CDC	Pending

* **Institutions distributing the candidate vaccine viruses:**

CDC - Centers for Disease Control and Prevention, USA
CDC/NIV - Centers for Disease Control and Prevention, USA/National Institute of Virology, India
CDC/CCDC - Centers for Disease Control and Prevention, USA/China Center for Disease Control and Prevention
FDA - Food and Drug Administration, USA
HKU – University of Hong Kong, China Hong Kong Special Administrative Region
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom
NIID - National Institute of Infectious Diseases, Japan
SJCRH - St Jude Children's Research Hospital, USA

Influenza A(H7N9)

Influenza A(H7) viruses have been detected in poultry populations worldwide with the associated disease ranging from mild to severe. Human infections with avian influenza A(H7N9) viruses were first reported to WHO on 31 March 2013.

Influenza A(H7N9) activity from 24 September 2014 to 23 February 2015

During this period, 148 human cases of avian influenza A(H7N9) virus infection were reported to WHO, bringing the total number of cases to 602 with 227 deaths reported[4]. All human cases were detected in China, or in travelers who visited China (2 in Canada). Increased genetic heterogeneity of HA and NA gene sequences was observed among recent viruses from humans, poultry and environmental samples. Comparison of these viruses using haemagglutination inhibition (HI) assays showed that the majority remained antigenically similar to the CVVs derived from A/Anhui/1/2013-like viruses.

Influenza A(H7N9) candidate vaccine viruses

Based on the current epidemiologic and virologic data, no new A(H7N9) CVVs have been proposed. Available A(H7N9) CVVs are shown in Table 6. National authorities may consider the use of one or more of these A(H7N9) CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need. As the viruses continue to evolve, new A(H7N9) CVVs may be developed.

Table 6. Status of influenza A(H7N9) candidate vaccine virus development

Candidate vaccine virus	Type	Institution*	Available
A/Anhui/1/2013 (H7N9) IDCDC-RG33A	Reverse Genetics	CDC	Yes
A/Anhui/1/2013 (H7N9) NIBRG-268	Reverse Genetics	NIBSC	Yes
A/Anhui/1/2013 (H7N9) NIIDRG-10.1	Reverse Genetics	NIID	Yes
A/Anhui/1/2013 (H7N9) SJ005	Reverse Genetics	SJCRH	Yes
A/Shanghai/2/2013 (H7N9) NIBRG-267	Reverse Genetics	NIBSC	Yes
A/Shanghai/2/2013 (H7N9) CBER-RG4A	Reverse Genetics	FDA	Yes
A/Shanghai/2/2013 (H7N9) IDCDC-RG32A	Reverse Genetics	CDC	Yes
A/Shanghai/2/2013 (H7N9) IDCDC-RG32A.3	Reverse Genetics	CDC	Yes

* **Institutions distributing the candidate vaccine viruses:**
CDC - Centers for Disease Control and Prevention, USA
FDA - Food and Drug Administration, USA
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom
NIID - National Institute of Infectious Diseases, Japan
SJCRH - St Jude Children's Research Hospital, USA

[4] Communication from WHO Collaborating Center, Beijing.

Influenza A(H9N2)

Influenza A(H9N2) viruses are enzootic in poultry populations in parts of Africa, Asia and the Middle East. The majority of viruses that have been sequenced belong to the A/quail/Hong Kong/G1/97 (G1), A/chicken/Beijing/1/94 (Y280/G9), or Eurasian clades. Since 1998, when the first human infection was detected, the isolation of A(H9N2) viruses from humans and swine has been reported infrequently. In all human cases the associated disease symptoms have been mild and there has been no evidence of human-to-human transmission.

Influenza A(H9N2) activity from 24 September 2014 to 23 February 2015

Three human cases of A(H9N2) infection have been reported in this period with no fatalities. An infection of a child was reported in Egypt. Sequencing of the HA and NA genes confirmed presence of A(H9N2) virus RNA genetically related to the G1 lineage viruses circulating in poultry in Egypt. Investigations revealed that the case had a history of contact with apparently healthy backyard poultry. Two human cases of A(H9N2) were detected in Sichuan and Guangdong Provinces, China. The viruses were genetically related to Y280-like viruses detected during environmental sampling around the same time in the same and neighbouring provinces (Figure 3).

Antigenic heterogeneity exists between viruses of different Y280 sublineages circulating in China with some recent viruses identified in environmental samples reacting less well to ferret antisera raised against A(H9N2) CVVs. Further antigenic characterization of recent human viruses compared to recently developed CVVs is pending. G1-like viruses detected in poultry in Bangladesh tested by HI assay remained antigenically similar to available CVVs.

Influenza A(H9N2) candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, no new CVVs are proposed. The available A(H9N2) CVVs are listed in Table 7. National authorities may consider the use of one or more of these A(H9N2) CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need. As the viruses continue to evolve, new A(H9N2) CVVs may be developed.

Table 7. Status of influenza A(H9N2) candidate vaccine virus development

Candidate vaccine viruses	Type	Clade	Institution*	Available
A/Hong Kong/1073/1999	Wild type	G1	NIBSC	Yes
A/chicken/Hong Kong/G9/1997 (NIBRG-91)	Reverse genetics	Y280/G9	NIBSC	Yes
A/chicken/Hong Kong/G9/1997 (IBCDC-2)	Conventional	Y280/G9	CDC	Yes
A/Hong Kong/33982/2009 (IDCDC-RG26)	Reverse genetics	G1	CDC	Yes
A/Bangladesh/994/2011 (IDCDC-RG31)	Reverse genetics	G1	CDC	Yes
Candidate vaccine viruses in preparation				
A/Hong Kong/308/2014-like	Reverse genetics	Y280/G9	SJCRH	Pending

* **Institutions distributing the candidate vaccine viruses:**
CDC - Centers for Disease Control and Prevention, USA
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom
SJCRH - St Jude Children's Research Hospital, USA

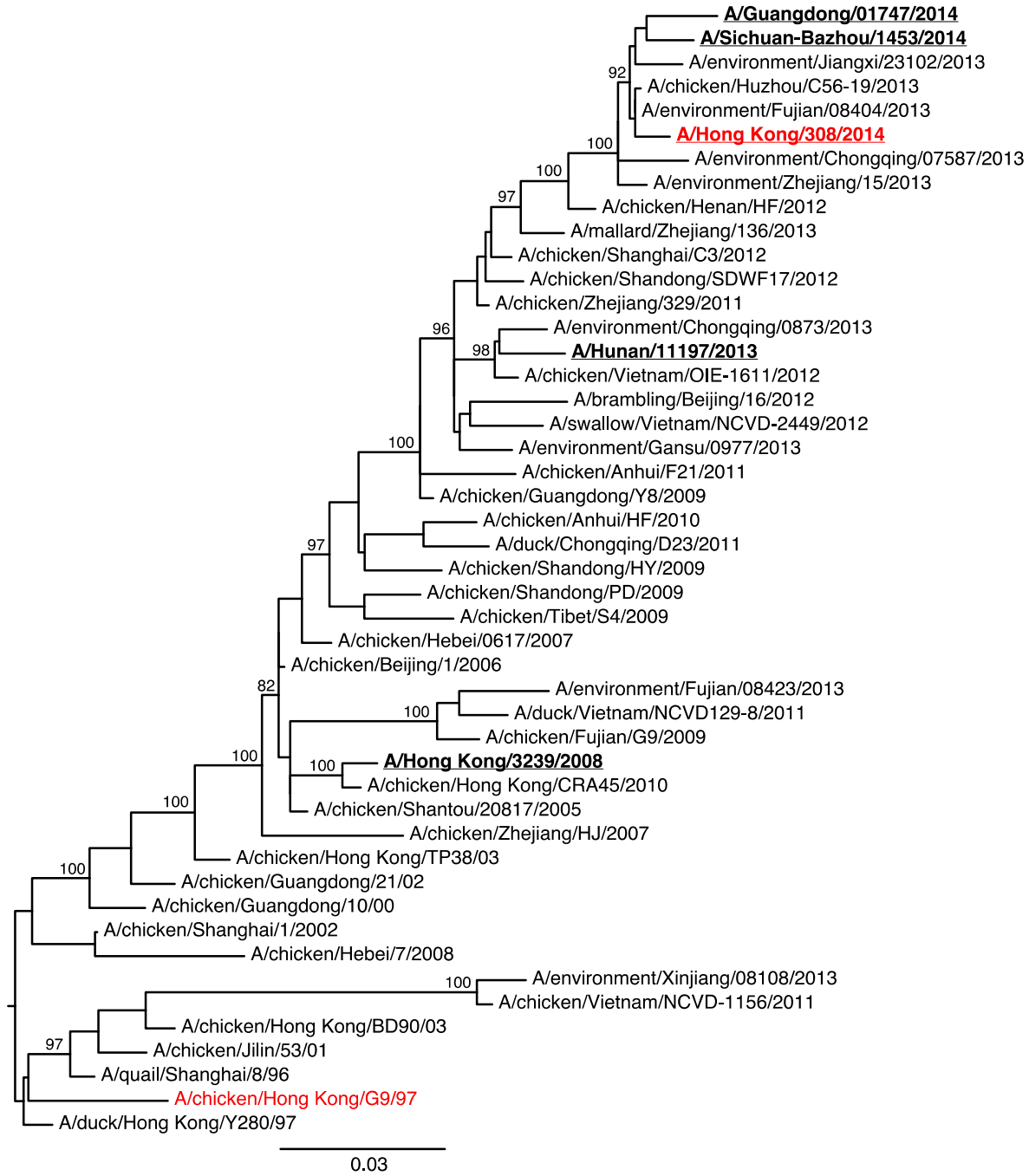

Figure 3. Phylogenetic relationships of A(H9N2) Y280-like HA genes. The available CVVs are in red. No new CVV is proposed. Human viruses are underlined and in bold font. The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes.

Influenza A(H1N1) and A(H1N2) variants (v)[5]

Influenza A(H1N1) and A(H1N2) viruses circulate in swine populations in many regions of the world. Depending on geographic location, the genetic characteristics of these viruses differ. Human infections with swine A(H1) viruses have been documented for many years. A total of three human infections with A(H1)v viruses have been detected in Sweden and USA. These viruses are genetically similar to viruses circulating in swine in these regions.

Influenza A(H1N1)v and A(H1N2)v activity from 24 September 2014 to 23 February 2015
One case of A(H1N1)v was identified in the USA in an adult with onset of influenza-like illness in October 2014. The case reported exposure to swine prior to illness onset. The HA gene of the A(H1N1)v is from the classical swine A(H1N1) lineage, which is frequently detected in pigs.

A report of two human cases of A(H1N2)v virus infection in Sweden was received during this period (although infection occurred in April 2014). The viruses were detected in nasal swabs from two pig farmers during an animal-human interface study. The virus detections in the pig farmers occurred after the same virus had been detected in pigs at the farm where the two farmers worked. The HA genes of these viruses were closely related to those of A(H1N1)pdm09.

Influenza A(H1)v candidate vaccine viruses
Based on the current understanding of the viruses and considering the existing immunity in the human population against the HAs of A(H1N1)pdm09 viruses and classical swine A(H1N1) viruses, the public health impact of these influenza A(H1)v viruses is expected to be low. CVVs are not proposed at this time.

Influenza A(H3N2)v

Influenza A(H3N2) viruses are enzootic in swine populations in most regions of the world. Depending on geographic location, the genetic and antigenic characteristics of these viruses differ. Human infections with swine A(H3N2) viruses have been documented in Asia, Europe and North America[6].

Influenza A(H3N2)v activity from 24 September 2014 to 23 February 2015
One human case of A(H3N2)v infection was reported in the USA during this reporting period[7]. The specimen was collected from a child in Wisconsin on October 13, 2014. Direct contact with swine prior to illness onset was reported. The virus was genetically similar to recently reported A(H3N2)v and swine A(H3N2) viruses. The virus was genetically and antigenically related to the A(H3N2)v CVV derived from A/Minnesota/11/2010.

Influenza A(H3N2)v candidate vaccine viruses
Based on the available antigenic, genetic and epidemiologic data, no new A(H3N2)v CVVs are proposed. The available A(H3N2)v CVVs are listed in Table 8. National authorities may consider the use of one or more of these A(H3N2)v CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need. As the viruses continue to evolve, new A(H3N2)v CVVs may be developed.

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

Candidate vaccine viruses	Type	Institution*
A/Minnesota/11/2010 (NYMC X-203)	Conventional reassortant	CDC
A/Indiana/10/2011 (NYMC X-213)	Conventional reassortant	CDC

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

[5] http://www.who.int/influenza/gisrs_laboratory/terminology_ah3n2v/en/
[6] Myers, KP. et al. Cases of Swine Influenza in Humans: A Review of the Literature. Clin Infect Dis. 44:1084. 2007
[7] http://www.cdc.gov/flu/swineflu/h3n2v-cases.htm