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

September 2013

The development of representative candidate influenza vaccine viruses, coordinated by the World Health Organization (WHO), remains an essential component of the overall global strategy for pandemic preparedness. Comparisons of the candidate vaccine viruses with respect to antigenicity and their relationship to newly emerging viruses are ongoing and will be reported periodically by WHO.

Influenza A(H5N1)

Since their re-emergence in 2003, highly pathogenic avian influenza A(H5N1) viruses have become enzootic in some countries and continue to cause outbreaks in poultry as well as sporadic human infections. The A(H5N1) viruses have diversified both genetically and antigenically leading to the need for multiple candidate vaccine viruses for pandemic preparedness purposes. This summary provides updates on the characterization of A(H5N1) viruses isolated from birds and humans, and the current status of the development of influenza A(H5N1) candidate vaccine viruses.

Influenza A(H5N1) activity from 19 February to 23 September 2013

A(H5N1) viruses have been detected in birds in Africa and Asia. Human infections have been reported to the WHO by Cambodia, Egypt, Indonesia, and Viet Nam, countries in which infections have been detected in birds (Table 1).

Table 1. Recent influenza A(H5N1) activity reported to international agencies

Country, area or territory	Host/source	Genetic clade
Bangladesh	Poultry/environment	2.3.2.1
Cambodia	Poultry	1.1
	Human (10)#	1.1
China	Poultry/environment	2.3.2.1, 2.3.4.2, 7.2
Democratic People's Republic of Korea	Poultry	2.3.2.1
Egypt	Poultry	2.2.1
	Human (3)	2.2.1
India	Poultry/wild birds	2.3.2.1
Indonesia	Poultry/wild birds	2.3.2.1*
	Human (1)	2.1.3.2
Nepal	Poultry/wild birds	2.3.2.1
Viet Nam	Poultry/wild birds	1.1/2.3.2.1/7.2
	Human (2)	1.1

# denotes number of human cases with illness onset dates falling within reporting period
* wild birds illegally imported into Europe from Indonesia were positive for A(H5N1) clade 2.3.2.1 virus

Antigenic and genetic characteristics of A(H5N1) viruses

The nomenclature for phylogenetic relationships among the haemagglutinin (HA) genes of A(H5N1) viruses is defined in consultation with representatives of the WHO, the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE) and academic institutions. The updated nomenclature report can be found at http://www.who.int/influenza/gisrs_laboratory/h5n1_nomenclature/en/.

Viruses circulating and characterized from 19 February to 23 September 2013 belonged to the following clades.

Clade 1.1 viruses were detected in poultry and humans in Cambodia and Viet Nam. Genetic characterization of the HA genes showed that these viruses were closely related to viruses detected previously in these countries (Figure 1). Some recent clade 1.1 viruses had reduced haemagglutination inhibition (HI) titres to post-infection ferret antisera raised against A/Viet Nam/1203/2004 and/or A/Cambodia/R0405050/2007 from which candidate vaccine viruses have been produced. Conversely, these viruses reacted well with post-infection ferret antisera raised against recent viruses isolated in Cambodia (Table 2). A new A/Cambodia/W0526301/2012-like candidate vaccine virus is proposed.

Table 2. Haemagglutination inhibition reactions of influenza A(H5N1) Clade 1.1 viruses

REFERENCE ANTIGENS	VN/1203	CB/R0405050	CK/VN/775	CB/W0526301	CB/W0329318
A/Viet Nam/1203/2004	**160**	40	320	320	160
A/Cambodia/R0405050/2007	40	**160**	5	20	20
A/duck/Viet Nam/NCVD-016/2007	160	10	160	80	80
A/chicken/Viet Nam/NCVD-775/2011	160	40	**320**	320	160
A/Cambodia/W0526301/2012	80	20	160	**320**	80
A/Cambodia /W0329318/2012	160	40	160	80	**160**
TEST ANTIGENS					
A/Cambodia/X0123311/2013	40	40	160	320	40
A/Cambodia/X0123312/2013	160	160	320	2560	160
A/Cambodia/X0125302/2013	160	160	160	1280	160
A/duck/Cambodia/33W2M3/2013	40	20	40	160	20
A/duck/Cambodia/59W3M1/2013	80	40	80	640	80
A/Viet Nam/VP12-3/2012	160	40	320	640	80

Clade 2.1.3.2 viruses continue to circulate in Indonesia. The HA gene sequence of a 2013 human virus was very similar to that of the candidate vaccine virus A/Indonesia/NIHRD11771/2011. No antigenic information is available.

Clade 2.2.1 viruses, similar to clade 2.2.1 viruses detected in previous years, were detected in poultry and humans in Egypt. These viruses reacted well with post-infection ferret antisera raised against available candidate vaccine viruses produced from A/Egypt/N03072/2010 and/or A/Egypt/2321-NAMRU3/2007.

Clade 2.3.2.1 viruses fall into three HA genetic groups as follows.

A/barn swallow/Hong Kong/D10-1161/2010-like viruses were detected in birds in China and Viet Nam but in reduced numbers compared to recent reporting periods. These viruses were genetically similar to viruses detected previously.

A/Hubei/1/2010-like viruses were detected in birds and/or environmental samples from Bangladesh, China, India, Nepal, and Viet Nam (Figure 2). While some viruses reacted well with post-infection ferret antisera raised against the available candidate vaccine virus produced from A/Hubei/1/2010, others did not (Table 3). Due to these observations and the widespread distribution of these viruses, a new A/duck/Bangladesh/19097/2013-like candidate vaccine virus is proposed.

A/Hong Kong/6841/2010-like viruses were detected in China, Democratic People's Republic of Korea, Indonesia (detected in birds illegally imported into Europe), and Viet Nam. Antigenically (Table 4) and genetically (Figure 3) some of these viruses have diverged from available candidate vaccine viruses, hence a new A/duck/Viet Nam/1584/2012-like candidate vaccine virus is proposed.

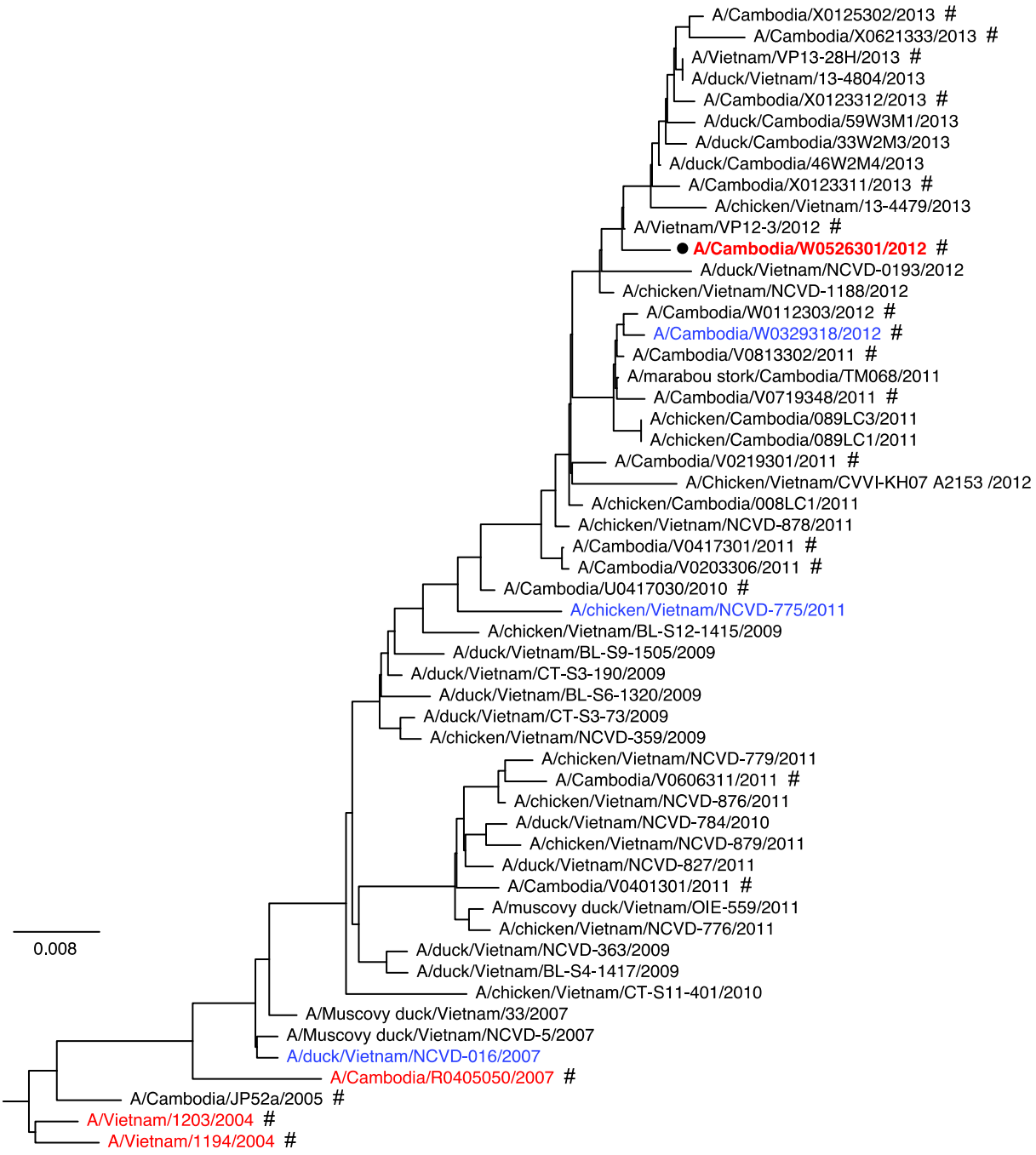

Figure 1. Phylogenetic relationships of A(H5N1) clade 1.1 virus HA genes. The available candidate vaccine viruses are in red and the HI reference viruses are in blue. The proposed vaccine candidate is indicated by a circle. Human viruses are indicated (#). The scale bar represents the number of substitutions per site.

Table 3. Haemagglutination inhibition reactions of influenza A(H5N1) Clade 2.3.2.1 Hubei-like viruses

REFERENCE ANTIGENS	HK/6841	Hubei (RG30)	CM/HK	CK/BG/ 15205	DK/BG/19 097
A/Hong Kong/6841/2010	**40**	10	40	40	160
A/Hubei/1/2010 (RG30)	40	**80**	80	40	320
A/common magpie/Hong Kong/5052/2007	40	10	**80**	40	160
A/chicken/Bangladesh/15205/2012	40	10	<10	**80**	320
A/duck/Bangladesh/19097/2013	40	<10	20	20	**160**
TEST ANTIGENS					
A/environment/Bangladesh/15131/2012	ND	40	80	20	ND
A/chicken/Bangladesh/15089/2012	ND	40	40	20	ND
A/chicken/Bangladesh/18061/2012	ND	20	<10	20	ND
A/duck/Bangladesh/18949/2013	40	20	80	10	320
A/duck/Bangladesh/18948/2013	20	<10	80	20	160
A/quail/Bangladesh/19254/2013	20	<10	80	10	160
A/chicken/Bangladesh/19338/2013	20	<10	20	<10	320
A/duck/Laos/507/2012	40	10	160	20	320

ND= not done

Table 4. Haemagglutination inhibition reactions of influenza A(H5N1) Clade 2.3.2.1 Hong Kong 6841-like viruses

REFERENCE ANTIGENS	CM/HK	HK/6841	DK/VN/1584	DK/VN/2848
A/common magpie/Hong Kong/5052/2007	**1280**	320	640	160
A/Hong Kong/6841/2010	160	**640**	160	160
A/duck/Viet Nam/NCVD-1584/2012	160	320	**160**	320
A/duck/Viet Nam /NCVD-2848/2013	40	320	160	**640**
TEST ANTIGENS				
A/duck/Viet Nam/NCDV-2745/2013	320	80	80	ND
A/swiftlet/Viet Nam/NCVD-3000/2013	80	320	40	80
A/duck/Viet Nam/NCVD-0145/2012	160	320	80	160
A/duck/Viet Nam/NCVD-0027/2012	160	640	160	2560
A/duck/Viet Nam/NCVD-0033/2012	160	640	160	160
A/duck/Viet Nam/NCVD-0130/2013	160	320	160	2560

ND= not done

Clade 2.3.4.2 viruses were isolated from birds and environmental samples in China. The HA genes of these viruses were genetically similar to those of viruses detected previously. Antigenic characterization of these viruses is pending.

Clade 7.2 viruses were detected in China and Viet Nam. Genetically these viruses were similar to viruses characterized previously. These viruses had reduced reactivity to post-infection ferret antisera raised against available candidate vaccine viruses and further analyses are proposed to determine if production of additional candidates is needed.

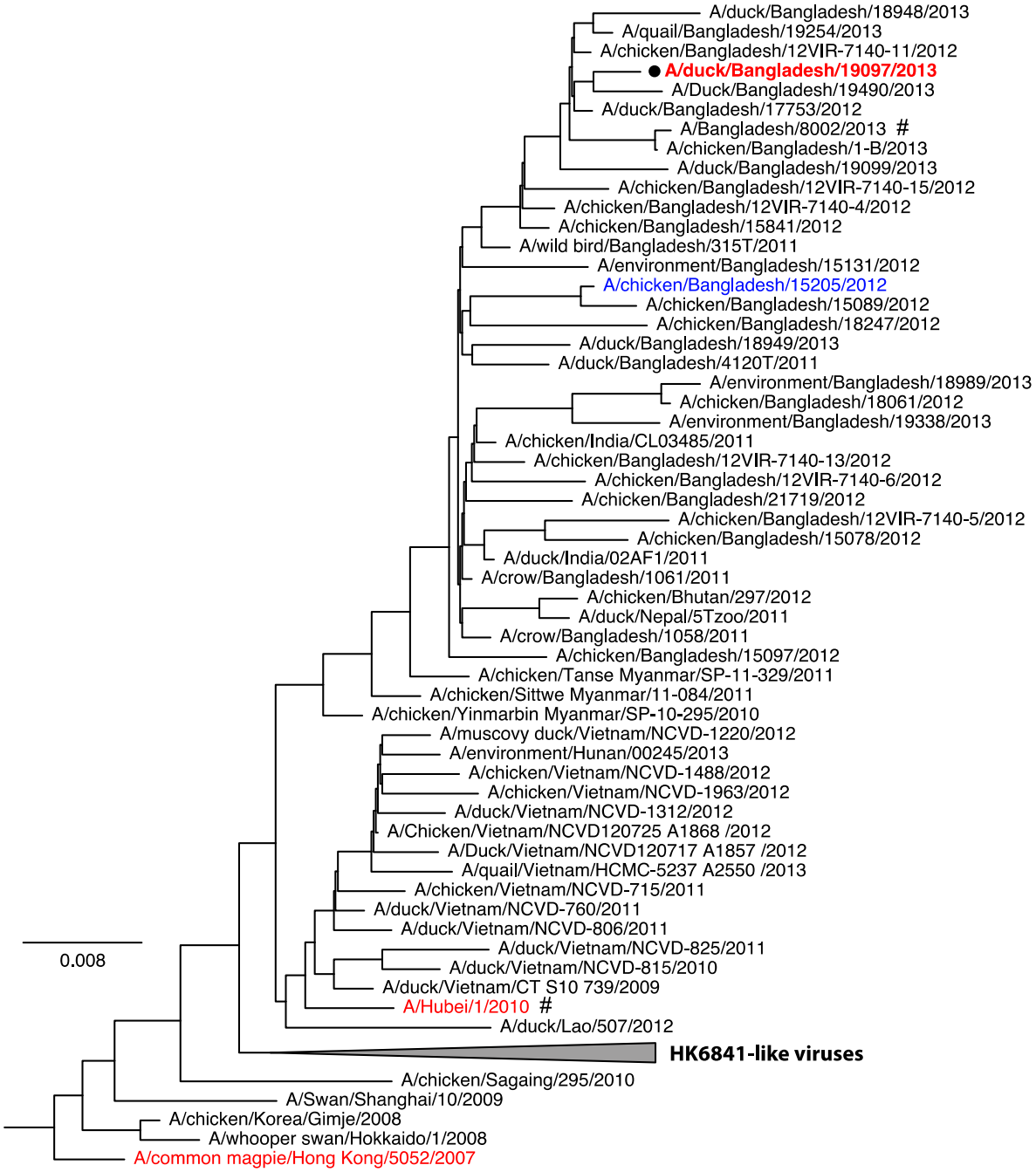

Figure 2. Phylogenetic relationships of A(H5N1) clade 2.3.2.1 A/Hubei/1/2010-like virus HA genes. The available candidate vaccine viruses are in red and the HI reference viruses are in blue. The proposed vaccine candidate is indicated by a circle. Human viruses are indicated (#). The scale bar represents the number of substitutions per site.

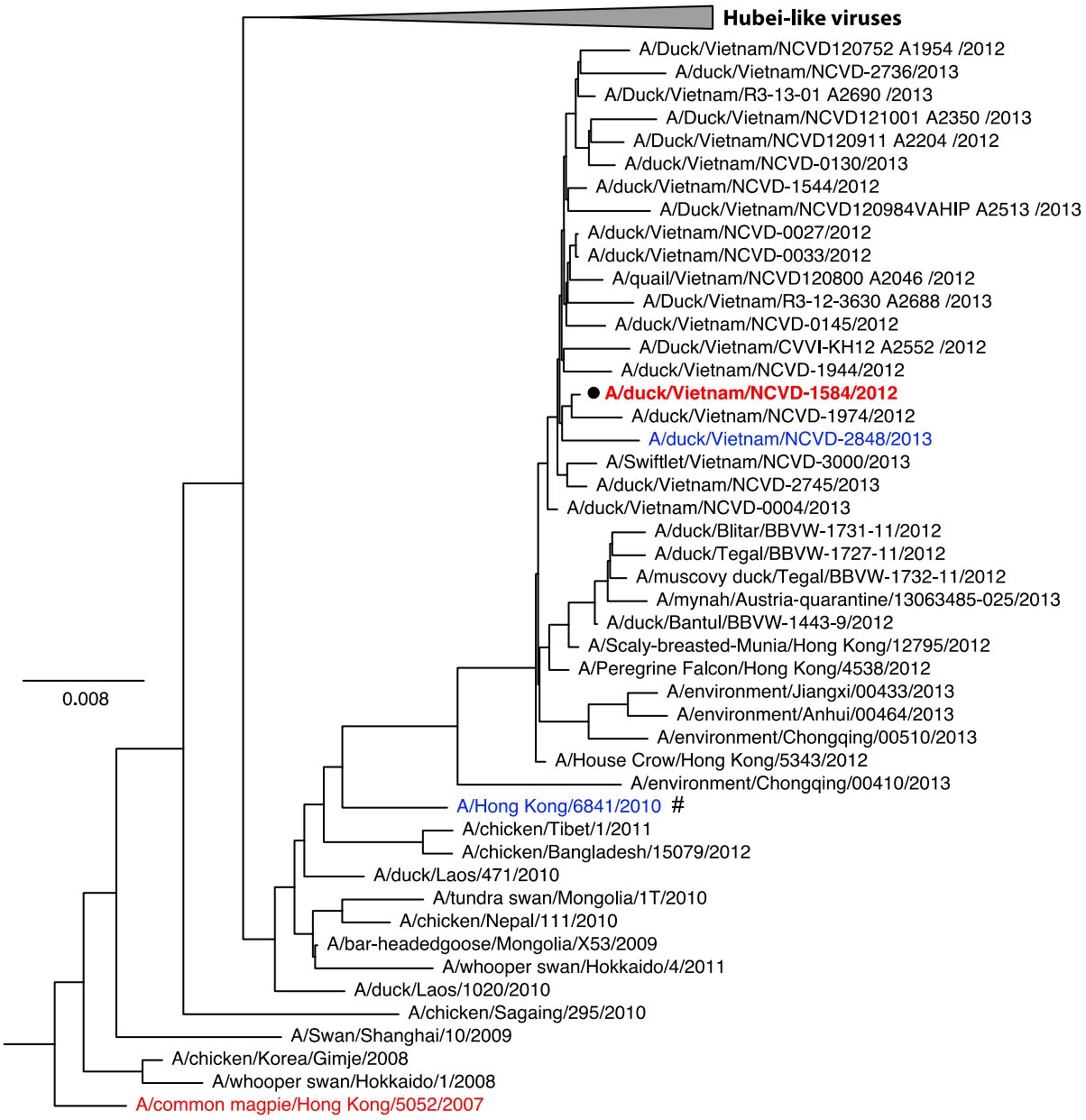

Figure 3. Phylogenetic relationships of A(H5N1) clade 2.3.2.1 A/Hong Kong/6841/2010-like virus HA genes. The available candidate vaccine viruses are in red and the HI reference viruses are in blue. The proposed vaccine candidate is indicated by a circle. Human viruses are indicated (#). The scale bar represents the number of substitutions per site.

Influenza A(H5N1) candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, A/duck/Bangladesh/19097/2013-like (clade 2.3.2.1), A/duck/Viet Nam/NCVD-1584/2012-like (clade 2.3.2.1) and A/Cambodia/W0526301/2012-like (clade 1.1) candidate vaccine viruses are proposed. The available and proposed candidate A(H5N1) vaccine viruses are listed in Table 5. On the basis of geographic spread, epidemiology and antigenic and genetic properties of A(H5N1) viruses in particular locations, national authorities may consider the use of one or more of these candidate vaccine viruses for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes.

As the viruses continue to evolve, new A(H5N1) candidate vaccine viruses will be developed and announced as they become available. Institutions that wish to receive these candidate vaccine viruses should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website[1].

Table 5. Status of influenza A(H5N1) 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/duck/Hunan/795/2002 (SJRG-166614)	2.1	SJCRH	Yes
A/Indonesia/5/2005 (CDC-RG2)	2.1.3.2	CDC	Yes
A/Indonesia/NIHRD11771/2011 (NIIDRG-9)	2.1.3.2	NIID	Yes
A/bar-headed goose/Qinghai/1A/2005 (SJRG-163222)	2.2	SJCRH	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	Yes
A/Hubei/1/2010 (IDCDC-RG30)	2.3.2.1	CDC	Yes
A/barn swallow/Hong Kong/D10-1161/2010 (SJ-003)	2.3.2.1	SJCRH	Yes
A/chicken/Hong Kong/AP156/2008 (SJ-002)	2.3.4	SJCRH	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	Yes
A/goose/Guiyang/337/2006 (SJRG-165396)	4	SJCRH	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/chicken/Bangladesh/11RS1984-30/2011-like	2.3.4.2	CDC	Pending
A/Guizhou/1/2013-like	2.3.4.2	CDC/CCDC	Pending
A/duck/Bangladesh/19097/2013-like	2.3.2.1	SJCRH	Pending
A/duck/Viet Nam/NCVD-1584/2012-like	2.3.2.1	NIBSC	Pending
A/Cambodia/W0526301/2012-like	1.1	CDC	Pending

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

CDC - Centers for Disease Control and Prevention, United States of America
CDC/NIV - Centers for Disease Control and Prevention, United States of America/National Institute of Virology, India
CDC/CCDC - Centers for Disease Control and Prevention, United States of America/China Center for Disease Control and Prevention
FDA - Food and Drug Administration, United States of America
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom of Great Britain and Northern Ireland
NIID - National Institute of Infectious Diseases, Japan
SJCRH - St Jude Children's Research Hospital, United States of America

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

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 G1, chicken/Beijing (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 19 February to 23 September 2013

No human cases of A(H9N2) infection have been reported in this period. A(H9N2) viruses continue to be isolated from birds in many regions of the world.

Influenza A(H9N2) candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, no new A(H9N2) candidate vaccine viruses are proposed. The available A(H9N2) candidate vaccine viruses are listed in Table 6. Institutions that wish to receive candidate vaccine viruses should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website[2].

Table 6. Status of 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 reassortant	Y280/G9	CDC	Yes
A/Hong Kong/33982/2009 (IDCDC-RG26)	Reverse genetics	G1	CDC	Yes
A/Bangladesh/0994/2011 (IDCDC-RG31)	Reverse genetics	G1	CDC	Yes

* **Institutions distributing the candidate vaccine viruses:**
CDC - Centers for Disease Control and Prevention, United States of America
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom of Great Britain and Northern Ireland

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

Influenza A(H7)

Influenza A(H7) viruses have been detected in poultry populations worldwide with the associated disease ranging from mild to severe. Occasionally, during outbreaks in poultry, human cases have been detected in those with direct poultry exposure. These infections often cause conjunctivitis or mild influenza-like-illness[3,4] but some H7 infections, notably A(H7N9)[5], can cause severe respiratory disease.

Influenza A(H7N9) activity from February to 23 September 2013

The first instance of A(H7N9) infecting humans was reported to WHO on 31 March 2013. There were 135 human cases including 44 deaths. Geographic distribution of these human cases (and genetically related avian and/or environmental samples) has been restricted to China. HA gene sequence and HI test comparison of A(H7N9) viruses isolated from humans and poultry suggest limited genetic and antigenic diversity among this group of viruses (Table 7 and Figure 4).

Table 7. Haemagglutination inhibition reactions of influenza A(H7N9) viruses

REFERENCE ANTIGENS	Subtype	AH1	SH2	PC360	NL12
A/Anhui/1/2013	H7N9	**320**	640	80	320
A/Shanghai/2/2013	H7N9	320	**640**	80	1280
A/wild gs/Dongting/PC0360/2012	H7N7	40	160	**160**	640
A/mallard/Netherlands/12/2000	H7N3	160	320	80	**640**
TEST ANTIGENS					
A/Shanghai/1/2013	H7N9	160	320	80	640
A/Jiangsu/01/2013	H7N9	320	640	80	640
A/Zhejiang/01/2013	H7N9	320	640	80	640
A/Beijing/01-A/2013	H7N9	320	640	80	640
A/Henan/01/2013	H7N9	160	320	80	320
A/Shandong/01/2013	H7N9	320	640	80	320
A/Fujian/01/2013	H7N9	320	640	80	640
A/Jiangxi/01/2013	H7N9	320	640	80	640
A/Hunan/01/2013	H7N9	160	640	80	640
A/Anhui/02/2013	H7N9	320	1280	80	640
A/Shandong/0068A/2013	H7N9	320	640	160	640
A/chicken/Shanghai/S1053/2013	H7N9	160	320	80	640
A/pigeon/Shanghai/S1069/2013	H7N9	320	640	80	640
A/environment/Shandong/1/2013	H7N9	320	640	160	1280

Influenza A(H7N9) candidate vaccine viruses

Based on the current epidemiologic data, A(H7N9) candidate vaccine viruses have been developed. Available A(H7N9) candidate vaccine viruses are shown in Table 8. Institutions that wish to receive candidate vaccine viruses should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website[6].

[3] Tweed, SA. et al. Human illness from avian influenza H7N3, British Columbia. 2004. Emerg Infect Dis. 10:2196.
[4] de Jong, MC. et al. Intra- and interspecies transmission of H7N7 highly pathogenic avian influenza virus during the avian influenza epidemic in the Netherlands in 2003. 2009. Rev Sci Tech. 28:333
[5] http://www.who.int/influenza/human_animal_interface/influenza_h7n9/en/
[6] http://www.who.int/influenza/vaccines/virus/en/

Table 8. 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/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

* **Institutions distributing the candidate vaccine viruses:**
CDC - Centers for Disease Control and Prevention, United States of America
FDA - Food and Drug Administration, United States of America
NIBSC - National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom of Great Britain and Northern Ireland
NIID - National Institute of Infectious Diseases, Japan

[#] downgrading of biosafety level pending WHO working group review

Influenza A(H7N3) activity from 19 February to 23 September 2013

Highly pathogenic A(H7N3) viruses continue to circulate in poultry in Mexico. No human cases have been reported during this period.

Influenza A(H7N7) activity from 19 February to 23 September 2013

Since 14 August 2013 there have been 6 outbreaks of highly pathogenic avian influenza A(H7N7) in poultry in Italy. Three cases of A(H7N7) conjunctivitis were documented in personnel involved in culling operations with one case developing influenza-like illness. All individuals recovered without treatment. Genetically, the A(H7N7) viruses were similar to low pathogenic viruses circulating in wild birds in Europe and those causing sporadic and limited outbreaks in poultry in Central and Northern Europe (Figure 4). Antigenically, the A(H7N7) virus reacted well to post-infection ferret antisera raised against the candidate vaccine viruses A/turkey/Virginia/4529/2002 (H7N2) IBCDC-5 and A/mallard/Netherlands/12/2000 (H7N7) IBCDC-1.

Influenza A(H7) candidate vaccine viruses

Available A(H7) candidate vaccine viruses are shown in Table 9 additional to those available for A(H7N9) described above (Table 8). Based on current data, no new A(H7N3) or A(H7N7) candidate vaccine viruses are proposed. Institutions that wish to receive candidate vaccine viruses should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website[7].

Table 9. Status of influenza A(H7) candidate vaccine virus development

Candidate vaccine viruses	Type	Institution*
A/turkey/Virginia/4529/2002 (H7N2) IBCDC-5	Conventional reassortant	CDC
A/mallard/Netherlands/12/2000 (H7N7) IBCDC-1	Conventional reassortant	CDC
A/mallard/Netherlands/12/2000 (H7N3) NIBRG-60	Reverse genetics	NIBSC
A/mallard/Netherlands/12/2000 (H7N1) NIBRG-63	Reverse genetics	NIBSC
A/Canada/RV444/2004 (H7N3)	Reverse genetics	SJCRH
A/New York/107/2003 (H7N2) NIBRG-109	Reverse genetics	NIBSC

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

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

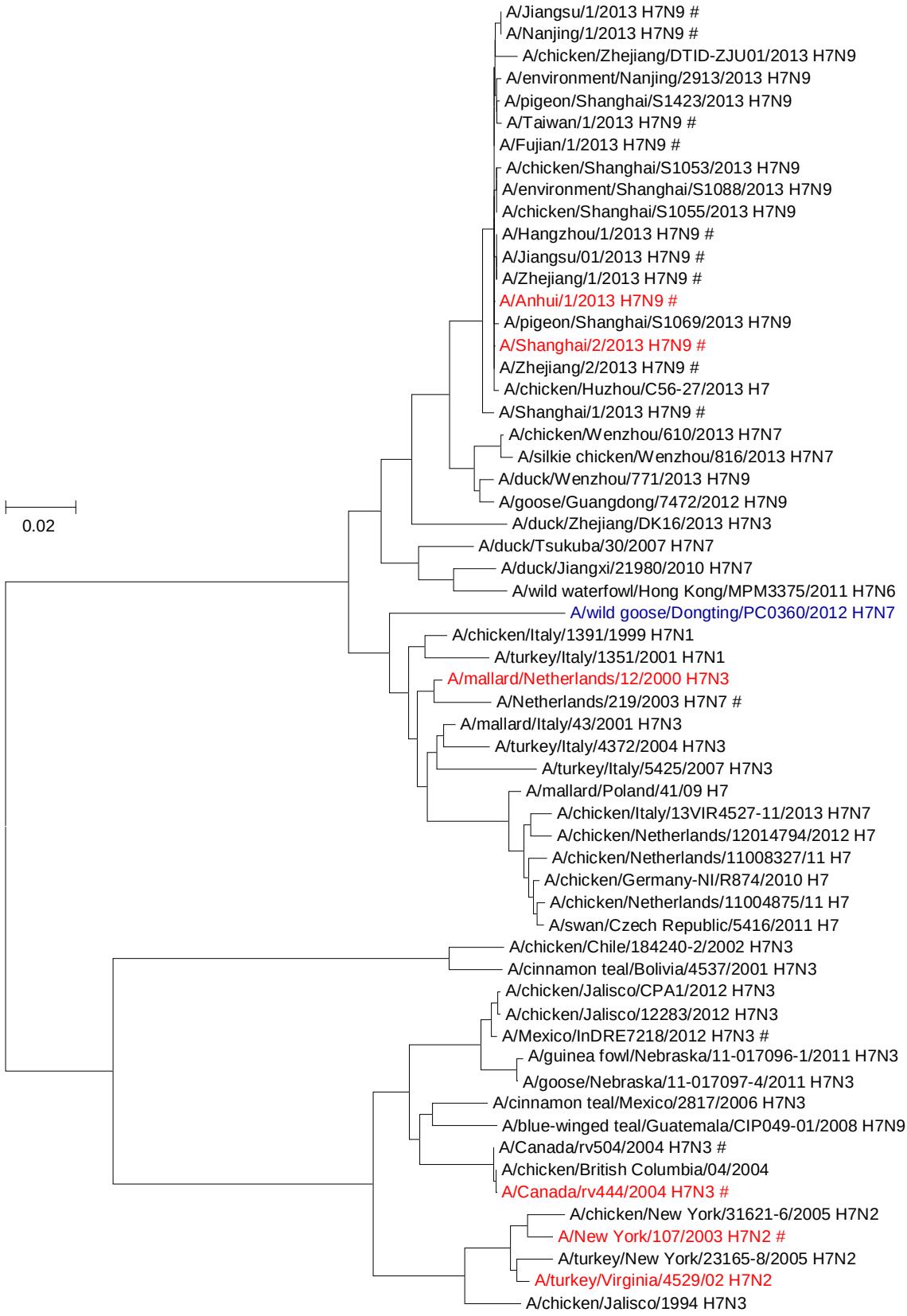

Figure 4. Phylogenetic relationships of A(H7) virus HA genes. The available candidate vaccine viruses are in red and the HI reference viruses are in blue. Human viruses are indicated (#). The scale bar represents the number of substitutions per site.

Influenza A(H3N2) variant (v)[8]

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[9].

Influenza A(H3N2)v activity from 19 February to 23 September 2013

Eighteen human cases of A(H3N2)v infection were reported in the United States of America during this reporting period[10]. These viruses were genetically and antigenically similar to previously characterized A(H3N2)v viruses. All cases had known exposure to swine at agricultural fairs. Similar viruses continue to be isolated from pigs in the United States of America.

Influenza A(H3N2)v candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, no new A(H3N2)v candidate vaccine viruses are proposed. Available candidate vaccine viruses are shown in Table 10. Institutions that wish to receive candidate vaccine viruses should contact WHO at gisrs-whohq@who.int or Centers for Disease Control and Prevention, United States of America.

Table 10. 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

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

Influenza A(H1N1)v

Influenza A(H1N1) 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[9,11]. Two human infections with A(H1N1)v viruses have been detected in the United States of America during the reporting period. These viruses are genetically similar to viruses circulating in swine in the region and to A(H1N1)v viruses detected in previous years.

Influenza A(H1N1)v candidate vaccine viruses

Based on a risk assessment of the antigenic and genetic characteristics of the A(H1N1)v viruses, candidate vaccine viruses are not proposed at this time.

Influenza A(H6N1)

A human infection with A(H6N1) virus was detected in Taiwan, China in May[12]. No human A(H6N1) infections had been detected previously. The virus was genetically similar to viruses isolated from chickens in Taiwan, China but different from A(H6N1) viruses circulating in poultry in other regions of Asia.

Influenza A(H6N1) candidate vaccine viruses

Based on a risk assessment, no candidate vaccine viruses have been proposed at this time.

[8] http://www.who.int/influenza/gisrs_laboratory/terminology_ah3n2v/en/index.html
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