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

February 2019

The development of influenza candidate vaccine viruses (CVVs), coordinated by WHO, remains an essential component of the overall global strategy for 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 genetically and antigenically, leading to the need for additional CVVs for pandemic preparedness purposes. Changes in the genetic and antigenic characteristics of these viruses relative to existing CVVs, and their potential risks to public health justify the need to select and develop new CVVs.

This document summarizes the genetic and antigenic characteristics of recent zoonotic influenza viruses and related viruses circulating in animals 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.

Influenza A(H5)

Since their emergence in 1997, highly pathogenic avian influenza (HPAI) A(H5) 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 viruses have diversified genetically and antigenically, including the emergence of viruses with replacement of the N1 gene segment by N2, N3, N5, N6, N8 or N9 gene segments, 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 current status of the development of influenza A(H5) CVVs.

Influenza A(H5) activity from 25 September 2018 to 17 February 2019

Three A(H5N6) human infections were detected in China during this period; no A(H5N1) human infections were reported. Since 2003 there have been 860 and 23 confirmed human infections with A(H5N1) and A(H5N6) viruses, respectively. A/goose/Guangdong/1/96-lineage A(H5) viruses were detected in poultry and wild birds in multiple countries (Table 1).

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1 For information relevant to other notifiable influenza virus infections in animals refer to http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home
2 http://www.who.int/influenza/vaccines/virus/candidates_reagents/home/en/
Table 1. Recent A(H5) activity

<table>
<thead>
<tr>
<th>Country, area or territory</th>
<th>Host</th>
<th>Genetic clade</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bangladesh</td>
<td>Poultry</td>
<td>2.3.2.1a (H5N1)</td>
</tr>
<tr>
<td>Bulgaria</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
</tr>
<tr>
<td>Cambodia</td>
<td>Poultry</td>
<td>unknown (H5)</td>
</tr>
<tr>
<td>China</td>
<td>Human (3)</td>
<td>2.3.4.4 (H5N6)</td>
</tr>
<tr>
<td></td>
<td>Poultry</td>
<td>2.3.4.4 (H5N6)</td>
</tr>
<tr>
<td>Taiwan, China</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N2)</td>
</tr>
<tr>
<td>Denmark</td>
<td>Wild birds</td>
<td>2.3.4.4 (H5N6)</td>
</tr>
<tr>
<td>Egypt</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
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<td>India</td>
<td>Wild birds</td>
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<td></td>
<td>Poultry</td>
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<tr>
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<td>Poultry</td>
<td>unknown (H5N1)</td>
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<tr>
<td>Iran (Islamic Republic of)</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
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<tr>
<td>Lao People’s Democratic Republic</td>
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<td>unknown (H5N1)</td>
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<tr>
<td>Namibia</td>
<td>Wild birds</td>
<td>unknown (H5N8)</td>
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<tr>
<td>Nigeria</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
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<tr>
<td>Russian Federation</td>
<td>Wild birds</td>
<td>2.3.4.4 (H5N6)</td>
</tr>
<tr>
<td></td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
</tr>
<tr>
<td>South Africa</td>
<td>Poultry</td>
<td>2.3.4.4 (H5N8)</td>
</tr>
<tr>
<td>Viet Nam</td>
<td>Poultry</td>
<td>unknown (H5N1); 2.3.4.4 (H5N6)</td>
</tr>
</tbody>
</table>

# denotes number of human cases reported to WHO within the reporting period (25 September 2018 to 17 February 2019)

Antigenic and genetic characteristics of influenza A(H5) viruses

The nomenclature for phylogenetic relationships among the 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.

A(H5) viruses circulating and characterized from 25 September 2018 to 17 February 2019 belong to the following clades:

**Clade 2.3.2.1a** viruses were detected in birds in Bangladesh and India. The majority of viruses tested reacted poorly with post-infection ferret antiserum raised against the CVV derived from A/duck/Bangladesh/19097/2013 and were genetically more similar to A/duck/Bangladesh/17D1012/2018, from which a CVV is in development.

**Clade 2.3.4.4** viruses were detected in three humans, birds and environmental samples in China, as well as birds in at least nine other countries in Africa, Asia and Europe (Table 1). Two of the three human infections were fatal. The HAs of the clade 2.3.4.4 viruses belonged to several genetic subgroups. Viruses from humans, an increasing number of poultry and environmental samples from China, some poultry in Viet Nam and a wild bird (common gull) in the Russian Federation belonged to an HA subgroup not currently represented by an existing CVV (Fig. 1). Correspondingly, viruses from this group reacted poorly to post-infection ferret antisera raised against available CVVs (Table 2). The detection in the Saratov region, Russian Federation, represents the first report of this 2.3.4.4 HA subgroup outside of Asia.

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Figure 1. Phylogenetic relationships of A(H5) clade 2.3.4.4 HA genes. The available CVVs are in red. The proposed CVV is indicated by a red dot (●). Human viruses are in bold font. The viruses tested in haemaglutination inhibition assay are indicated by hashes (#). NA subtypes other than N1 are specified. 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. A/Anhui/1/2005 (clade 2.3.4) is used to root the tree.
Table 2. Haemagglutination inhibition assays of clade 2.3.4.4 A(H5N6) influenza viruses

<table>
<thead>
<tr>
<th>Reference Antigens</th>
<th>Clade</th>
<th>SC/26221</th>
<th>HB29578</th>
<th>FJ/21099</th>
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</thead>
<tbody>
<tr>
<td>A/Sichuan/26221/2014</td>
<td>2.3.4.4</td>
<td>160</td>
<td>&lt;20</td>
<td>40</td>
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<tr>
<td>A/Hubei/29578/2016</td>
<td>2.3.4.4</td>
<td>&lt;20</td>
<td>320</td>
<td>&lt;20</td>
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<tr>
<td>A/Fujian-Sanyuan/21099/2017</td>
<td>2.3.4.4</td>
<td>40</td>
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<td>80</td>
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</table>

**Test antigens**

<table>
<thead>
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<th>HB29578</th>
<th>FJ/21099</th>
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<tr>
<td>A/Guangxi/13486/2017</td>
<td>2.3.4.4</td>
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<td>&lt;20</td>
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<td>A/Jiangsu/32888/2018</td>
<td>2.3.4.4</td>
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<tr>
<td>A/Guangdong/18SF020/2018</td>
<td>2.3.4.4</td>
<td>&lt;20</td>
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<td>A/Guangxi/32797/2018</td>
<td>2.3.4.4</td>
<td>&lt;20</td>
<td>80</td>
<td>&lt;20</td>
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<tr>
<td>A/environment/Chongqing/31755/2018</td>
<td>2.3.4.4</td>
<td>&lt;20</td>
<td>&lt;20</td>
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<tr>
<td>A/environment/Guangdong/33285/2018</td>
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<td>A/environment/Guangdong/33225/2018</td>
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</table>

**Influenza A(H5) candidate vaccine viruses**

Based on the current antigenic, genetic and epidemiologic data, a new A/Guangdong/18SF020/2018-like A(H5N6) CVV is proposed. The available and pending A(H5) CVVs are listed in Table 3.
Table 3. Status of influenza A(H5) candidate vaccine virus development

<table>
<thead>
<tr>
<th>Candidate vaccine viruses (like virus)</th>
<th>Clade</th>
<th>Institution*</th>
<th>Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>CDC-RG (A/Viet Nam/1203/2004)</td>
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<td>CDC</td>
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<tr>
<td>SJRG-161052 (A/Viet Nam/1203/2004)</td>
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<td>SJCRH</td>
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<tr>
<td>NIBRG-14 (A/Viet Nam/1194/2004)</td>
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<td>NIBSC</td>
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<tr>
<td>NIBRG-88 (A/Cambodia/R0405050/2007)</td>
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<td>NIBSC</td>
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<tr>
<td>IDCDC-RG34B (A/Cambodia/X0810301/2013)</td>
<td>1.1.2</td>
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<tr>
<td>SJRG-166614 (A/duck/Hunan/795/2002)</td>
<td>2.1.1</td>
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<tr>
<td>CDC-RG2 (A/Indonesia/5/2005)</td>
<td>2.1.3.2</td>
<td>CDC</td>
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<tr>
<td>NIIIDRG-9 (A/Indonesia/NHRD11771/2011)</td>
<td>2.1.3.2a</td>
<td>NIDD</td>
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<tr>
<td>SJRG-163222 (A/bar-headed goose/Qinghai/1A/2005)</td>
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<td>SJCRH/HKU</td>
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<tr>
<td>IBCDC-RG7 (A/chicken/India/NIV33487/2006)</td>
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<td>CDC/NIV</td>
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<tr>
<td>SJRG-163243 (A/whooper swan/Mongolia/244/2005)</td>
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<td>SJCRH</td>
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<tr>
<td>IDCDC-RG11 (A/Egypt/2321-NAMRU3/2007)</td>
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<tr>
<td>NIBRG-23 (A/turkey/Turkey/1/2005)</td>
<td>2.2.1</td>
<td>NIBSC</td>
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<tr>
<td>IDCDC-RG29 (A/Egypt/N03072/2010)</td>
<td>2.2.1</td>
<td>CDC</td>
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<tr>
<td>IDCDC-RG13 (A/Egypt/3300-NAMRU3/2008)</td>
<td>2.2.1.1</td>
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<td>NIBRG-306 (A/Egypt/N04915/2014)</td>
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<td>SJRG-166615 (A/common magpie/Hong Kong/5052/2007)</td>
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<td>IDCDC-RG30 (A/Hubei/1/2010)</td>
<td>2.3.2.1a</td>
<td>CDC</td>
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<tr>
<td>SJ007 (A/duck/Bangladesh/19097/2013)</td>
<td>2.3.2.1a</td>
<td>SJCRH</td>
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<tr>
<td>SJ003 (A/barn swallow/Hong Kong/D10-1161/2010)</td>
<td>2.3.2.1b</td>
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<tr>
<td>NIBRG-301 (A/duck/Viet Nam/NCVD-1584/2012)</td>
<td>2.3.2.1c</td>
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<tr>
<td>SJ002 (A/chicken/Hong Kong/AP156/2008)</td>
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<td>SJCRH/HKU</td>
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<tr>
<td>IBCDC-RG6 (A/Anhui/1/2005)</td>
<td>2.3.4</td>
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<td>CBER-RG1 (A/duck/Laos/3295/2006)</td>
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<td>SJRG-164281 (A/Japanese white eye/Hong Kong/1038/2006)</td>
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<td>IDCDC-RG36 (A/chicken/Bangladesh/11rs1984-30/2011)</td>
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<td>IDCDC-RG35 (A/Guizhou/1/2013)</td>
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<td>IDCDC-RG42A (A/Sichuan/26221/2014)</td>
<td>2.3.4.4</td>
<td>CDC/CCDC</td>
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<tr>
<td>CNIC-29578 (A/Hubei/29578/2016)</td>
<td>2.3.4.4</td>
<td>CDC/CCDC</td>
<td>Yes</td>
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<tr>
<td>IDCDC-RG43A (A/gyrfalcon/Washington/41088-6/2014) (H5N8)</td>
<td>2.3.4.4</td>
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<tr>
<td>NIID-001 (A/duck/Hyogo/1/2016)</td>
<td>2.3.4.4</td>
<td>NIID</td>
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<tr>
<td>CNIC-21099 (A/Fujian-Sanyuan/21099/2017) (H5N6)</td>
<td>2.3.4.4</td>
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<td>SJRG-165396 (A/goose/Guiyang/337/2006)</td>
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<td>IDCDC-RG12 (A/chicken/Viet Nam/NCVD-016/2008)</td>
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<td>IDCDC-RG25A (A/chicken/Viet Nam/NCVD-03/2008)</td>
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<table>
<thead>
<tr>
<th>Candidate vaccine viruses in preparation</th>
<th>Clade</th>
<th>Institution</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/duck/Bangladesh/17D1012/2018-like</td>
<td>2.3.2.1a</td>
<td>CDC</td>
<td>Pending</td>
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<tr>
<td>A/chicken/Guiyang/1153/2016-like</td>
<td>2.3.2.1c</td>
<td>SJCRH/HKU</td>
<td>Pending</td>
</tr>
<tr>
<td>A/chicken/Ghana/20/2015-like</td>
<td>2.3.2.1c</td>
<td>CDC</td>
<td>Pending</td>
</tr>
<tr>
<td>A/chicken/Viet Nam/NCVD-15A59/2015 (H5N6)-like</td>
<td>2.3.4.4</td>
<td>SJCRH</td>
<td>Pending</td>
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<tr>
<td>A/environment/Hubei/950/2013-like</td>
<td>7.2</td>
<td>CCDC</td>
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<tr>
<td>A/Guangdong/18SF020/2018 (H5N6)-like</td>
<td>2.3.4.4</td>
<td>CCDC/HKU</td>
<td>Pending</td>
</tr>
</tbody>
</table>

* Institutions developing and/or distributing the candidate vaccine viruses:
  
  CCDC – Chinese Center for Disease Control and Prevention
  CDC – Centers for Disease Control and Prevention, United States of America
  FDA – Food and Drug Administration, United States of America
  HKU – University of Hong Kong, Hong Kong Special Administrative Region, China
  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
  NIV – National Institute of Virology, India
  SJCRH – St Jude Children’s Research Hospital, United States of America
**Influenza A(H7)**

A(H7) viruses have caused zoonotic infections on multiple occasions in previous years. Most zoonotic infections have been caused by A(H7N9) viruses of the A/Anhui/1/2013 HA lineage, which was first detected in a human in March 2013 with 1566 subsequent cases. A genetically and antigenically distinct low pathogenicity avian influenza A(H7N4) virus caused a severe human infection in China in January 2018. This summary provides updates on the characterization of A(H7) viruses related to these zoonotic viruses and the current status of the development of corresponding CVVs.

**Influenza A(H7) activity from 25 September 2018 to 17 February 2019**

No human cases of A/Anhui/1/2013 HA lineage A(H7N9) viruses have been detected since March 2018 and no viruses were detected in poultry or the environment during this reporting period.

In Asia, low pathogenicity avian influenza A(H7) viruses of the Eurasian lineage were detected in birds and/or environmental samples in Cambodia, China, Republic of Korea and Viet Nam.

**Antigenic and genetic characteristics of influenza A(H7) viruses**

The A(H7) viruses from China and Viet Nam were representatives of the Eurasian lineage of A(H7) viruses. The HAs of these viruses were similar to the A(H7N4) human virus, A/Jiangsu/1/2018, and waterfowl viruses detected recently in the region (Fig. 2). Compared to the genetically closest CVV, derived from A/mallard/Netherlands/12/2000, the viruses had 8 to 13 amino acid differences in HA1. These A(H7) viruses had NA genes of multiple subtypes and were antigenically distinct from available CVVs (Tables 4-5).

**Table 4. Haemagglutination inhibition assays of A(H7) Eurasian influenza viruses**

<table>
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<tr>
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<tbody>
<tr>
<td>A/Netherlands/219/2003</td>
<td>H7N7</td>
<td>160</td>
<td>80</td>
<td>40</td>
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<td>A/mallard/Netherlands/12/2000</td>
<td>H7N3</td>
<td>160</td>
<td>160</td>
<td>80</td>
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<tr>
<td>A/turkey/Italy/5425/2007</td>
<td>H7N3</td>
<td>160</td>
<td>80</td>
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</table>

<table>
<thead>
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<th>Test antigens</th>
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<tbody>
<tr>
<td>A/duck/Viet Nam/NCVD-TG3V3S6/2018</td>
<td>H7N6</td>
<td>40</td>
<td>40</td>
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<td>A/duck/Viet Nam/NCVD-TG3-V3-S1/2017</td>
<td>H7N6</td>
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**Table 5. Haemagglutination inhibition assays of A(H7) Eurasian influenza viruses**

<table>
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<th>Reference Antigens</th>
<th>Subtype</th>
<th>AH/1/2013</th>
<th>SH/2/2013</th>
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<td>1280</td>
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<table>
<thead>
<tr>
<th>Test antigens</th>
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<th></th>
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</thead>
<tbody>
<tr>
<td>A/duck/Jiangsu/13141/2018</td>
<td>H7N9</td>
<td>80</td>
<td>320</td>
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<tr>
<td>A/duck/Jiangsu/13160/2018</td>
<td>H7N7</td>
<td>80</td>
<td>320</td>
</tr>
<tr>
<td>A/duck/Jiangsu/13171/2018</td>
<td>H7N3</td>
<td>40</td>
<td>160</td>
</tr>
<tr>
<td>A/wild bird/Jiangsu/27068/2018</td>
<td>H7N4</td>
<td>40</td>
<td>160</td>
</tr>
<tr>
<td>A/wild bird/Jiangsu/32492/2018</td>
<td>H7N7</td>
<td>80</td>
<td>320</td>
</tr>
</tbody>
</table>
Figure 2. Phylogenetic relationships of A(H7) Eurasian HA genes. The available CVVs are in red. The proposed CVV is indicated by a red dot (●). Human viruses are in bold font. The viruses tested in haemaglutination inhibition assay are indicated by hashes (#). NA subtypes other than N9 are specified. 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. A/duck/Hong Kong/293/78 (N2) is used to root the tree.
**Influenza A(H7) candidate vaccine viruses**

Based on the current antigenic, genetic and epidemiologic data, a new A/chicken/Jiangsu/1/2018 (H7N4)-like CVV is proposed. The available and pending A(H7) CVVs are listed in Table 6.

**Table 6. Status of influenza A(H7) candidate vaccine virus development (excluding A/Anhui/1/2013 lineage A(H7N9) viruses)**

<table>
<thead>
<tr>
<th>Candidate vaccine virus</th>
<th>Subtype</th>
<th>Type</th>
<th>Institution*</th>
<th>Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>NIBRG-63 (A/mallard/Netherlands/12/2000)</td>
<td>H7N1</td>
<td>Reverse genetics</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>A/turkey/Italy/3889/99</td>
<td>H7N1</td>
<td>Wild type</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>IBCDC-5 (A/turkey/Virginia/4529/2002)</td>
<td>H7N2</td>
<td>Reverse genetics</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>NIBRG-109 (A/New York/107/2003)</td>
<td>H7N2</td>
<td>Reverse genetics</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>SJRG-161984 (A/Canada/rv444/2004)</td>
<td>H7N3</td>
<td>Reverse genetics</td>
<td>SJCRH</td>
<td>Yes</td>
</tr>
<tr>
<td>NIBRG-60 (A/mallard/Netherlands/12/2000)</td>
<td>H7N3</td>
<td>Reverse genetics</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>IBCDC-1 (A/mallard/Netherlands/12/2000)</td>
<td>H7N7</td>
<td>Conventional</td>
<td>CDC</td>
<td>Yes</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Candidate vaccine viruses in preparation</th>
<th>Subtype</th>
<th>Type</th>
<th>Institution</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/chicken/Jiangsu/1/2018-like</td>
<td>H7N4</td>
<td>Reverse genetics</td>
<td>CCDC/HKU</td>
<td>pending</td>
</tr>
</tbody>
</table>

* **Institutions distributing the candidate vaccine viruses:**
  - CCDC – Chinese Center for Disease Control and Prevention
  - CDC – Centers for Disease Control and Prevention, United States of America
  - HKU – University of Hong Kong, Hong Kong Special Administrative Region, China
  - 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, United States of America
Influenza A(H9N2)

Influenza A(H9N2) viruses are enzootic in poultry in parts of Africa, Asia and the Middle East. The majority of viruses sequenced from these regions belongs to the A/quail/Hong Kong/G1/97 (G1) or A/chicken/Beijing/1/94 (Y280/G9) lineages. Since the late 1990s, when the first human infection was identified, the detection of A(H9N2) viruses from humans and swine has been reported infrequently. In most human cases, the associated illness has been mild and there has been no evidence of human-to-human transmission.

Influenza A(H9N2) activity from 25 September 2018 to 17 February 2019

Five human cases of A(H9N2) virus infections were reported in China in this period. The Y280/G9 lineage A(H9N2) viruses continue to predominate in environmental and poultry samples in China and Viet Nam and were detected in poultry in the Russian Federation. As in previous reporting periods, G1-lineage viruses were detected in poultry in a number of countries in Africa and Asia.

Antigenic and genetic characteristics of influenza A(H9N2) viruses

Genetic and antigenic data were generated for viruses from three of the five human cases. All recent A(H9N2) human and poultry infections in China, and all poultry infections in Viet Nam, were caused by viruses of the Y280/G9 lineage. Representatives of these recent viruses, including the three human viruses, reacted well to post-infection ferret antiserum raised against A/Anhui-Lujiang/39/2018, from which a CVV is in development. A subset of viruses detected in Viet Nam and China was not well inhibited by this post-infection ferret antiserum but reacted well with post-infection ferret antiserum raised against the A/chicken/Hong Kong/G9/97 CVV.

The majority of poultry viruses from the G1 lineage was antigenically and/or genetically similar to those detected in previous periods and to available CVVs

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 7.

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

<table>
<thead>
<tr>
<th>Candidate vaccine viruses (like virus)</th>
<th>Type</th>
<th>Clade</th>
<th>Institution*</th>
<th>Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/Hong Kong/1073/99</td>
<td>Wild type</td>
<td>G1</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>NIBRG-91 (A/chicken/Hong Kong/G9/97)</td>
<td>Reverse genetics</td>
<td>Y280/G9</td>
<td>NIBSC</td>
<td>Yes</td>
</tr>
<tr>
<td>IBDCDC-2 (A/chicken/Hong Kong/G9/97)</td>
<td>Conventional</td>
<td>Y280/G9</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>IDCDC-RG26 (A/Hong Kong/33982/2009)</td>
<td>Reverse genetics</td>
<td>G1</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>IDCDC-RG31 (A/Bangladesh/994/2011)</td>
<td>Reverse genetics</td>
<td>G1</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>SJ008 (A/Hong Kong/308/2014)</td>
<td>Reverse genetics</td>
<td>Y280/G9</td>
<td>SJCRH</td>
<td>Yes</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Candidate vaccine viruses in preparation</th>
<th>Type</th>
<th>Clade</th>
<th>Institution</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/Anhui-Lujiang/39/2018-like</td>
<td>Reverse genetics</td>
<td>Y280/G9</td>
<td>CCDC</td>
<td>Pending</td>
</tr>
<tr>
<td></td>
<td>Conventional</td>
<td>Y280/G9</td>
<td>NIBSC</td>
<td>Pending</td>
</tr>
</tbody>
</table>

* Institutions distributing the candidate vaccine viruses:
- CCDC – Chinese Center for Disease Control and Prevention
- CDC – Centers for Disease Control and Prevention, United States of America
- HKU – University of Hong Kong, Hong Kong Special Administrative Region, China
- 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, United States of America
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 influenza A(H3N2) viruses have been previously documented in Asia, Europe and North America.

Influenza A(H3N2)v activity from 25 September 2018 to 17 February 2019

A human case of A(H3N2)v influenza virus infection was detected in Australia during routine screening of influenza positive samples. The case was a 15-year-old female with likely exposure at a livestock exhibition. This is the first documented case of a variant influenza virus human infection in Australia.

Antigenic and genetic characteristics of influenza A(H3N2)v viruses

Phylogenetic analyses of the HA and NA genes of the Australian virus, A/South Australia/85/2018, showed that it grouped with A(H3N2) swine influenza viruses detected in Australia and Asia, which were likely derived from seasonal A(H3N2) viruses that circulated in the late 1990s. The six internal genes of A/South Australia/85/2018 were derived from A(H1N1)pdm09 viruses circulating in pigs. Antigenic characterization of this virus is pending.

Influenza A(H3N2)v candidate vaccine viruses

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

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

<table>
<thead>
<tr>
<th>Candidate vaccine viruses (like virus)</th>
<th>Type</th>
<th>Institution*</th>
<th>Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>NYMC X-203 (A/Minnesota/11/2010)</td>
<td>Conventional</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>NYMC X-213 (A/Indiana/10/2011)</td>
<td>Conventional</td>
<td>CDC</td>
<td>Yes</td>
</tr>
<tr>
<td>IDCDC-RG55C (A/Ohio/28/2016-like)</td>
<td>Reverse genetics</td>
<td>CDC</td>
<td>Yes</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Candidate vaccine viruses in preparation</th>
<th>Type</th>
<th>Institution</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/Ohio/13/2017-like</td>
<td>Reverse genetics</td>
<td>CDC</td>
<td>Pending</td>
</tr>
</tbody>
</table>

* Institution distributing the candidate vaccine viruses:
  CDC – Centers for Disease Control and Prevention, United States of America

Acknowledgements

We acknowledge the WHO Global Influenza Surveillance and Response System (GISRS) which provides the mechanism for detection and monitoring of emerging 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 comprehensive analysis of viruses; and WHO H5 Reference Laboratories for their complementary analyses. We thank the OIE/FAO Network of Expertise on Animal Influenza (OFFLU) laboratories and other national institutions for contributing information and viruses. We also acknowledge the Global Initiative on Sharing All Influenza Data (GISAID) for the EpiFlu database, and other sequence databases which were used to share gene sequences and associated information.

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