Identification, Genetic Analysis and Pathogenicity of Classical Swine H1N1 and Human-Swine Reassortant H1N1 Influenza Viruses from Pigs in China

Yafen Song¹, Yong Zhang¹, Bing Zhang¹, Ling Chen¹, Min Zhang¹, Jingwen Wang¹, Ying Jiang¹, Chenghuai Yang¹, Taozhen Jiang¹*

¹ China Institute of Veterinary Drug Control, Beijing 100081, China

* Taozhen Jiang is the Corresponding author:

Dr. Taozhen Jiang, China Institute of Veterinary Drug Control, 8 Nandajie, Zhongguancun, Haidian District, Beijing, 100081, China.

Tel: (+86) 010-62103518; Fax: (+86) 010-61255380; E-mail: taozhen_jiang@163.com
Table S1. The nucleotide homology between the AV1522 virus and the A/swine/Hubei/02/2008(H1N1) virus, when analyzing each gene fragment.

<table>
<thead>
<tr>
<th>virus</th>
<th>gene</th>
<th>virus with similarity</th>
<th>Homology (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/swine/Shandong/AV1522/2011(H1N1)</td>
<td>HA</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.5</td>
</tr>
<tr>
<td></td>
<td>NA</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>100</td>
</tr>
<tr>
<td></td>
<td>PB2</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.7</td>
</tr>
<tr>
<td></td>
<td>PB1</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.9</td>
</tr>
<tr>
<td></td>
<td>PA</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.6</td>
</tr>
<tr>
<td></td>
<td>NP</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.5</td>
</tr>
<tr>
<td></td>
<td>M</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>99.9</td>
</tr>
<tr>
<td></td>
<td>NS</td>
<td>A/swine/Hubei/02/2008(H1N1)</td>
<td>100</td>
</tr>
</tbody>
</table>
Figure S1. Phylogenetic analysis of the NA(A), PB2 (B), PB1 (C), PA (D), NP (E), M (F), and NS (G) genes. The trees were constructed by using the neighbor-joining method with the Maximum Composite Likelihood model and MEGA version 4.0 with 1,000 bootstrap replicates. Our viruses were indicated by triangle marker “▲”.
Figure S1A

[Diagram of phylogenetic tree showing relationships between different strains of influenza viruses including Human, Avian, Classical swine, and Triple Reassortant branches]
Figure S1B

Classical swine

Human

Triple Reassortant

Avian
Figure S1C

Classical swine

Human

Avian

Triple Reassortant
Figure S1G

A/England/5/2007(H1N1)
A/England/10/2007(H1N1)
A/Japan/AI/07/2008(H1N1)
A/Japan/AI/07/2006(H1N1)
A/England/494/2006(H1N1)
A/Auckland/619/2009(H1N1)
A/New York/241/2001(H1N1)
A/Ohio/36/1996(H1N1)
A/Chili/1/1983(H1N1)
A/Alaska/1935(H1N1)
A/Shandong/AV1522/2011(H1N1)
A/Singapore/5/2009(H1N1)
A/Swine/Hong Kong/CX484/2016(H1N2)
A/Swine/Hong Kong/S19/2010(H1N2)
A/Swine/Hong Kong/S104/2011(H1N2)
A/Swine/Hong Kong/S777/2010(H1N2)
A/Swine/Hong Kong/666/2011(H1N2)
A/Swine/Hong Kong/S320/2011(H1N2)
A/Swine/Hong Kong/320/2011(H1N2)
A/Swine/Hong Kong/NS3954/2011(H1N2)
A/Swine/Hong Kong/NS3969/2011(H1N2)
A/Swine/Hong Kong/S202/2011(H1N2)
A/Swine/Hong Kong/S3976/2011(H1N2)
A/Swine/Hong Kong/NS3969/2011(H1N2)
A/Swine/Hong Kong/S3977/2011(H1N2)
A/Swine/Hong Kong/S3978/2011(H1N2)
A/Swine/Hong Kong/2421/2012(H1N1)
A/Swine/Hong Kong/1683/2005(H1N1)
A/Swine/Hong Kong/559/2007(H1N1)
A/Swine/Hong Kong/851/2007(H1N1)
A/Swine/Sweden/1021/2009(H1N1)
A/swine/Italy/671/1987(H1N1)
A/mallard/Ohio/171/1990(H1N1)
A/duck/Alberta/35/1976(H1N1)
A/Swine/Shandong/AV1523/2011(H1N1)