

WHO recommendation on influenza A(H7N9) vaccine virus

26 September 2013

Since 31 March 2013, public health authorities in China have reported a total of 135 human cases of novel avian influenza A(H7N9) infection, including 44 deaths¹. To date, there has been no evidence of sustained human-to-human transmission.

Because the A(H7N9) virus seems to transmit from animals to humans more readily than the highly pathogenic avian influenza A(H5N1) viruses, and little or no immunity against the novel virus A(H7N9) exists in the human population, WHO is actively working with its Member States and partners on effective responses and preparedness. As part of these efforts, candidate vaccine viruses² are being developed and made available by the WHO GISRS.

To date, the HA sequences of 123 A(H7N9) viruses (54 viruses from 44 human cases and 69 avian/environmental viruses) have been deposited in genetic sequence databases. Genetic analysis of the HA genes indicated limited heterogeneity among these viruses (see Figure). Antigenic analyses of 45 viruses from humans, animals and environment with post-infection ferret antisera indicated that the provisionally recommended vaccine virus, A/Anhui/1/2013-like virus³, elicits antibodies that react well with all viruses tested (see Table).

Based on genetic and antigenic analysis, it is recommended that:

- An **A/Anhui/1/2013-like*** virus be used for the development of influenza A(H7N9) vaccines for pandemic preparedness purposes.

* A/Shanghai/2/2013 is an A/Anhui/1/2013-like virus.

Status updates on the development and availability of influenza A(H7N9) candidate vaccine viruses⁴, as well as biosafety requirements⁵ on handling the A(H7N9) candidate vaccine viruses, are available on the WHO website.

The A(H7N9) viruses, including candidate vaccine viruses, are considered PIP Biological Materials and are being shared under the PIP Framework.⁶

For more information, please contact gisrs-whohq@who.int.

¹ http://www.who.int/influenza/human_animal_interface/influenza_h7n9/en/index.html

² http://www.who.int/entity/influenza/vaccines/virus/candidates_reagents/summary_a_h7n9_cvv_20130813.pdf

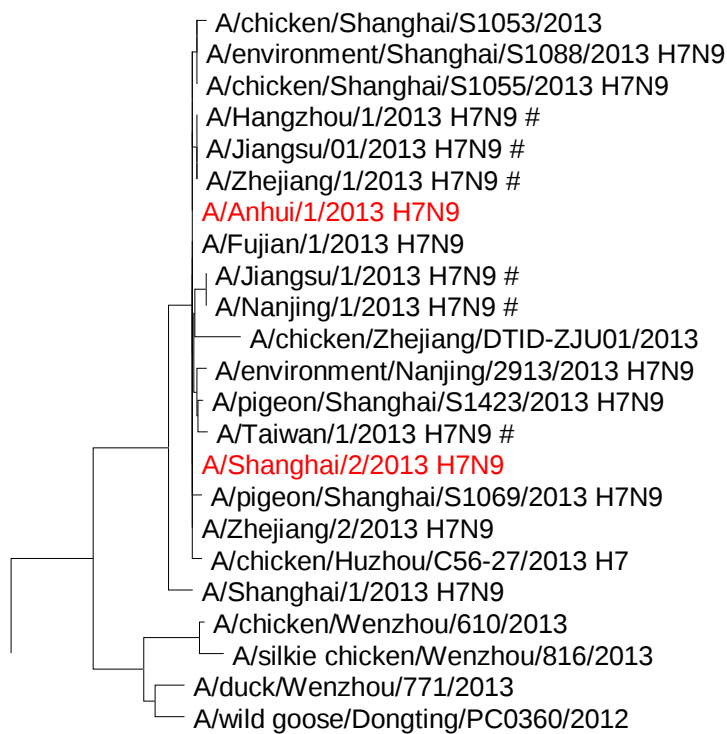
³ http://www.who.int/influenza/human_animal_interface/influenza_h7n9/ProvisionalRecommendation_H7N9_31May13.pdf

⁴ http://www.who.int/influenza/vaccines/virus/candidates_reagents/a_h7n9/en/index.html

⁵ http://www.who.int/entity/biologicals/BIOSAFETY_RISK_ASSESSMENT_21_MAY_2013.pdf

⁶ http://www.who.int/influenza/resources/pip_framework/en/index.html

Figure



Phylogenetic relationships of A(H7) virus HA genes. The available candidate vaccine viruses are in red characters. Human viruses are indicated (#).

Table

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/1/2013	H7N9	320	640	80	640
A/Zhejiang/1/2013	H7N9	320	640	80	640
A/Beijing/1-A/2013	H7N9	320	640	80	640
A/Henan/1/2013	H7N9	160	320	80	320
A/Shandong/1/2013	H7N9	320	640	80	320
A/Fujian/1/2013	H7N9	320	640	80	640
A/Jiangxi/1/2013	H7N9	320	640	80	640
A/Hunan/1/2013	H7N9	160	640	80	640
A/Anhui/2/2013	H7N9	320	1280	80	640
A/Shandong/68A/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