Author's response to reviews

Title: One Family Cluster of avian influenza A(H7N9) virus infection in Shandong, China

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Author's response to reviews: see over
Dear Editor,

Here within enclosed is our paper for consideration to be published on “BMC Infectious Disease” as “Case Report”. The further information about the paper is in the following: The Title: One Family Cluster of Avian influenza A(H7N9) Virus infection in Shandong, China. The Authors: Ti Liu, Zhenqiang Bi, Xianjun Wang, Zhong Li, Shujun Ding, Zhenwang Bi, Liansen Wang, Yaowen Pei, Shaoxia Song, Songyang Zhang, Jianxing Wang, Dapeng Sun, Bo Pang, Lin Sun, Xiaolin Jiang, Yulu Wang, Jie Lei, Qun Yuan, Zengqiang Kou, Bin Yang, Yuelong Shu, Lei Yang, Xiyan Li, Kaishun Lu, Jun Liu, Tao Zhang, Aiqiang Xu. The authors claim that none of the materials in the paper has been published or is under consideration for publication elsewhere. And the authors claim that we all saw the final manuscript and the paper are not being submitted to any other journals. The study was approved by the institutional review board of Shandong Provincial Center for Disease Control and Prevention; The patient or guardian were provided written informed consent form before specimen collection and testing and clinical information publication.

We believe the paper may be of particular interest to the readers of your journal because the study reports the epidemiological analysis of one family cluster of human infection with Avian Influenza A (H7N9) Virus in Shandong, China.

Correspondence and phone calls about the paper should be directed to Aiqiang Xu at the following address, phone fax number, and E-mail address.
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The revised part

The first reviewer

1# Abstract # Case Presentation# “rRT-PCR” should be modified to “RT-PCR”.

In the text, we detected the sample with real-time RT-PCR, so we revised in the abstract# Case Presentation# rRT-PCR: Both of the two cases were confirmed to infect with H7N9 virus by the results of real-time reverse transcriptase-polymerase-chain reaction (rRT-PCR)

2# Abstract # Case Presentation# respectively. 11 close: The middle needs space.

I have revised in the text according to the suggestion.

3# Background : most affected patients had a history: “affected” should be modified to “infected”.

I have revised in the text according to the suggestion.

4# Background : human H7N9 case who is the son of the index case was confirmed: “is” should be modified to “was”.

I have revised in the text according to the suggestion.

5# Case Presentation : Patients : to Zaozhuang Shili Hospital on April 21: “Shili” should be modified to city.

I have revised in the text according to the suggestion.

6# Case Presentation : Patients : April 14. He was given: The middle needs space.

I have revised in the text according to the suggestion.

The second reviewer

The authors describe the cases of a father and his son being infected with the novel H7N9 virus. They conclude that the infection of the index case probably resulted from contact with 3 environmentally contaminated material. For the son, the probable infection source was from the index case during unprotected exposure, but the possibility from the environment or other sources could not be completely ruled out. As for both cases virus was isolated and RT-PCR was performed, the authors are advised to include the sequence analysis of the
isolated viruses (particularly the HA gene) as this may provide more solid data on the ability of the virus to be transmitted from the father to the son.

We revised the paper according to the reviewer’s suggestion, the revised parts were seen below:

In the abstract#case presentation: The homologous analysis of the full genome sequence indicated that both viruses from the patients were almost genetically identical.

In the case presentation: Complete genomic sequencing of SD/01, SD/0068A and Ev/SD/01 were analyzed. The homologous analysis showed that they were 99.82% to 100% identical in all eight gene segments and the two human A (H7N9) viruses were 100% identical in HA, PB1, PA, NS and M genes (Table 2). There are only four amino acid substitutions between the two human A (H7N9) viruses, two in the PB2 (E341K and R427Q substitutions), one in NA (L399S substitution) and one in NP (M191V substitution), respectively. The full-length gene sequence number in GISAID are EPI 1447715-1447721 and 1447618 [SD/01], EPI 1457428-1457435 [SD/0068A], EPI1447645-651 and 1447628 [Ev/SD/01].

In the discussion part about the infection sources of the son: Last, the sequence analysis showed that both virus from patients possessed high degrees of similarity between nucleotide (99.8% - 100.0%) and amino acid (99.7% - 100.0%) sequence.

Thank you very much for consideration!

Sincerely Yours,

Aiqiang Xu