Infection With Multiple Avian Influenza Viruses in a Man Without Poultry-Handling Practices Suggesting an Increased Probability of Emergent Pandemic Influenza Virus in General Population

To the Editor—Avian influenza viruses are occasionally able to cross species barrier to infect humans, and this infection depends on behavioral, environmental, and genetic factors. Previous studies have demonstrated that contact with poultry, especially sick or dead poultry, was the risk factor for infection with avian influenza [1, 2]. Because the general population is much less likely than poultry workers to come into close contact with poultry, the risk of infection with avian influenza is deemed to be insignificant in the general population. Nonetheless, even without poultry-handling practices, residents of general population dwellings in rural areas should not be neglected by investigators, because these residents may come into contact with wild birds that carry avian influenza viruses, particularly aquatic birds, which frequently appear in rural areas [3, 4]. To examine infection with avian influenza in general population dwellings in rural areas of Beijing, China, we conducted a serological survey among residents of 6 rural districts of Beijing in March 2011.

This serological survey was carried out in 605 participants without poultry-handling practices and randomly selected from 24 villages of Beijing, in which there was no poultry raising. Blood samples were collected to test for antibodies against H5, H7, and H9 avian influenza viruses with hemagglutination inhibition assay [5]. One participant (0.17%) tested seropositive for H5 virus, none were positive for H7 virus, and 5 (0.83%) were positive for H9 virus. Of the participants who tested seropositive for avian influenza viruses, a 55-year-old man tested seropositive for both H5 and H9 virus. His son also tested seropositive for H9 virus, but neither his wife nor his daughter-in-law tested seropositive.

Our findings demonstrated a risk of infection with avian influenza in the general population dwelling in a rural area. Of the 5 infected participants, 1 man was infected with both H5 and H9 viruses, possibly owing to a high genetic susceptibility to avian influenza virus. Some individuals in the general population, like our male subject, may have high genetic susceptibility to avian influenza, with a much higher than normally expected probability of infection with avian influenza virus; this would increase the likelihood of coinfection with avian influenza virus and human influenza virus, reassortment of these viruses, and even emergence of pandemic influenza virus. In addition, infection with avian influenza was found only in a blood relative of this man, further suggesting the possibility of genetic susceptibility to the infection [6].

Given the possibility of increased genetic susceptibility to avian influenza, the risk of emergence of pandemic influenza virus in the general population, and the large size of this population, standard surveillance systems for preparedness and response to pandemic influenza, focusing mainly on poultry workers, seem insufficient. Our findings warrant enhanced surveillance of general populations in the future, especially of populations dwelling in rural areas.

Note

Financial support. This work was supported by grants from the National High Technology Research and Development Program of China (863 Program, 2008AA02Z416) and the Public Service Institute Program of the Beijing Center for Preventive Medical Research.

Potential conflicts of interest. All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

Peng Yang,1,3 Weixian Shi,1,3 Shujuan Cui,1,3 Yi Zhang,1,3 Xiujun Liu,2 and Quanyi Wang1,3

1Institute for Infectious Disease and Endemic Disease Control, Beijing Center for Disease Prevention and Control, 2Institute for Infectious Disease and Endemic Disease Control, Tongzhou District Center for Disease Prevention and Control, and 3Capital Medical University School of Public Health and Family Medicine, Beijing, China

References


Correspondence: Quanyi Wang, MD, MPH, Institute for Infectious Disease and Endemic Disease Control, Beijing Center for Disease Prevention and Control, Capital Medical University School of Public Health and Family Medicine, No. 16 He Pingli Middle St, Dongcheng District, Beijing 100013, China (bjcdcxm@126.com).

Clinical Infectious Diseases 2012;54(2):307

© The Author 2011. Published by Oxford University Press on behalf of the Infectious Diseases Society of America. All rights reserved. For Permissions, please e-mail: journals.permissions@oup.com.

DOI: 10.1093/cid/cir844