

# International Forum on Ecology & Evolution of Avian Influenza

*A webinar series over the period of 5/2021 - 12/2024*

June 22, 2021, Tuesday, 9am – 10am, China

June 21, 2021, Monday, 9pm – 10pm, EDT, USA



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[http://cvm.cau.edu.cn/art/2011/12/26/art\\_19968\\_142.html](http://cvm.cau.edu.cn/art/2011/12/26/art_19968_142.html)

Juan Pu is a Professor at College of Animal Medicine, China Agricultural University and the Director of Infectious Diseases and Microbiology Teaching and Research Group. She, as a visiting scholar, worked at Nottingham University, UK and St. Jude Children's Research Hospital, USA. She was awarded the excellent youth fund of National Natural Science Foundation of China (NSFC). She is Principal Investigator for the NSFC projects and other national projects. She is interested in the epidemiology and ecology of animal influenza virus and its transmission mechanism, focusing on the impact of animal influenza virus on domestic animals and its public health hazards, tracking the epidemic and transmission of animal influenza virus in animal, environment and human, revealing the mechanism of virus pathogenicity and interspecies transmission, so as to explore the key elements of influenza virus transmission in the ecosystem, and to provide a theoretical basis for scientific prevention and control of zoonotic diseases such as animal influenza.

## Role of Chicken farms in the evolution and emergence of Avian Influenza Viruses in China

Emerging animal borne zoonoses are mostly transmitted through the chain of wild animal - livestock/poultry - human. Livestock and poultry are important intermediate hosts in the infection of humans with animal borne viruses, and they are also key indicators for early warning of animal borne zoonosis. H9N2 and H7N9 subtypes of avian influenza viruses are important zoonosis pathogens, which are widely prevalent in Chinese chicken flocks and cause human infections. Through epidemiological investigation, gene evolution analysis and biological characteristics evaluation, we found that the epidemic advantage of H9N2 virus in chicken flocks was gradually enhanced, the antigenicity variation was accelerated, and the adaptability of H9N2 virus to chicken flocks and mammals was continuously enhanced, which led to two large-scale epidemics of H9N2 virus in chicken flocks (2010-2017) and increased the gene exposure opportunities of H9N2 virus that promoted the generation and evolution of H7N9 virus. Therefore, through gene reassortment, H7N9 obtained key genes from H9N2 virus and enhanced its infectivity to mammals, which was an important reason for the first and fifth wave of H7N9 epidemic. In a word, our research confirmed that chicken flocks can provide an important early warning signal for the occurrence of human avian influenza virus epidemic, which will move the control gate forward. It is necessary to strengthen the monitoring and control of AIVs epidemic in chickens.

Registration at <http://eomf.ou.edu/workshops/current/>

**Organizers:** University of Oklahoma, St. Jude Children's Research Hospital, USGS EESC;  
Sun Yat-sen University, China Agricultural University, China CDC CNIC,

**Organizing Committee Chairs:** Xiangming Xiao (University of Oklahoma, USA), and Yuelong Shu (Sun Yat-sen University, China)