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Epidemiological analysis of H9N2 virus in China

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In our lab, systemic surveillance and epidemiological investigation on H9N2 influenza were conducted. From January 2008 to August 2014, 6569 clinical samples had been collected and tested, and the positive rate of H9N2 influenza was 25.12%. More than 1,000 H9N2 virus strains were isolated. The genome sequences of the virus were determined, and the biological characters were tested. The results showed the mutation speed of HA gene became faster. New clade virus were emerging nearly year by year. Different clade virus was circulating at the same time and same location. The H9N2 virus isolated after 2008 displayed higher virulence to embryonated eggs, and the virulence with higher virulence in embryonated eggs also showed higher pathogenicity in chickens, and caused systemic infection. The antigenicity of H9N2 changed quickly, and formed different antigenic groups, some of which showed significant antigenic difference, compared with earlier vaccine strains. Our study also showed when HA amino acid sequence mutations reached a point (more than 7%), the antigenicity change could be significant. The study results emphasized that the vaccine strain should be updated in a timely manner through surveillance and accompanying laboratory evaluation of contemporary viruses for antigenic similarity with existing vaccine strains, and the genetic and pathogenic variation of H9N2 virus should be closely monitored.

Biography

Yanbo Yin has completed his PhD from China Agricultural University. He is a Member of Avian Diseases Branch, Executive Member of Veterinary Pathology Branch, Chinese Association of Animal Science and Veterinary Medicine; The avian diseases prevention duty expert of Shandong Modern Agricultural Technology & Industry System. He is a Professor of Qingdao Agricultural University and has trained more than 30 graduate students. He has published more than 200 peer-reviewed papers in English and Chinese.

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