

Emergence of a young case infected with avian influenza A (H5N6) in Anhui Province, East China during the COVID-19 pandemic

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Abstract

In the context of the COVID-19 pandemic, we investigated the epidemiological and clinical characteristics in a young patient infected by avian influenza A (H5N6) virus in Anhui Province, East China, and analyzed genomic features of the pathogen. Through the cross-sectional investigation of external environment monitoring (December 29-December 31, 2020), 1 909 samples were collected from Fuyang City. It was found that the positive rate of H5N6 in Tianma poultry market was higher than other areas obviously, where the case appeared. The virus was the clade 2.3.4.4, which was most likely formed by genetic reassortment between H5N6 and H9N2 viruses. This study found that the evolution rates of HA gene and NA gene of the virus were higher than those of common seasonal influenza viruses. The virus was still highly pathogenic to poultry, and had a preference for avian receptor binding.

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