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H7 highly pathogenic avian influenza A virus genomes from the first half of the 20th century

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Highly pathogenic avian influenza viruses (HPAIV) cause severe outbreaks in poultry, leading to high mortality, economic losses, and occasional human infections. While H5 and H7 subtypes have dominated poultry outbreaks in the 20th century, the genomic diversity of HPAIV before widespread surveillance in the 1980s remains poorly characterized. So far, only a few complete genomes from before 1950 have been sequenced.

Historical pathology collections provide a unique window into the evolutionary history of pathogens and are a valuable resource for studying ancient HPAIV. To explore early HPAIV diversity, we analyzed 30 formalin-fixed avian tissue samples from the 1920s to 1960s, sourced from four historical pathology collections.

Using shotgun RNA sequencing, we detected HPAIV reads in five samples and reconstructed two near-complete genomes: H7N1 (1927) and H7N7 (undated). Three additional samples (1942–1960) yielded lower coverage genome-wide data. Interestingly, three specimens originally diagnosed as avian influenza only contained Newcastle disease virus sequences.

We are currently working to complete genome recovery from all HPAIV-positive samples. The resulting dataset will support phylodynamic analyses to reconstruct the history of HPAIV lineages and refine the evolutionary timeline of avian influenza viruses.

Keywords

avian influenza, subtype H7, ancient viral genomes, viral evolution

Registration ID

123

Professional Status of the Speaker

Postdoc

Junior Scientist Status

No, I am not a Junior Scientist.

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