



# AVIAN H3N8 HUMAN CASE

April 2022

## A/Henan/4-14/2022

On the 26th of April there were reports of a human H3N8 infection in a 4 year old male in Henan province, China. Whole genome sequence data is available on GISAID for samples taken on the 10th April 2022 and 14th April 2022. Full genome analysis was undertaken for A/Henan/4-14/2022.

Each segment was blasted for the 100 closest matches, aligned using MAFT v7.475 (Kato and Standley, 2013) and maximum likelihood phylogenetic trees were generated using IQ-TREE 2.1.3 default settings (Nguyen et al., 2015). Molecular changes were screened using Fludb's sequence feature identifier, Fluserver's mutations app <http://fluserver.bii.a-star.edu.sg>, Inventory of molecular changes (Suttie et al. 2019) and a general literature search to identify genetic changes that determine viral phenotypic characteristics of importance that may increase virulence, signal adaptation to mammalian species or alter susceptibility to existing antivirals.

### Summary:

The virus is an H3 low pathogenic reassortant virus of avian origin with genes from viruses which have been detected previously in poultry and wild birds. The internal genes are from H9N2 eurasian lineage poultry viruses and the NA of American wild bird lineage poultry viruses. There is evidence of the presence of molecular changes associated with mammalian adaption.

The amino acid change E627K (PB2) was identified which is associated with adaption to mammalian infection and increased virulence in mammals and the amino acid change 31N (M) was identified which is reported to increase resistance to the antiviral amantadine and rimantadine.

There are a total of 3 amino acid changes linked to statistical host specificity shifts in the HA1 (S8N, T144A, T147S) compared to the closest blast result and 3 amino acid changes in N. On the 26th April there were reports of a human H3N8 infection in a 4 year old male in Henan province, China. Whole genome sequence data is available on GISAID for samples taken on the 10th April 2022 and 14th April 2022. Full genome analysis was undertaken for A/Henan/4-14/2022.

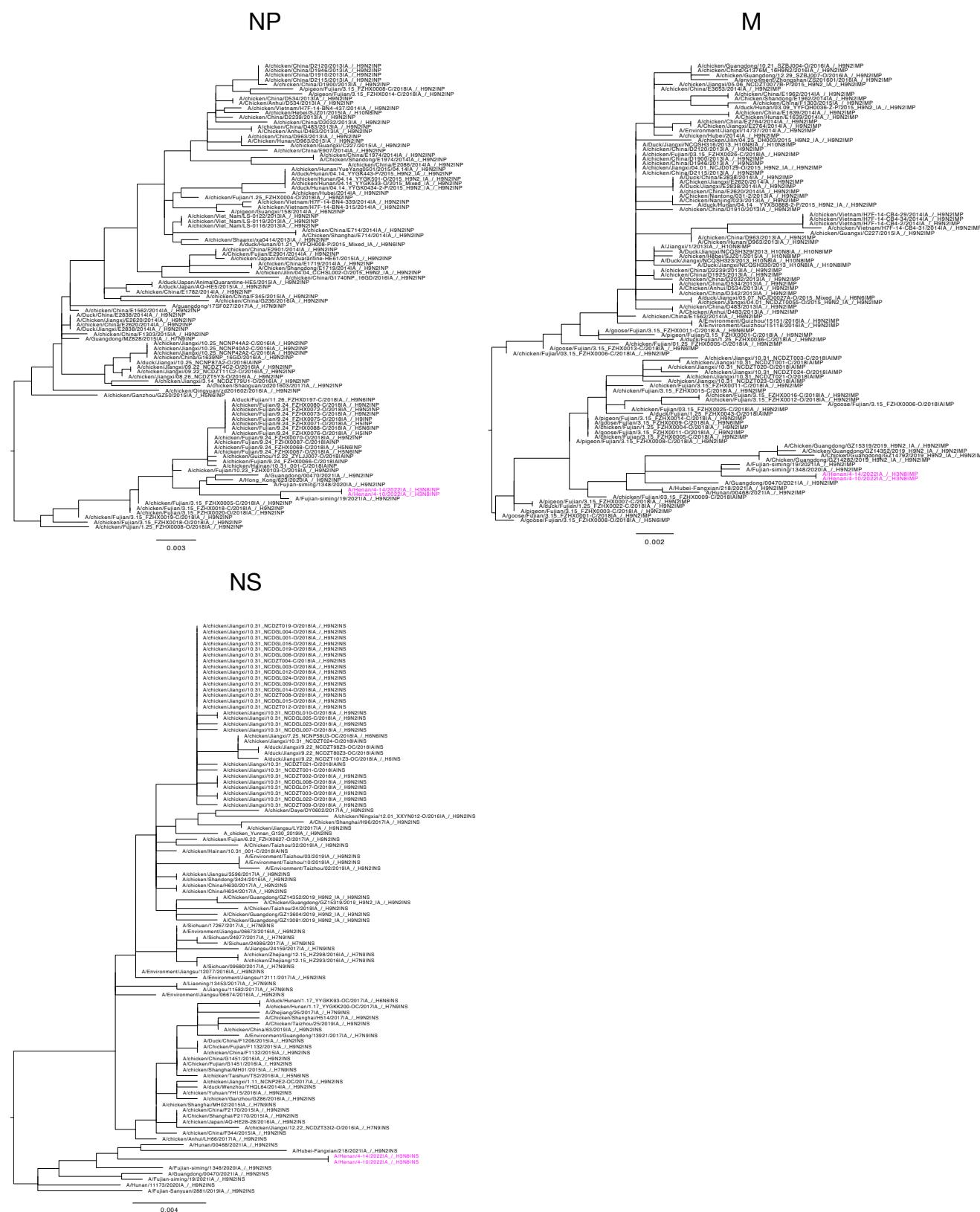
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# HA



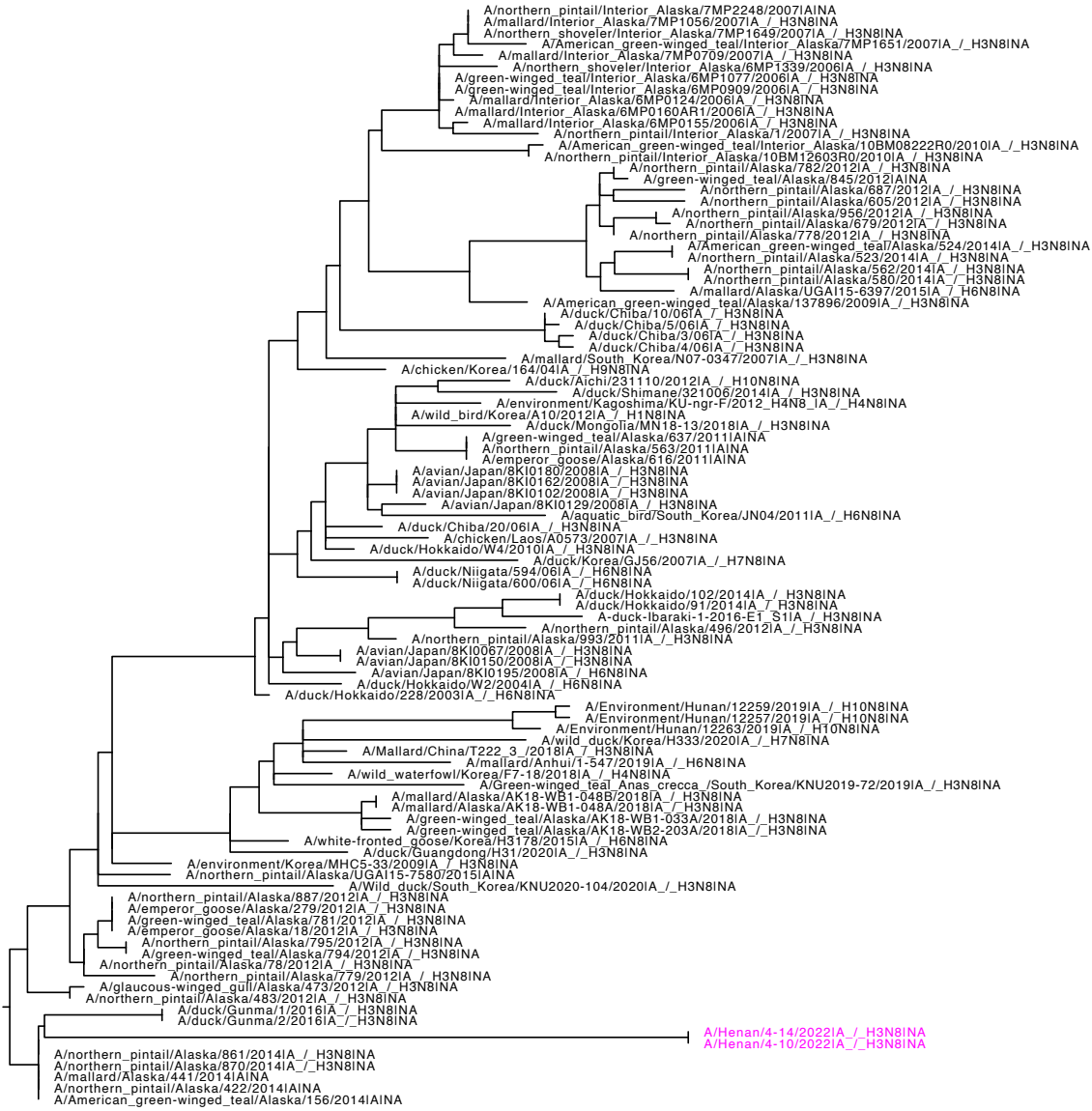
0.02

# NP, M and NS: H9N2 eurasian lineage poultry virus with ancestry to human H9N2 cases in China in 2021 and H5 reassortants in poultry



NA: North American West Pacific/Pacific America flyway H3N8 wild birds and ducks

NA



0.004

PA: H9N2 eurasian lineage poultry virus ancestry to environmental H9N2 viruses

PA

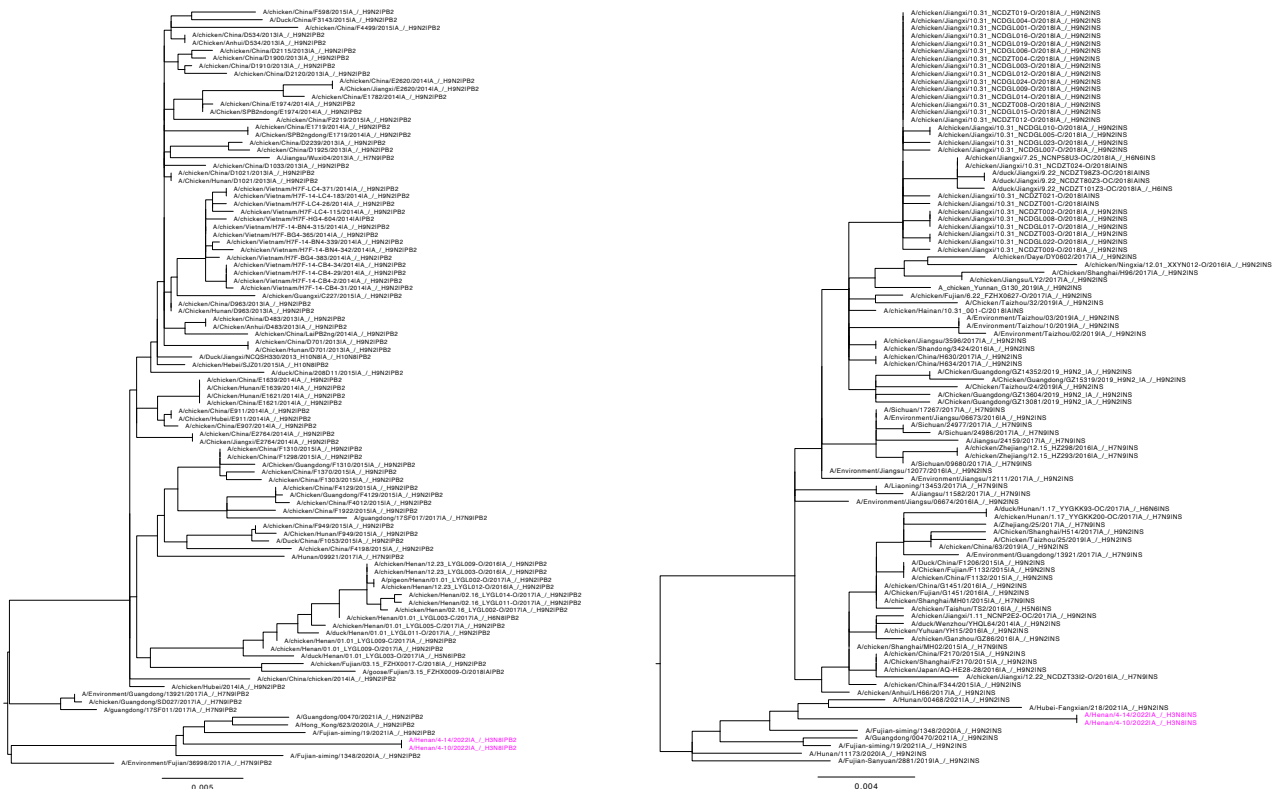


0.002

# PB1 and PB2: Eurasian lineage poultry virus with ancestry to human H9N2 viruses

## PB2

## PB1



## Whole genome mutation analysis A/Henan/4-14/2022 H3N8

<b>Protein</b>	<b>Motif</b>	<b>Reported effect</b>	<b>Reference</b>
<b>HA</b>	99K	Host specificity shift	Fluserver
	144A	Host specificity shift	Fluserver
	147S	Antigenic drift / escape variant	Fluserver
	160A	Increased replication in upper respiratory tract of ferrets	Wang et al 2010
<b>PA</b>	295P	Virulence	Ducatez et al 2012
	476A	Increased polymerase activity	Cauldwell et al 2014
	630E	Increased polymerase activity	Cauldwell et al 2014
<b>PB2</b>	292V	Host specificity shift	Gao et al 2019
	588V	Mammalian adaption	Xiao et al 2016
	627K	Increased polymerase activity in mammalian cell line, increased virulence in mice	Nilsson et al 2017
	473M, 598V	Altered polymerase activity in mammalian cells	Xu et al 2012
	676V	Virulence	Li et al 2009
<b>PB1</b>	375S	Decreased virulence in ferrets	Salomon et al 2006
	383D	Mamalian Adaption	Song et al 2015
<b>NA</b>	38R	Mild drug resistance	Fluserver
<b>M2</b>	31N	Increased resistance to amantadine and rimantadine in H9N2	Lan et al 2015
	30D 215A	Introduction of Asn30Asp and Thr215Ala substitutions in the A/duck/Guangxi/53/2002 backbone conferred increased virulence in mice indicated by survival rate in H5N1	Fan et al 2008
<b>NS1</b>	226V	Virulence	Fluserver
	227K	Virulence	Fluserver