

PRESS RELEASE

Avian Flu, from 'FluWarning' early alerts for virus spillovers

A system developed by Researchers at the Politecnico di Milano and the University of Milan detects changes that may indicate cross-species transmission and anticipate possible epidemics

Milan, 20 November 2025 – How can we monitor the cross-species transmission of avian flu? The answer is **FluWarning**, a digital system that reports abnormal changes in flu viruses, developed by a research team from the **Politecnico di Milano** and the **University of Milan**. The system analyses the genetic code of flu viruses, looking for **subtle but significant changes that could indicate cross-species transmission (for example, from birds to cattle or to humans)**, a process known as *spillover*.

The study, which was recently published in the prestigious journal **Science Advances**, was developed under the NRRP-funded PRIN 2022 – SENSIBLE project (*Small-data Early warNing System for viral pathogens In puBLic hEalth*). The *FluWarning* research team includes three members from **DEIB – Department of Electronics, Information and Bioengineering** at the Politecnico di Milano, SENSIBLE's Principal Investigator **Anna Bernasconi**, Professor **Stefano Ceri** and Researcher **Tommaso Alfonsi**, along with **Matteo Chiara**, Professor in the **Department of Biosciences** at the University of Milan.

The study relied on data from GISAID, a platform for sharing virus sequences and the related metadata produced by laboratories all around the world. **FluWarning was developed using data from the H1N1 swine flu pandemic** in 2009, a well-documented example of a virus being transmitted from animals to humans. It **was then applied to H5N1 bird flu**, a highly pathogenic strain among birds, which in the past year has also begun to spread among US cattle.

The system **uses a statistical method to recognise anomalies**. Depending on the settings, it can be used to recognise individual anomalous sequences or groups of anomalous sequences. *FluWarning* learns the normal sequences of influenza viruses and issues an alert whenever the code of the sequences changes significantly. **For each alert, virologists analyse the corresponding sequences** and confirm or reject the presence of spillover.

'With its simple installation and analysis that can be done for specific locations and over specific time periods, the *FluWarning* software can potentially be used by many laboratories or regional genomic surveillance institutions, enabling important discoveries on both small and large scales,' **Anna Bernasconi** notes. 'In fact, the system is perfectly operational. It can give feedback on these changes day by day.'

In 2024–2025, **two H5N1 genotypes were linked to independent outbreaks in the US**, where numerous heads of dairy cattle were found to be infected with bird flu. '*FluWarning* identified clusters of viral activity in several US states, particularly in California, where a state of emergency was declared on 18 December 2024 due to the risk of bird flu contamination in cattle. Surprisingly,

some *FluWarning* alerts appeared before official reports were published. The system also detected specific mutations in the haemagglutinin (HA) gene, a key protein that affects the way the virus infects the host cells,' **Matteo Chiara** says. The tool monitored the evolution of the virus and identified characteristic markers of the California strains.

'*FluWarning* is an important step towards more effective detection of viral changes that could pose a risk to animals or humans. **By making this technology widely available, we hope to strengthen global surveillance** on a health issue of global significance' **Stefano Ceri** concludes.

[LINK TO THE STUDY HERE](#)

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FOR MORE INFORMATION:

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