

Predicting avian Influenza spillover through innovative tools to support public health decision-making

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Highly pathogenic avian influenza (HPAI) H5N1 viruses from clade 2.3.4.4b represent a major threat to animal and public health. Since 2021, these viruses have undergone unprecedented ecological and epidemiological changes characterized by global dissemination and expansion of the range of susceptible bird and mammal species. Also, sustained mammal-to-mammal transmission has been documented in multiple settings and sporadic human infections raise concerns about their pandemic potential.

In this context, we are developing an integrated pipeline to assess the risk of HPAI H5N1 spillover into humans by combining genomic analyses with a panel of complementary in vitro assays designed to characterize viral adaptation to human. Specifically, these assays evaluate the capacity of the virus to replicate in human airway models, including air-liquid interface cultures and respiratory organoids, as well as key determinants of host adaptation, such as hemagglutinin receptor-binding preference, the pH threshold for HA-mediated membrane fusion, and viral polymerase activity in human cells.

The pipeline is currently being benchmarked using seasonal human and representative avian influenza viruses to define reference phenotypic profiles associated with human and avian adaptation. Ultimately, this framework aims to strengthen the early identification of H5N1 viruses with increased zoonotic potential and to provide experimental evidence supporting public health risk assessment and preparedness.

Keywords

Professional status of the speaker

PhD student

Junior scientist status

No, I am not a junior scientist.

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