

Avian H5N1 spillover into mammals in Finland: Evolutionary pathways and early signs of human adaptation

Inhalt

Avian influenza A/H5N1 is driving a severe panzootic, with increasing spillover from avian reservoirs to wild mammals. Outbreaks in fur farms in Spain and Finland (2022–23) demonstrated high susceptibility of these mammals to avian influenza, while infections in dairy cattle in the USA highlighted the virus's expanding host range. These developments emphasize the need to understand mechanisms of cross-species transmission. This project aims to investigate avian H5N1 and seasonal H3N2 virus infections and host immune responses in human upper airway epithelial and immune cells. Recent Finnish H5N1 isolates (2021–23) from fur farms and wildlife were propagated for study. Human primary nasal epithelial (HNE) cells were differentiated at air-liquid interface (ALI), providing a physiologically relevant model for early virus–host interaction. Phylogenetic analysis showed the Finnish isolates clustered into three distinct branches, indicating divergent evolutionary paths. Network analysis revealed close genetic relationships between viruses from wild birds and fur animals within the 2023 epizootic, while strains from different farms were more distant, suggesting multiple introductions. Despite mutations between avian and mammalian isolates, no differences in replication were observed in human dendritic cells. However, mammalian-origin H5N1 showed slightly reduced replication in HNE cells compared with seasonal H3N2. Further studies on early virus–host interactions are ongoing.

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No, I am not a junior scientist.

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