



ID der Kurzfassung : 250

Genomic Characterization of Highly Pathogenic H5N1 Avian Influenza Viruses in Wild and Domestic Animals in Argentina Using a One Health Approach

Inhalt

In 2022, HPAI H5N1 clade 2.3.4.4b (B3.2 genotype) reached South America, causing poultry outbreaks, mass die-offs in marine mammals, and a severe human case in Chile, highlighting its zoonotic potential. Through collaborative efforts between virologists, ecologists, and public/veterinary health agencies, full-genome sequences of H5N1 viruses in Argentina were generated and we identified two distinct B3.2 introductions. The first, in Feb 2023, via wild birds in the northwest, spreading southward and mainly affecting poultry (limited wildlife spillover). The second, in Aug 2023, entered via marine mammals in southern Argentina, spread north along the Atlantic coast, and caused mass mortality in elephant seals and sea lions. We showed that viruses from this second wave belong to a distinct “marine mammal” subclade, carrying mammalian-adaptive mutations (PB2-Q591K, D701N) that may enhance transmission among them. We further identified that these viruses diversified into two sublineages with different geographic patterns and retained the ability to infect seabirds, indicating an expanding host range. In Feb 2025, after nearly a year without outbreaks, we detected a novel triple reassortant H5N1 virus in backyard poultry. Our phylogenetic analysis revealed the first reassortment between H5N1 B3.2 and South American low pathogenicity avian influenza viruses, underscoring the need for continued surveillance and genome sequencing to monitor zoonotic HPAI H5N1 evolution in the region.

Keywords

HPAI H5N1, Genotype B3.2, H5N1 Marine mammal subclade, Spatial diffusion of H5N1, Sublineage diversification, Reassortment, South American LPAI virus, Viral genome

Registration ID

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

Track Klassifizierung: One Health in Public Health

Typ des Beitrags: Oral presentation

Kommentare:

The One Health approach is essential for studying HPAI H5N1, particularly in resource-limited countries where sustained active surveillance is challenging. Here, we present key data on H5N1

in Argentina, South America, generated through coordinated cross-sectoral efforts that optimize resources, enhance early detection, and accelerate the generation of genomic information on emerging H5N1 viruses.