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Migratory shorebirds as key drivers of North American avian influenza virus introduction, spread, and evolution in South America

Inhalt

Wild aquatic birds are reservoirs of avian influenza virus (AIV), yet genomic surveillance in South America remains limited. In Argentina, studies in wild ducks revealed high AIV subtype diversity with internal gene constellations exclusively from South American (SA) lineage, despite frequent HA and NA reassortment with North American (NA) lineages. Migratory shorebirds connect breeding and nonbreeding grounds across the Americas and may facilitate the introduction of NA AIV lineages, as recently seen with H5N1 HPAI incursion. To assess their role in AIV evolution, we sampled migratory shorebirds in central Argentina and obtained the first AIV genomes from these hosts: H1N8 and HxNx from *Calidris fuscicollis* and H11N2 from *C. himantopus*. H11N2 possessed all eight gene segments of NA lineage, representing the first such detection in Argentina. In contrast, H1N8 and HxNx were reassortant viruses with internal genes from both NA and SA lineages, revealing an undocumented mechanism of viral genetic exchange. The PB1 segment of H1N8 formed a sister clade to PB1 genes linked to the 2022 H5N1 HPAI incursion and clustered with viruses from shorebirds in Brazil, suggesting regional circulation. These findings show that migratory shorebirds contribute to the introduction, spread, and evolution of AIV in South America, highlighting their importance for genomic surveillance as an early warning system for novel AIV incursions with potential implications for animal and human health.

Keywords

Avian influenza virus; migratory shorebirds; genomic surveillance; reassortment

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No, I am not a Junior Scientist.

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