

Can we blame the cranes? In-depth analyses of HPAIV H5N1 whole genome sequences in a densely poultry populated area

Inhalt

In 2025, HPAIV H5N1 led to massive losses among wild birds and poultry. Cranes were particularly affected, and in Lower Saxony, roughly 1.5 million poultry were lost due to HPAI. The aim of this study was to investigate the genetic relationships between H5N1 viruses detected in wild birds and those circulating in poultry. Illumina whole genome sequencing generated complete viral sequences from 60 wild birds and 85 poultry flocks.

All viral sequences were assigned to the H5N1 euDI.2.1 genotype. Notably, H5N1 viruses recovered from cranes formed a distinct monophyletic group, regardless of the geographic location of sampling. In contrast, no comparable species-specific clustering was observed among other wild bird species. Instead, phylogenetic analyses suggested a regional rather than host-associated clustering pattern. The same applied to poultry-derived viruses in municipalities with exceptionally high poultry densities.

To further investigate viral dissemination, phylogeographic analyses were conducted for both the crane-associated and other wild bird and poultry-associated clusters. The crane-associated cluster exhibited a broad geographic distribution across northern Germany. In contrast, a poultry-associated cluster was largely confined to the major poultry production area of western Lower Saxony. Reconstruction of viral migration pathways revealed numerous links among geographically proximate poultry holdings, indicating predominantly local transmission dynamics.

Keywords

HPAIV H5N1, wild birds, poultry, genome sequencing, virus transmission pathways

Registration ID

INF26- 72

Professional status of the speaker

Senior Scientist

Junior scientist status

No, I am not a junior scientist.

Track Klassifizierung: Epidemiology and emerging viruses

Typ des Beitrags: Poster presentation