

## Emerging Infections

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### Phylogenetic analysis of avian influenza H9N2 viruses from recent outbreaks in poultry and wild birds in Germany

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**Question:** Recently, influenza virus H9N2 infections in turkeys in Germany were reported. The subtype is known to circulate in the European wild bird population but is also endemic in poultry in Asia. The origin, transmission pathways and zoonotic potential of these strains remained unclear.

**Methods:** Hemagglutinin- and neuraminidase genes of recent H9N2 isolates from Germany were sequenced. Phylogenetic analyses were carried out in maximum likelihood and Bayesian frameworks. Antigenic properties were examined by hemagglutination inhibition assays (HI).

**Results:** H9N2 isolates from poultry and wild birds in Germany formed a monophyletic group together with further viruses of this subtype from Europe. No specific European "poultry lineage" was identified. Instead, sequences of viruses from wild birds and poultry were interspersed within the European lineage.

The European wild bird/poultry lineage was distinct from viruses circulating predominantly in poultry in Middle and Far Eastern countries of Asia.

Antigenic analysis by HI did not reveal gross differences between viruses of the European lineage.

**Conclusions:** Outbreaks of H9N2 infection in turkeys in Germany were caused by viruses with close phylogenetic and antigenic relationships to viruses circulating in the European wild bird population. Since available surveillance data do not point towards endemic H9N2 infections in European poultry, and H9N2 infections have been detected continuously over years in wild birds in Europe, spill-over transmission of virus from the wild bird population is likely to have caused sporadic outbreaks in poultry.

European H9N2 viruses are clearly distinct from Asian lineages. The latter also hold viruses which are capable to infect (man) and transmit among mammals (swine). Currently no data on related zoonotic potential in European H9N2 viruses is available.

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