Avian influenza: New aspects of an old threat

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In Europe, epidemics of highly pathogenic avian influenza (HPAI) used to be a seasonal phenomenon associated with migratory waterfowl that were returning to their overwintering sites in the autumn. Since 2020, however, this picture has changed. HPAI viruses, particularly of the influenza A(H5) subtype, have caused the worst epidemics in birds

observed to date, with more than 14,000 reported outbreaks and culling of roughly 96 million farmed birds in Europe.

In their editorial published in *Eurosurveillance*, Cornelia Adlhoch (European Centre for Disease Prevention and Control, ECDC) and Francesca Baldinelli (European Food Safety Authority, EFSA) look at the rapid HPAI development in recent years with a move away from seasonality which has been accompanied by a large geographical extension: from west to east along the migratory bird routes towards south-east Asia.

Recently, A(H5N1) virus introductions from Europe to North America was observed in an east to west spread via Iceland and Greenland for the first time from Europe to North America, progressing rapidly across large areas of Canada and the United States (US). Respectively, a north (Europe and North America) to south (Africa and Central/South America) spread during autumn bird migration occurred to as far down as the southern tip of Chile.

They note that risk for human health is currently limited but warn that introduction of avian influenza viruses into mammalian populations could increase the risk of reassortment of influenza viruses that could adapt to mammals and spread among them: "With the ongoing global presence of A(H5) HPAI viruses, further sporadic spill-over events to humans cannot be excluded."

Avian influenza: From virus evolution and diversification

The authors summarize that the recent "rapid spread of A(H5N1) viruses to many previously unaffected areas globally and their successful persistence during the summer months was likely facilitated by the

ongoing evolution and reassortment with local low pathogenic avian (LPAI) viruses, leading to their adaptation to newly or previously very rarely affected wild bird species such as barnacle geese or sea birds."

With this rapid and extensive spread, HPAI viruses affect wild bird populations e.g. in South America, where influenza A(H5N1) led to the death of more than 40% of the pelican population in Chile and Peru. In addition, Adlhoch and Baldinelli refer to reports from across the globe about transmission of HPAI to mammals such as minks and sea lions. Such events also increase the risk of the virus spilling over to pet animals through contact with for example dead or sick wild birds or mammals such as foxes.

So far, human infections with A(H5N1) have been reported only in a few countries with no or just mild symptoms (United Kingdom, Spain and the United States), related to exposure to infected birds or culling activities but also severe disease or even death (Chile, China, Ecuador and Vietnam) after exposure to sick or dead backyard poultry or to contaminated environment.

The authors highlight that "although currently circulating avian influenza viruses retain a preference for avian-type receptors, different mutations associated with transmission to and pathogenicity in mammals have been observed. These mutations were detected sporadically in infected wild and domestic birds and more often emerged upon transmission events to mammals."

To tackle the threat of avian influenza, they conclude "a One Health approach is needed through: rapid sharing of information about outbreaks, provision of sequence data and reference viruses, and close collaboration between the different sectors locally and globally. Communication campaigns may help to increase awareness in the population and recognize avian influenza viruses as a threat to animal

and human health, in order to reduce the risk of contact with potentially infected animals."

More information: Cornelia Adlhoch et al, Avian influenza, new aspects of an old threat, *Eurosurveillance* (2023). DOI: 10.2807/1560-7917.ES.2023.28.19.2300227

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