ASSESSMENT OF H5N1 HPAI RISK AND THE IMPORTANCE OF WILD BIRDS

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ABSTRACT: The role of wild birds in the transmission of highly pathogenic avian influenza virus H5N1 is still unclear. Risk-assessment techniques can be used to identify the most important epidemiological mechanisms potentially leading to transmission to domestic poultry and to synthesize existing knowledge as risk estimates with associated uncertainty. As an example, a qualitative risk assessment was conducted by the European Food Safety Authority at the request of the European Commission to determine the risk of introduction of the virus through migratory wild birds into the European Union. Further techniques that can be used to inform risk management include quantitative risk factor analyses as well as simulation modeling.

Key words: Avian influenza, epidemiology, risk assessment, wild birds.

Avian influenza caused by the highly pathogenic H5N1 pathotype of the avian influenza (H5N1 HPAI) virus has now spread over several years from East Asia across Asia to Europe and Africa, despite extensive control efforts in affected countries in Southeast and East Asia.

The zoonotic implications and the risk of possible mutation/reassortment that might enable effective transmission between humans resulted in a high level of global alert in an attempt to prevent a human influenza pandemic. The need for implementing effective disease surveillance systems has been emphasized as a key measure in the management of this current threat to livestock industries and humans (Sims et al., 2005). The complex epidemiology of H5N1 HPAI, particularly the involvement of wild bird populations, requires a mix of measures tailored to the importance of different potential transmission paths. The World Organization for Animal Health’s (OIE) risk analysis framework provides an agreed basis for a structured assessment of risks and the subsequent development of risk management procedures (Murray et al., 2004). The relevance of this approach and in particular its risk assessment component in the context of H5N1 HPAI control is described herein.

The risk analysis framework consists of four components, namely, hazard identification, and risk assessment, management, and communication (Murray et al., 2004). This paper focuses primarily on the risk assessment component, with the use of a risk assessment recently conducted by the European Food Safety Authority (EFSA) for the European Commission as an example (Pfeiffer et al., 2006). The process starts with stakeholders and risk managers defining the hazard and risk question(s). In our example, the hazard was H5N1 HPAI. A risk assessment is aimed at answering a specific risk question, which in the current case was the likelihood of introducing the virus into defined populations of wild birds and domestic poultry through migratory wild birds. This risk question had to be clearly defined and agreed upon with risk managers, in this situation the European Commission. The first step in risk assessment is a description of the risk pathway through development of a diagram describing the possible mechanisms for introducing the hazard into the population of interest. It usually is stratified into the pathways leading to release, exposure, and consequence of the hazard. The process of defining the pathway diagram is essential for producing a risk assessment that will
cover all relevant aspects of the risk question, and it requires input from a range of areas of scientific expertise. It is desirable that the risk assessment involves a multidisciplinary team of experts, as was the case with the EFSA expert Working Group, which consisted of ornithologists, virologists, veterinarians, epidemiologists, and risk assessors (see Acknowledgments section). The first meeting of the expert group resulted in a series of path diagrams describing the mechanisms underlying this risk question. An example is presented as Figure 1. It shows the various paths through which H5N1 HPAIV could be introduced by migratory birds into the European Union.

To answer the risk question, an analysis is then conducted based on the pathway diagram and related data compiled from the scientific literature and possibly expert knowledge. The quality of the data will determine whether the risk assessment is conducted in a qualitative or quantitative fashion. A key concept for emphasis and acceptance by stakeholders and risk managers is the conditionality of the sequential likelihoods defined in the pathway diagrams. The qualitative approach is more transparent to the majority of stakeholders who typically are less experienced in working with quantitative models. The outcomes of the risk assessment are expressed as qualitative probability statements, which describe the likelihood of the event occurring. These estimates should be associated with an estimate of uncertainty that expresses the lack of knowledge about the mechanisms used to generate the probability estimate. Although it is difficult to communicate the meaning of likelihood, it is even harder to explain it in the context of the estimated uncertainty. In the EFSA assessment, there was a low to medium probability of transmission of the virus from migratory birds to poultry kept under free-range or backyard husbandry conditions in the EU, but this estimate was associated with a high degree of uncertainty. For other poultry species, the transmission risk was defined as very low to negligible with low uncertainty (Table 1). It is notable, but not surprising, that many of the probabilities are associated with medium to high levels of uncertainty, reflecting our limited understanding of the underlying epidemiological processes. As explained above, the summary conclusions are the result of

![Figure 1. Release pathway diagram for introduction of H5N1 HPAIV through migratory birds into the European Union (Pfeiffer et al., 2006).](image-url)
Table 1. Summary conclusions from a qualitative risk assessment of the introduction of H5N1 HPAI through migratory birds into the EU (Pfeiffer et al., 2006).

<table>
<thead>
<tr>
<th>Risk pathway</th>
<th>Probability</th>
<th>Uncertainty</th>
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<tbody>
<tr>
<td>(A) Input from release assessment:</td>
<td>Low to high(^a)</td>
<td>High</td>
</tr>
<tr>
<td>Conditional probability of migratory birds infected with Asian-lineage H5N1 HPAI reaching EU.</td>
<td></td>
<td></td>
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<tr>
<td>(B) Input from exposure assessment:</td>
<td>Low to high</td>
<td>High</td>
</tr>
<tr>
<td>Conditional probability of Asian-lineage H5N1 HPAI becoming endemic in migratory and nonmigratory European wild birds.</td>
<td></td>
<td></td>
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<tr>
<td>(C.1) Exposure of free-range or backyard flocks.</td>
<td>High(^b)</td>
<td>Medium</td>
</tr>
<tr>
<td>(C.2) Exposure of intensively-reared or indoor flocks.</td>
<td>Negligible to very low(^b)</td>
<td>Low</td>
</tr>
<tr>
<td>(C.3) Transmission of Asian-lineage H5N1 HPAI to poultry.</td>
<td>High</td>
<td>Low</td>
</tr>
<tr>
<td>(C.4) Detection of Asian-lineage H5N1 HPAI in poultry.</td>
<td>Very high</td>
<td>Low</td>
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Summary: Conditional probability of Asian-lineage H5N1 HPAI being transmitted from wild birds to poultry in free-range and backyard flocks in Europe or indoor flocks without high biosecurity standard. | Low to medium\(^b\) | High |

Summary: Conditional probability of Asian-lineage H5N1 HPAI being transmitted from wild birds to indoor poultry flocks kept under conditions of high biosecurity standard in a high-density poultry population area. | Very low | Low |

Summary: Conditional probability of Asian-lineage H5N1 HPAI being transmitted to poultry in Europe from wild birds to indoor poultry flocks kept under conditions of high biosecurity standard and in a low to moderately high-density poultry population area. | Negligible\(^c\) | Low |

\(^a\) Depending on wild bird species.

\(^b\) Depending on proximity to wetlands.

\(^c\) Depending on density of farms and adherence to biosecurity measures.

conditional sequential interpretation of the outcomes of release (A in Table 1), exposure (B in Table 1), and consequence assessments (C in Table 1).

In the presence of better-quality data, quantitative risk assessments can convert the specified risk pathways into a probabilistic model. Multicriteria decision-making models can potentially be adapted for risk assessment, as they can account for uncertainty associated with the model parameters (Clements et al., 2006). Parameters included in the knowledge-driven models often are generated by data-driven models, such as regression analyses. The H5N1 HPAI infection risk for domestic poultry posed by wild birds has not been measured directly. But assuming that congregations of water birds likely represent an important spatial focus for transmission, wetland or other surface water areas can be used as proxy variables for likely locations of spatially clustered wild bird infection. This approach was used in retrospective analyses of H5N1 HPAI outbreaks in poultry in Indonesia and Vietnam. In both cases, the percentage of irrigated land was associated with increased risk of outbreaks (Pfeiffer, 2006; Pfeiffer et al., In press). But it is very likely that in these poultry production systems this variable is confounded with the presence of domestic ducks, which often graze on rice paddy fields (Gilbert et al., 2006). Georeferenced maps of wetland areas also can be used to generate appropriate proxy variables. But the relative importance of wild bird exposure and therefore the ability to detect relevant statistical associations will depend on the importance of other exposure pathways not related to wild birds, and indeed the latter appear to be more important in Southeast Asian countries.
Simulation models typically are used to describe the dynamics of H5N1 HPAI transmission. They are particularly useful for evaluating the impact of risk management strategies, but usually take some time to develop. Also, specific parameter values can be generated as needed in quantitative risk assessments. In the context of H5N1 HPAI, simulation has not been used to model the epidemiology of infection in wild birds explicitly. Instead, published work has focused on the spread of a potential human pandemic (Ferguson et al., 2005, 2006; Germann et al., 2006).

The outputs generated by the risk assessment provide one of several factors to consider in the development of risk management strategies. The function of risk assessment is therefore to inform risk managers in an objective fashion about key factors important for the occurrence of outbreaks. In the EFSA risk assessment, the conclusion indicated a high risk of introducing H5N1 HPAI through selected migratory wild bird species and for the infection to become enzootic in some wild bird species within the EU. Transmission to domestic poultry was considered low risk for domestic poultry kept under conditions other than free range and backyard husbandry.

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LITERATURE CITED


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