Comparing introduction to Europe of highly pathogenic avian influenza viruses A(H5N8) in 2014 and A(H5N1) in 2005

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Since the beginning of November 2014, nine outbreaks of highly pathogenic avian influenza virus (HPAIV) A(H5N8) in poultry have been detected in four European countries. In this report, similarities and differences between the modes of introduction of HPAIV A(H5N1) and A(H5N8) into Europe are described. Experiences from outbreaks of A(H5N1) in Europe demonstrated that early detection to control HPAIV in poultry has proven pivotal to minimise the risk of zoonotic transmission and prevention of human cases.

Highly pathogenic avian influenza virus A(H5N1) and A(H5N8) outbreaks in domestic poultry and wild birds in Europe

Outbreaks of highly pathogenic avian influenza virus (HPAIV) A(H5N8) in domestic poultry and wild birds in Europe in 2014 have some similarities to the previous introduction of HPAIV A(H5N1). Since beginning of November 2014, nine outbreaks have been detected in four countries in Europe. Comparisons between these incursions may help to better understand potential risks to public health.

In autumn 2005, Romania and Croatia were the first European countries reporting influenza A(H5N1) virus infections in wild birds and domestic poultry; hereafter, it spread rapidly across central Europe starting in February 2006 [1]. When HPAIV A(H5N1) finally disappeared in 2010, it had been detected in wild birds and poultry in 21 European countries (Table) [2]. Prior to the introduction into Europe, HPAIV A(H5N1) was extensively circulating in poultry, with recurrent spill-overs to wild birds, in Asia [3].

Influenza A(H5N8) virus is a complex reassortant virus carrying genes from A(H5N1) as one of its parental viruses. An ancestral strain was first reported in China in 2010 [4]. In 2014, following further virus evolution via reassortment, several outbreaks with HPAIV A(H5N8) viruses occurred in aquatic migratory birds, chickens, geese and ducks in China, Japan, and Republic of Korea [2,5-10]. Between 5 November and 16 December 2014, Germany, Italy, the Netherlands, and the United Kingdom (UK) reported HPAIV A(H5N8) outbreaks in nine holdings in total, with turkeys, chickens or ducks [11] (Figure, Table).

In November and December 2014, HPAIV A(H5N8) was detected in a healthy common teal (*Anas crecca*) in Germany and in two faecal samples from Eurasian wigeons (*Anas penelope*) in the Netherlands. The region in Germany currently affected by HPAIV A(H5N8) largely matches the area that was first affected by HPAIV A(H5N1), whereas in the UK, cases of A(H5N1) were initially located in eastern and southern regions and in Italy in central and southern regions, but not in the areas affected in November 2014. The Netherlands had not been affected by HPAIV A(H5N1) at all [12].

Influenza A(H5N8) virus infection does not appear to be associated with severe illness or excessive mortality in wild mallard ducks [10]. In contrast, in galliform poultry (turkey, chickens), HPAIV A(H5N8) causes mass mortality as seen in affected holdings [2]. The low to moderate virulence of HPAIV A(H5N8) in domestic ducks seen in the UK resembles the situation in wild mallards [2]. Many strains of HPAIV A(H5N1), in contrast, cause high mortality not only in galliformes but also in anseriform poultry and in wild birds [13,14].

Routes of introduction into Europe

The spread of HPAIV A(H5N1) from east Asia to Europe via central Asia may have occurred by a complex mixture of activities associated with poultry production,

Table

European countries with reported outbreaks of influenza A(H5N1) and influenza A(H5N8) virus infection in domestic poultry and wild birds, 2003 to 2014[a]

Country	Detections of influenza A(H5N1) virus infection in domestic poultry/wildlife 2003–2010	Number of outbreaks of influenza A(H5N1) virus infection in domestic poultry 2003–2010	Number of outbreaks of influenza A(H5N8) virus infection in domestic poultry 2014	Detections of influenza A(H5N8) virus infection in wildlife 2014
Albania	Yes	3	0	0
Austria	Yes	0	0	0
Bosnia and Herzegovina	Yes	0	0	0
Bulgaria	Yes	0	0	0
Croatia	Yes	0	0	0
Czech Republic	Yes	4	0	0
Denmark	Yes	1	0	0
France	Yes	1	0	0
Germany	Yes	8	2	1
Greece	Yes	0	0	0
Hungary	Yes	9	0	0
Italy	Yes	0	1	0
Netherlands	No	0	5	2
Poland	Yes	10	0	0
Romania	Yes	164	0	0
Serbia	Yes	1	0	0
Slovakia	Yes	0	0	0
Slovenia	Yes	0	0	0
Spain	Yes	0	0	0
Sweden	Yes	1	0	0
Switzerland	Yes	0	0	0
United Kingdom	Yes	2	1	0

[a] Data available from [2].

illegal poultry transports, spill-over infections to wild birds, and migratory bird dispersal, but no consistent route of infection into poultry holdings within Europe has been identified [15]. The sudden occurrence of HPAIV A(H5N1) in central Europe in 2006 was probably associated with cold spells in western Russia that drove out substantial numbers of putatively infected wild birds further west [16].

Mutual transmission of HPAIV between migratory birds and domestic poultry might occur through direct or indirect contacts [7]. Genetic analyses of the recent European influenza A(H5N8) viruses revealed very high similarity to Japanese wild bird isolates suggesting a common source of infection [17].

Import of live poultry and live captive birds as well as poultry commodities from affected Asian regions to the European Union (EU) is illegal but cannot be formally excluded as route of introduction for HPAIV A(H5N8); however, this seems unlikely considering the simultaneous nature and geographic spread of the outbreaks. No epidemiological links have been identified between the initially affected holdings in Germany, the Netherlands and the UK. Findings of HPAIV A(H5N8) in wild birds in Europe also open a possibility for an importation from Asia to Europe via migratory wild birds although this remains hypothetical until the virus would be found in further wild bird populations in central and western Asia.

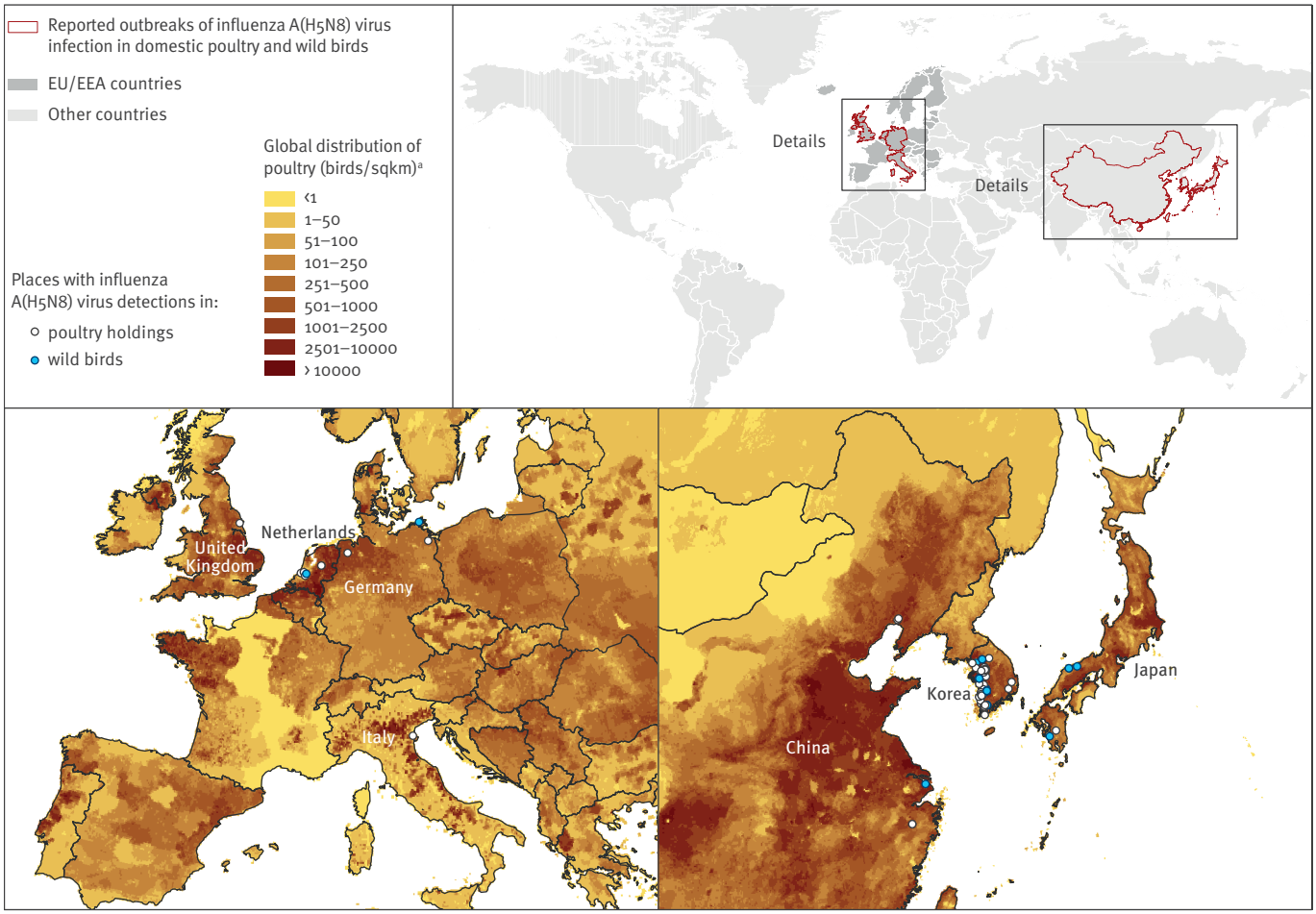
Affected holdings in Europe so far were indoor facilities with nominally good biosecurity, yet indirect contact between wild birds and poultry (via any material contaminated by infected wild birds, e.g. faeces) might be possible. The fact that in several of the holdings, stable units closest to the entrance of the compound were the first affected in the outbreak, might suggest the introduction of A(H5N8) from a focal source close to the compound

Surveillance of highly pathogenic avian influenza viruses in the European Union

The experience of large HPAIV outbreaks of in the Netherlands, Belgium and Germany, e.g. A(H7N7) in 2003, prompted the EU to better prepare for large scale incursions of HPAIV [18]. The establishment and implementation of surveillance systems, diagnostic tools for

Figure

Countries reporting outbreaks of influenza A(H5N8) virus infection in domestic poultry and wild birds, 2014



EU/EEA: European Union/European Economic Area.

[a] Recently published Gridded Livestock of the World (GLW) 2.0, May 2014.

early detection of HPAIV and harmonised restriction and control measures was laid down in the EU legislation [19]. This included introducing programmes of passive surveillance of wild bird populations as an early warning system, which proved to be a useful tool in detecting presence of HPAIV A(H5N1). This was complemented by active monitoring of poultry. In the current epizootic, enhanced wild bird monitoring might also help to further elucidate the role of wild birds transmitting A(H5N8), although the apparently asymptomatic presentation in wild bird species in Europe indicates potentially scaling up elements of targeted active rather than passive surveillance may be appropriate to better understand the distribution, prevalence and introduction pathways into Europe.

Risk for human transmission and resulting public health measures

Although to date, HPAIV A(H5N1) has caused 676 human cases worldwide, including 398 deaths [20], no human cases have ever been reported in Europe and these viruses lack the capability for sustained human-to-human transmission. Cats and mustelids were the only mammals found to be infected in Europe [13]. No human cases due to A(H5N8) have so far been reported anywhere. Mammals such as mice, ferrets, dogs and cats proved to be susceptible to experimental A(H5N8) infection, yet, only mild clinical disease, if any, ensued and so their role as amplification or reservoir hosts appears less likely [21].

Binding of avian influenza viruses to mammalian α2–6 sialic acid receptors is a prerequisite for transmission to humans. HPAIV A(H5N8) binds strongly to avian α2–3 receptors and, to a markedly lesser degree, to α2–6 receptors indicating limited zoonotic potential [21]. Antiviral resistance has not been described in the recent isolates [17]. Candidate vaccine viruses for human use have been proposed for pandemic preparedness [22].

People at risk of spill-over infections are those directly exposed to infected birds and their carcasses, e.g. during culling measures in affected holdings. Personal

protective equipment and other protective measures are a prerequisite for preventing zoonotic transmission. Passive or active monitoring of exposed persons enables early identification of transmission events. There is no evidence of human infection through consumption of contaminated food [23]. Recommended diagnostic tests for animal and human samples showed reliable detection of HPAIV A(H5N8).

Conclusions

The current simultaneous occurrence of A(H5N8) in different European countries is comparable to the introduction of A(H5N1) around a decade ago. These similarities may point to common routes of introduction into Europe, although these are not fully understood and the exact sources of infection of the affected indoor poultry holdings have not been identified yet. More outbreaks seem possible. Although HPAIV A(H5N8) might have the potential to transmit to humans, no human cases have been detected so far. Based on the experience from HPAIV A(H5N1) in Europe, efficient biosecurity, early detection, and stringent control measures are able to minimize risks of spill-over transmission to humans. The rapid geographic dispersion of yet another reassortant highly pathogenic avian influenza A virus underlines the need for enhanced preparedness.

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Authors' contributions

CA: study initiation, compilation of data, drafting the manuscript

CG: critical review and drafting of the manuscript

GK & RB: data provision from outbreaks in the Netherlands, critical review and approval of the manuscript

IB: providing data from the UK and EUR Lab, critical review and approval of the manuscript

FV: providing EFSA data, critical review and approval of the manuscript

PP: critical review and approval of the manuscript

TH: study concept and providing German data, manuscript draft, critical review and approval

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