

REVIEW ARTICLE

Global patterns of avian influenza A (H7): virus evolution and zoonotic threats

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One sentence summary: H7 avian influenza virus causes infections in birds and mammals and is of pandemic concern; our review brings together data from the ecology, veterinary and human health points of view and demonstrates the importance of 'One Health' in the long-term management of this virus.

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ABSTRACT

Avian influenza viruses (AIVs) continue to impose a negative impact on animal and human health worldwide. In particular, the emergence of highly pathogenic AIV H5 and, more recently, the emergence of low pathogenic AIV H7N9 have led to enormous socioeconomical losses in the poultry industry and resulted in fatal human infections. While H5N1 remains

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infamous, the number of zoonotic infections with H7N9 has far surpassed those attributed to H5. Despite the clear public health concerns posed by AIV H7, it is unclear why specifically this virus subtype became endemic in poultry and emerged in humans. In this review, we bring together data on global patterns of H7 circulation, evolution and emergence in humans. Specifically, we discuss data from the wild bird reservoir, expansion and epidemiology in poultry, significant increase in their zoonotic potential since 2013 and genesis of highly pathogenic H7. In addition, we analysed available sequence data from an evolutionary perspective, demonstrating patterns of introductions into distinct geographic regions and reassortment dynamics. The integration of all aspects is crucial in the optimisation of surveillance efforts in wild birds, poultry and humans, and we emphasise the need for a One Health approach in controlling emerging viruses such as AIV H7.

Keywords: avian influenza; influenza A virus; H7; One Health; virus evolution; zoonosis

INTRODUCTION

Influenza A virus is a multihost virus and one of the most significant viruses affecting wildlife, domestic animals and human health (Webby and Webster 2001). Wild birds of the order Anseriformes (mainly ducks, swans and geese) and Charadriiformes (mainly gulls, terns and waders) appear to be central in the maintenance of influenza A virus, so-called avian influenza virus (AIV) (Webster et al. 1992; Olsen et al. 2006). From wild birds, AIV can be transmitted to domestic birds, causing a significant socioeconomical damage, and sporadically followed by transmission to humans, so-called zoonotic infections (Krammer et al. 2018).

Influenza A viruses belong to the family of *Orthomyxoviridae* and contain a single-stranded ribonucleic acid (RNA) genome composed of 8 gene segments encoding at least 11 viral proteins (Tollis and Di Trani 2002; Cheung and Poon 2007). The influenza A virus proteins can be categorised as 'surface proteins' (hemagglutinin [HA], neuraminidase [NA] and matrix protein 2 [M2]), 'internal proteins' (tripartite polymerase consisting of polymerase basic protein 2 [PB2], polymerase basic protein 1 [PB1], polymerase acidic protein [PA], nucleoprotein [NP], matrix protein 1 [M1] and nuclear export protein [NEP]) and 'non-structural proteins' (NS1 and PB1-F2) (Webster et al. 1992; Brown 2000; Cheung and Poon 2007). Influenza A viruses are categorised based on their surface proteins, HA and NA, into 18 and 11 subtypes, respectively. Currently, AIVs of 16 HA (H1–H16) and 9 NA (N1–N9) subtypes have been identified in birds (Fouchier et al. 2005; ICTVdB 2006; Webster et al. 1992); however, the new HA (H17 and H18) and NA (N10 and N11) subtypes have been reported only in bats. Furthermore, AIVs can be categorised as low pathogenic AIVs (LPAIVs) or highly pathogenic AIVs (HPAIVs) based on their pathogenicity in chickens. This far, only AIVs of the H5 and H7 subtypes have shown the potential to mutate from LPAIV into HPAIV (Deshpande et al. 1987; Capua and Alexander 2007; Bonfanti et al. 2014).

Interspecies transmission is an important event in the evolution and ecology of AIV H7 (Joseph et al. 2017). These viruses are able to infect a broad range of species, from an array of wild bird species to poultry and mammals, including seals, pigs, horses and humans (Abdelwhab, Veits and Mettenleiter 2014; Fereidouni et al. 2016; Mostafa et al. 2018). In poultry, LPAIV H7 can circulate asymptotically, and evolve into HPAIV H7, causing severe systemic diseases and mortality (Belser et al. 2018). From poultry, humans have shown to become infected sporadically with either LPAIV or HPAIV H7. These infections were mostly limited to ocular and/or mild respiratory signs, with one human death during an HPAIV H7N7 outbreak in the Netherlands in 2003 (Fouchier et al. 2004). In February 2013, LPAIV H7N9 emerged in poultry and humans in China. LPAIV H7N9 has caused seasonal waves of zoonotic infections in China and has led to lethal human infections. Human infections with H7N9 since 2013 has

been far more severe than all other prior sporadic H7 human infections (i.e. 1567 confirmed human cases; 615 deaths; case fatality rate 39%) (as of March 2019) (Belser et al. 2018; WHO 2019a). So far, humans have become infected upon direct exposure to infected poultry, and no sustained interhuman transmission has been confirmed.

In this review, we address the current understanding of the evolution and emergence of AIV H7 in wild birds, poultry and humans. Specifically, we interrogate features of the wild–domestic bird interface, global virus evolution patterns and distributions, including a list of genetic changes associated with altered virus replication, pathogenesis and transmission in mammals. Overall, we demonstrate that AIV H7 is a One Health problem, requiring a One Health solution, including the control of AIV H7 in poultry and decreasing the potential for zoonotic transmission.

H7 VIRUS GENESIS

Different pathotypes and cleavage sites within H7 viruses

The characterisation of AIV as LPAIV or HPAIV is based on their capacity to cause disease in chickens upon experimental exposure and scored on an intravenous pathogenicity index (OIE 2019). Currently, the more common method to identify pathogenicity is by sequencing the HA gene segment as the presence of multiple basic amino acids at the HA cleavage site (HACS) [referred to as MBCS (Multiple Basic Cleavage Site)] indicates high pathogenicity (OIE 2019). Thus, while LPAIVs harbour a single basic amino acid (either arginine 'R' or lysine 'K') at of the cleavage site of the HA gene segment, HPAIVs possess motifs with more than one R and/or K (Table S1, Supporting Information) (OFFLU and OIE/FAO 2018). The insertion of an MBCS results in a broader tissue tropism of the virus, with HPAIVs being able to cause systemic infections (Garten and Klenk 2008), in contrast to LPAIVs, which are limited to the respiratory or digestive tract in birds or ocular and respiratory tract in mammals (Böttcher-Friebertshäuser et al.).

From low to high pathogenicity

Based on poultry outbreaks, a number of conceivable mechanisms for the emergence of HPAIV H7 from ancestral LPAIV H7 by converting a single basic cleavage site to an MBCS have been suggested (Table 1). *In vitro*, *in vivo* and/or *in ovo* experiments—including multiple virus passages and/or the use of reverse genetics—have been performed to investigate potential mechanisms involved in the emergence of HPAIV (Brugh 1988; Horimoto and Kawaoka 1995; Ito et al. 2001; Munster et al. 2010; Gohrbandt et al. 2011; Soda et al. 2011; Böttcher-Friebertshäuser et al. 2014; Abdelwhab et al. 2016). Furthermore, in both natural

Table 1. Overview of the proposed mechanism of H7 highly pathogenic AIVs detected during poultry outbreaks, which emerged from known ancestral low pathogenic AIVs, modified from Seekings (2017).

Subtype	Country	Year	Host	Proposed mechanism
H7N1	Italy	1999–2000	Turkeys; chickens; other	Recombination; minor variants in the LPAIV progenitor quasispecies
H7N3	Pakistan	1994–95	Chicken	Nucleotide substitution and insertion
	Chile	2002	Chicken	Non-homologous recombination with NP
	Canada	2004	Chicken	Recombination with M1, nucleotide substitution mutation
H7N7	Canada	2007	Chicken	Recombination with host RNA
	Mexico	2012	Chicken	Recombination with host 28s rRNA
	Australia	1976	Duck; chicken	Duplication insertion
	Netherlands	2003	Chicken	Presumed reassortment with LPAIV H7N3 2003 (HA) and LPAIV H10N7 2000 (NA)
	UK	2008	Chicken	Nucleotide substitution and insertion
	Spain	2009–2010	Chicken	Insertion of foreign nucleotides
	UK	2015	Chicken	Nucleotide substitution and insertion
H7N8	USA	2016	Turkey	Insertion
		2017	Chicken	Insertion

and experimental settings, next-generation sequencing (NGS) has shown to be a useful technique to identify HPAIV minor variants among LPAIV quasispecies (Monne et al. 2014; Dietze et al. 2018).

So far, three molecular mechanisms for HPAIV genesis have been described. The most frequently described mechanism for HPAIV genesis from ancestral LPAIVs is the duplication of an existing AIV template by a polymerase stuttering mechanism (Pasick et al. 2005). This results in the insertion of series of A and G nucleotides, encoding basic amino acids at the HACS. This mechanism has been described in several occasions, including the Chinese LPAIV H7N9 outbreak in 2013, which mutated to HPAIVs in 2017 (Shi et al. 2017), and HPAIV H7N7 outbreaks in Germany in 2015, in the UK in 2008 and 2015, and in Spain in 2009–2010 (Defra 2008; Iglesias et al. 2010; Dietze et al. 2018; Seekings et al. 2018), HPAIV H7N8 outbreak in the USA in 2016 (Killian et al. 2016) and HPAIV H7N3 outbreaks in Pakistan in 1994–1995 and 2003 (Abbas et al. 2010). Another mechanism for HPAIV genesis is based on the non-synonymous mutation of one or more nucleotides in the HACS, leading to the coding of an R or K. However, this mechanism has only been observed in association with the insertion of nucleotides, as described for the HPAIV H7N7 outbreaks in the UK in 2008 and 2015 (Defra 2008; Seekings et al. 2018) and for the HPAIV H7N3 outbreak in Pakistan in 1994–1995 (Abbas et al. 2010). A third mechanism for HPAIV genesis is based on a non-homologous recombination. This mechanism is characterised by an insertion of nucleotides from another viral gene segment or other non-viral sources (e.g. host) into the HACS. Insertions of varying lengths have been described for multiple instances. For instance, the HACS of LPAIV H7N3 detected in Chile in 2002 and in Canada in 2004 had acquired several nucleotides from the M and the NP genes (Suarez et al. 2004; Pasick et al. 2005; Berhane et al. 2009). The HACS of LPAIV H7N3 as detected in Canada in 2007 and in Mexico in 2012 had acquired several nucleotides from chicken 28S rRNA (FAO 2012; Maurer-Stroh et al. 2013). Finally, the HACS of an LPAIV H7N1 in Italy mutated into unique HPAIV HACS motifs (PEIPKRSRVRR*GLF and PEIPKGSRMRR*GLF) in 1999–2000 and resulted in the insertion of four amino acids from an unknown source (Banks et al. 2001; Capua et al. 2002; Monne et al. 2014).

Remarkably, the emergence of HPAIV H7 appears to be mainly associated with the adaptation of LPAIV to poultry, especially chickens or turkeys (Richard et al. 2017). The majority of HPAIVs that emerged are of the H7 subtype compared to a relatively few of the H5 subtype (Richard et al. 2017); yet, the reason for this is still unknown. However, it highlights the risk of HPAIV H7 emergence and remains a major concern for the poultry industry globally, as the subclinical LPAIVs are continuing to circulate in wild birds.

WILD–DOMESTIC BIRD INTERFACE OF H7 VIRUSES

Wild birds, in particular dabbling ducks, shorebirds and gulls, form the natural reservoir for most AIV subtypes (H1–H16, N1–N9). In wild birds, H7 has been detected in combination with N1–N9 (Olson et al. 2014). LPAIV H7 has been detected in wild birds in six continents and predominantly in autumn and winter, which is consistent with the ecology of all LPAIV subtypes in wild birds (Latorre-Margalef et al. 2014; Zhang et al. 2017). LPAIV H7 is most frequently reported in dabbling ducks, including mallards (*Anas platyrhynchos*), Northern pintails (*Anas acuta*), Northern shovelers (*Spatula clypeata*) and shorebirds, particularly ruddy turnstones (*Arenaria interpres*) (the latter at the AIV hotspot in Delaware Bay in North America only) (Zhang et al. 2017). Nevertheless, LPAIV H7 are relatively uncommon in wild birds, constituting only a small proportion of isolates in long term study systems (De Marco et al. 2003; Munster et al. 2005; Latorre-Margalef et al. 2014). Remarkably, no HPAIV H7 has been isolated from wild birds, in contrast to HPAIV H5, which has been detected in wild birds in association with outbreaks in poultry (Verhagen, Herfst and Fouchier 2015). Yet, avian influenza surveillance programmes are severely biased towards certain bird species—in particular mallards (Olsen et al. 2006)—leaving a wide range of bird species unexplored. Regardless, based on online sequence databases, LPAIV H7 has been detected in at least 65 bird species, demonstrating that a broad avian host range may be involved in the epidemiology of AIV H7 (Zhang et al. 2017).

LPAIV H7 detected in poultry has their origin in wild waterfowls (Munster et al. 2005; Campitelli et al. 2008), and, globally, viruses of the H7 subtype are frequently detected in poultry (Senne, Pedersen and Panigrahy 2005). This may be due to a bias in poultry diagnostics towards H7 (and H5) viruses compared to other HA subtypes (Olson et al. 2014). HPAIV H7 emerges from LPAIVs in poultry; there is no evidence that HPAIVs have ever emerged in wild birds (Rohm et al. 1995). Furthermore, LPAIV H7 has been detected in poultry in six continents (Zhang et al. 2017). HPAIV H7 outbreaks in poultry have been observed year round, with varying severity (Alexander 2000; Capua and Marangon 2000; Naeem 2003; Hirst et al. 2004; Munster et al. 2005) and varying time intervals between the detection of ancestral LPAIVs and HPAIVs (e.g. less than one month for H7N3 in Chile and more than eight months for H7N1 in Italy) (Capua et al. 2002; Suarez et al. 2004; de Jong et al. 2009). Despite the regular emergence of H7 outbreaks in poultry, individual outbreaks appear to be limited in space and time (de Wit et al. 2004), with the exception of LPAIV H7N2 and LPAIV H7N9. LPAIV H7N2, which emerged in 1994, has been isolated across several years from birds sampled at live bird markets (LBMs) in Northeastern USA (Spackman et al. 2003; Suarez, Spackman and Senne 2003; Senne, Pedersen and Panigrahy 2005). LPAIV H7N9 has been maintained in the poultry population in China since 2013 and has been detected primarily in chickens and less frequently in domestic ducks, pigeons and quails (Chen et al. 2013; Pantin-Jackwood et al. 2014; Wang et al. 2014a; Millman et al. 2015). LPAIV H7N9, which is endemic in China (see the section titled 'H7N9'), contains genes solely of avian origin (Gao et al. 2013); yet, a virus with the same gene constellation has not been identified in wild birds, including waterfowls thus far (Zhao et al. 2014). This suggests that LPAIV H7N9 infection may not be widespread in wild birds (Millman et al. 2015). Furthermore, experimental infections suggest that there may be host-specific adaptations of LPAIV H7 in wild birds and chickens (Lebarbenchon and Stallknecht 2011; Kim et al. 2012; Lebarbenchon, Brown and Stallknecht 2013).

LPAIVs and HPAIVs of different avian origins have been studied experimentally to investigate virulence, pathogenesis, transmission and host range. Tissue tropism and receptor-binding profiles of LPAIV and HPAIV H7 have been characterised in different bird species (Mo et al. 1997; Hooper and Selleck 2003; Gambaryan et al. 2012). LPAIVs H7 of different origins have been shown to infect wild waterfowls (including mallards) (Ferreira et al. 2010; Pantin-Jackwood et al. 2016) and domestic birds (Lu and Castro 2004; Kaleta and Honicke 2005; Jourdain et al. 2010; Spackman et al. 2010). LPAIV H7N1 originating from chickens has been successfully transmitted to chickens via direct contact (Claes et al. 2013, 2015), and HPAIVs H7 of different origins have been shown to infect mallards (Pantin-Jackwood et al. 2016). With respect to the Chinese LPAIV H7N9, virus excretion was higher in chickens and quails than in rock pigeons (*Columba livia*), pekin ducks (*Anas platyrhynchos domesticus*), mallards, muscovy ducks (*Cairina moschata*) and emden geese (*Anser anser domesticus*). Furthermore, quails transmitted the virus through direct contacts, while pigeons and pekin ducks did not, which may suggest a limited ability to spread in these species (Pantin-Jackwood et al. 2014). Finally, LPAIV H7N9 was transmitted from finches to quails and chickens (Jones et al. 2015), suggesting that passerines cannot be excluded from the epidemiology of AIV H7.

The introduction and emergence of an AIV in poultry—in this case LPAIV H7N9—is not surprising. In China, chicken and duck meat production has increased by more than 600% from 1990 to 2015 (Gilbert, Xiao and Robinson 2017). Globally, the

domestic chicken constitutes 70% of the bird biomass. Remarkably, the domestic duck constitutes a far greater biomass than the most common wild duck, the mallard (*Anas platyrhynchos*) (Gilbert, Xiao and Robinson 2017). This creates an enormous ecological niche for AIVs. Furthermore, LBMs are the primary source for poultry production and trading activities in China, where in 2013, 63% of the 190 million chickens consumed annually were purchased from LBMs (Wu et al. 2017b). Finally, the frequent contact between wild and domestic birds facilitates virus introduction and virus gene movement in and between the domestic and wild ecosystems. Despite the recognition that the wild–domestic bird interface is porous, there is a limited understanding of factors affecting viral introduction and the frequency of AIV gene movement across the interface. For instance, it was shown that contact rates between wild and domestic birds at a local scale varied per season (Cappelle et al. 2011), and that the proximity and abundance of water and wetlands have been associated with AIVs in poultry farms (Roche et al. 2009; Bouwstra et al. 2017; Verhagen et al. 2017). Currently, most studies limit their findings to an association in time between the presence of AIV and arrival of migratory birds in the area (e.g. the HPAIV H7N3 virus in poultry in Pakistan in December 1994 was associated with the arrival of migratory birds) (Naeem 2003). Thus, a combination of intensification of the poultry industry, poultry trade and close contact between wild and domestic birds creates a vulnerable system.

ZOONOTIC AIV H7 INFECTIONS AND RELATED AMINO ACID SUBSTITUTIONS

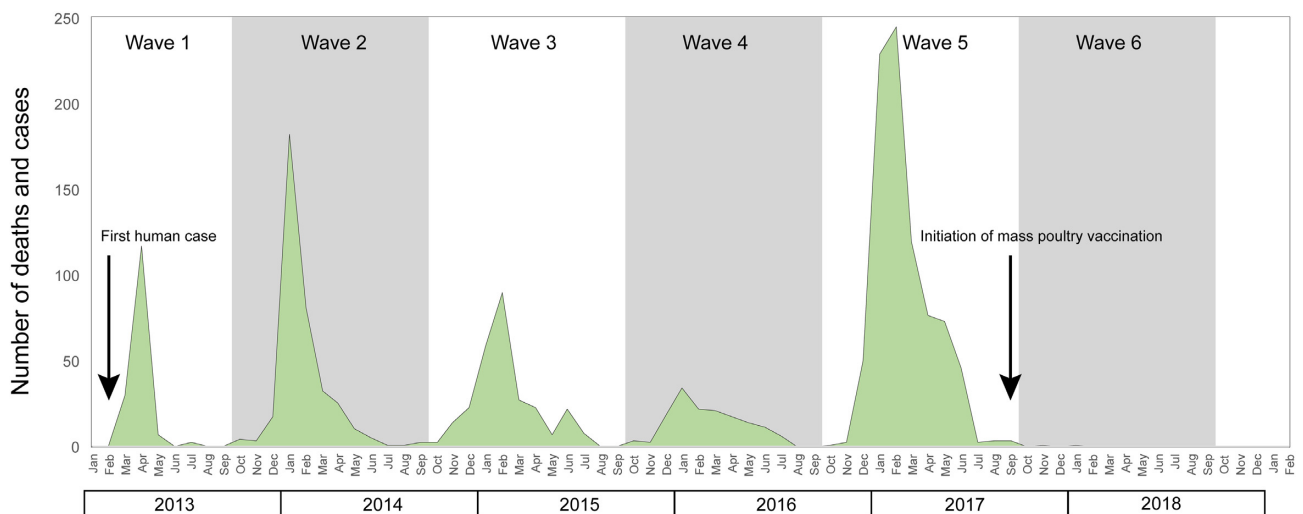
Human infections caused by AIV H7 are placed on the top priority list among other zoonotic AIVs, including HPAIV H5N1 and LPAIV H9N2 (WHO 2018b). To date, reported human infections with AIV H7 have been caused by LPAIV H7N2, H7N3, H7N4, H7N7 and H7N9 and HPAIV H7N3, H7N7 and H7N9 (Fouchier et al. 2004; Abdelwhab, Veits and Mettenleiter 2014; Ke et al. 2017) (Table 2). More than 1600 LPAIV H7 human infections have been reported, in contrast to 840 HPAIV H5N1 and 55 LPAIV H9N2 human infections (WHO 2018c, 2019b; Ali et al. 2019). The ancestral viruses of LPAIV and HPAIV H7 isolated from humans were found in a variety of bird species, both wild and domestic (Elbers et al. 2004; Fouchier et al. 2004; Lam et al. 2013; ProMED-mail).

H7N9

Since the emergence of LPAIV H7N9 in China in March 2013, a total of 1567 laboratory-confirmed human cases (case fatality rate 615/1567, 39%) have been reported, including 40 instances of two to three human cases infected by a shared source (as of March 2019) (WHO 2019a). Human infections were acquired directly from poultry, which shed LPAIV H7N9 with no clinical signs of disease. Most of these transmission events from poultry to humans occurred in association with LBMs (Wu et al. 2017b). The vast majority of human H7N9 cases were detected in China, with two main epicentres: cities in the Yangtze River Delta and Pearl River Delta areas. In addition, cases have been detected in Malaysia (one case, imported from China) and Canada (two cases, imported from China) (WHO 2018b). Since 2013, there have been repeated waves of human infection of LPAIV H7N9 (Guo et al. 2018; FAO 2019), occurring mostly in the winter and spring months. Between March 2013 and March 2019, there have been seven waves of infection, although there have been no human, environmental or animal cases associated with the seventh wave to date (Fig. 1). Zoonotic LPAIV H7N9 orig-

Table 2. Reported human infections with AIVs of the H7 subtype from 1959 to 2018.

Pathotype	Subtype	Country	Year	Symptoms	Cases (deaths)	Reference
HP	H7N7	USA	1959	Respiratory	1	(Belser et al. 2009)
HP	H7N7	Australia	1977	Conjunctivitis	1	(Belser et al. 2009)
LP	H7N7	USA	1979	Conjunctivitis	4	(Webster et al. 1981)
LP	H7N7	UK	1996	Conjunctivitis	1	(Kurtz et al. 1996)
LP	H7N2	USA	2002	Respiratory	1	(Terebuh et al. 2018)
LP	H7N2	USA	2003	Respiratory	1	(Prevention 2004)
HP	H7N7	Netherlands	2003	Conjunctivitis, pneumonia, fatal respiratory failure	89 (1)	(Fouchier et al. 2004)
HP	H7N3	Canada	2004	Conjunctivitis	2	(Tweed et al. 2004)
LP	H7N3	UK	2006	Conjunctivitis	1	(Nguyen-Van-Tam et al. 2006)
LP	H7N2	UK	2007	Conjunctivitis	4	(Editorial-team-Collective 2007)
HP	H7N3	Mexico	2012	Conjunctivitis	2	(Lopez-Martinez et al. 2013)
HP	H7N7	Italy	2013	Conjunctivitis	3	(Puzelli et al. 2014)
LP	H7N2	USA	2016	Respiratory	1	(Marinova-Petkova et al. 2017)
LP/ HP	H7N9	China	2013-2018	Severe illness, fatal respiratory failure	1567 (615)	(WHO 2018a)
LP	H7N4	China	2018	Cough, fever, chills	1	(Tong et al. 2018)

**Figure 1.** Seasonal waves of human infections with low pathogenic AIV H7N9 in China from 2013 to 2018. Data taken from Flutrackers.com (FluTrackers 2019), collated by Ian Mackay (Mackay 2019).

inated from multiple reassortment events between three different AIV subtypes: H7N7 (HA), H7N9 (NA) and H9N2 (internal segments) (Lam et al. 2013) (see the section titled ‘Reassortment of LPAIV and HPAIV H7N9 affecting LBMs and humans in China’). Most AIV H7N9 cases reported have been of low pathogenicity; however, one fatal case of a patient in the Guangdong province in China was reported in January 2017 (fifth wave) with an H7N9 that had an MBCS at its HA cleavage site representing the first human HPAIV H7N9 case (Ke et al. 2017) (Fig. 1). In total, 32 human cases were identified to have HPAIV H7N9 (FAO 2019).

In response to the emergence of HPAIV H7N9, the closure of LBMs in several Chinese cities implemented in early waves, has shown a significant impact on the virus spread and reduced the incidence of human cases associated with LPAIV H7N9 (Fournie and Pfeiffer 2014); in September 2017, vaccination of poultry was initiated using a bivalent H5/H7 vaccine. This may consolidate the impact of closure of LBM in limiting LPAIV H7N9 spread in both poultry and humans (Zeng et al. 2018; Wu et al. 2019).

H7N7

LPAIV H7N7 was detected in a 43-year-old woman with conjunctivitis in the UK in 1996 (Kurtz, Manvell and Banks 1996). Human infections with HPAIV H7N7 have been mostly associated with conjunctivitis, and have been reported in 1959, 1977 and 1979 (Webster et al. 1981; Belser et al. 2009). In the spring of 2003, HPAIV H7N7 was detected in commercial poultry farms in the Netherlands, resulting in a massive, country-wide poultry outbreak. During the outbreak, 89 humans became infected with HPAIV H7N7. The majority of the patients suffered from conjunctivitis and a few had mild influenza-like illness. This outbreak included the first reported human death (a veterinarian) due to HPAIV H7N7 infection (Fouchier et al. 2004). The genes of the Dutch HPAIV H7N7 were of avian origin, genetically related to previously reported LPAIVs in ducks in the same region in 2000 (Table 1) (Fouchier et al. 2004). In 2013, three human cases of HPAIV H7N7 were detected among poultry workers in Italy associated with the culling of HPAIV H7N7 infected poultry and clinical signs were limited to conjunctivitis (Puzelli et al. 2014).

Genetically, all gene segments of this virus were closely related to the H7N7 viruses isolated from affected chicken farms (Puzelli et al. 2014).

H7N4

In February 2018, LPAIV H7N4 was isolated from a 68-year-old woman in Jiangsu Province in China (Tong et al. 2018), representing the first human LPAIV H7N4 case. It was suggested that the infection was acquired after direct exposure to poultry in an LBM (Tong et al. 2018). The genes of the LPAIV H7N4 were of avian origin (Gao et al. 2018; Tong et al. 2018).

H7N3

LPAIV H7N3 has been detected in one poultry worker associated with an LPAIV H7N3 outbreak in poultry in the UK in 2006. Symptoms were limited to conjunctivitis (Nguyen-Van-Tam et al. 2006). There is serological evidence of a separate LPAIV H7N3 in poultry workers during the H7N3 epizootic in Italy in 2003 (Puzelli et al. 2005), although no symptoms were reported at that time. HPAIV H7N3 caused two human infections in British Columbia, Canada, which were laboratory-confirmed and isolated in 2004 (Tweed et al. 2004). In 2012, two laboratory-confirmed mild infections of humans with HPAIV H7N3 were reported to be associated with exposure to infected poultry in Jalisco, Mexico (Lopez-Martinez et al. 2013).

H7N2

Evidence of human infections with LPAIV H7N2 was first reported based on a positive serological analysis of workers with a history of exposure to infected poultry in the USA in 2002 (Terebuh et al. 2018). LPAIV H7N2 was first isolated from an immunocompromised man who suffered from fever and acute respiratory symptoms in the USA in 2003 (Ostrowsky et al. 2012). LPAIV H7N2 was also detected in four humans showing clinical signs, including conjunctivitis and influenza-like illness, in Wales, UK, in 2007 (Editorial-team-Collective 2007). In December 2016, LPAIV H7N2 led to an outbreak in a cat shelter in the USA, during which a veterinarian exposed to the infected cats in this animal shelter became infected, representing the first human infection with LPAIV H7N2 in North America since 2003 (Belser et al. 2017; Marinova-Petkova et al. 2017).

Amino acid substitution of H7 viruses associated with mammalian adaptation

While H7N9 is an avian-adapted virus, a main concern is the emergence of sustained human-human transmission; amino acid substitutions are required for the adaptation from avian to mammalian hosts (de Vries et al. 2017; Shao et al. 2017). Regardless of subtype, key amino acid substitutions are critical in (1) changing receptor specificity from avian-type to human-type receptors, α 2.3-to α 2.6-linked sialic acids (SAs), respectively; (2) increased HA thermostability and pH stability; (3) increased replication of influenza viruses *in vitro* and *in vivo* at temperatures equivalent to those of the mammalian upper respiratory tract; and (4) changing the expression of RNA transcripts by the viral polymerase complex, resulting in increased replication (Wang et al. 2014b). Many of these changes were described as early as 2014, and Wang et al. proposed a system of 'genetic tuning' in the emergence of H7N9, whereby there were continuous substitutions mediating adaptation to mammalian hosts (Wang

et al. 2014a). To date, substitutions falling into all of the above categories have been described in both field isolates and animal experiments, suggesting it is imperative to continue to closely monitor the evolution of this virus (Table S2, Supporting Information).

SPATIAL DIFFUSION OF H7 VIRUSES

As with other AIV subtypes, there is strong evidence of geographically structured viral diffusion of H7, both on a global and a regional scale. Using a dataset of 606 nucleotide sequences of the full HA gene segment of LPAIV and HPAIV H7 isolated from avian and mammalian hosts [obtained from the Genbank and Global Initiative on Sharing All Influenza Data (GISAID) platforms], Bayesian phylogeographic analysis was conducted to investigate the spatial diffusion and routes of transmission of this subtype (see Supporting Information for details). From a global perspective, currently circulating AIV H7 may have expanded from Europe to East Asia, and represent a separate gene pool from AIV H7 in North America (Figs 2 and 3). Across all AIV subtypes and segments, there are two different geographically segregated gene pools: North American and Eurasian. This genetic segregation is driven by patterns of bird migration, wherein waterfowl, the main reservoir for AIVs, tend to have migratory patterns within each continental region (Olsen et al. 2006). There are, of course, exceptions, often driven by trans-hemispheric introductions followed by a competitive exclusion of previously circulating lineages (Bahl et al. 2009). Based on online databases (Shu and McCauley 2017; GenBank 2019), the most common H7 subtype combinations in the European and North American wild bird reservoirs are H7N7 and H7N3, respectively, whereas there has been a transition in the East Asian reservoir from H7N7 prior to 2013 to H7N9 thereafter (see Table S3, Supporting Information). These regional-specific dominating HA-NA subtypes are highly correlated to, and hence feed, the evolution of other subtypes within each reservoir (see Fig. S2, Table S4, Supporting Information) (Banks et al. 2000; Escalera-Zamudio et al. 2018). This spatially independent evolution may also result in the parallel evolution of HPAIVs from their LPAIV counterparts (Escalera-Zamudio et al. 2018). That is, we see the genesis of HPAIV H7 as a reoccurring event, rather than a single transition to HPAIV H7 followed by a global spread (see the section titled 'Wild-domestic bird interface of H7 viruses').

Within Eurasia, AIV H7N7 sampled in European countries are more likely to constitute the ancestral viruses from which new lineages have evolved compared to AIV H7N7 isolated in other regions, linking viruses sampled in European and East Asian countries and guiding the worldwide viral diffusion. There is an important caveat here, whereby H7N7 sequences from Europe (2002–2009) predate the ever-increasing number of sequences generated in China since 2013 with the emergence of LPAIV H7N9. Within Asia, AIV H7N7 in Japan and South Korea drives the spatial transmission pattern, with bidirectional gene flow between the two countries, and diffusions to the Yangtze River area of China (see Fig. S1, Tables S5 and S6, Supporting Information). The substantial H7N9 human infections occurring in China since 2013 (see the section titled 'H7N9') correspond in time and space with the shift of the most prevalent subtype in East Asia from H7N7 to H7N9. Both Yangtze River and Pearl River Delta regions have a relatively high probability of being the origin of viruses within China, indicating the establishment of two epicentres (Wang et al. 2016; Li et al. 2018). In particular, AIVs H7N9 isolated in the Yangtze River area form significant

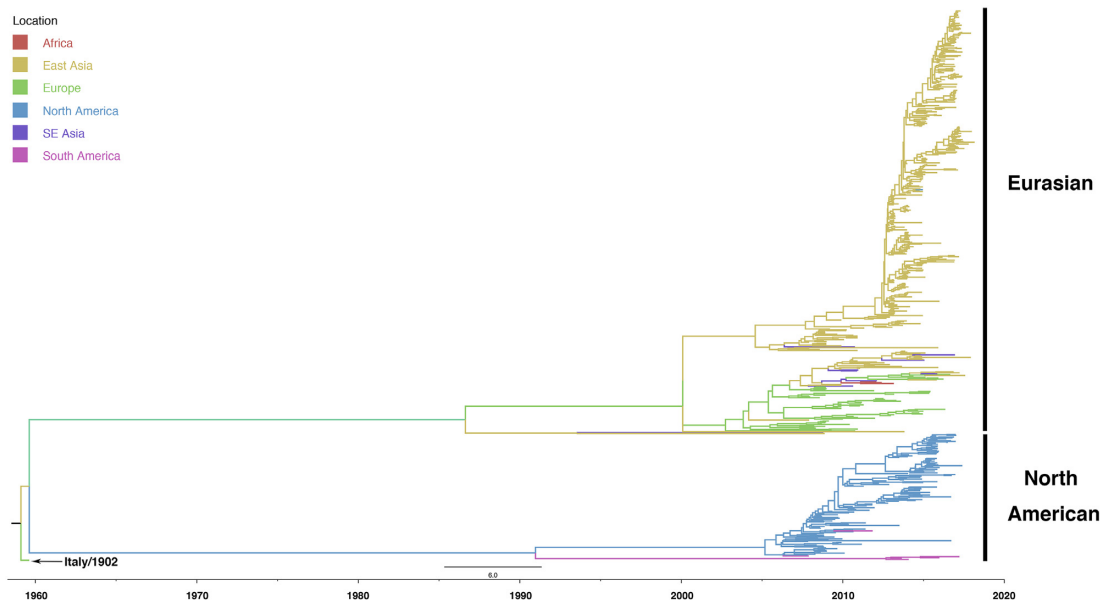


Figure 2. Phylogenetic relationship of the HA gene segment of H7 AIVs isolated from different geographical regions. The whole HA gene segment was used from viruses reported from 2008 to 2018, with ancestral virus A/chicken/Brescia/1902 (H7N7). The locations of virus isolation are classified into different regions. Branches are distinguished by different colours based on the region of viruses.

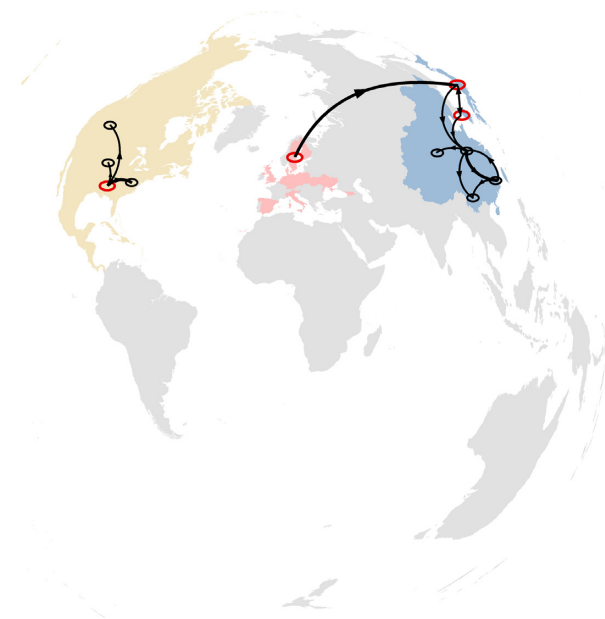


Figure 3. Hierarchical transmission network of H7 AIVs in the period from 2008 to 2018. Based on available sequences, three viral reservoirs located in Europe (pink), East Asia (blue) and North America (yellow) were identified (as shown in Fig. 2) and indicated here. Statistically supported pathways among regions on the global level and among subregions within two viral reservoirs are shown by arrow lines. The corresponding pairwise locations are shown using circles. Pathways with the highest significance and locations with the highest probability as transmission origins are highlighted by thick arrow lines and red circles.

transmission routes to other parts of China, including Southern, Southwest, Northeast and the Yellow River areas. Of these diffusions, dissemination from the Yangtze River to the Pearl River Delta region is more probable than from the Pearl River Delta area to the Yangtze River Delta (see Table S4, Supporting Information). In contrast, the viral evolution and gene flow within the North American reservoir depicts a more compact

pattern, which can be characterised by expansions from the Mississippi to other flyways (see Fig. S2, Tables S5 and S6, Supporting Information). Differences in transmission patterns between Asia and North America of AIV H7 may be due, in part, to the specific epidemiological and socioeconomic conditions of each region, indicating its role in the maintenance of virus on the local scale. Based on the intensive poultry population and high demand/consumption of live poultry in Southern and Eastern China, LBMs and poultry trading have been considered a major driver in the dissemination of the most prevalent AIV subtypes, including H5N1, H5N6, H7N9 and H9N2 viruses (Soares Magalhaes *et al.* 2012; Jin *et al.* 2014; Zhou *et al.* 2015; Bi *et al.* 2016). Correspondingly, the higher density of commercial poultry farms in the Mississippi flyways also serves as one of the prerequisites for the increased number of poultry outbreaks (Belkhiria, Alkhamis and Martinez-Lopez 2016) and, hence, viral transmissions.

EVOLUTIONARY GENETICS OF AIV H7

Reassortment of LPAIV H7 in wild birds

Reassortment is the process whereby, following co-infection, viral progeny may contain various combinations of gene segments from the different parental viruses. Thus, given an infection with two AIVs, each with eight segments, 256 different genetic progenies are theoretically possible, generating a significant viral diversity. In wild birds, reassortment of LPAIVs is frequent and occurs among co-circulating viruses (Wille *et al.* 2013).

As noted in the section titled ‘Wild-domestic bird interface of H7 viruses’, H7 is a naturally occurring virus in wild birds, and is consistently detected in surveillance schemes, albeit at low frequencies (Sharp *et al.* 1997; Munster *et al.* 2007; Wilcox *et al.* 2011; Latorre-Margalef *et al.* 2014). Reassortment of LPAIV H7 from wild birds has been assessed in two studies. First, it was demonstrated that like other LPAIV subtypes, there is large incongruence across phylogenetic trees of each segment, and genome constellations with the H7 HA are transient rather than stable (Xu *et al.* 2016). Lu *et al.* further demonstrated that LPAIV

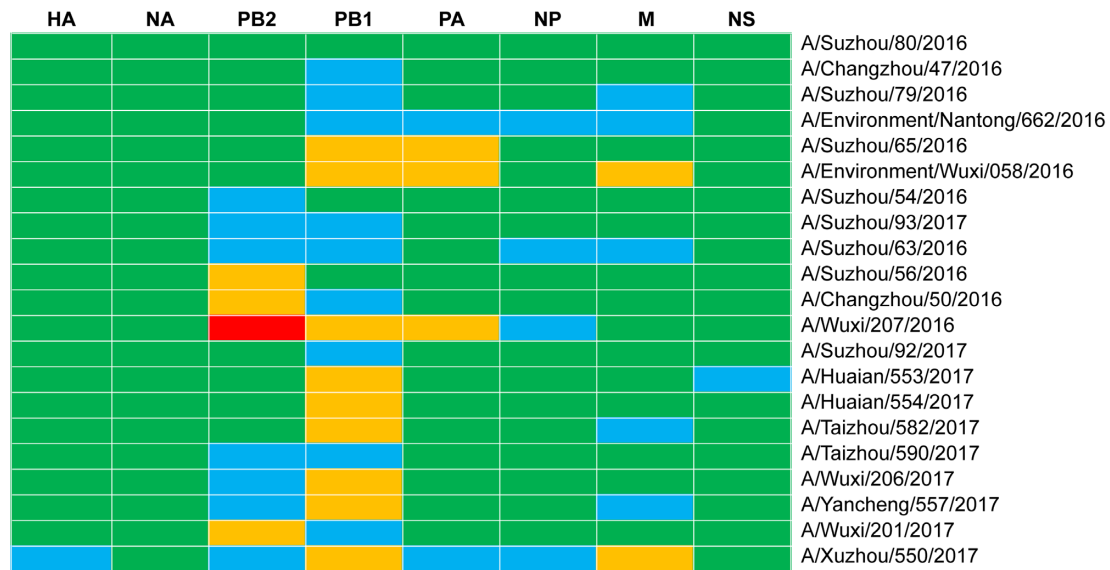


Figure 4. Reassortment patterns with H7 low pathogenic AIVs. Co-circulation of 21 different genome constellations of H7N9 in humans and LBMs of China in 2016–2017. Genome segments are arranged by HA and NA, followed by the ‘internal’ segments in order of size. Each colour corresponds to a unique genetic lineage. Adapted from (Qi et al. 2018a).

H7 reassort no more frequently or infrequently than other AIV subtypes. Interestingly, reassortment rates were correlated to prevalence in anseriform (waterfowl) vs gallinaceous (chickens, quail) birds, such that LPAIV H7N3, found mostly in gallinaceous birds, had a lower reassortment rate than LPAIV H7N7, found mostly in anseriform birds (Lu, Lycett and Brown 2014).

Reassortment of LPAIV and HPAIV H7N9 affecting LBMs and humans in China

The genesis of LPAIV H7N9 in China is a story of reassortment. Prior to the emergence of H7N9, H9N2 had been circulating in domestic birds in Asia for many years (Li et al. 2005; Bahl et al. 2016). It has been hypothesised that LPAIV H7N9 was the result of numerous reassortment events, whereby the six internal protein genes were derived from at least two separate H9N2 lineages, with wild-bird origin H7 and N9 segments (Gao et al. 2013; Wu et al. 2013; Lam et al. 2013; Pu et al. 2015; Wang et al. 2016). Despite the maintenance of the HA and NA subtypes, LPAIVs H7N9 detected in LBMs and human infections have a high degree of diversity in the internal genes. Cui et al. (2014) described a remarkable diversity, reporting 27 genotypes within three months of emergence. They further proposed a dynamic reassortment model for LPAIV H7N9 evolution (Cui et al. 2014). This reassortment and diversity have not abated since the first wave, although the number of genotypes has decreased. An analysis by Qi et al. demonstrated that in the fifth wave there were 18 genotypes present in 41 sequenced viruses from the Yangtze River Delta clade (Ding et al. 2017; Qi et al. 2018a,b). This diversity is likely maintained due to reassortment combined with the diversity of AIV in poultry markets and farms (Shi et al. 2018). Indeed, there has been reported reassortment between H5N6, H6N6 and H7N9, suggesting not all internal genes are derived from the H9N2 internal gene cassette (Jin et al. 2017; Wu et al. 2017a) (Fig. 4).

In mid-2016, HPAIV H7N9 emerged in mainland China in poultry. Phylogenetic analysis demonstrated that the HA and NA sequences of these HPAIVs clustered together. However the internal genes did not cluster together, suggesting that these

HPAIVs H7N9 had undergone complex reassortment with LPAIVs H7N9/H9N2 and that multiple genotypes were co-circulating in poultry (Shi et al. 2018; Qi et al. 2018a,b). Alternatively, this was due to a number of independent transitions from LPAIV to HPAIV.

Despite continued circulation for five years and presumably high levels of reassortment of the internal genes, the HA–NA subtype combination has remained stable. However, this lineage of H7 has been with N9 for a number of years, and other lineages of LPAIV H7 are indeed promiscuous. As outlined in the WHO Candidate Vaccine Virus report (2018/10) and previous studies, LPAIV H7N6 in China and Chile, and LPAIV H7N3 in Japan, has been evolved from the H7N9 gene pool (Wu et al. 2017a; WHO 2018a; Jimenez-Bluhm et al. 2019; Shibata et al. 2019). Similar recent evidence has been noted with H5 viruses (2.3.4.4 lineage), where a number of different NAs have been detected (Claes, Morzaria and Donis 2016).

Evolutionary rates of H7 viruses

In addition to genetic reassortment, AIVs evolve through genetic drift. Genetic drift is the process of mutation, which is due to an error-prone RNA-dependant RNA polymerase, which lacks proof-reading ability, resulting in genetic changes. Influenza A viruses have an extraordinary rapid rate of mutations, with an average of 3.41×10^{-3} substitutions per site per year (subs/site/year) (Chen and Holmes 2006). To put this in perspective, the rate of RNA virus mutation is a million times greater than that of vertebrates (Pybus and Rambaut 2009). Different factors can affect nucleotide substitution rates within the viral genome. For example, Worobey et al. demonstrated that influenza A viruses have different mutation rates in different broad host groups (Worobey, Han and Rambaut 2014), and, crucially, that there are different rates between poultry and wild birds (Fourment and Holmes 2015). Lebarbenchon, Brown and Stallknecht (2013) found that rates obtained for viruses circulating in wild birds were higher than for those isolated from domestic birds, albeit this study was undertaken prior to the emergence of LPAIV H7N9 (Lebarbenchon and Stallknecht

2011). Ward et al. (2013) showed no differences in evolutionary rates of AIVs H7 across different host types (waterfowl vs galliformes), and, furthermore, found no difference between LPAIVs and HPAIVs H7 (Ward et al. 2013). A study by Rejmanek et al. (2015) showed that the nucleotide substitution rate of H7N7 and H7N3 (11.62×10^{-3} subs/site/year and 8×10^{-3} subs/site/year, respectively) was significantly higher than that of LPAIV H3N8, a very common LPAIV subtype combination found in wild birds (1.43×10^{-3} subs/site/year) (Rejmanek et al. 2015). Focussing on only H7N9, there are different rates across the different reported lineages (Lu et al. 2018; Zhu et al. 2018). These rates range from 0.60 (lineage A) to 3.12 (lineage C2) adaptive substitutions per year, suggesting a faster adaption in the 2C clades compared to the A and B lineages (Lu et al. 2018). Furthermore, the evolutionary rate of the 2C clades is higher than for seasonal human influenza (H1N1, 1.02 adaptive substitutions per year; H3N2, 1.52 adaptive substitutions per year) (Bhatt, Holmes and Pybus 2011). Despite high rates of substitutions, it is mutations occurring at key regions, many of which are adjacent to or in the receptor binding site of the HA protein that allows for an antigenic drift, as shown for human H3N2 viruses (Koel et al. 2013). Antigenic drift allows for escape from antibody-mediated neutralisation acquired following infection (Koel et al. 2013) or vaccination (Lee, Senne and Suarez 2004; Escorcia et al. 2008; Nguyen et al. 2017). As such, one important concern with the reports of elevated rates, particularly in H7N9, is the potential of these viruses to escape from the vaccine-induced immunity, which is an ongoing problem in global efforts to contain HPAIV H5 (Connie Leung et al. 2013). Nevertheless, a conserved motif at the antigenic site A was found in the HA of all H7 sequences. It has been shown that mouse monoclonal antibodies produced from hemagglutinin of A/Shanghai/1/2013 (H7N9) do cross-react with different H7 isolates of the North American and Eurasian lineages, including the recent Chinese H7N9 virus from 2016–2017 (Stadlbauer et al. 2018). This suggests that the existing H7N9 vaccine candidate could protect against divergent H7 strains (Krammer et al. 2014; Tan et al. 2016).

CONCLUSION AND FUTURE PERSPECTIVES

The emergence of HPAIV H5 of the goose/Guangdong lineage put AIV, colloquially referred to as ‘Bird Flu’, on the map. These viruses caused the destruction of millions of domestic birds with large socioeconomic ramifications. However, these viruses resulted in limited human cases, which is in stark contrast to AIV H7. Given repeated spillover into mammals, particularly humans, there has been an increasing concern that human AIV H7 infections may lead to local epidemics or, given transmissibility between humans, a global pandemic. Influenza pandemics in the last century, for example, H2N2/1957 and H3N2/1968, arose from reassortment events between two or more viruses, including AIVs (Fuller et al. 2013). Therefore, even if AIV H7 with a complete avian genome never does become transmissible between humans, reassortment of human seasonal influenza with AIV H7 may allow the emergence of a new influenza virus variant in the human population (Zhu et al. 2013; Zhang et al. 2015; Huo et al. 2017).

The current reservoir for LPAIV H7N9 is commercial poultry, particularly in LBMs in China, despite ancestral LPAIVs circulating among wild birds. It has been suggested that LPAIV H7N9 emerged in LBMs (Wu et al. 2017b), and in the initial years, it was entirely restricted to cities. As such, combined with other factors, these viruses have not expanded into wild birds, and the

control and surveillance in LBMs played a crucial role in controlling this virus. To control LPAIV H7N9 and other emerging AIVs, it is imperative to reconsider poultry management and practices on a global scale. Measures such as increased biosecurity and hygiene controls throughout the entire poultry supply chain and improved biosecurity in live poultry retail markets may help to reduce the risk for human exposure to AIV, and further to other zoonotic pathogens. More drastically, poultry vaccination strategies are crucial in decreasing the viral burden, therefore lowering potential human contact with poultry viruses, although imperfect vaccination does drive viral evolution. Interventions in the reservoir are crucial to limit zoonotic spillover; of note is that the seventh wave of H7N9 has not materialized in poultry, the environment or humans, and this may be attributable to strict LBM control and massive poultry vaccination schemes, which may also be important in decreasing the viral burden, therefore lowering potential human contact with poultry viruses. This clearly demonstrates that a ‘One Health’ approach—including wildlife, domestic animal and human health—is critical in controlling zoonotic viruses, such as AIV H7.

To get ahead of AIV H7, we will need to continue surveillance of birds, the environment and humans. From surveillance, virus characterisation and timely sharing of virus sequence data remains imperative, which can be integrated into models of virus epidemiology and evolution. Timely data sharing has played a central role in managing and understanding outbreaks, with notable examples in the outbreak of Zika Virus in the Americas (De Carvalho et al. 2016) and Ebola Virus in West Africa (Diehl et al. 2016, Urbanowicz et al. 2016). Real-time epidemiological and sequence data were rapidly fed into models to demonstrate transmission patterns and virus evolution, and platforms such as Nextstrain (Hadfield et al. 2018), which allows for dissemination to researchers and the general public. To better understand the interspecies transmission of AIV H7, comparative *in vitro* and *in vivo* studies are required to reveal H7 virulence, pathogenesis, transmission and to identify genetic markers (van Riel et al. 2006; Koel et al. 2013), which are key to the interpretation of sequence and surveillance data. Studies from ecology are crucial in better describing the host range and bird migration patterns and strategies. Studies tracking wild birds have demonstrated their extraordinary capacity to link broad geographical regions and potentially disperse viruses (Gilbert et al. 2010; Van Toor et al. 2018). A multifaceted One Health approach is imperative for creating early warning systems to detect emerging, re-emerging and endemic viruses, particularly AIVs, that are prone to cross-species barriers.

SUPPLEMENTARY DATA

Supplementary data are available at [FEMSRE](https://www.femsre.com) online

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REFERENCES

- Abbas MA, Spackman E, Swayne DE et al. Sequence and phylogenetic analysis of H7N3 avian influenza viruses isolated from poultry in Pakistan 1995–2004. *Virology* 2010;**7**:137.
- Abdelwhab EM, Veits J, Mettenleiter TC. Prevalence and control of H7 avian influenza viruses in birds and humans. *Epidemiol Infect* 2014;**142**:896–920.
- Abdelwhab EM, Veits J, Tauscher K et al. A unique multibasic proteolytic cleavage site and three mutations in the HA2 domain confer high virulence of H7N1 avian influenza virus in chickens. *J Virol* 2016;**90**:400–11.
- Alexander DJ. A review of avian influenza in different bird species. *Vet Microbiol* 2000;**74**:3–13.
- Ali M, Yaqub T, Mukhtar N et al. Avian influenza A (H9N2) virus in poultry worker, Pakistan, 2015. *Emerg Infect Dis* 2019;**25**:136–9.
- Bahl J, Pham TT, Hill NJ et al. Ecosystem interactions underlie the spread of avian influenza A viruses with pandemic potential. *PLoS Pathog* 2016;**12**:e1005620.
- Bahl J, Vijaykrishna D, Holmes EC et al. Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. *Virology* 2009;**390**:289–97.
- Banks J, Speidel EC, McCauley JW et al. Phylogenetic analysis of H7 haemagglutinin subtype influenza A viruses. *Arch Virol* 2000;**145**:1047–58.
- Banks J, Speidel ES, Moore E et al. Changes in the haemagglutinin and the neuraminidase genes prior to the emergence of highly pathogenic H7N1 avian influenza viruses in Italy. *Arch Virol* 2001;**146**:963–73.
- Belkhiria J, Alkhamis MA, Martinez-Lopez B. Application of species distribution modeling for avian influenza surveillance in the United States considering the North America migratory flyways. *Sci Rep* 2016;**6**:33161.
- Belser JA, Bridges CB, Katz JM et al. Past, present, and possible future human infection with influenza virus A subtype H7. *Emerg Infect Dis* 2009;**15**:859–65.
- Belser JA, Lash RR, Garg S et al. The eyes have it: influenza virus infection beyond the respiratory tract. *Lancet Infect Dis* 2018;**18**:e220–e7.
- Belser JA, Pulit-Penalzo JA, Sun X et al. A novel A (H7N2) influenza virus isolated from a veterinarian caring for cats in a New York City animal shelter causes mild disease and transmits poorly in the ferret model. *J Virol* 2017;**91**.
- Berhane Y, Hisanaga T, Kehler H et al. Highly pathogenic avian influenza virus A (H7N3) in domestic poultry, Saskatchewan, Canada, 2007. *Emerg Infect Dis* 2009;**15**:1492–5.
- Bhatt S, Holmes EC, Pybus OG. The genomic rate of molecular adaptation of the human influenza A virus. *Mol Biol Evol* 2011;**28**:2443–51.
- Bi Y, Chen Q, Wang Q et al. Genesis, evolution and prevalence of H5N6 avian influenza viruses in China. *Cell Host Microbe* 2016;**20**:810–21.
- Bonfanti L, Monne I, Tamba M et al. Highly pathogenic H7N7 avian influenza in Italy. *Vet Rec* 2014;**174**:382.
- Bottcher-Friebertshausen E, Garten W, Matrosovich M et al. The hemagglutinin: a determinant of pathogenicity. *Curr Top Microbiol* 2014;**385**:3–34.
- Bouwstra R, Gonzales JL, de Wit S et al. Risk for low pathogenicity avian influenza virus on poultry farms, the Netherlands, 2007–2013. *Emerg Infect Dis* 2017;**23**:1510–6.
- Brown EG. Influenza virus genetics. *Biomed Pharmacother* 2000;**54**:196–209.
- Bugh M. Highly pathogenic virus recovered from chickens infected with mildly pathogenic 1986 isolates of H5N2 avian influenza-virus. *Avian Dis* 1988;**32**:695–703.
- Campitelli L, Di Martino A, Spagnolo D et al. Molecular analysis of avian H7 influenza viruses circulating in Eurasia in 1999–2005: detection of multiple reassortant virus genotypes. *J Gen Virol* 2008;**89**:48–59.
- Cappelle J, Gaidet N, Iverson SA et al. Characterizing the interface between wild ducks and poultry to evaluate the potential of transmission of avian pathogens. *Int J Health Geogr* 2011;**10**:60.
- Capua I, Alexander DJ. Avian influenza infections in birds - a moving target. *Influenza Other Resp* 2007;**1**:11–8.
- Capua I, Marangon S. The avian influenza epidemic in Italy, 1999–2000: a review. *Avian Pathol* 2000;**29**:289–94.
- Capua I, Mutinelli F, Pozza MD et al. The 1999–2000 avian influenza (H7N1) epidemic in Italy: veterinary and human health implications. *Acta Trop* 2002;**83**:7–11.
- Centers for Disease Control and Prevention (CDC). Update: influenza activity—United States and worldwide, 2003–04 season, and composition of the 2004–05 influenza vaccine. *Centers for Disease Control and Prevention* 2004;**53**:547–52.
- Chen R, Holmes EC. Avian influenza virus exhibits rapid evolutionary dynamics. *Mol Biol Evol* 2006;**23**:2336–41.
- Chen Y, Liang W, Yang S et al. Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: clinical analysis and characterisation of viral genome. *Lancet* 2013;**381**:1916–25.
- Cheung TK, Poon LL. Biology of influenza A virus. *Ann N Y Acad Sci* 2007;**1102**:1–25.
- Claes F, Morzaria SP, Donis RO. Emergence and dissemination of clade 2.3.4.4 H5Nx influenza viruses—how is the Asian HPAI H5 lineage maintained. *Curr Opin Virol* 2016;**16**:158–63.
- Claes G, Lambrecht B, Dewulf J et al. Extended transmission of two H5/H7 low pathogenic avian influenza viruses in chickens. *Epidemiol Infect* 2015;**143**:781–90.
- Claes G, Welby S, Van Den Berg T et al. The impact of viral tropism and housing conditions on the transmission of three H5/H7 low pathogenic avian influenza viruses in chickens. *Epidemiol Infect* 2013;**141**:2428–43.
- Connie Leung YH, Luk G, Sia SF et al. Experimental challenge of chicken vaccinated with commercially available H5 vaccines reveals loss of protection to some highly pathogenic avian influenza H5N1 strains circulating in Hong Kong/China. *Vaccine* 2013;**31**:3536–42.
- Cui L, Liu D, Shi W et al. Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. *Nat Commun* 2014;**5**:3142.
- De Carvalho NS, De Carvalho BF, Fugaca CA et al. Zika virus infection during pregnancy and microcephaly occurrence: a review of literature and Brazilian data. *Braz J Infect Dis* 2016;**20**:282–9.
- Defra. Highly pathogenic avian influenza – H7N7 in egg laying poultry in Oxfordshire. *Epidemiology report*. 2008. <http://webarchive.nationalarchives.gov.uk/20130402151656/http://archive.defra.gov.uk/foodfarm/farmanimal/diseases/atoz/ai/documents/epireport-080711.pdf> (26 September 2016, date last accessed).

- de Jong MC, Stegeman A, van der Goot J et al. Intra- and interspecies transmission of H7N7 highly pathogenic avian influenza virus during the avian influenza epidemic in the Netherlands in 2003. *Rev Sci Tech* 2009;**28**:333–40.
- De Marco MA, Foni E, Campitelli L et al. Long-term monitoring for avian influenza viruses in wild bird species in Italy. *Vet Res Commun* 2003;**27** Suppl 1:107–14.
- Deshpande KL, Fried VA, Ando M et al. Glycosylation affects cleavage of an H5N2 influenza-virus hemagglutinin and regulates virulence. *Proc Natl Acad Sci USA* 1987;**84**:36–40.
- de Vries RP, Peng W, Grant OC et al. Three mutations switch H7N9 influenza to human-type receptor specificity. *PLoS Pathog* 2017;**13**:e1006390.
- de Wit JJ, Koch G, Fabri TH et al. A cross-sectional serological survey of the Dutch commercial poultry population for the presence of low pathogenic avian influenza virus infections. *Avian Pathol* 2004;**33**:565–70.
- Diehl WE, Lin AE, Grubaugh ND et al. Ebola virus glycoprotein with increased infectivity dominated the 2013–2016 epidemic. *Cell* 2016;**167**:1088–98 e6.
- Dietze K, Graaf A, Homeier-Bachmann T et al. From low to high pathogenicity—characterization of H7N7 avian influenza viruses in two epidemiologically linked outbreaks. *Transbound Emerg Dis* 2018;**00**:1–12.
- Ding X, Luo J, Quan L et al. Evolutionary genotypes of influenza A (H7N9) viruses over five epidemic waves in China. *Infect Genet Evol* 2017;**55**:269–76.
- Editorial-team-Collective. Avian influenza A(H7N2) outbreak in the United Kingdom. *Euro Surveill* 2007;**12**:E070531.2.
- Elbers AR, Fabri TH, de Vries TS et al. The highly pathogenic avian influenza A (H7N7) virus epidemic in the Netherlands in 2003—lessons learned from the first five outbreaks. *Avian Dis* 2004;**48**:691–705.
- Escalera-Zamudio M, Gutierrez B, Theze J et al. Parallel evolution and the emergence of highly pathogenic avian influenza A viruses. *bioRxiv* 2018, 10.1101/370015: 370015.
- Escorcía M, Vázquez L, Méndez ST et al. Avian influenza: genetic evolution under vaccination pressure. *Virology* 2008;**5**:15.
- FAO. H7N9 situation update. 2019. <http://www.fao.org/ag/againfo/programmes/en/empres/H7N9/situation.update.html> (10 March 2019, date last accessed).
- FAO. Highly pathogenic avian influenza in Mexico (H7N3) - a significant threat to poultry production not to be underestimated. *EMPRES WATCH*. 2012. <http://www.fao.org/3/a-an395e.pdf> (March 31, 2016, date last accessed: 10 March 2019).
- Fereidouni S, Munoz O, Von Dobschuetz S et al. Influenza virus infection of marine mammals. *Ecohealth* 2016;**13**:161–70.
- Ferreira HL, Pirlot JF, Kaspers B et al. Development of specific enzyme-linked immunosorbent assays to evaluate the duck immune response after experimental infection with H5N1 and H7N1 low pathogenic avian influenza viruses. *Avian Dis* 2010;**54**:660–7.
- FluTrackers. FluTrackers 2013-18: Human Case List of Provincial/Ministry of Health/Government Confirmed Influenza A(H7N9) Cases with Links. 2019. Available online at <https://flutrackers.com/forum/forum/china-h7n9-outbreak-tracking/143874-flutrackers-2013-18-human-case-list-of-provincial-ministry-of-health-government-confirmed-influenza-a-h7n9-cases-with-links?t=202713> (15 March 2019, date last accessed).
- Fouchier RA, Munster V, Wallensten A et al. Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. *J Virol* 2005;**79**:2814–22.
- Fouchier RA, Schneeberger PM, Rozendaal FW et al. Avian influenza A virus (H7N7) associated with human conjunctivitis and a fatal case of acute respiratory distress syndrome. *Proc Natl Acad Sci* 2004;**101**:1356–61.
- Fourment M, Holmes EC. Avian influenza virus exhibits distinct evolutionary dynamics in wild birds and poultry. *BMC Evol Biol* 2015;**15**:120.
- Fournie G, Pfeiffer DU. Can closure of live poultry markets halt the spread of H7N9? *Lancet* 2014;**383**:496–7.
- Fuller TL, Gilbert M, Martin V et al. Predicting hotspots for influenza virus reassortment. *Emerg Infect Dis* 2013;**19**:581–8.
- Gambaryan AS, Matrosovich TY, Philipp J et al. Receptor-binding profiles of H7 subtype influenza viruses in different host species. *J Virol* 2012;**86**:4370–9.
- Gao P, Du H, Fan L et al. Human infection with an avian-origin influenza A (H7N4) virus in Jiangsu: a potential threat to China. *J Infect* 2018;**77**:249–57.
- Gao R, Cao B, Hu Y et al. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med* 2013a;**368**:1888–97.
- Garten W, Klenk HD. Cleavage activation of the influenza virus hemagglutinin and its role in pathogenesis. In: Klenk HD, Matrosovich MN, Stech J (eds). *Avian Influenza*, Monogr Virolog. Basel, Karger, V ol. 27. 2008, 156–67.
- GenBank. National Center for Biotechnology Information. 2019.
- Gilbert M, Newman SH, Takekawa JY et al. Flying over an infected landscape: distribution of highly pathogenic avian influenza H5N1 risk in South Asia and satellite tracking of wild waterfowl. *Ecohealth* 2010;**7**:448–58.
- Gilbert M, Xiao X, Robinson TP. Intensifying poultry production systems and the emergence of avian influenza in China: a ‘One Health/Ecohealth’ epitome. *Arch Public Health* 2017;**75**:48.
- Gohrbandt S, Veits J, Hundt J et al. Amino acids adjacent to the haemagglutinin cleavage site are relevant for virulence of avian influenza viruses of subtype H5. *J Gen Virol* 2011;**92**:51–9.
- Guo Z, Xiao D, Li D et al. The temporal distribution of new H7N9 avian influenza infections based on laboratory-confirmed cases in Mainland China, 2013–2017. *Sci Rep* 2018;**8**:4051.
- Hadfield J, Megill C, Bell SM et al. Nextstrain: real-time tracking of pathogen evolution. *Bioinformatics* 2018;**34**:4121–3.
- Hirst M, Astell CR, Griffith M et al. Novel avian influenza H7N3 strain outbreak, British Columbia. *Emerg Infect Dis* 2004;**10**:2192–5.
- Hooper P, Selleck P. Pathology of low and high virulent influenza virus infections. *Avian Dis* 2003;**47**:134–41.
- Horimoto T, Kawaoka Y. Molecular-changes in virulent mutants arising from avirulent avian influenza-viruses during replication in 14-day-old embryonated eggs. *Virology* 1995;**206**:755–9.
- Huo X, Chen L, Qi X et al. Significantly elevated number of human infections with H7N9 virus in Jiangsu in Eastern China, October 2016 to January 2017. *Euro Surveill* 2017;**22**:pii:30496.
- ICTVdB(International Committee on Taxonomy of Viruses). Index of viruses, index of viruses: orthomyxoviridae. In: Büchen-Osmond CE (ed.). *ICTVdB - The Universal Virus Database, version 4*. New York: Columbia University, 2006.
- Iglesias I, Martínez M, Muñoz MJ et al. First case of highly pathogenic avian influenza in poultry in Spain. *Transboundary Emerg Dis* 2010;**57**:282–5.
- Ito T, Goto H, Yamamoto E et al. Generation of a highly pathogenic avian influenza A virus from an avirulent field isolate by passaging in chickens. *J Virol* 2001;**75**:4439–43.

- Jimenez-Bluhm P, Bravo-Vasquez N, Torchetti MK et al. Low pathogenic avian influenza (H7N6) virus causing an outbreak in commercial Turkey farms in Chile. *Emerg Microbes Infections* 2019;**8**:479–85.
- Jin Y, Ren H, Teng Y et al. Novel reassortment of avian influenza A (H7N9) virus with subtype H6N6 and H5N6 viruses circulating in Guangdong Province, China. *J Infect* 2017;**75**: 179–82.
- Jin Y, Yu D, Ren H et al. Phylogeography of avian influenza A H9N2 in China. *BMC Genomics* 2014;**15**:1110.
- Jones JC, Sonnberg S, Webby RJ et al. Influenza A(H7N9) virus transmission between finches and poultry. *Emerg Infect Dis* 2015;**21**:619–28.
- Joseph U, Su YC, Vijaykrishna D et al. The ecology and adaptive evolution of influenza A interspecies transmission. *Influenza Other Respir Viruses* 2017;**11**:74–84.
- Jourdain E, Gunnarsson G, Wahlgren J et al. Influenza virus in a natural host, the mallard: experimental infection data. *PLoS One* 2010;**5**:e8935.
- Kaleta EF, Honicke A. Review of the literature on avian influenza A viruses in pigeons and experimental studies on the susceptibility of domestic pigeons to influenza A viruses of the hemagglutinin subtype H7. *Dtsch Tierarztl Wochenschr* 2005;**111**:467–72.
- Ke C, Mok CKP, Zhu W et al. Human infection with highly pathogenic avian influenza A (H7N9) virus, China. *Emerg Infect Dis* 2017;**23**:1332–40.
- Killian ML, Kim-Torchetti M, Hines N et al. Outbreak of H7N8 low pathogenic avian influenza in commercial turkeys with spontaneous mutation to highly pathogenic avian influenza. *Genome Announc* 2016;**4**:e00457–16.
- Kim HR, Park CK, Lee YJ et al. Low pathogenic H7 subtype avian influenza viruses isolated from domestic ducks in South Korea and the close association with isolates of wild birds. *J Gen Virol* 2012;**93**:1278–87.
- Koel BF, Burke DF, Bestebroer TM et al. Substitutions near the receptor binding site determine major antigenic change during influenza virus evolution. *Science* 2013;**342**:976–9.
- Krammer F, Albrecht RA, Tan GS et al. Divergent H7 immunogens offer protection from H7N9 virus challenge. *J Virol* 2014;**88**:3976–85.
- Krammer F, Smith GJD, Fouchier RAM et al. Influenza. *Nature Rev Disease Primers* 2018;**4**:3.
- Kurtz J, Manvell RJ, Banks J. Avian influenza virus isolated from a woman with conjunctivitis. *Lancet* 1996;**348**:901–2.
- Lam TT, Wang J, Shen Y et al. The genesis and source of the H7N9 influenza viruses causing human infections in China. *Nature* 2013;**502**:241–4.
- Latorre-Margalef N, Tolf C, Grosbois V et al. Long-term variation in influenza A virus prevalence and subtype diversity in migratory mallards in Northern Europe. *Proc Biol Sci* 2014;**281**:20140098.
- Lebarbenchon C, Brown JD, Stallknecht DE. Evolution of influenza A virus H7 and N9 subtypes, Eastern Asia. *Emerg Infect Dis* 2013;**19**:1635–8.
- Lebarbenchon C, Stallknecht DE. Host shifts and molecular evolution of H7 avian influenza virus hemagglutinin. *Virology* 2011;**8**:328.
- Lee CW, Senne DA, Suarez DL. Effect of vaccine use in the evolution of Mexican lineage H5N2 avian influenza virus. *J Virol* 2004;**78**:8372–81.
- Li C, Yu K, Tian G et al. Evolution of H9N2 influenza viruses from domestic poultry in Mainland China. *Virology* 2005;**340**:70–83.
- Li R, Zhang T, Bai Y et al. Live poultry trading drives China's H7N9 viral evolution and geographical network propagation. *Frontiers Public Health* 2018;**6**:210.
- Lopez-Martinez I, Balish A, Barrera-Badillo G et al. Highly pathogenic avian influenza A(H7N3) virus in poultry workers, Mexico, 2012. *Emerg Infect Dis* 2013;**19**:1531–4.
- Lu H, Castro AE. Evaluation of the infectivity, length of infection, and immune response of a low-pathogenicity H7N2 avian influenza virus in specific-pathogen-free chickens. *Avian Dis* 2004;**48**:263–70.
- Lu J, Raghwanji J, Pryce R et al. Molecular evolution, diversity, and adaptation of influenza A (H7N9) viruses in China. *Emerg Infect Dis* 2018;**24**:1795–805.
- Lu L, Lycett SJ, Brown AJL. Reassortment patterns of avian influenza virus internal segments among different subtypes. *BMC Evol Biol* 2014;**14**, DOI: 10.1186/1471-2148-14-16.
- Mackay IM. Influenza A(H7N9) virus: detection numbers and graphs . 2019. Virology Down Under Blog <https://virologydownunder.blogspot.com/2014/11/influenza-ah7n9-virus-detection-numbers.html>.
- Marinova-Petkova A, Laplante J, Jang Y et al. Avian influenza A (H7N2) virus in human exposed to sick cats, New York, USA, 2016. *Emerg Infect Dis* 2017;**23**:2046–9.
- Maurer-Stroh S, Lee RT, Gunalan V et al. The highly pathogenic H7N3 avian influenza strain from July 2012 in Mexico acquired an extended cleavage site through recombination with host 28S rRNA. *Virology* 2013;**10**:139.
- Millman AJ, Havers F, Iuliano AD et al. Detecting spread of avian influenza A (H7N9) virus beyond China. *Emerg Infect Dis* 2015;**21**:741–9.
- Mo IP, Brugh M, Fletcher OJ et al. Comparative pathology of chickens experimentally inoculated with avian influenza viruses of low and high pathogenicity. *Avian Dis* 1997;**41**:125–36.
- Monne I, Fusaro A, Nelson MI et al. Emergence of a highly pathogenic avian influenza virus from a low-pathogenic progenitor. *J Virol* 2014;**88**:4375–88.
- Mostafa A, Abdelwhab EM, Mettenleiter TC et al. Zoonotic potential of influenza A viruses: a comprehensive overview. *Viruses* 2018;**10**:497.
- Munster VJ, Baas C, Lexmond P et al. Spatial, temporal, and species variation in prevalence of influenza A viruses in wild migratory birds. *PLoS Pathog* 2007;**3**:e61.
- Munster VJ, Schrauwen EJA, de Wit E et al. Insertion of a multibasic cleavage motif into the hemagglutinin of a low-pathogenic avian influenza H6N1 virus induces a highly pathogenic phenotype. *J Virol* 2010;**84**:7953–60.
- Munster VJ, Wallensten A, Baas C et al. Mallards and highly pathogenic avian influenza ancestral viruses, northern Europe. *Emerg Infect Dis* 2005;**11**:1545–51.
- Naeem K. The Avian Influenza H7 N3 Outbreak in South Central Asia. *Avian Dis* 2003;**47**:31–5.
- Nguyen-Van-Tam JS, Nair P, Acheson P et al. Outbreak of low pathogenicity H7N3 avian influenza in UK, including associated case of human conjunctivitis. *Euro Surveill* 2006;**11**:E060504.2.
- Nguyen LT, Nishi T, Shichinohe S et al. Selection of antigenic variants of an H5N1 highly pathogenic avian influenza virus in vaccinated chickens. *Virology* 2017;**510**:252–61.
- OFFLU, OIE/FAO. Network of expertise on animal influenza. Influenza A cleavage sites, Vol. 2018. Paris/Rome: OIE/FAO. 2018. http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/Influenza_A_Cleavage_Sites.pdf(31 January 2018, date last accessed).

- OIE. Avian influenza. Infection with avian influenza viruses. OIE *terrestrial manual Chapter 104* Available online: http://www.oie.int/fileadmin/Home/eng/Health_standards/tahc/current/chapitre_avian_influenza_viruses.pdf 2019.
- Olsen B, Munster VJ, Wallensten A et al. Global patterns of influenza A virus in wild birds. *Science (New York, NY)* 2006;**312**:384–8.
- Olson SH, Parmley J, Soos C et al. Sampling strategies and biodiversity of influenza A subtypes in wild birds. *PLoS One* 2014;**9**:e90826.
- Ostrowsky B, Huang A, Terry W et al. Low pathogenic avian influenza A (H7N2) virus infection in immunocompromised adult, New York, USA, 2003. *Emerg Infect Dis* 2012;**18**:1128–31.
- Pantin-Jackwood MJ, Costa-Hurtado M, Shepherd E et al. Pathogenicity and transmission of H5 and H7 highly pathogenic avian influenza viruses in mallards. *J Virol* 2016;**90**:9967–82.
- Pantin-Jackwood MJ, Miller PJ, Spackman E et al. Role of poultry in the spread of novel H7N9 influenza virus in China. *J Virol* 2014;**88**:5381–90.
- Pasick J, Handel K, Robinson J et al. Intersegmental recombination between the haemagglutinin and matrix genes was responsible for the emergence of a highly pathogenic H7N3 avian influenza virus in British Columbia. *J Gen Virol* 2005;**86**:727–31.
- ProMED-mail. Avian influenza.
- Pu J, Wang S, Yin Y et al. Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. *Proc Natl Acad Sci USA* 2015;**112**:548–53.
- Puzelli S, Di Trani L, Fabiani C et al. Serological analysis of serum samples from humans exposed to avian H7 influenza viruses in Italy between 1999 and 2003. *J Infect Dis* 2005;**192**:1318–22.
- Puzelli S, Rossini G, Facchini M et al. Human infection with highly pathogenic A(H7N7) avian influenza virus, Italy, 2013. *Emerg Infect Dis* 2014;**20**:1745–9.
- Pybus OG, Rambaut A. Evolutionary analysis of the dynamics of viral infectious disease. *Nat Rev Genet* 2009;**10**:540–50.
- Qi W, Jia W, Liu D et al. Emergence and adaptation of a novel highly pathogenic H7N9 influenza virus in birds and humans from a 2013 human-infecting low-pathogenic ancestor. *J Virol* 2018b;**92**: e00921–17.
- Qi X, An X, Jiao Y et al. Co-circulation of multiple genotypes of influenza A (H7N9) viruses in Eastern China, 2016–2017. *Arch Virol* 2018a;**163**:1779–93.
- Rejmanek D, Hosseini PR, Mazet JA et al. Evolutionary dynamics and global diversity of influenza A virus. *J Virol* 2015;**89**:10993–1001.
- Richard M, Fouchier R, Monne I et al. Mechanisms and risk factors for mutation from low to highly pathogenic avian influenza virus. 2017. <https://efsa.onlinelibrary.wiley.com/doi/pdf/10.2903/sp.efsa.2017.EN-1287> (9 August 2017, date last accessed).
- Roche B, Lebarbenchon C, Gauthier-Clerc M et al. Water-borne transmission drives avian influenza dynamics in wild birds: the case of the 2005–2006 epidemics in the Camargue area. *Infect Genet Evol* 2009;**9**:800–5.
- Rohm C, Horimoto T, Kawaoka Y et al. Do hemagglutinin genes of highly pathogenic avian influenza viruses constitute unique phylogenetic lineages? *Virology* 1995;**209**:664–70.
- Seekings AH, Slomka MJ, Russell C et al. Direct evidence of H7N7 avian influenza virus mutation from low to high virulence on a single poultry premises during an outbreak in free range chickens in the UK, 2008. *Infect Genet Evol* 2018;**5**:13–31.
- Seekings AH. Emergence of H7 highly pathogenic avian influenza virus from low pathogenicity avian influenza virus. 2017. <http://hdl.handle.net/10044/1/52910> (05 March 2019, date last accessed).
- Senne DA, Pedersen JC, Panigrahy B. Live-bird markets in the Northeastern United States: a source of avian influenza in commercial poultry. In: Schrijver RS, Koch G. *Avian Influenza: Prevention and Control*. Netherland: Springer, 2005, 19–24.
- Shao W, Li X, Goraya MU et al. Evolution of influenza A virus by mutation and re-assortment. *Int J Mol Sci* 2017;**18**.
- Sharp GB, Kawaoka Y, Jones DJ et al. Coinfection of wild ducks by influenza A viruses: distribution patterns and biological significance. *J Virol* 1997;**71**:6128–35.
- Shibata A, Harada R, Okamoto M et al. Characterization of a novel reassortant H7N3 highly pathogenic avian influenza virus isolated from a poultry meat product taken on a passenger flight to Japan. *J Vet Med Sci* 2019;**81**:444–8.
- Shi JZ, Deng GH, Kong HH et al. H7N9 virulent mutants detected in chickens in China pose an increased threat to humans. *Cell Res* 2017;**27**:1409–21.
- Shi JZ, Deng GH, Ma SJ et al. Rapid evolution of H7N9 highly pathogenic viruses that emerged in China in 2017. *Cell Host Microbe* 2018;**24**:558–68.
- Shu Y, McCauley J. GISAID: Global Initiative on Sharing All Influenza Data - from vision to reality. *Euro Surveill* 2017;**22**:pii:30494.
- Soares Magalhaes RJ, Zhou X, Jia B et al. Live poultry trade in Southern China provinces and HPAIV H5N1 infection in humans and poultry: the role of Chinese New Year festivities. *PLoS One* 2012;**7**: e49712.
- Soda K, Cheng MC, Yoshida H et al. A low pathogenic H5N2 influenza virus isolated in Taiwan acquired high pathogenicity by consecutive passages in chickens. *J Vet Med Sci* 2011;**73**:767–72.
- Spackman E, Gelb J, Jr., Preskenis LA et al. The pathogenesis of low pathogenicity H7 avian influenza viruses in chickens, ducks and turkeys. *Virol J* 2010;**7**:331.
- Spackman E, Senne DA, Davison S et al. Sequence analysis of recent H7 avian influenza viruses associated with three different outbreaks in commercial poultry in the United States. *J Virol* 2003;**77**:13399–402.
- Stadlbauer D, Amanat F, Strohmeier S et al. Cross-reactive mouse monoclonal antibodies raised against the hemagglutinin of A/Shanghai/1/2013 (H7N9) protect against novel H7 virus isolates in the mouse model. *Emerg Microbes Infections* 2018;**7**:110.
- Suarez DL, Senne DA, Banks J et al. Recombination resulting in virulence shift in avian influenza outbreak, Chile. *Emerg Infect Dis* 2004;**10**:693–9.
- Suarez DL, Spackman E, Senne DA. Update on molecular epidemiology of H1, H5, and H7 influenza virus infections in poultry in North America. *Avian Dis* 2003;**47**:888–97.
- Tan GS, Leon PE, Albrecht RA et al. Broadly-reactive neutralizing and non-neutralizing antibodies directed against the H7 influenza virus hemagglutinin reveal divergent mechanisms of protection. *PLoS Pathog* 2016;**12**:e1005578.
- Terebuh P, Adija A, Edwards L et al. Human infection with avian influenza A (H7N2) virus-Virginia, 2002. *Influenza Other Respir Viruses* 2018;**12**:529–32.
- Tollis M, Di Trani L. Recent developments in avian influenza research: epidemiology and immunoprophylaxis. *Vet J* 2002;**164**:202–15.
- Tong XC, Weng SS, Xue F et al. First human infection by a novel avian influenza A (H7N4) virus. *J Infect* 2018;**77**:249–57.

- Tweed SA, Skowronski DM, David ST et al. Human illness from avian influenza H7N3, British Columbia. *Emerg Infect Dis* 2004;**10**:2196–9.
- Urbanowicz RA, McClure CP, Sakuntabhai A et al. Human adaptation of Ebola virus during the West African outbreak. *Cell* 2016;**167**:1079–87 e5.
- van Riel D, Munster VJ, de Wit E et al. H5N1 Virus attachment to lower respiratory tract. *Science* 2006;**312**:399.
- Van Toor ML, Avril A, Wu G et al. As the duck flies—estimating the dispersal of low-pathogenic avian influenza viruses by migrating mallards. *Front Ecol Evol* 2018;**6**:208.
- Verhagen JH, Herfst S, Fouchier RA. Infectious disease. How a virus travels the world. *Science* 2015;**347**:616–7.
- Verhagen JH, Lexmond P, Vuong O et al. Discordant detection of avian influenza virus subtypes in time and space between poultry and wild birds; Towards improvement of surveillance programs. *PLoS One* 2017;**12**:e0173470.
- Wang C, Wang J, Su W et al. Relationship between domestic and wild birds in live poultry market and a novel human H7N9 virus in China. *J Infect Dis* 2014a;**209**:34–7.
- Wang D, Yang L, Gao R et al. Genetic tuning of the novel avian influenza A(H7N9) virus during interspecies transmission, China, 2013. *Euro Surveill* 2014b;**19**:pii:20699.
- Wang DY, Yang L, Zhu WF et al. Two outbreak sources of influenza A (H7N9) viruses have been established in China. *J Virol* 2016;**90**:5561–73.
- Ward MJ, Lycett SJ, Avila D et al. Evolutionary interactions between haemagglutinin and neuraminidase in avian influenza. *BMC Evol Biol* 2013;**13**:222.
- Webby RJ, Webster RG. Emergence of influenza A viruses. *Philos T Roy Soc B* 2001;**356**:1817–28.
- Webster RG, Bean WJ, Gorman OT et al. Evolution and ecology of influenza A viruses. *Microbiol Rev* 1992;**56**:152–79.
- Webster RG, Geraci J, Petursson G et al. Conjunctivitis in human beings caused by influenza A virus of seals. *N Engl J Med* 1981;**304**:911.
- WHO. Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness (September 2018 Update). In: World Health Organization(ed.). Geneva: WHO, 2018a.
- WHO. Avian influenza weekly update number 679. 2019a. <https://iris.wpro.who.int/bitstream/handle/10665.1/14328/AI-20190308.pdf> (15 March 2019, date last accessed).
- WHO. Cumulative number of confirmed human cases for avian influenza A (H5N1) reported to WHO, 2003–2019. 2019b. https://www.who.int/influenza/human_animal_interface/2019_02_12_tableH5N1.pdf?ua=1 (10 March 2019, date last accessed).
- WHO. Human infection with avian influenza A(H7N9) virus China: update. 2018b. <https://www.who.int/csr/don/05-september-2018-ah7n9-china/en/> (10 March 2019, date last accessed).
- WHO. Influenza at the human-animal interface. 2018c. https://www.who.int/influenza/human_animal_interface/Influenza_Summary_IRA_HA_interface_13_12_2018_FINAL.pdf?ua=1 (10 March 2019, date last accessed).
- Wilcox BR, Knutsen GA, Berdeen J et al. Influenza A viruses in ducks in Northwestern Minnesota: fine scale spatial and temporal variation in prevalence and subtype diversity. *PLoS One* 2011;**6**:e24010.
- Wille M, Tolf C, Avril A et al. Frequency and patterns of reassortment in natural influenza A virus infection in a reservoir host. *Virology* 2013;**443**:150–60.
- Worobey M, Han GZ, Rambaut A. A synchronized global sweep of the internal genes of modern avian influenza virus. *Nature* 2014;**508**:254–7.
- Wu A, Su C, Wang D et al. Sequential reassortments underlie diverse influenza H7N9 genotypes in China. *Cell Host Microbe* 2013;**14**:446–52.
- Wu H, Lu R, Peng X et al. Molecular characterization of a novel reassortant H7N6 subtype avian influenza virus from poultry in Eastern China, in 2016. *Arch Virol* 2017a;**162**:1341–7.
- Wu J, Ke C, Lau EHY et al. Influenza H5/H7 virus vaccination in poultry and reduction of zoonotic infections, Guangdong Province, China, 2017–18. *Emerg Infect Dis* 2019;**25**:116–8.
- Wu T, Perrings C, Kinzig A et al. Economic growth, urbanization, globalization, and the risks of emerging infectious diseases in China: a review. *Ambio* 2017b;**46**:18–29.
- Xu YF, Bailey E, Spackman E et al. Limited antigenic diversity in contemporary H7 avian-origin influenza A viruses from North America. *Sci Rep-Uk* 2016;**6**:20688.
- Zeng X, Tian G, Shi J et al. Vaccination of poultry successfully eliminated human infection with H7N9 virus in China. *Sci China Life Sci* 2018;**61**:1465–73.
- Zhang W, Zhu D, Tian D et al. Co-infection with avian (H7N9) and pandemic (H1N1) 2009 influenza viruses, China. *Emerg Infect Dis* 2015;**21**:715–8.
- Zhang Y, Aevermann BD, Anderson TK et al. Influenza research database: an integrated bioinformatics resource for influenza virus research. *Nucleic Acids Res* 2017;**45**:D466–74.
- Zhao B, Zhang X, Zhu W et al. Novel avian influenza A (H7N9) virus in tree sparrow, Shanghai, China, 2013. *Emerg Infect Dis* 2014;**20**:850–3.
- Zhou X, Li Y, Wang Y et al. The role of live poultry movement and live bird market biosecurity in the epidemiology of influenza A (H7N9): a cross-sectional observational study in four eastern China provinces. *J Infect* 2015;**71**:470–9.
- Zhu W, Dong J, Zhang Y et al. A gene constellation in avian influenza A (H7N9) viruses may have facilitated the fifth wave outbreak in China. *Cell Rep* 2018;**23**:909–17.
- Zhu Y, Qi X, Cui L et al. Human co-infection with novel avian influenza A H7N9 and influenza A H3N2 viruses in Jiangsu Province, China. *Lancet* 2013;**381**:2134.