

Conservation implications of avian influenza

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Executive summary

- 1 Information on the outbreaks of the H5N1 highly pathogenic avian influenza virus in south-east and central-southern Asia is reviewed with respect to pathogenicity to wild and domestic birds, modes of transmission, efficacy of culling wild birds in disease management and human activities that might assist the spread of the virus among wild birds, domestic animals and humans.
- 2 The disease is of huge economic, social, public health and wildlife conservation concern. The outbreaks in south-east Asia have already led to major economic losses and social disruption, and to some human infections, with over 50% mortality. Fears are constantly expressed that this virus could develop into the next human pandemic. Some scientists, international agencies and governments maintain that wild birds are implicated in the spread of the virus.
- 3 Avian influenza viruses circulate widely in wild bird populations, especially waterfowl, but infections are usually benign. Viruses that are highly pathogenic to poultry (HPAI) evolve in poultry from low pathogenicity avian influenza (LPAI) viruses that have probably been acquired from wild birds. HPAI viruses do not normally occur in wild birds. In the south-east Asian outbreaks, however, mutations led the virus to become highly pathogenic to domestic and wild waterfowl. Deaths of wild birds at some locations have led many people to believe that wild birds are responsible for spread among poultry but the evidence is circumstantial and unconvincing.
- 4 The current outbreaks were first recorded in 1997 in Hong Kong but the virus had presumably been circulating in the region, especially in southern China, before that. The disease has subsequently spread to Vietnam, Thailand, Cambodia, Lao PDR, Malaysia, Indonesia, Japan and Korea, and in 2005 north and north-west to northern China, Mongolia, Kazakhstan and Siberia. Over 150 million poultry have died or been slaughtered. Many wild birds have been found dead, including up to 10% of the world population of bar-headed geese, and fatal infections have been recorded in pigs, zoo animals and in humans. There is continuing evidence of change in the virus, through mutation and genetic re-assortment, leading to concern over the potential for the evolution of human-human transmission, raising the possibility of a human pandemic.
- 5 The general patterns of bird migration in Eurasia are described. Most migration flyways are north-south but some species, and individuals of some species, undertake migrations across longitudes. The opportunities for the spread of influenza virus between the major flyways are limited, however, and on this basis it seems unlikely that migrating birds will introduce the virus to western Europe. This risk is further reduced because at present H5N1 has been isolated only from dead or moribund wild birds, suggesting that it is highly lethal and that infected birds are unlikely to be capable of migration.
- 6 Evidence for the transmission of H5N1 to poultry by wild birds is entirely circumstantial, based on the isolation of the virus from dead wild birds, the similarity of virus strains in poultry and wild birds, limited association of some outbreaks in poultry with the time of bird migration, and the failure to find other possible sources of infection. Within south-east Asia, movements of poultry and poultry products are known to have been involved in the virus's spread among flocks and between countries. Evidence is presented here that show outbreaks to the north and west, including to Lake Quinghai (China), and in Kazakhstan and southern Russia, are all associated with connecting major road and rail routes. While this does not apply to outbreaks in Mongolia, this country imports poultry and poultry products from China and Russia, raising the possibility of the import of infection. The outbreaks in Kazakhstan, Mongolia and Russia occurred in summer, when most birds would be moulting and not undertaking long migrations.

- The involvement of wild birds in these outbreaks thus seems highly unlikely, whereas movements of poultry and poultry products seem to be a more plausible source of infection.
- 7 There is no evidence that H5N1 infection in humans has been acquired from wild birds. Human infections have occurred in people who have been closely associated with poultry. The virus has not proved efficient at passing from poultry to human and it remains unable to pass from human to human, with one possible exception.
 - 8 Culling has rarely been successful in eliminating or significantly reducing problems caused by wild birds. Culling is generally inefficient at reducing the size of bird populations and promotes the dispersal of survivors and potential recruits. We do not have the techniques to impose sufficiently high mortality, and sufficiently quickly, to manage disease outbreaks by killing wild bird hosts. Most of the techniques for culling are restricted in their use to specific periods of the birds' annual cycle and those techniques with the potential to kill large numbers of birds generally have associated environmental hazards.
 - 9 Contact activities that could promote the dissemination of H5N1 among wild birds include trapping, hunting, ringing and the keeping and movement of birds, especially waterfowl, in captivity and in outdoor collections where captive and wild birds can intermix. The risk of cross-infections between poultry and wild birds – in both directions – is facilitated by the keeping of poultry outdoors where food and water supplies attract wild birds, where drainage from poultry facilities enters wetland and when poultry are allowed to range into wetlands. If the H5N1 virus changes in a way that dramatically increases its host range to include passerines, pigeons and game birds, activities such as garden bird feeding, pigeon shows and racing and game rearing and release will need to be evaluated to maintain a clear separation from poultry. Similarly, if the virus attains the ability to pass readily from these birds to humans, the contact between these birds and their products and people must be minimised. Where contact is unavoidable, the need for personal hygiene measures will be paramount.

Remit and data sources

I was approached by Dr Andy Evans from the RSPB to review the outbreak of avian influenza in south-east Asia in order to assess its implications for wild birds there and, in the event of the disease spreading further afield, in the UK. The review covers two broad topics: A – the current outbreak of H5N1 and methods of spread, and B – a risk assessment including the potential and practicality of culling wild birds in disease management and human activities that could promote infections of wild birds and humans. Specific questions were asked and I have adopted these, with some minor changes, as section headings in the review below.

The H5N1 outbreak in south-east Asia is a recent event, probably commencing in 2002 with the emergence of a new strain of the virus, and the virus continues to evolve. As a result, recent observations have yet to appear in the peer-reviewed scientific literature. In order to make this review as up-to-date as possible I have relied extensively on material made available on the internet, especially by the agencies most actively involved in monitoring and controlling the spread of the virus. These are the Food and Agriculture Organisation and the World Health Organisation, both agencies of the United Nations, dealing respectively with agricultural and public health implications, together with the International Organisation for Animal Welfare. In addition, I have made use of current news items, both on the internet and in the popular press, such as the magazine *New Scientist*, which report events as soon as information becomes available. However, many of these reports are from unsubstantiated sources and are admittedly preliminary, awaiting further studies, especially the confirmation of identity of Influenza A sub-types and genetic variants. Where I refer to these, I make clear which facts are not substantiated.

Section A: a review of the current situation and events leading up to it

1 The disease and its causes

Influenza viruses exist in three basic types, A, B and C, which are recognised as separate genera within the Orthomyxoviridae (Alexander in press). Types B and C are normally infections of humans, whereas Influenza A viruses are typically infections of birds, with wild birds being the natural hosts of these viruses, but some can also infect mammals, including humans.

The taxonomy of Influenza A viruses is based on antigenic responses to two surface proteins, haemagglutinin (H) and neuraminidase (N). At present, 16 haemagglutinin and nine neuraminidase sub-types of these surface proteins are known, and are designated H1-16 and N1-9. Each virus contains one of each surface protein sub-type but any combination is apparently possible. The current outbreak in south-east Asia is of the H5N1 sub-type. Further separation of each sub-type is possible and is based on genetic variations found within the RNA genome of the virus.

Another separation of the sub-types is based on their pathogenicity to domestic poultry. Most sub-types are of relatively low pathogenicity and are designated Low Pathogenicity Avian Influenza (LPAI), while others, of H5 and H7 sub-types, regularly inflict massive mortality on poultry and are designated High Pathogenicity Avian Influenza (HPAI). Some H10 viruses fulfil the *in vivo* laboratory test for HPAI viruses. The East Asian H5N1 is a HPAI virus. It is not clear how the LPAI and HPAI categories relate to risk of infection in people but it is notable that the major pandemics of which we are aware have so far been caused by influenza A viruses of LPAI sub-types.

LPAI viruses circulate widely in wild bird populations and are also found in birds held as pets. Generally, wild birds do not become ill as a result of these infections but some HPAI viruses can inflict mortality in wild birds. Some species, notably ducks, show few or no signs of disease when infected with HPAI viruses. Virus is shed through faeces, saliva and nasal excretions and birds acquire infection through contact with these. Contraction of HPAI viruses by domestic poultry (chickens, turkeys, waterfowl) can lead to illness and death on a huge scale, as is occurring in some south-east Asian countries at present. Contraction of infection from wild birds requires contact between them and/or their excretions with poultry. As a result, the most vulnerable poultry flocks are those that are housed in the open and those that, although housed indoors, are accessible to wild birds or receive food and water from sources open to wild birds.

The disease can have three impacts on humans. In decreasing order of likely concern, these are:

- **Public health:** the imminence of a human pandemic was first mooted in 1997 and virologists, international agencies and others have continued to raise alarm over the likelihood of such an event. This will depend upon the virus evolving into a form that can pass readily from human to human. If this happens, and there is no sign at present, it has been predicted that many millions of people, especially young adults, will die worldwide, with at least 700,000 deaths in Britain.
- **Economy:** losses of poultry are already significant with >150 million (including both terrestrial and aquatic breeds) having died or been slaughtered so far. In countries that have the virus, this has had significant financial and social consequences, including the failure of poultry and associated businesses, especially smaller, village and private concerns, and food shortages. A consequence of slaughter policies has been the alleged hiding of sick and dead poultry in some countries in order to avoid loss of entire flocks. Further economic consequences arise from the banning by currently uninfected countries of poultry and poultry products from countries that are known to have the virus.

- **Wildlife conservation:** the virus at present appears to be lethal to some species of wild birds and its infection of endangered species could be catastrophic – it is estimated that up to 10% of the world population of bar-headed geese died at Lake Qinghai in China (discussed below). The most direct effect of human responses to outbreaks could be the call for culls of wild birds with the belief by many that wild birds are responsible for spreading the disease within and between countries. Such culls could reduce numbers of currently protected species, with potentially dangerous co-lateral consequences for some endangered species. Fear of the disease could engender fear of wild birds in the human population and widespread outbreaks in wild birds would limit the activities of researchers and conservation organisations.

2 Temporal and spatial analysis of the spread of the current outbreak

2.1 Earlier pandemics and outbreaks in poultry

In the 1970s, much interest was focused on the occurrence of influenza viruses in birds following the realisation that human pandemics might originate from avian influenza viruses (Webster & Laver 1975). The Influenza A pandemics of 1918–19 (H1N1), 1957–58 (H2N2), 1968–69 (H3N2) and 1977 (H1N1) all led to high human mortality and the last two of these outbreaks are known to have been caused by viruses containing a combination of genes from both human and avian influenza viruses (Alexander in press); the origin of the 1918 pandemic is unknown (CDC2005). These pandemics were first reported in Spain (but this pandemic probably originated elsewhere in Europe or in the USA – D Alexander, pers.comm), China, Hong Kong and Russia respectively. None of these three pandemics was caused by H5 or H7 viruses, which can be highly pathogenic in poultry.

In poultry, 29 outbreaks of HPAI viruses have been reported since 1959 (Table 1)(FAO 2005a). These outbreaks have covered all continents and 21 have occurred since 1990, 11 since 2000. However, there has been only one recorded outbreak in Africa, this occurring in farmed ostriches.

In addition to the data in Table 1, in China H5N1 viruses were reported from apparently healthy domestic ducks in 1999–2002, healthy poultry in markets in 2001–2004, from humans that had visited Fujian Province in 2003, and from pigs in 2001 and 2003 (FAO 2005a).

Since the initial outbreak in southern China, the epidemic has been seasonal, rather than continuous. Li *et al* (2004) noted the reduced survival of AI viruses at ambient temperatures above 20°C and the restriction of outbreaks to the northern winter.

Table 1 shows that the incidence of detected outbreaks of HPAI in poultry has apparently increased in recent years and that, since 2001, H5N1 viruses have become widespread in south-east Asian countries. FAO (2005) details six factors that have contributed to these trends:

- improved detection and surveillance
- changes in the virus and its host range
- increases in poultry populations in south-east Asia
- increase in intensification of poultry production
- increase in the severity of outbreaks associated with intensification
- possible influence of some climatic factors, especially localised drought.

These factors will be discussed in more detail below.

In addition to H5N1 sub-types, other AI sub-types have circulated in other parts of the world, most of low pathogenicity to poultry (Alexander 2002). In 2003, however, HPAI H7N7 caused extensive mortality in poultry in The Netherlands, along with infections, and a death, in humans (Koopmans *et al* 2004).

Table 1 Recorded outbreaks of HPAI in poultry since 1959

Date	Location	Virus sub-type	Crossed international or state boundaries?
1959	Scotland	H5N1	No
1963	England	H7N3	No
1966	Ontario, Canada	H5N9	No
1976	Victoria, Australia	H7N7	No
1979	Germany	H7N7	No
1983	Ireland	H5N8	No
1983	Pennsylvania, USA	H5N2	Yes
1985	Victoria, Australia	H7N7	No
1991	England	H5N1	No
1992	Victoria, Australia	H7N3	No
1994	Queensland, Australia	H7N3	No
1994	Mexico	H5N2	No
1995	Pakistan	H5N2	No
1996	China	H5N1	No
1997	NSW, Australia	H7N4	No
1997	Italy	H5N2	No
1997	Hong Kong	H5N1	No
1999	Italy	H7N1	No
2001–2005	China (incl. Hong Kong)	H5N1	Yes
2001–2004	Pakistan	H7N3	No
2002	Chile	H7N3	No
2003	Netherlands, Germany, Belgium	H7N7	Yes
2003–2004	Japan, Korea ¹	H5N1	Yes
2003–2005	China, Thailand, Vietnam, Cambodia, Lao PDR, Malaysia Indonesia, Mongolia, Kazakhstan, Russia ¹	H5N1	Yes
2004	South Africa	H5N2	No
2004	BC, Canada	H7N3	No
2004	Texas, USA	H5N2	No

¹The Japan/Korea and Thailand/Vietnam/Cambodia/Lao PDR/Malaysia outbreaks are considered to be separate since they involved different H5N1 genotypes.

2.2 Current outbreak – history and current status

The failure of the outbreak of H5N1 in poultry in Hong Kong in 1997 to spread further is considered to have been due to the prompt culling of the entire poultry population (WHO 2004), an action that was not taken on mainland China or elsewhere (FAO 2005a). Nevertheless, it is apparent that in China H5N1 viruses were circulating from 1996 to 2004 in apparently healthy domestic ducks and chickens, pigs and humans (FAO 2005a). Improved surveillance led to the discovery of avian influenza viruses prior to 2003 in bird markets in southern China and Vietnam (Chen *et al* 2002, Li *et al* 2004, Nguyen *et al* 2005) and subsequent studies have revealed that virus was likely to have been circulating at the same time in Thailand and Malaysia (FAO 2005a). Surveillance was further improved after the discovery of H5N1 in ducks and humans from late 2002 onwards.

The first recorded occurrence of the H5N1 HPAI virus subtype involved in the present outbreak followed the death of geese in Guangdong province, China, in 1996. The origin of this virus is unknown but is thought to have evolved from an LPAI virus that was circulating in wild waterbirds.

In the 1997 Hong Kong outbreak in poultry, several genotypes were already found to be present, indicating at this early stage the ability of the virus to mutate and also indicating the likelihood that the virus had already been circulating for some time. This outbreak involved chickens, inflicting mortality over 75%, but in addition 18 people in Hong Kong became infected, with six deaths (Sturm-Ramirez *et al* 2004). Further genetic changes have continued since then, accompanied by behavioural changes relating to variations in pathogenicity and host species infected (FAO 2005a).

Domestic ducks normally carry H5N1 HPAI viruses without showing signs of infection. A significant change in the virus in late 2002/early 2003 led to high pathogenicity to ducks, including wild ones, representing the first report of pathogenicity in wild aquatic birds of avian influenza viruses since 1961 (Sturm-Ramirez 2004). This was accompanied by systemic and respiratory infections, leading ducks to shed virus through nasal and salivary media, in addition to faeces. A subsequent further change has led to a reversion to asymptomatic infection of ducks, with an extension of the duration of shedding virus, up to 17 days (Hulse-Post *et al* 2005). In some south-east Asian countries, duck flocks are moved over considerable distances, including over provincial and international boundaries, to allow free-ranging flocks to graze on harvested rice fields (FAO 2005d). This allows them to contribute to weed, volunteer seed and snail control but also plays a major role in the transmission and maintenance of the HPAI virus (FAO (2005d). Reversion to asymptomatic infection within ducks has not been accompanied by any reduction of pathogenicity in chickens, while pathogenicity in mammals (experimental mice) has increased (Chen *et al* 2004). Such asymptomatic infection in ducks increases the risk of failure to detect virus spread in the absence of comprehensive surveillance and the extent of surveillance is highly variable in different south-east Asian countries.

The dominant form of the H5N1 sub-type that is responsible for most current outbreaks was christened the 'Z-genotype'. This was first seen in 2001 in a duck in Guangxi province, China, and this genotype, with continuing mutations, was found in domestic waterfowl in 2002–2004 (Li *et al* 2004). Variants of this genotype, and others, have circulated in poultry from at least 2001 in southern China and Hong Kong. Continuing evolution of H5N1 sub-types is thought to have been facilitated by the keeping of poultry in mixed species flocks of chickens and ducks/geese on farms and in markets, and the rearing of both terrestrial and aquatic poultry at high density and in close proximity in small enterprises where little biosecurity exists.

In Asia, the number of poultry has increased dramatically in recent years, and in some countries small enterprises have increased the size of their flocks without improving biosecurity. The HPAI infections have been demonstrated to be more prevalent in smaller village enterprises than in larger, industrial schemes where biosecurity is tighter. However, the distribution of outbreaks was related, in a study in Thailand, to the presence of free-ranging ducks rather than to the density of chickens (Gilbert *et al*, in preparation, cited in FAO 2005a). This could explain why HPAI outbreaks have been more prevalent in southern China, where poultry husbandry is mainly small-scale and in open premises, than further north where production is more industrial with better biosecurity.

The major outbreak of 2004, continuing into 2005, has resulted in a wider international spread of infections but the genetic constitution of the viruses has differed between regions. For example, the Z-genotype prevalent in southern China in 2004 differs from that found in the outbreak in Thailand/Vietnam/Lao PDR/Cambodia/Malaysia at the same time (FAO 2005a). As mentioned above, the virus prevalent in Korea and Japan differed further (V-genotype) and its origin is unknown. At present (August 2005), HPAI H5N1 viruses have been reported from China (including Hong Kong), Cambodia, Lao PDR, Vietnam, Thailand, Indonesia, Malaysia, Korea and Japan, with the most recent developments in July/August being north-west spread into Tibet (actually reported in June 2005), Mongolia, Kazakhstan and to six territories in Russia: Altai, Novosibirsk, Omsk, Tyumen, Kurgan, and Chelyabinsk (OIE 2005); this extends the range of the virus west to the southern Urals (WHO

2005b). The outbreak in Mongolia at Lake Ehrel is now known to have involved wild birds – a bar-headed goose and three whooper swans *Cygnus cygnus* (OIE 2005). Although there have been changes in the virus, viruses in all outbreaks are considered to be derived from the goose virus isolated in Guangdong province in 1996. Japan, Republic of Korea and Peninsular Malaysia are now (August 2005) reported to be clear of HPAI H5N1, but both Japan and Korea have now (2005) had outbreaks of LPAI H5N2 (OIE 2005).

In addition to birds and humans, south-east Asian H5N1 viruses have affected zoo animals. In Thailand, two tigers and two leopards died in a zoo at Suphanburi, Thailand, in December 2004, and were confirmed to have H5N1. In 2005, more than 100 Bengal tigers were claimed to have died in a zoo in Bangkok (Wilson 2004) but these deaths and their cause need confirmation. Anecdotal reports of fatal infection in domestic cats were explored by Kuiken *et al* (2004), who demonstrated experimentally that domestic cats could become infected, and that they excreted virus and could pass the infection horizontally. In addition, ferrets that were experimentally inoculated with H5N1 viruses of human and poultry origin became infected, some lethally, indicating that some other mammalian groups might be at risk (Govorkova *et al* 2005).

An important characteristic of the south-east Asian H5N1 virus is that it appears to have crossed directly from poultry to humans without prior evolution in another mammal. Earlier pandemics are believed to have arisen after AI underwent reassortment in pigs (Claas *et al* 1998), although direct evidence for this is still lacking (Peiris *et al* 2001). Pigs are susceptible to both avian and human viruses and this allows reassortment between them. In south-eastern China, contemporary human H3N2 viruses are now endemic in pigs and can reassort with H5N1 viruses in this intermediate host (Guan *et al* 2004). In addition, avian H9N2 viruses are circulating in pigs. H9N2 viruses are also circulating in poultry in the area and one of the strains, isolated from a quail *Coturnix coturnix*, is of particular concern since it contains internal genes that are closely related to the H5N1 sub-type isolated in 1997 in Hong Kong (Guan *et al* 2000) and led to infection in two humans (Lin *et al* 2000). A strain of H5N1 was isolated from pigs in Fujian province in 2001 and 2003, possibly acquired through contact with infected poultry or waterfowl or water contaminated by them (FAO 2005a). The role of pigs in current outbreaks is uncertain but the ability of viruses to reassort in them is cause for concern in relation to the prospect of H5N1 entering Europe, and of a human pandemic.

D Alexander (pers.comm) has summarised the problem in relation to pigs: 'Experimental and field evidence indicates that pigs are susceptible to avian influenza viruses. Genetic analyses of viruses currently circulating in the pig populations of most countries suggest their origins may be pig, avian or human. However, to date only viruses of H1 and H3 subtypes have been shown to become established in pig populations and readily pass from pig to pig causing disease. Evidence of other avian influenza subtypes infecting pigs does exist [H4, H5, H7, H9], but to date these infections have been transitory and the viruses have not become established in pig populations. Nevertheless there is still concern that such infections occur since if the pig infected with one of these was also infected with a human virus there is the theoretical possibility that reassortment of genes between the two could occur with the emergence of a virus potentially capable of causing a pandemic in humans. In East Asia there is evidence of infections of pigs with H5N1 virus, although, in view of the prevalence of the infections in poultry, surprisingly few reports. But the degree of surveillance in pigs is not known.'

In the UK, pig farmers are already concerned about the presence of birds feeding at piggeries, both in relation to the amount of food eaten by birds (eg rooks *Corvus frugilegus* – Feare 1974) and to the risk of disease (eg from starlings – Summers *et al* 1984). Many pig farmers operate biosecurity measures but in the event of H5N1 reaching Britain these should be reconsidered and extended. As with poultry, farmers who keep pigs outdoors would be particularly at risk. However, open-air piggeries

do not normally attract wildfowl but gulls sometimes feed there when food is broadcast on the ground, and could return to water bodies shared with waterfowl. The birds most commonly associated with open-air piggeries are corvids and starlings and these are not among the principal avian hosts for H5N1.

3 Occurrence of avian flu viral sub-types (especially H5N1) in wild birds and the risks they pose

The normal hosts of Influenza A viruses are wild birds and such viruses have been recorded in most bird families (Alexander 2000, 2002). Sub-types of most possible combinations of H1-16 and N1-9 have been recorded in wild birds where they are generally asymptomatic. The HPAI forms of sub-types H5 and H7, however, have not generally been found in wild birds (apart from H5N3 in common terns *Sterna hirundo* that died in South Africa – Becker 1966). In most wild bird families, avian influenza viruses occur at low incidences. In the Anseriformes (ducks, geese and swans), on the other hand, both the incidence of virus occurrence, and the range of sub-types found, by far exceed these parameters in other families. Hinshaw *et al* (1980) found that 60% of juvenile ducks, prior to their autumn migration, were positive for avian influenza viruses. Influenza A viruses occur at lower but nevertheless elevated frequencies also in the Charadriiformes (gulls, terns, waders etc). Kawaoka *et al* (1988) found that about half of sub-types present in Charadriiformes were capable of infecting ducks, but that the remainder were not. Nevertheless, Kawaoka *et al* concluded that shorebirds might be involved in disseminating the viruses to wild ducks and poultry. In relation to wild birds, the factor that makes the current H5N1 sub-type circulating in south-east Asia exceptional is its ability to kill aquatic birds, for the first time since 1961 (Sturm-Ramirez *et al* 2004).

The H5N1 strain that has been isolated from bar-headed geese *Anser indicus*, brown-headed gulls, *Larus brunneicephalus* great black-headed gulls *Larus ichthyaetus*, great cormorants *Phalacrocorax carbo* and ruddy shelducks *Tadorna ferruginea* that died at Lake Qinghai in north-central China has now been confirmed to be related to the genotypes circulating in poultry in southern China, as has the virus isolated from poultry around Novosibirsk in Russia (Niman 2005). Chen *et al* (2005) and Liu *et al* (2005) suggested that the virus was likely to have been picked up by some of the birds further south from contact with infected poultry or water used by them but D Alexander (pers.comm) thinks it is unlikely that infected and dying waterbirds could travel so far, and therefore that the infection was likely to have been contracted more locally. This is discussed in greater detail in section 5 below.

Other wild bird species that have been recorded with H5N1 in the current south-east Asian outbreak are the little cormorant *Phalacrocorax niger*, peregrine *Falco peregrinus*, little egret *Egretta garzetta*, grey heron *Ardea cinerea*, Chinese pond heron *Ardeola bacchus*, Asiatic open-billed stork *Anastomus oscitans*, black-headed gull *Larus ridibundus*, feral pigeon *Columba livia*, red-collared dove (? = red turtle dove *Streptopelia tranquebarica*), scaly-breasted munia *Lonchura punctulata*, black drongo *Dicrurus macrocercus*, tree sparrow *Passer montanus*, magpie *Pica pica* and crows *Corvus* sp (Ellis *et al* 2004, FAO 2005a). Of these, the little egret, Chinese pond heron and black-headed gull are migrants or partial migrants in south-east Asia, whereas the remainder are largely resident. This list includes six waterbird species and eight land birds; four of the latter are commensal with man and likely to abundant at poultry farms.

In relation to the risk of infection in other birds, it is notable that Ellis *et al* (2004) reported deaths from H5N1 of the following species in captivity in bird parks in Hong Kong: greater flamingo *Phoenicopterus ruber*, white-faced whistling duck *Dendrocygna viduata*, red-crested pochard *Netta ruffina*, wood duck *Aix sponsa*, Brazilian teal *Anas brasiliensis*, Bahama pintail *Anas bahamensis*, chestnut-breasted teal *Anas castanea*, Argentine shoveler *Anas platalea*, chiloe wigeon *Anas sibilatrix*, Puna teal *Anas versicolor*, ringed teal *Callonetta leucophrys*, maned wood duck *Chenonetta jubata*, rosybill pochard *Netta peposaca*, Hawaiian goose *Nesochen sandvicensi*, Canada goose *Branta canadensis*,

bar-headed goose *Anser indicus*, Coscoroba swan *Coscoroba coscoroba* and black-necked swan *Cygnus melanocoryphus*. The H5N1 strain circulating in Hong Kong in 2002–2003 was clearly highly pathogenic to a wide range of wildfowl species, along with flamingos.

In Europe, avian influenza viruses are also found predominantly in waterfowl. Fouchier *et al* (2003) isolated AI viruses of many sub-types from Anseriformes and Charadriiformes, but not other families, in a sample of 8,787 birds examined. Overall, 1% of birds were infected, but 10.6% of mallards *Anas platyrhynchos* (n = 132) were infected at one location in the Netherlands and 60% (n = 10) of black-headed gulls *Larus ridibundus* were infected in August at Ottenby, Sweden. In Denmark, AI infections have been detected in gulls, ducks and light-bellied brent geese *Branta bernicla hrota* (Therkildsen *et al* 2005). Arenas *et al* (1990) examined 331 birds in Spain and found 43% of waterbirds, 43% of greater flamingos and 31% of house sparrows *Passer domesticus* to be infected. The infected waterbird species included greylag goose *Anser anser*, shelduck *Tadorna tadorna*, mallard, pintail *Anas acuta*, gadwall *Anas strepera*, shoveler *Anas clypeata*, teal *Anas crecca*, pochard *Aythya ferina*, red-crested pochard *Netta rufina*, coot *Fulica atra* and black-headed gull. They also found antibodies in spoonbill *Platalea leucorodia*, crane *Grus grus*, grey heron and gulls. In Italy, de Marco *et al* (2003) found up to 80% of mallard to be seropositive for AI (mainly H1N1) in different flocks, and isolated virus from mallard and shelduck. The high proportion of mallard infected may have resulted from the rearing of mallard for hunting, so that some of the birds sampled could have been reared in captivity. These authors thought that the wintering areas of waterfowl in the Mediterranean area could be important in the circulation of viruses in migratory waterfowl in Europe.

Alexander (2002) noted that, although wild birds provide a widespread reservoir of influenza virus sub-types, the evidence for transmission to domestic poultry is largely circumstantial. This includes: higher infection rates in poultry on waterfowl migration routes and in poultry exposed to contact with wild waterfowl, the similarity of virus sub-types identified in poultry to those identified in waterfowl in the same area, and the seasonality of outbreaks coinciding with migration times. Where contact between wild birds and poultry is possible, however, transmission of influenza virus can be in both directions. The general absence of HPAI sub-types H5 and H7 in wild birds suggests that these sub-types evolve in poultry through mutations/recombinations of LPAI sub-types. Where wild birds have become infected with HPAI viruses these are (apart from the tern outbreak mentioned above) believed to have been acquired through contact with infected poultry or with facilities used by them.

In wild birds, indigenous influenza viruses appear to be largely benign; reports of mortality of wild birds from influenza are rare. In most cases where influenza-related deaths of wild birds have been reported, the pathogenic sub-types have been acquired from domestic poultry. However, since HPAI viruses in poultry evolve from LPAI viruses most likely acquired from wild birds, it could be argued that all influenza virus sub-types in wild birds are potentially dangerous in that they can, when introduced into poultry flocks, evolve into HPAI viruses. This is an extreme argument since, until the recent and ongoing outbreak in south-east Asia and north-west into Russia, such evolution has been relatively rare worldwide with relatively few HPAI outbreaks (see Table 1 above). The reason for this is that certain conditions in poultry management appear to favour the mutation/recombination necessary to produce the HPAI sub-types. In the current outbreak initiated in and centred upon southern China, factors that appear to have favoured the evolution of the H5N1 sub-types and genotypes include: small village enterprises in which poultry are maintained in the open with no biosecurity, close juxtaposition of flocks of chickens and waterfowl, maintenance of chickens and waterfowl at high density, further mixing of live chickens and waterfowl from different origins in bird markets (FAO 2005a). These conditions have been met in south-east Asia following a large increase in poultry production that has involved small producers as well as large industrial concerns.

A few studies have investigated the survival of AI viruses outside the bird host. Fitchner (1984) recorded a survival time of 105 days for HPAI H5N2 in a slurry pit in winter in Pennsylvania. Stallknecht *et al* (1990) examined the survival of four sub-types (H3N8, H4N6, H12N5 and H10N7 from ducks) in distilled water. At 28°C viruses survived up to 102 days, whereas at 17°C survival up to 207 days was recorded. There was a significant variation between sub-types, but the authors concluded that AI viruses were adapted to transmission among waterfowl on the wintering grounds, where mixing with poultry could be hazardous for the industry.

4 Migration patterns of bird species hosts

Migratory birds migrate in a wide variety of ways, including using different routes, timings, modes of migration and, especially relevant to the risks of transmitting avian influenza, different forms of social behaviour during their migrations. The principal reservoirs and potential vectors of AI, waterfowl, are to some extent constrained in their migration routes by the need for staging areas, where they can feed to renew energy for the next stage of the journey. Waterfowl are also highly social, migrating and feeding in flocks. The availability of places suitable for staging is limited and is becoming even more so as inland and coastal wetlands are reclaimed for various forms of human use. The migration routes of waterfowl are thus determined by the availability of staging areas and these staging areas are generally used also by other species of waterbird, such as herons/egrets, gulls/terns and shorebirds. Staging areas thus constitute places where large numbers of waterbirds assemble, with individuals spending some days there as they replenish their energy. These sites are sometimes used additionally for human activities, such as the rearing of fish and aquatic poultry (eg Mai Po marshes, Hong Kong). The limited geographical availability of staging areas means they are used by migrants from many origins and with many destinations, leading to a temporal and spatial mixing of birds on their flyways. Staging areas can therefore represent sites where conditions are favourable for the transmission of AI viruses, with the potential that these can then be transported by infected birds to the next staging area on the migration route, assuming that infected birds attempt to make that journey and survive it.

The potential for mixing of birds from widely different origins is, however, limited, because global migration routes have evolved along certain flyways (McClure 1974). These routes presumably maximise the birds' survival prospects through the availability of staging sites, favourable meteorological conditions and minimisation of energy expenditure. Eight major global flyways are recognised for northern migrants, four in Eurasia and four in the Americas: east Asian, Indo-Asian, Eastern European and western European in Eurasia, and Atlantic, Mississippi, central and Pacific in the Americas. In the Americas, all four flyways are channelled by geographical features through the Central America/Caribbean region. Here, birds from a wide range of longitudes in the nearctic and with a wide range of wintering areas in South America have the potential to mix at some stopover places.

The Eurasian situation differs in that migration routes remain largely separate in each of the flyways (McClure 1974). This reduces the risk of cross-flyway transmission of HPAI H5N1. Nevertheless, some birds have been recorded moving between flyways, eg the ringed pintail *Anas acuta* switching between the east Asian and American Pacific flyways (McClure 1974). Some migration routes do not conform to the standard flyways, eg broad-billed sandpipers *Limicola falcinellus* breeding in the north of the western European flyway and wintering in the eastern European and/or Indo-Asian flyways Hayman *et al* (1986). Generally, waterbirds do follow the accepted flyways and in Eurasia this limits the extent to which avian influenza viruses can be spread across longitudes by these migrants. Some waterfowl do nevertheless migrate across recognised flyways and in Europe the dark-bellied brent goose *Branta bernicla bernicla* and Bewick's swan *Cygnus bewickii* breed in northern Siberia but winter in western Europe; their migration route, however, takes them far to the north of the current outbreak of H5N1 in the southern Urals and staging areas tend to be coastal (Gibbons *et al* 2002). Recoveries of

ringed white-fronted geese *Anser albifrons* and bar-tailed godwits *Limosa lapponica* indicate that some individuals of these species originate from areas near to the current outbreak and reach Britain but most recoveries are from the west of the Urals. Several species of duck, eg mallard, teal *Anas crecca*, pintail, wigeon *Anas penelope*, shoveler *Anas clypeata*, tufted duck *Aythya fuligula* and pochard *Aythya ferina*, have recoveries indicating that a small proportion of birds that spend part of the year in Britain reach locations to the east and south of the Urals, but the numbers are small and most of the birds with connections to Britain remain within Europe (Wernham *et al* 2002). However, if small numbers from this region reach Britain, more are likely to reach eastern and central European countries. Most waders and gulls that reach Britain do not range to the east of the Urals. On this evidence, it seems unlikely that the spread of H5N1 to the east of the southern Urals poses an immediate threat of wildfowl or other waterbirds bringing the virus to the UK.

The spread of H5N1 to the southern Urals has brought the virus within the range of the eastern European flyway where the red-breasted goose *Branta ruficollis*, white-fronted and lesser white-fronted geese *Anser erythropus*, various species of duck (mallard, teal, pintail, wigeon, shoveler, tufted and pochard) and lapwing *Vanellus vanellus* migrate mainly south in winter. In addition, the eastern subspecies of the starling *Sturnus vulgaris poltaratskyi*, a numerous bird that feeds and roosts in flocks often in association with farm stock, migrates south to Afghanistan, Iran and the Middle East, reaching the eastern Mediterranean basin (Feare 1984). The current H5N1 outbreak thus presents greater potential risks to these regions than to western Europe.

Claims that the deaths of bar-headed geese from H5N1 in central China can, through their autumn migration to their wintering sites in Pakistan, India and Myanmar, pose a threat of the virus spreading to Europe (Chen *et al* 2005) are highly speculative and unlikely.

Transmission south along the east Asian flyway could, if birds survive the journey, take the virus toward Australasia (Liu *et al* 2005) but this would be via shorebirds, rather than waterfowl (Tracey *et al* 2004).

Birds that do not migrate in flocks, do not share stopover places for feeding and do not form localised concentrations at different stages of their journeys are less likely to become infected and to transmit AI viruses.

Along migration routes, conditions for the survival and transmissibility of the virus may vary. Li *et al* (2004) highlighted the seasonality of outbreaks in China, showing that all occur in the northern winter and stating that avian influenza viruses survive best when temperatures fall below 20°C. There are two implications of this for the prediction of likely spread of virus and the interpretation of associations of outbreaks with migration. First, poor survival above 20°C will reduce the risk of outbreaks on tropical staging areas of migrant waterfowl, and in neighbouring domestic poultry flocks. Second, outbreaks that are coincident with autumn southward migration may not be associated with wild bird movements, but may rather represent resurgences of viral transmission in already affected area as ambient temperature decline in autumn.

5 Evidence of transmission of avian flu from wild birds to domestic poultry and between infected flocks

As mentioned above, the evidence for the transmission of avian influenza in the current outbreak from wild birds to poultry is circumstantial (Alexander 2002). Despite claims by international agencies (eg FAO 2005f), governments and popular press, and even some scientists, that migrant wild birds have been responsible for the spread of H5N1, there is still no incontrovertible evidence that wild birds have been responsible for any outbreaks in poultry. Nevertheless, as wild birds constitute the principal reservoir of influenza viruses worldwide, it is assumed that the initial transfer to poultry

of an LPAI virus was indeed from wild birds. The HPAI H5N1 sub-type that is responsible for the current outbreak in domestic poultry is considered to have evolved within poultry, and is thus not likely to have been spread from wild birds in the first place.

Although there is now clear evidence of mortality in wild birds from H5N1 (Chen *et al* 2005, Liu *et al* 2005), there is currently no unequivocal evidence that H5N1 sub-types have been spread among poultry flocks by wild birds. The only case of H5N1's being identified from living birds involved two crested hawk-eagles *Spizaetus nipalensis* smuggled from Thailand to Belgium (van Borm *et al* 2005); all other isolates from wild birds have involved dead or moribund birds. The deaths of a large number of waterbirds of five species at Lake Qinghai, Qinghai Province in central China (Chen *et al* 2005, FAO 2005b, Liu *et al* 2005), and of bar-headed geese and whooper swans at Lake Erhel, Mongolia (OIE 2005), indicates that the virus sub-type is lethal to wild waterbirds. Mortality of captive waterbirds of a wide range of species had earlier been reported in Hong Kong parks (Ellis *et al* 2004). The incubation period in the wild waterbirds, the interval between initial infection and death and the proportion of birds that are killed and whether some wild birds carry the virus without perceivable sickness or change in behaviour are unknown. The fact that it is lethal to wild birds might reduce the extent of environmental contamination, compared with a non-lethal virus, and thus reduce the risk of spread via wild birds. This is a crucial point, and it is notable that H5N1 has so far only been isolated from *dead* wild birds (D Alexander, pers. comm.). Events following the Lake Qinghai outbreak, however, reveal a spread considerably further north-west into Siberia where the relative roles of wild birds and poultry or human movements are unclear (see below), but where wild birds have been widely assumed to have been responsible.

Sick and dead birds were first recorded at Lake Qinghai on 30 April 2005, and all birds involved at this stage were bar-headed geese, all on a single islet. By 4 May an estimated 100 birds were dying per day and by 20 May around 1,500 birds had died, some on other islets and 10% of other species (Chen *et al* 2005). The other species were brown-headed and great black-headed gulls (Chen *et al* 2005), ruddy shelducks and great cormorants (FAO 2005b). The later deaths of the gulls, ducks and cormorants suggest that they could have contracted the virus from the geese, but the possibility that they could have contracted the virus from the same source of the geese cannot be excluded. By July 2005, more than 6,000 birds were reported to have been killed (FAO 2005c). These dates suggest that birds died at the lake over a period of at least two months but there appears to have been no subsequent news from the area. Whether birds bred successfully this year does not appear to be known, nor does there appear to be information on the number of birds that have survived into the migration season. Chen *et al* (2005) concluded that the genotypes of the viruses isolated from the Lake Qinghai birds suggested that the geese had contracted the virus from domestic poultry in southern China. Chen *et al* (2005) claimed that there were no domestic poultry in the vicinity of the lake and yet some popular reports indicated that poultry in the area had been killed and that China was attempting to vaccinate three million birds in Qinghai province (CBC News 2005), clearly indicating the presence of poultry much closer than southern China. D Alexander (pers. comm) thinks that the geese are most likely to have picked up the virus locally from poultry. Further credence for this possibility comes from Chen *et al's* (2005) statement that they compared the viruses isolated from dead wild birds at Lake Qinghai with isolates collected in 2005 from poultry markets in Fujian, Guangdong, Hunan and Yunnan provinces: no outbreaks have been reported from these provinces by the Chinese authorities in 2005, suggesting that there could be significant under-reporting of such outbreaks. In support of this, in August 2005 an outbreak was reported near Lhasa, Tibet (OIE 2005), that had first been found in early June. This outbreak is on the migration route of bar-headed geese from India to its breeding grounds in north-west China and Mongolia, but even the Lhasa outbreak is a long way (c1,200 km) from Lake Qinghai. The outbreaks in southern China are well off the migration route of bar-headed geese (Cheng Tso-Hsin 1976, Madge & Burn 1988) but may be on the

routes used by the other four species found dead at lake Qinghai; the nearest reported outbreaks to the south for these birds are probably those in Thailand and Vietnam, c1,900 km away.

Lake Qinghai is an important breeding site for waterbirds and also an important staging area for waterbirds on the east Asian flyway. This raises the possibility of virus spread to Australasia, mainly by shorebirds as east Asian ducks do not reach Australasia (Tracey *et al* 2004), and to Myanmar and India, especially by bar-headed geese, when these birds migrate south. However, this contention must be regarded with caution at this stage since we do not know whether infected birds that are shedding virus will survive until the autumn migration, or if they do whether they will be able to travel long distances or whether the lethality of the virus will restrict its spread.

FAO (2005b) reported that there had been an outbreak of H5N1 in domestic geese from Tacheng, in the north of Xinjiang Province on the Kazakhstan border, in early June 2005 and by July H5N1 had been confirmed from four villages in the north of Kazakhstan in the Pavlovar area. According to WHO (2005b), 89 migratory birds (species not given) were found dead in early August 2005 at two lakes in northern Mongolia. The timing of this event does not coincide with migration from further south. The proximity of these waterfowl deaths to poultry enterprises has not been reported. Reports of an outbreak of avian influenza poultry in Russia in July have been confirmed as H5N1 and by late August this had included 35 localities in six Russian territories (WHO 2005b), extending west to the southern Ural Mountains. According to WHO (2005b), Russian poultry outbreaks have been blamed on wild birds, with poultry allegedly contracting the virus from shared water sources. At some Russian villages where outbreaks occurred in poultry, these poultry were apparently kept in homes close to wetlands where dead wild ducks had been found (OIE 2005). In the descriptions available so far, however, it appears that the virus has reached a few localities in Russia by unknown routes, but quickly spread from these foci around the local area in a manner that suggests human agency, eg poultry movements. A Yanovsky, of the Russian Academy of Sciences, reported that in the Novosibirsk region domestic ducks and geese are taken by day to forage in open water bodies where they mix with wild waterbirds, and are then taken back to their owners' premises at night, where they mix with chickens (Yanovsky, 2005, unpublished report sent to Richard Thomas, BirdLife UK). According to a RIA Novosti news report (12 August), local poultry farmers were hiding poultry in woodland in order to prevent veterinarians from finding them.

These areas are remote from the areas where H5N1 is now endemic in southern China and nearby countries, and the time of year and direction from earlier outbreaks suggest that bird migration was not involved; in fact at the time of the Russian and Kazakhstan outbreaks, most wild birds would be moulting and not undertaking long-distance movements. At this stage, the involvement of wild birds in the initiation of this outbreak cannot be completely ruled out but neither can spread by human agency. For example, it may not be coincidence that the localities with H5N1 of Novosibirsk, Kurgan and Omsk in Russia all lie along the Trans-Siberian Railway and also have good road links. The remaining three localities with outbreaks in Russia, Chelyabinsk, Tyumen and Altai, all have good rail and road connections with the Trans-Siberian Railway. The location of the H5N1 outbreak in Kazakhstan, Pavlovar, lies on major rail and road routes connecting the area with Altai. Kazakhstan also has main rail and road routes to the south-east that pass through Qinghai province in China; this major route passes through the city of Lanzhou, which has rail and road connections to towns that surround Lake Qinghai. Another of these road links passes through Tacheng, a Chinese border town that reported an outbreak in June 2005. There are thus possibilities for long-distance transport of poultry and poultry products between many of the centres that have had outbreaks of H5N1 during the summer of 2005. The possible exception is Lake Erhel, in Hövsgöl province, Mongolia, which has few road connections and no rail connection with other major routes. Nevertheless, the lake is very close to the Russian border and only about 200 km from industrial centres around Lake Baikal and major roads and the Trans-Siberian Railway that skirt the south of this lake. Mongolia has only a

small poultry industry but efforts are underway to increase production. At present, the country is a net importer of poultry and poultry products, including annual averages of 30 million eggs from China and 144 million eggs from Russia. Egg boxes are re-used without disinfection and, as poultry food is considered to be a major limiting factor for the industry (FAO 2005e), much of this is doubtless imported. The importation of poultry, eggs and food presents possibilities for the introduction of avian influenza from neighbouring countries and the possibility of acquisition of infection by wild waterbirds from local sources should not be dismissed.

The overwhelming evidence is that transmission of H5N1 between poultry flocks in south-east Asia stems from man's activities, involving:

- a big increase in poultry husbandry and its intensification in south-east Asia, including ducks, leading to high densities of poultry farms
- extensive movements of live and dead poultry and their products across provincial and national borders, both legally and illegally (includes eggs, which have been found to carry H5N1 [FAO 2005b])
- extensive movements of duck flocks to graze rice fields for volunteer, weed and snail control
- mixing of birds from different origins in live bird markets
- failure to ensure biosecurity – relates especially to small village enterprises
- failure to report poultry sickness and deaths and thus to facilitate speedy identification of virus and culling of infected flocks – this due to regular poultry losses from disease and possibly reluctance to risk having entire flock culled if H5N1 found
- failure to decontaminate transport media and people involved in transportation.

The occurrence of most outbreaks in central-southern Asia along major transport routes, and along directions and at times that do not correspond with wild bird movements, suggests that unrecorded movements of poultry and products must be considered seriously as likely factors in the summer spread of H5N1 infections to the north and west of known outbreaks in south-east Asia. Remarkably, this possibility was not mentioned in the most recent FAO report (2005f), which highlighted the 'potential', 'possible' and 'probable' involvement of migratory birds in the dissemination of HPAI over both long and short distances, saying only that 'unexplained factors other than shedding of AI viruses by migratory wild birds could possibly be at play in the dissemination of AI viruses'. Furthermore, the FAO model of HPAI spread in (FAO 2005f) did not include a possibility of spread from poultry to wild birds!

6 Evidence of transmission of the virus (especially H5N1) by wild birds between countries

There is currently no certain evidence of the spread of H5N1 by wild birds between countries (FAO 2005a). However, wild birds, rather than poultry, were killed at Lake Qinghai, China, and at Lake Erhel, Mongolia, and these outbreaks, in May and June 2005, were reported when wildfowl might have been migrating north. On the other hand, the Russian and Kazakhstan outbreaks, in July-August, were late for the arrival of migrants, especially at the relatively low latitudes involved (approx 50–55°N), and other potential sources could have been involved, as suggested above. Insufficient details are known about movements of poultry and their products, and of people, within and between these areas to exclude the possibility of human agency in these outbreaks. Nevertheless, the direction of passage of the virus between poultry and wild birds remains uncertain at this stage but human agency seems likely to have been involved in outbreaks in Kazakhstan and Russia, and cannot be totally excluded elsewhere.

An initial claim by Chinese authorities that bar-headed geese had brought AI into China from their wintering areas in India (Anon 2005a) was erroneous: there have been no reports of AI from India and

the genotype of the H5N1 sub-type found in the dead geese was subsequently found to be allied to viruses isolated from poultry in southern China (Chen *et al* 2005, Liu *et al* 2005).

The origin of the H5N1 outbreak in Japan and Korea is unknown. Viruses with the characteristics of the genotype in that outbreak have not been found in wild birds (apart from some crows found dead at affected farms), and the timing of the outbreak did not match the time of bird migration from the south; no infections with this virus strain are known from regions to the north. Up to the January before the March 2003 outbreak in Japan, however, there had been imports of poultry from China (D Alexander, pers. comm).

7 Evidence of transmission of the virus (especially H5N1) from wild birds to humans

There is no evidence that the viruses circulating in south-east Asia have been transmitted from wild birds to humans (FAO 2005). Unequivocal demonstration of such transmission is difficult, however, since the acquiring of an infection by a human is usually not traceable to a specific contact with a wild bird (Feare *et al* 1999) and many cases of bird-human disease transmission must go unrecorded. In the current outbreak, however, most cases have clearly been through contact with poultry (see below).

8 Description of the outbreaks among human populations in the last five years

As mentioned above, the four major human Influenza A pandemics were caused by H1N1 (1918–19), H2N2 (1957–58), H3N2 (1968–69), and H1N1 (1977), none of which are HPAI sub-types (Alexander in press). The 1997 H5N1 outbreak in Hong Kong was an indication that avian influenza viruses could be transmitted to man without prior reassortment in a mammalian host or with a human virus and could cause severe disease in humans (Sturm-Ramirez *et al* 2004); examples of this are rare (Alexander, in press). During this outbreak, 18 humans were infected and six of these died. During the 2002–2003 outbreak in Hong Kong, two more human cases were confirmed and one of these died; these people had recently visited a poultry area in Fujian province, China. By 23 July 2005, there had been 110 reported cases of confirmed H5N1 infection in humans, with 55 fatalities, from December 2003 to the present (Table 2). These were in Vietnam, Thailand, Cambodia and Indonesia. The apparent absence of cases from China is surprising but may result from failure to report human infections either unwittingly or deliberately.

In addition to H5N1, an outbreak of HPAI H7N7 in the Netherlands in 2003 led to the death of a veterinarian and mild illness in 83 other people, and in Hong Kong mild cases of LPAI H9N2 occurred in children in 1999 (two cases) and 2003 (one case) (WHO 2004, Alexander, in press).

Table 2 - number of confirmed human cases of H5N1 infection in south-east Asia up to 5 August 2005 (FAO 2005b, WHO 2005a)

Date of onset	Vietnam		Thailand		Cambodia		Indonesia		Total	
	Cases	Deaths	Cases	Deaths	Cases	Deaths	Cases	Deaths	Cases	Deaths
Dec 03–Mar 04	23	16	12	8	0	0	0	0	35	24
Jul 04–Oct 04	4	4	5	4	0	0	0	0	9	8
Dec 04–Aug 05	63	20	0	0	4	4	1	1	68	25
Total	90	40	17	12	4	4	1	1	112	57

9 Evidence for transmission of the virus between infected poultry and humans

I have not found a breakdown of human cases of H5N1 infection relating them to possible sources of infection. However, general statements indicate that the majority of human infections have been in people who have regular contact with poultry, and in particular people who have been in the vicinity of sick or dying poultry (CDC2004, FAO 2005a). WHO (2004) states that, 'Extensive investigation of that [Hong Kong 1997] outbreak determined that close contact with live infected poultry was the source of human infection'.

Given the number and distribution of outbreaks in domestic poultry and waterfowl, the number of human cases is very small, indicating that the transmission of the virus from poultry to man remains inefficient.

10 Evidence for human to human transmission

Efficient human to human transmission of AI is a prerequisite for a pandemic. So far, human to human transmission appears inefficient (Wilson 2005) and there is only one likely example, involving two cases in a family cluster. Ungchusak *et al* (2005) reported that in Thailand, in September 2004, an 11-year-old child had become ill 3–4 days after playing and sleeping in an area that had housed dying chickens. Before her death, the child was cared for in hospital by her mother and an aunt, neither of whom had had recent contact with poultry. Both carers became ill and the mother died; both were confirmed positive for H5N1, the genotype of which was closely similar to strains that were circulating in Thai poultry.

A second possible case of human to human transmission has been reported in 2005 from Indonesia; this case also represents the first fatal human case from Indonesia. Two young girls became ill with pneumonia in late June 2005 and both died. Their father became ill on 2 July and died on 12 July, and was confirmed to have been infected with H5N1. Samples from the two daughters are still awaiting analysis (as at 23 July 2005). Four other members of the household have not shown any symptoms so far and the source of the infection has yet to be traced (WHO 2005a).

WHO (2004) reported that limited transmission from infected humans to healthcare workers had occurred but no details were given.

Section B: risk analysis

1 General

Before answering the questions posed, I think some general points must be made. First, if H5N1 reaches Europe, there is likely to be a general panic, fuelled especially by statements from ill-informed politicians and the popular press, who will doubtless look for any scapegoats which will include wild birds. The degree of alarm will to some extent be related to the stage of evolution of the virus when it arrives. The RSPB, and others, will need to be able to counter inevitable calls for culls.

If first reports of the virus emanate from surveillance of wild birds, and the infections are asymptomatic, a risk of transfer to poultry, with potentially huge economic ramifications, and to humans, raising major public health concerns, will both be raised. Both will create alarm and are likely to lead to calls for culls of wild birds. If wild birds die in large numbers from the infections, the demand for culls will be more immediate, while at the same time there will be concern from the standpoint of declining bird populations and the risk of further declines.

If infections are first recorded in poultry, either asymptotically or with mortality, there will be widespread culls of affected and nearby poultry flocks (Defra contingency plan). Farmers, and possibly vets, are likely to call for culls of wild birds, as in the last foot-and-mouth epidemic in the UK. There are also likely to be similar calls from the wider public due to perceived risks to human health.

If, on the other hand, H5N1 is first recorded in the human population, this is likely to be a reflection of the evolution in the virus of a capability of human to human infection and the realistic emergence of a pandemic. Under this scenario, isolation of infected people and immunisation (assuming the availability of vaccines) will take precedence. However, the association of the virus with wild birds will doubtless still be raised, but I suspect that calls for culls will be lower key as infected people will be the feared source of virus.

In my responses to the questions raised by the RSPB, I shall group those relating to culls together and add a section on the objectives and feasibility of culls, since this discussion will influence the responses to later questions on human contact with wild birds and the possible impacts of various H5N1 scenarios on RSPB policy.

2 Questions relating to culls

2.1 Is there any evidence that wild birds can spread avian influenza between poultry flocks within or between countries?

In section A, I concluded that there is no incontrovertible evidence that birds can spread AI between poultry flocks and between countries, and that most of the spread in south-east Asia is likely to have been the result of human activity. However, in the outbreaks in poultry at Tacheng, in the north of Xinjiang Province, and in Siberia even further to the north, both to the north of Lake Qinqhai, Qinqhai Province where deaths of wild geese and other birds were recorded, a role for wild birds cannot be excluded. As wild birds, especially waterfowl and shorebirds, are the primary reservoir of AI viruses, wild birds can theoretically be implicated in transmission, a hypothesis given more credence in the current epidemic where this H5N1 virus has certainly been transmitted to wild birds from poultry.

2.2 Is there any evidence that wild birds can transmit the virus to humans?

No. However, as with other diseases, it is very difficult to link an infection in a human with that in a wild bird. Infection by this route is feasible, although currently remains a remote possibility.

2.3 If wild bird culls were to be implemented in infected countries/regions, which species would be most at risk from a conservation standpoint?

As waterbirds are the species most widely infected with AI viruses, these are the groups that would be most likely to be targeted in the event of an outbreak. In Thailand there have already been calls by the Prime Minister for culls of Asian open-billed storks, despite lack of any facts implicating their involvement in virus spread (BirdLife 2004), and measures taken to control the outbreak in Kazakhstan include 'control of wildlife reservoirs' but no details have been given (OIE 2005). So far, most deaths of waterbirds have occurred on inland wetlands. The virus can survive in water for prolonged periods (Fichner 1984), especially at low temperatures (Stallknecht *et al* 1990). Virus survival has not, however, been assessed under natural conditions in wetlands or in brackish or sea water. AI viruses might be capable of surviving between seasons in some wintering areas but in estuaries and on coasts tidal flushing might reduce virus survival or dilute concentrations to the extent that infection of birds would be rare. It therefore seems most likely that waterbirds that prefer inland wetlands will become infected, and it is therefore here that attempted culls are most likely to be targeted.

In terms of conservation, species with small populations (especially declining), localised distribution and use of inland wetland habitats shared by man and poultry at some stage of their life cycle would be most vulnerable to the effects of culls. Risks to resident species with these characteristics would be especially severe, whereas threats of culls of migrants would have an international perspective, particularly as some countries along the migration route might support culls while other countries might object. It is unlikely that rare birds would be specifically targeted but some rare species could be vulnerable to non-selective large-scale culls aimed at reducing numbers of more abundant species (Table 3).

Table 3. Rare waterbirds that could be vulnerable to population reductions due to infection with avian influenza H5N1 or to non-selective culls, on the assumption that AI infections and culls are most likely at inland wetlands.

Europe and central Asia	East Asia
Pygmy cormorant <i>Phapacrocorax pygmaeus</i>	Bar-headed goose <i>Anser indicus</i>
Dalmatian pelican <i>Pelecanus crispus</i>	Swan goose <i>Anser cygnoides</i>
Red-breasted goose <i>Branta ruficollis</i>	Mandarin <i>Aix galericulata</i>
White-headed duck <i>Oxyura leucocephala</i>	Black-faced spoonbill <i>Platalea minor</i>
Marbled teal <i>Marmonetta angustirostris</i>	Spotted greenshank <i>Tringa guttifer</i>
Crested coot <i>Fulica cristata</i>	Asiatic dowitcher <i>Limnodromus semipalmatus</i>
Slender-billed curlew <i>Numenius tenuirostris</i>	Spoon-billed sandpiper <i>Eurynorhynchus pygmaeus</i>
	Saunders' gull <i>Larus saundersi</i>

If the virus evolves the ability to infect a wider range of bird species, more species could be threatened with culls. For example, several species of farmland bird in Europe have undergone significant declines in the latter part of the 20th century and some of these declines continue. Species that feed in association with domestic stock, especially poultry and pigs, are likely to be regarded by farmers as suspect. This could affect species such as starlings, house sparrows, rooks, jackdaws and, especially in coastal areas, gulls and geese. Of these, the starling, house sparrow and herring gull *Larus argentatus* are already in serious decline. If the virus did change, however, the main threat to these species would be from infection with the virus, rather than from attempted culls.

2.4 The practice of culling – objectives, techniques, efficacy, hazards

2.4.1 Objectives and legitimacy of culling

The objective of culling birds is to reduce a problem, not to reduce the number of birds for its own sake. There have been many attempts to reduce the number of birds on the assumption that removing individuals will reduce a problem. Rarely, however, has the effect of attempts to reduce numbers on problem reduction been measured and where it has, the problems have rarely been reduced (Feare 1991). In the EU, all wild birds, together with their nests and eggs, are protected under the Birds Directive of 1979. Exemptions from total protection are permitted, especially for the hunting of certain species. Member states may also derogate from parts of the legislation to accommodate local specific needs, which can include the control of birds that are causing problems. In the UK, such problems include risks to human and animal health. Under the UK derogation, birds on a list of 11 species may be killed under a general licence where there is no alternative to resolving the problems. Wildfowl, however, are not included in this list and special licences would be needed to kill them on public or animal health grounds. In addition, techniques other than shooting and trapping would require special licences.

2.4.2 Culling techniques

When birds are killed in an attempt to resolve problems that they are alleged to cause, the aim of pest controllers (which can include professional pest controllers, government or international agencies, together with farmers, landowners and sometimes private individuals) is generally to kill as many as possible of the offending species in the belief that reduction in damage will be proportional to the reduction in numbers achieved. Even though there has been an acceptance among scientists that killing generally fails to produce a level of mortality capable of reducing pest populations over large areas (Ward 1979, White *et al* 1985, Dolbeer 1988, Haag-Wackernagel 1995, Feare 1991, 2004), outbreaks of damage are still frequently accompanied by calls for the killing of birds believed to be responsible, as in the recent foot-and-mouth outbreak in the UK and the current avian influenza outbreak in Thailand. The techniques available vary in sophistication and efficacy, and in the number of birds that are likely to be killed. Individual birds, local populations responsible for damage (eg roosts, colonies) or entire populations may be targeted. In the discussion below, I shall omit consideration of egg and nest removal, and also of chemo- and immuno-sterilants, since by their nature these can at best only be long-term population reduction measures, which would be inappropriate in the event of an avian influenza outbreak.

2.4.2.1 Shooting

Shooting, by means of shotguns or rifles, is generally capable of controlling only small numbers of birds. It can be useful in killing individuals, for example birds that appear to specialise in predation of particular prey or of prey at particular locations, or for eliminating individuals that are particularly aggressive to humans, e.g. some gulls and geese. Larger numbers can sometimes be killed using more specialist shooting techniques, eg the shooting of 'brancher' rooks *Corvus frugilegus* [pulli that have left the nest but still cannot fly well] or the night shooting of feral pigeons, both using small calibre rifles, ideally with telescopic sights and, for night shooting, some form of target illumination. More general shooting is limited in its efficacy by the ability of birds to learn quickly to associate the sight and sound of guns with danger and thus to avoid their proximity. This can lead to bias in the kinds of bird that can be killed, with naïve, young or underweight individuals being most susceptible. While shooting offers a degree of selectivity, as long as the shooters can identify the target species, it is not a useful technique for killing large numbers of birds in order to reduce numbers quickly.

2.4.2.2 Trapping

Trapping involves the attraction of birds to bait within a trap or within a catching area of a net. Once caught, target birds can be humanely killed while non-target species can be released; trapping thus offers selectivity. However, the enticement birds to bait within or adjacent to a novel object raises two problems. First, the bait must be of sufficient attractiveness and acceptability to divert birds from their usual foods in the surrounding area and, second, the bait must be sufficiently attractive for the birds to overcome their natural wariness of novel objects. As a result of these constraints, birds are most easily trapped when natural foods are in short supply and the birds that are caught tend to be biased towards the hungriest and youngest members of the population, which may well be those that would in any case starve during periods of food shortage (Dunnet & Patterson 1968, Murton 1968, Feare *et al* 1974). In terms of responding to a disease outbreak, therefore, trapping is unsuitable as it catches relatively small numbers and is time-dependent in its efficacy.

2.4.2.3 Round-up and kill (waterfowl)

During their annual moult, waterfowl are unusual among birds in that they moult their primaries and secondaries simultaneously, rendering them flightless for a short period. At this time, they can be herded on the water bodies where they are moulting, driven into corrals and humanely killed. The main constraints on this technique are its extreme time-dependency, a window of only 2–3 weeks per year, and the specialist people needed both for the round-up and the killing, especially where large

waterfowl are involved. These problems would render such round-ups of limited value in killing large numbers of waterfowl during a disease outbreak.

2.4.2.4 Explosives

Explosives have been used in Europe in attempts to reduce starling *Sturnus vulgaris* numbers in cherry-growing regions of Belgium, and are used to kill red-billed queleas *Quelea quelea* in Africa to reduce crop damage. In Belgium, dynamite was exploded within the night roosts of starlings, mainly juveniles, and some amelioration of local damage was believed to have been achieved (Tahon 1986). Insufficient birds were killed, however, to achieve any long-term reduction in the starling population of the area of the country concerned and in the damage caused (Feare 1991). In many parts of sub-Saharan African savanna, queleas are subjected to a barrage of lethal techniques, now aimed at reducing populations close to vulnerable crops (see 'Poisons' below). Large numbers can be killed using explosives and the method has the advantage in Africa of requiring less specialised techniques and staff than poisoning. The proportion of a roosting assemblage that can be killed using explosives is highly variable (Meinzingen *et al* 1989) and they do not offer a reliable way of reducing local populations, let alone achieving long-term reduction of numbers. In Belgium, the use of dynamite apparently caused little damage to the habitats where starlings roosted (Tahon 1986) but damage to quelea roosts in wetlands might have longer term implications for other wildlife (but this must be considered in relation to perhaps more immediate food needs in parts of Africa).

2.4.2.5 Poisons

Poisons are used in the Americas and in Africa in attempts to resolve agricultural and public health concerns. Species that feed in flocks and/or roost communally at night are targeted, both while feeding and roosting. In Africa, granivorous birds, especially quelea, are sprayed with contact poisons from the air in breeding colonies or communal roosts, while in the Americas the main targets are 'blackbirds', including icterids (mainly the red-winged blackbird *Ageialius phoeniceus*) and starlings as they assemble in large flocks prior to returning to the night roost.

The spraying of quelea, from fixed-wing aircraft or helicopters, is accomplished using the organophosphorus compound fenthion. Huge numbers can be killed, offering temporary alleviation of damage to crops within the commuting range of the colony or roost, but achieving no long-term reduction in the overall quelea population (Ward 1979), so that treatments must be repeated if immigration leads to further damage while crops are vulnerable, or if crops are damaged in succeeding years. Failure to achieve adequate kills can result from disturbance caused by the aircraft, failure to delineate areas to be sprayed accurately, and wind drifting spray away from the target area, but especially from inability to locate all roosts and colonies. A variety of non-target wildlife is susceptible to both primary and secondary poisoning.

In the US, culls of blackbirds are achieved mainly by baiting pre-roost assembly areas with seed treated with a toxicant DRC-1339 (3-chloro-4-methylalanine), often called 'starlicide' on account of its initial development in the 1960s to control starling numbers. Prior to returning to the night roost site, 'blackbirds' and starlings feed intensively on abundances of energy-rich seeds and can be attracted to treated baits, resulting in extensive mortality. Death is through kidney failure and can take 3–4 days, so that birds do not develop an aversion to the bait (Besser *et al* 1967). Other seed-eating birds are susceptible to primary poisoning (Blackwell *et al* 2003), but the compound is completely metabolised and is not regarded as a secondary poisoning threat. DRC-1339 is currently being considered to kill red-winged blackbirds in the Dakotas, where they damage ripening sunflower crops. An intention, which is probably achievable, to kill c2 million birds annually (out of an estimated 27 million birds) close to roosts on their spring staging areas, has been evaluated by Blackwell *et al* (2003), who concluded that economic benefits to the sunflower industry from these culls would be negligible.

Smaller-scale programmes aimed at killing starlings in winter roosts by aerial spraying in France (ACTA/INRA/SPV 1987) similarly failed to achieve the intended aim of reducing agricultural damage (Feare *et al* 1992).

The failure of these mass-killing programmes to achieve their management goals stems from man's inability to kill sufficient of the target birds to overcome compensatory responses in the species' demography. With common birds that have a high natural turnover (high fecundity and high annual mortality), we do not have the technology to achieve rates of killing that exceed the birds' capacity to replace the numbers killed, in the short-term through immigration and in the longer term through their fecundity.

2.4.2.6 Stupeficients

Stupeficients are chemicals that on ingestion by a bird induce sleep. Narcotised birds can be picked up and humanly killed but the technique offers some selectivity in that non-target birds that are affected can often be revived by keeping them warm and subsequently released. Stupeficients, notably alphachloralose, can sometimes be used to catch particular nuisance individuals, eg unusually aggressive Canada geese or gulls that pester humans for food but more usually they are used in the UK in attempts to reduce local populations of birds that cause damage, eg feral pigeons and house sparrows in food stores and roof-nesting gulls in towns, or gulls in colonies where they are believed to interfere with other, 'more desirable', birds. The main problem lies in the need for the chemical to be ingested. As with other baits, target birds need to be lured from their natural foods to take the stupeficient-treated bait and in many situations, eg food stores and on farms, this can be difficult as the birds' usual food can be superabundant. Additionally, alphachloralose and other stupeficient chemicals have distinctive tastes, detection of which can render target birds averse to the baits. Furthermore, affected birds take time, usually c0.5 h, to succumb, during which they may disperse, and when affected they behave abnormally, especially in flight, which can lead to public concern. In an experiment on a farm where starlings were taking cattle food, the removal of c50% of the birds failed to resolve the problem as within days of the stupeficient treatment, immigration from other areas led to the recovery of the farm population of starlings (Feare *et al* 1981). These problems have led to reduced usage of this technique, caused by reduced demand for it and by increased reluctance of licensing authorities to permit its use.

2.4.2.7 Surfactants

Surfactants are chemicals that remove the waterproofing/insulation properties of birds' feathers so that subsequent wetting induces hypothermia and death. They can be sprayed on to roosting birds at night, in the expectation of subsequent cold ambient temperature and rainfall, or followed by spraying with water. During 19 years of use in the USA, an estimated 38.2 million 'blackbirds' and starlings were killed, but this represented less than 1.3% of the populations. There was no effect on national winter populations or on regional breeding populations (Dolbeer *et al* 1997). The technique was, however, considered useful for elimination roosts close to human habitation, where the guano in these roosts constituted a health hazard through providing a growth medium for the fungus *Histoplasma capsulatum*, which can cause respiratory disease in humans (Tosh *et al* 1970, Garner 1978). The spraying of surfactants does cause disturbance and some birds escape the treatment; these are available to move elsewhere and establish new foci of *Histoplasma* infection. The use of surfactants is limited by dependence on time (large numbers can be killed only when communal night roosts are large, ie in winter) and to some extent on weather (cold nights are usually needed).

2.4.3 Culling efficacy and side effects

If killing wild birds were to be used to eliminate potential sources of infection of H5N1, the killing would have to eliminate the majority of affected populations very quickly before they could spread the disease further. None of the techniques available for killing wild birds is capable of achieving this.

Even where mass-killing techniques have been used over several years they have generally failed to reduce overall population size, and have even failed to reduce local populations for any significant length of time due to the birds' abilities to repopulate attractive areas very quickly through immigration. At waterbird staging areas, any killing programme would need to be repeated at regular intervals in order to remove birds as they arrived on their migration. This could lead to regular severe disturbance, leading arriving birds to avoid the traditional staging areas in search of alternative, thereby spreading the risk of infection.

Dispersal has been demonstrated to follow attempts to reduce local gull populations through culling. Breeding adult gulls that avoid being killed tend to remain in the colony, but birds that are about to recruit to a colony being culled may be deterred by reduced nest density of surviving birds and decide to seek nest sites elsewhere. While the target colony may decline, colonies elsewhere may increase or be established within the dispersal range of the target colony (Coulson 1991, Bosch *et al* 2000). In addition to effects on dispersal, Duncan (1978) and Coulson *et al* (1982) found significant effects on demographic and morphological parameters of gulls that were thought to represent responses to reduced density-dependent factors. The consequences of killing breeding gulls can therefore be wide ranging and long lasting, but the dispersal of birds about to recruit can be immediate, leading to the dispersal of infected birds, should these survive long enough to be able to disperse. Biases in the age, sex and social status of birds that are killed may reduce the efficiency of culls in terms of population reduction, but if weaker birds are more susceptible to infection (this is not known for H5N1), techniques such as trapping and shooting might select for infected birds. However, the inefficiency of these techniques in killing large numbers of birds renders them unusable in disease management.

Most killing techniques involve severe disturbance and none of the techniques is totally efficient. Varying numbers of surviving birds are thus able to respond quickly by moving to less disturbed areas where they may establish new foci of infection, again assuming that infected birds survive long enough to do so.

Finally, killing techniques that permit the culling of large numbers of birds are unselective, rendering any birds within the target area to be killed, posing potential dangers for rare birds, such as those in Table 3, whose rarity renders them an unlikely source of infection. Additionally, the use of poisons and surfactants can have important secondary effects leading to environmental contamination lasting longer than that required for the culls.

2.4.4 Conclusion

Several techniques are available for killing wild birds, varying in the number of birds that can be killed, the selectivity of the target species, side-effects on the demography of the target species, and effectiveness in resolving the perceived problem. In addition, there is wide variation in the cost of the different techniques and in the expertise and technology required to use them. In general, the simplest and cheapest techniques offer the greatest selectivity but these are the least effective in killing large numbers of target species. Most techniques are to a greater or lesser extent time-specific, in that target birds are amenable to capture/killing only at certain stages of their life cycle. The more specialised techniques require staff trained in their use. These impose serious constraints on the utility of killing in order to combat a disease outbreak, when calls from politicians and the public would be for immediate action.

If H5N1 reaches Britain and the disease in wildlife follows patterns seen earlier, the species most likely to be affected, and thus the species most likely to be considered a threat in terms of further spread, are waterfowl, gulls and waders. Waterfowl, especially geese, are a special case in that it is possible, with adequate trained staff and appropriate equipment, to catch and kill large numbers

during the annual moult, with little chance of disturbance causing significant dispersal. At other times of year, and with waterfowl that do not flock together to the same extent for the moult, alternative killing techniques would be required. These would be less effective and less selective.

In summary, the killing of wild birds, in attempts to remove a perceived threat of the spread of avian influenza among poultry or to humans, is very unlikely to achieve this objective owing to the practical difficulties of achieving adequate kills of the target species over a very short period. We simply do not have the ability to kill birds to reduce their numbers sufficiently, and over a large enough geographical area, to remove such a threat, if indeed this threat really exists. The primary mechanism of spread of avian influenza viruses at present is via movements of poultry and poultry products, and contamination of people and vehicles used for transport or of water sources at poultry-rearing facilities. In view of this mode of spread, the most effective means of containing the virus is to ensure adequate biosecurity at all stages of the poultry production and distribution cycle. In most parts of the EU, biosecurity is already an integral part of poultry production, to guard against AI and other diseases. The most vulnerable part of the industry would be the free-range sector; here, improvements in biosecurity, for example by erecting enclosures of sufficient size over outdoor ranging areas and ensuring disinfection of all incoming materials, would again be more reliable in reducing the threat of AI infection than attempted palliative culls of wild birds. According to WHO (2005b), the major international agencies, WHO, FAO and OIE, involved in the monitoring and eradication of the H5N1 virus agree that the control of avian influenza in wild birds is not feasible *and should not be attempted*.

2.5 What contact activities could facilitate the spread of avian flu from wild birds to humans? Possibilities include hunting, trapping, ringing etc.

2.5.1 Hunting, trapping and ringing

All of these activities involve handling wild birds, leading to direct exposure to faeces, which may dry on skin and clothing, and to respiratory aerosols. Without appropriate protection, such as disposable protective clothing, the wearing of respirators and adequate washing, there is a risk of ingestion or inhalation of infective material from birds excreting influenza virus. In areas where H5N1 (and other sub-types known to transmit directly from birds to man) is known to occur, people indulging in these activities must be aware of the risks and advised to take necessary precautions or curtail these activities.

2.5.2 Bird keeping

Bird keeping takes many forms, including indoor caged (for most of the time) pets, the maintenance of raptors for falconry, the rearing of game birds for hunting, the keeping of birds in zoos and waterfowl collections and the breeding and maintenance of pigeons for show and racing. The keeping of birds as pets, and the trade associated with this practice, is the subject of a separate report for the RSPCA by Dennis Alexander.

The keeping of birds in captivity presents risks to humans, especially their keepers, of acquiring infections if the birds are not isolated from infected wild birds. Thus birds kept within houses are likely to be more secure than birds kept in outdoor aviaries where contact with wild birds and their products is feasible. Birds that are kept in a free-flying condition pose an even greater risk, for such birds can mix with similarly free-flying flocks of the same species, with wild birds, and can share food and water supplies with wild birds.

2.5.3 Waterfowl collections

Given the propensity of Anseriform species to host avian influenza viruses, waterfowl collections that have free-flying birds, and which also attract wild waterfowl, could represent potential threats to

keepers and visitors. Waterfowl collections could thus receive infection from wild birds and also act as foci of infection for wild birds and humans. Waterfowl in collections should, in the event of an H5N1 outbreak, resort to biosecurity measures ranging from provision of protective wear for all staff and closure of facilities to the public, to capture and confinement of birds and, if deemed necessary by veterinary/public health authorities, destruction of the birds and disinfection of the premises.

2.5.4 Birds in recreation areas

Studies of potential human pathogens in the droppings of Canada geese and of the behaviour of these birds in urban parks showed that pathogenic bacteria could be deposited over large areas of park grassland which humans (and sometimes their companion animals) use for recreation (Feare *et al* 1999, Kullas *et al* 2002). Should these birds become infected with an AI virus, virus could be shed on grassland until infected birds died, or in the event of asymptomatic infection, until the birds ceased to shed virus in their faeces. Other species of goose that forage at some distance from the water could pose similar risks, whereas with waterfowl that foraged near to the water's edge, risks of human infection would be concentrated closer to the water. Defaecation by birds into the water may present potential risks for people using the water for recreation, especially given the long survival of the virus in water (Stallknecht *et al* 1990).

Various species of gull feed and roost on open areas of water, many of which are used for recreation and as a source of domestic and industrial water supplies. Water in these roosts can be contaminated with bacteria pathogenic to humans (Gould & Fletcher 1978, Jones *et al* 1978, Benton *et al* 1983, Girdwood *et al* 1985, Monaghan *et al* 1985, Levesque *et al* 1993, Bosch & Muniesa 1996) and avian influenza viruses would be shed and may survive here.

In both of these cases, an outbreak of an influenza sub-type pathogenic to man would necessitate prohibition of recreational activities in these sites as long as the risk persisted. In addition, water treatment would need to be adequate to kill/filter avian influenza viruses. Ideally, birds should be deterred from using aquatic sites such as these but, while the use of scarers and overhead wires can be successful in reducing the number of birds (Blokpoel & Tessier 1983, 1984), birds cannot be totally excluded.

2.5.5 Bird feeding in gardens

The feeding of birds in gardens has become widespread in Europe and North America, and is actively promoted by bird conservation organisation such as the RSPB and BTO. This encourages birds to feed in proximity to humans and leads to direct contact between humans and bird products when bird feeders are replenished and cleaned. The birds that are attracted to garden bird feeders, however, are not those species that are currently the main carriers of AI and are thus unlikely to pose a significant threat unless the virus evolves to become less species specific. In the event that the virus becomes transmissible by pigeons, the exclusion of pigeons from garden bird feeding stations, using mesh barriers of appropriate size, could reduce the risk of infection to smaller wild birds (see below).

The feeding of birds in gardens is already recognised as having risks to both human and wild bird health and basic hygiene procedures are recommended by the RSPB and others. This advice should be re-stated, but members should be informed that unless the virus changes to become infective for a wider range of bird species, there is little risk of human infection and bird feeding should continue.

2.5.6 Racing, show and feral pigeons

The discovery in late 2002 of H5N1 in a dead feral pigeon *Columba livia* in Kowloon Park, Hong Kong (Ellis *et al* 2004), and reports from Thailand, allegedly of hundreds of dead pigeons carrying HPAI H5N1 (Anon 2004, FAO 2005a) suggest that feral pigeons might act as carriers for the virus. However, with only two recorded instances of infection in feral pigeons, only one of which has been confirmed,

at this stage the feral pigeon cannot be regarded as a serious threat to human health any more than it is for other human pathogens (Haag-Wackernagel & Moch 2003), or to poultry. Should the virus change to become infective in pigeons, especially with low morbidity, then pigeons may become of particular concern.

Feral pigeons, which are abundant in many urban areas throughout the world, have the potential to interact with pigeons kept in free-flying flocks, often for racing but in some areas also to provide food for humans, and also with pigeons bred for their plumage and behaviour characteristics and exhibited at bird shows. Urban feral pigeons have been considered to be largely resident birds with small home ranges, but with interchange between feeding flocks (Lefebvre & Giraldeau 1984, Sol & Senar 1995). In some places they can commute long distances between urban feeding areas and rural roosting/breeding sites, or between urban roosting and breeding areas and rural feeding sites (Johnson & Janiga 1995, Baldaccini *et al* 2000, Feare 2004). Haag (pers. comm) tracked urban pigeons using GPS transmitters located by satellite (Rose *et al* 2005), and found that the home range of these birds was greater, up to 151 ha, than values obtained by direct observations of individually marked birds.

Some members of the public deliberately place themselves in close contact with pigeons, through feeding them, and other people come into contact with pigeons or their products through pest control activities, or through living in or passing through areas inhabited by pigeons.

Racing pigeons are frequently encouraged to fly long distances, sometimes over international boundaries, and prior to release are often transported in containers housing flocks of birds from many owners. Some pigeons fail to return home and some of these join urban flocks as revealed by the presence of ringed pigeons in these flocks, especially in parts of the country, such as north-west England, where racing is a regular activity (Feare, pers. obs.). At pigeon shows, birds from different origins are housed close to each other and are handled by owners and judges. All of these activities provide opportunities for pigeons of different origins to mix, and for some humans to experience close contact with them. This was clearly demonstrated in 1982–1984 when a new variant of avian paramyxovirus (APMV-1) spread rapidly through pigeon populations across Europe. Although APMV-1 does not affect humans, this case illustrates how an infectious, sometimes fatal, virus of pigeons can spread among the pigeons and from them infect other taxa, in this case poultry.

The new variant APMV-1 was first reported in 1981 from two racing pigeons imported to Belgium from Italy. It was subsequently identified in Italy and then spread rapidly across Europe from south-east to north and west (Alexander *et al* 1984a, Table 4), eventually reaching Britain in 1983, despite the imposition of a ban on races from the continent to Britain in March 1983 (Alexander *et al* 1984a). Here, it entered the poultry food chain when sick and dying feral pigeons contaminated rice bran and possibly other constituents, destined to be incorporated into poultry food, in a large storage facility in Liverpool docks. This led to 23 outbreaks of Newcastle Disease in poultry flocks in 1984 (D Alexander, pers. comm), costing £0.75 million in losses and compensation (Feare 1985).

Alexander *et al* (1984b) identified the kinds of contact that were believed to have led to outbreaks of the disease. Of the 192 outbreaks among pigeons in Britain, 133 were traceable to contacts involved in racing: birds in the same race, birds placed in the same crate, travelling in the same transporter, or that had been trained together. Fourteen outbreaks were attributable to the purchase, exchange or gift of racing pigeons. Seven outbreaks resulted from the taking of stray birds into lofts and 38 outbreaks were of unknown origin.

Table 4. – dates of reporting of Avian Paramyxovirus Type 1 (APMV-1) outbreaks in Europe, 1981–1983 (from Alexander et al 1985) and types of pigeon involved.

Country	Date (month(s)/year	Types of pigeon
Italy	12/81–8/82	Racing
Portugal	8/82	Racing
Germany	12/82–5/83	Racing, show
Belgium	2–10/83	Racing
Netherlands	4–5/83	Racing
Czechoslovakia	6–8/83	Racing, feral, show
Great Britain	6/83–6/84	Racing, feral
Hungary	7/83–1/84	Racing
France	7/83–2/84	Racing, feral
Denmark	8/83	Racing
Switzerland	8-10/83	Racing
Sweden	9-10/83	Racing

This illustrates the ease and rapidity with which a virus infectious to pigeons can spread through their populations, including captive, free-flying and feral. The British experience further demonstrates the capacity of a virus, with appropriately infective properties, to cause disease and death in other bird species.

In the event that HPAI H5N1 evolves these capabilities of spread among pigeons, and is also capable of cross-infection to other species, some particular risks are apparent:

- **Waterfowl collections:** waterfowl collections often attract large numbers of feral pigeons (and racing pigeons that fail to return to their lofts) due to the large amounts of grain that are broadcast for the wildfowl. Waterfowl collections also attract non-captive resident native waterfowl and also migrant waterfowl. Introduction of AI by feral pigeons could therefore generate foci of waterfowl infection that could have serious implications for the captive birds, but could also spread more widely through waterfowl movements. Some waterfowl collection managers undertake control (trapping) of feral pigeons but if the threat through feral pigeons increases, such control should be given high priority. However, collections would also be susceptible to the introduction of virus through the immigration of waterfowl and the general biosecurity of such collections would require examination and re-evaluation.
- **Garden bird feeding stations:** in urban and suburban areas, feral pigeons are attracted to garden bird feeding stations where food is placed on birdtables or placed on the ground. Placement of food on the ground can also attract rats and thus this practice should always be discouraged. Pigeons can be prevented from feeding at birdtables by covering the table with a net of suitable mesh size that will exclude pigeons but allow smaller birds to access the table. Suitable barriers are already available and their use should be recommended.
- **Poultry:** major poultry farms in the UK and in many other parts of Europe already practice high levels of biosecurity, maintaining the birds and their food in premises proofed against the entry of wild birds and mammals. Free-range poultry farms, however, do not have this protection and are thus susceptible to use by feral pigeons. For economic reasons (loss of food), feral pigeons should be discouraged from visiting free-range poultry farms but possible infection with HPAI should stimulate poultry farmers to examine their biosecurity.
- **Risk to humans:** the presence of feral pigeons, infected with AI, at waterfowl collections, garden bird feeding stations and poultry farms would bring pigeons and their products into close contact with humans, especially the staff of waterfowl collections and poultry farms. This could provide opportunities for acquisition of infection by people. This is a further incentive for managers to control feral pigeon numbers at their premises. Their role should also include education of staff so that they are aware of risks and staff should be provided with adequate

protective clothing and other equipment to reduce the risks of contraction of disease and also of spreading virus to other facilities or people. More casual contact with pigeons, such as walking through parks where pigeons are fed, is less likely to put people at risk, as with other human pathogens carried by pigeons (Haag-Wackernagel & Moch 2004). Nevertheless, the public should be informed of the risks of close contact with pigeons and feeding them should be actively discouraged.

- If waterfowl in collections open to the public and flocks of racing and urban pigeons become infected with a readily transmissible strain of H5N1 there are likely to be calls for culls of these birds and alarm will most probably be created by the popular press. However, the chance of the virus spreading further will depend upon its lethality to these birds. If highly lethal, killing infected birds within a few hours or days of infection, this will reduce the rate of spread. But if the virus is not lethal, it is likely to spread further. Infected geese have been recorded shedding virus in their faeces for up to 19 days, which can potentially lead to extensive environmental contamination. Nevertheless, it is important to note that a human pandemic is likely only when a virus strain evolves that can be readily passed from human to human – if/when this occurs, this form of transmission will drive infection in wild birds into insignificance with regard to concern for human health.

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