The risks from H5N1 to wild birds from captive-reared mallard

Quick scoping review

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Foreword

Natural England evaluated the risks from high pathogenicity avian influenza (HPAI) to wild birds associated with the release of captive-reared mallards for recreational shooting in winter 2023/24. At this time, the background risk of HPAI in wild birds was considered by Defra to be medium i.e. event occurs regularly.

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Executive summary

We assessed the evidence relating to the risks to wild birds of increased spread of high pathogenicity avian influenza (HPAI) H5N1 associated with releasing juvenile mallards for wildfowl shooting in England. We conclude that there is a very high likelihood of major consequences to populations of wild birds associated with mallard releases.
Due to the widespread prevalence of HPAI in England, and high incidence in waterfowl species, there is a very high likelihood that captive-reared mallards will be exposed to H5N1 after release. In addition, due to the species' known susceptibility to infection, high densities in release ponds, and the predominance of immunologically naive juveniles in the released populations, there is a very high likelihood that captive-reared mallards will be infected with H5N1 following exposure. Once infected, mallards are likely to shed higher viral loads and for longer durations than other species of waterfowl. Shedding is highest in juvenile birds.

There is high uncertainty as to the numbers of captive-reared mallards released annually and the trend compared to other gamebirds. However, the number is likely to be well in excess of the wild population and therefore to add substantially to the abundance and density of waterfowl on some inland watercourses.
The gregarious nature of waterfowl, post-release feeding and predator control means that there is a very high likelihood of wild mallards and other waterfowl being actively attracted to ponds where captive-reared mallards are released, creating many opportunities for direct and indirect interactions between wild waterfowl and formerly captive mallards. In addition, potential bridging species such as gulls may forage at ponds used by released mallards creating multiple routes of exposure to H5N1 amongst wild birds. Mammals and birds that predate on or scavenge ducklings may also be exposed to H5N1 by eating infected mallards.

Once exposed, there is a very high likelihood of widespread morbidity and mortality in wild birds as most species appear to be susceptible to infection and severe disease associated with H5N1 infection.

It is therefore our view that captive-reared juvenile mallards have potential to act as both a reservoir and amplifier of H5N1 and to play a major role in H5N1's continued persistence and dissemination. Our confidence in these conclusions is high as there is extensive literature on avian influenza in mallards.

Contents

Introduction

The mallard (*Anas platyrhynchos*) is one of 17 waterfowl quarry species in the United Kingdom with a resident, breeding population estimated at up to 145,000 pairs (RSPB, 2023a). This population is supplemented in summer by releases of captive-reared birds and in winter by an estimated 675,000 migrating birds from northern Europe (RSPB, 2023a). Although common and widespread, the mallard is amber-listed (BoCC 5) due to recent declines in the number of non-breeding birds.

Wild aquatic birds, in particular dabbling ducks such as mallards, are considered a natural reservoir of low pathogenic avian influenza viruses (LPAIV; Jourdain et al, 2010). For the past 20 years, dabbling ducks have additionally acted as a reservoir and vector for high pathogenicity avian influenza (HPAI) viruses which they host with only mild or absent clinical signs (Ahrens et al, 2022).

Since 2021, the UK has experienced an unprecedented outbreak of the H5N1 strain of HPAI which has caused high levels of mortality in both captive poultry and wild birds. In the current season, from 1 October 2023 to date, there have been 6 cases in kept birds in the UK, compared to 207 cases in 2022/23 and 158 in 2021/22. The Animal and Plant Health Agency (APHA) wild bird surveillance scheme has confirmed HPAI infection in 24 wild birds of 13 species in Great Britain, primarily waterfowl, seabirds, pheasants and birds of prey, in the year to date (1 October 2023 to 23 February 2024). These data compare to 1595 cases in 62 species of wild birds in 2022/23 and 1727 cases in 59 species in 2021/22. Even though case numbers are substantially lower than in the two previous years of the outbreak, the risk to wild birds is currently assessed as medium i.e. event occurs regularly. This risk level is based on the continued circulation of the HPAI virus in wild birds in Great Britain and Europe and the potential for an increase in cases with wild bird movements.

Notably, since the start of the outbreak in 2021, substantial levels of mortality have been reported in amber- and red-listed (BoCC5) species including the sandwich tern (*Thalasseus sandvicensis*) and roseate tern (*Sterna dougallii;* 55% of the UK's breeding population found dead in 2022). In addition, mortalities in association with HPAI infection have been reported in the hen harrier (*Circus cyaneus*), white-tailed eagle (*Haliaeetus albicilla*) and Eurasian curlew (*Numenius arquata*). Extremely high levels of mortality, approaching 50% in some cases, were reported in breeding colonies of black headed gulls (*Chroicocephalus ridibundus)* in 2023. H5N1 of avian origin has also been detected in the red fox (*Vulpes vulpes*), Eurasian otter (*Lutra lutra*), harbour seal (*Halichoerus grypus*), grey seal (*Phoca vitulina*), harbour porpoise (*Phocoena phocoena*) and common dolphin (*Delphinus delphis*) since the current outbreak began in 2021, all of which are thought to have been infected by the ingestion of infected prey species.

Strain sequencing of LPAIV harboured by captive and free-living mallards in Denmark has demonstrated the presence of the same strain in both populations confirming the potential for transmission of avian influenza viruses between captive and wild mallards (Handberg et al, 2010; Therkildsen et al, 2011). It has therefore been proposed that releases of captive-reared mallards may be involved in the epidemiology of the current outbreak of H5N1 in the UK with similar spillover and spillback between captive and wild birds.

Method

In order to evaluate whether releases of captive-reared mallards might increase the likelihood of dissemination of H5N1 into wild bird populations, we conducted a review of published literature on avian influenza in waterfowl, including mallards; the rearing and release of mallards for shooting; and H5N1 epidemiology, using the internet search engines of CABDirect, Scopus and Google Scholar. Keywords utilised in searches were: mallard, duck, anatid, *Anas platyrhynchos* AND avian influenza, HPAI, LPAI, H5N1, captive-reared, behaviour.

The risk questions considered each step in the epidemiological pathway potentially linking captive-reared mallards and wild birds and assessed the likelihood at each step using the criteria at Table 1. Following determination of the level of risk, the certainty level of this decision was described using the reasoning outlined in Table 2.

Table 1: Interpretation of hazard probability categories used in this risk assessment (table taken from The EFSA Journal 2006, adapted from Murray *et al*. (2004)

Hazard Category	Interpretation
Negligible	Event is so rare that it does not merit to be considered
Very Low	Event is very rare but cannot be excluded
Low	Event is rare but does occur
Medium	Event occurs regularly
High	Event occurs very often
Very High	Event occurs almost certainly

Table 2: Interpretation of certainty categories used in this risk assessment (table adapted from The EFSA Journal 2006)

Certainty Category	Interpretation
Low	There are scarce or no data available on the species and/or event in question; evidence is not provided in references but rather in unpublished reports or based on observations, or personal communication; authors report conclusions that vary considerably between them
Medium	There are some but no complete data available on the species and/or event in question; conclusions have been extrapolated from closely related species; evidence is provided in small number of references; authors report conclusions that vary from one another.
High	There are solid and complete data available for the species and/or event in question; strong evidence is provided in multiple references; authors report similar conclusions

Results

The online searches generated a total of 5530 records. A first screen of title only removed duplications and papers describing: mallard diet, other avian species, other pathogens, viral characteristics, anatid biology, sociology, reproductive behaviour, case studies outside Europe, toxicology, vaccination and infection testing methods. 171 records were selected for a second screen and the abstract of each paper was read. From this group, 87 papers were considered relevant and read in full.

Review question 1: How many captive-reared mallards are released annually?

There is considerable uncertainty as to how many captive-reared mallards are released in Great Britain annually, but numbers have been rising rapidly since the practice started in the 1950s (Champagnon 2011) and potentially by nearly 50% in the past 20 years (Aebischer, in prep.). Recently, there may have been some decline in release numbers due to greater focus on pheasant and red-legged partridge rearing (Glynn Evans, pers. comm) although anecdotal reports suggest that many estates released more mallards than normal in 2022 to compensate for the temporary unavailability of gamebird poults due to avian influenza.

Madden (2021) analysed 12 datasets, mainly from 2016, to calculate an annual release of 2.6 million (range 0.9-6.0 million) mallards in the UK. The Game and Wildlife Conservation Trust (GWCT) national gamebird census (NGC) indicates that about 1 million mallards were shot in the UK in the 2022 season based on voluntary returns from 491 estates and that this is likely to equate to a release of approximately 1.3 million mallards (range 890,000 to 1.9million; (Aebischer, in prep). NGC data also suggest that release numbers and densities are increasing on those estates that release mallards (Aebischer, in prep.).

Conclusion: The estimated number of captive-reared mallards released annually in the UK has wide confidence intervals, but it is likely that annual releases are well in excess of the wild population and consequently released mallards are likely to make a substantial contribution to wildfowl population numbers and densities (medium certainty).

Review question 2: What is the likelihood that captive-reared mallards will be exposed to H5N1 following release?

Captive-reared mallards are released during the summer months until July 31 either directly onto ponds or, less commonly, into temporary rearing pens. Once released, they may be shot until January 31 (February 20 in areas below the high-water mark of ordinary spring tides). Estates may also manage flight ponds to attract wild waterfowl by feeding and/or the use of flightless decoy birds.

H5N1 cases in wild birds have been reported at a wide range of locations across the country with positive submissions to APHA from 457 locations in 90 counties in 2022/23, including: mute swan (*Cygnus olor*), pink-footed goose (*Anser brachyrhynchus*), Canada goose (*Branta canadensis*), greylag goose (*Anser anser*), barnacle goose (*Anser leucopsis*), mallard, teal (*Anas crecca*), whooper swan (*Cygnus cygnus*), black-headed gull, common gull (*Larus canus*), great black-backed gull (*Larus marinus*), lesser black-backed gull (*Larus fuscus*), herring gull (*Larus argentatus*) and common tern (*Sterna hirundo*). The migratory and wide-ranging behaviour of such species and incidence of H5N1 in many locations means that there is a high likelihood that infected birds have visited ponds used by captive-reared mallards in the past year.

H5N1 has been recovered from both cloacal and oropharyngeal swabs from infected birds and it is likely that the virus is transmitted between birds either directly or indirectly via contaminated water and surfaces in nasal secretions, saliva and faeces. Several studies have demonstrated the potential for HPAI viruses including H5N1 to survive for prolonged periods in the environment: for example, Shortridge et al (1998) demonstrated that H5N1 viruses can persist in wet faeces with no detectable loss of infectivity after 40 days at 4˚C and Nazir et al (2010) showed that H5N1 may remain viable for up to seven months in freshwater at 0˚C or two months at 10˚C and 19 days at 20˚C. Survival of HPAI viruses may be particularly prolonged in surface water as viral persistence is favoured at pH 7.4 to 8.2 (Stallknecht and Brown, 2009) and pond surface water pH is typically 7.5 to 8.5 (Fondriest, 2023).

Waterfowl, including released mallards, are likely to be exposed to HPAI due to their feeding behaviours in shallow water and at pond margins and while drinking and preening.

Conclusion: As H5N1 is known to be persistent in the environment, particularly in freshwater, and cases in wild waterfowl have been reported year-round, there is a very high likelihood that captive-reared mallards will be exposed to H5N1 following release (high certainty).

Review question 3: What is the likelihood that captive-reared mallards will be infected following exposure to H5N1?

In a large study by Gaidet et al (2012) of avian influenza virus (AIV) prevalence in waterfowl (n=8413), Anas species had higher prevalence than non-Anas species even when accounting for variations in foraging behaviour or geographic origin. Similarly, Torrontegi et al (2019) used DNA sequencing to identify host species from faecal samples (n=3392) collected at 16 wetland sites in northern Spain over two three-year periods. All AIV-positive samples that could be DNA-sequenced (25/52) were from anatids, with mallard accounting for 92% and greylag geese 8% of positive samples. In addition, nearly all possible combinations of the antigenic subtypes of AIV have been detected in wild dabbling ducks (van Dijk, 2014) and several experimental studies have indicated that mallards are highly susceptible to infection with HPAI (Hulse-Post al, 2005; Keawcharoen et al 2008; Ahrens et al, 2022). Further, James et al (2023) demonstrated in an experimental study on Pekin ducks that clade 2.3.4.4b, the currently circulating strain of H5N1, is highly adapted to ducks: all experimentally infected ducks (n=18) became infected with H5N1, even at low doses, with onward transmission to all naïve ducks (n=18) by 6 days post inoculation.

In addition, mallards are likely to be susceptible to infection with HPAI by many routes. Experimental studies by França et al (2012) have demonstrated that mallards can be infected with LPAIV by all potential routes: intranasal, intratracheal, intraocular, intracloacal and intragluvial and the same is likely to be true for HPAI viruses. Wille et al (2018) additionally report infection of mallards with LPAIV via allo-preening of conspecifics with contaminated feathers.

Prior infection with LPAIV may reduce susceptibility to infection with HPAI (Jourdain et al, 2010) but juvenile mallards are very unlikely to have been infected with LPAIV before release due to their young age and low likelihood of exposure while in captivity. Transient immunity to infection with AIV might be conferred by maternal antibodies. However, it has been demonstrated that maternal antibodies reduce rapidly after hatching in mallards (van Dijk, 2014), with a reported maximum duration of less than five weeks at 33 days (Dirsmith et al, 2018). Mallard ducklings are therefore likely to lack immunity to AIV at the time of release (typically six weeks onwards). In addition, in common with other species, juvenile mallards are likely to be less immunocompetent than adult birds. This has been demonstrated through several studies reporting higher infection prevalence or disease severity following infection with HPAI in juvenile ducks (Pantin-Jackwood et al, 2007; Hill et al, 2012). Further, Ahrens et al (2022) demonstrated experimentally that sub-adult mallards (10 to 13 weeks old; n=4) were infected with HPAI even at very low viral loads (0.1 $TCID_{50}$/mL). Similarly, Aiello et al (2013) detected H5N1 viruses more commonly and for longer durations in feather samples from 4-week-old Pekin duck (*Anas platyrhynchos* var. *domestica*) compared to adult ducks. A year-long study of avian influenza infection in mallards (n=266) in the Netherlands (van Dijk, 2014) found that prevalence peaked in late summer prior to the arrival of migratory mallards, indicating further confirmation of the importance of juvenile recruits to mallard populations in the epidemiology of avian influenza viruses.

Infection prevalence may also be higher in captive mallards when compared to wild counterparts due to higher stocking densities (Bragstad et al, 2005). Gaidet et al (2012) found that avian influenza prevalence was positively correlated with bird density in a study of 16 waterfowl species (n=8413). Similarly, Vittecoq et al (2012) found that avian influenza prevalence was consistently higher in captive mallards compared to wild mallards in the same area where water was free flowing between pens and ponds used by both. It is not known what mallard release densities are in practice. Until fledging (50 to 60 days; RSPB, 2023b) ducklings can be kept in outdoor, well-grassed rearing pens at densities of up to 5000 ducklings per hectare, or 1 duck per $2m^2$, or indoors on slatted floors at a maximum stocking rate of 8 ducklings per m^2 (GOV.UK, 2023). Following release, the BASC Code of Practice recommends a density appropriate to the size and characteristics of the pond with a suggested maximum density of 600 birds per hectare of water. For comparative purposes with wild mallards, analysis of data collected at 12 sites by BTO for the Wetland Birds Survey (BTO, 2023) between 2017 and 2022 suggests a wide variation in five-year average densities of mallards (range 0.1 to 49.7 mallards per hectare).

Captive-reared ducks are also likely to be in better body condition than wild equivalents which has been observed to increase prevalence of infection with avian influenza in a small (n=40) experimental study of wild and captive mallards in the USA (Arsnoe et al, 2011). Arsnoe et al (2011) speculated that the negative association between body condition and immunocompetence in the mallards in their study may be due to variations in protein intake, with high protein (either from dietary sources or muscle breakdown) associated with increases in immunocompetence.

Conclusion: As mallards are highly susceptible to infection with H5N1 via many routes and susceptibility is increased in juvenile birds, and at the high densities associated with captivity, there is a very high likelihood that captive-reared mallards will be infected if exposed to H5N1 (high certainty).

Review question 4: How likely is it that infected released mallards will disseminate H5N1?

Dabbling ducks, and in particular mallards, are believed to play a major role in the dissemination of AIV due to: high concentrations of virus in faeces, prolonged viral shedding, and defecation into water and muddy pond margins, environments where, as described above, AIV can persist for prolonged periods (Stallknecht and Brown 2009). In addition, AIV isolation data suggests that genetic relatedness in mallards may be associated with enhanced transmission potential (de Marco et al, 2014). Captive-reared mallards may be less genetically diverse than wild equivalents which could therefore further enhance their transmission potential.

Costa et al (2011) compared AIV shedding in 10- to 16-week-old experimentally-infected American species of mallard, redhead (*Aythya americana*), wood duck (*Aix sponsa*) and laughing gull (*Leucophaeus atricilla*). Mallards were found to exhibit the most extensive viral shedding of all species based on the number of infected birds shedding virus and the duration of shedding. Similarly, in a small study (n=46), Keawcharoen et al (2008) demonstrated high viral shedding in mallards experimentally infected with HPAI H5N1 when compared to five other species of duck including 3 dabbling duck species: common teal, Eurasian wigeon (*A. Penelope*) and gadwall (*A. strepera*).

Hulse-Post et al (2005) demonstrated that viral shedding by mallards experimentally infected with 14 different H5N1 strains and in-contact ducks (n=56) is prolonged, with viable virus shed for up to 17 days post-inoculation. Notably, Hulse-Post et al (2005) also reported that viral titres in the mallards studied were higher in tracheal than cloacal swabs suggesting an additional route of viral dissemination via respiratory secretions which is likely to be of importance when birds are at high density. In a recent experimental study, Stackman et al (2023) report that 65% of ducks (n= 12) naturally infected with H5N1 at 2 weeks of age were still shedding virus cloacally 13 days post-exposure. This is consistent with a previous study by Jourdain et al (2010) which found that juvenile mallards experimentally infected with LPAIV shed virus continuously for 12 days post-inoculation and a further 3.7 days intermittently.

Mallards reinoculated with the same virus in the study by Jourdain et al (2010) were reinfected and found to shed AIV transiently for up to six days post-inoculation suggesting potential for mallards to recirculate and amplify AIV over prolonged periods in contaminated environments, particularly as mallards rarely experience morbidity and mortality when infected with AIV (Keawcharoen et al, 2008). Additionally, James et al (2023) found in a study of Pekin ducks (n=18) experimentally infected with H5N1 that viral shedding by ducks and consequent environmental contamination was frequent: viral DNA was detected daily in pond and drinking water used by the infected birds for 13 days, despite daily water changes. In addition, 100% of naïve ducks (n=18) housed with three infected ducks became infected with H5N1.

AIV shedding is highest in juvenile mallards and declines with age (van Dijk, 2014) which may be a result of juvenile birds' increased susceptibility to infection and severity of disease as noted above. Markwell and Shortridge (1982) observed that AIV contamination of ponds in Hong Kong was maintained by the introduction of new batches of ducklings and only declined once the ducks were at least 70 to 80 days old.

Transmission potential in ponds might also be facilitated if ponds are small and contain a high number of released mallards. Pérez-Ramírez et al (2012) demonstrated a higher prevalence of LPAIV in waterfowl on small waterbodies in Spain compared to larger areas and concluded that AIV may be concentrated in small watercourses, particularly if birds congregate at high densities. Modelling by René and Bicout (2007) indicated a risk of transmission of HPAI in shallow water (0.2m) ponds which increased with duck density. Similarly modelling by Papp et al (2017) has shown that AIV transmission risk increases when dabbling duck densities increase due to higher frequencies of contact between susceptible and infected birds.

In addition to viral dissemination via shedding in faeces and respiratory secretions, infected mallards moving between watercourses may also act as mechanical vectors for viral particles both on their feet and plumage. Ahrens et al (2022) found viral RNA on the breast plumage of infected mallards while Delogu et al (2010) demonstrated experimentally in mallards that uropygial gland secretions (preen oil) attract and concentrate avian influenza viral particles in water. Karunakaran et al (2019) showed that the presence of preen oil prolongs HPAI viral persistence on duck feathers, with infectivity and viral load significantly higher in naturally preened feathers compared to controls.

Conclusion: As juvenile mallards shed high AIV loads and for longer durations than older mallards and other waterfowl infected with AIV, and AIV shed by mallards can be disseminated via several routes, there is a very high likelihood that infected released mallards will disseminate HPAI (high certainty).

Review question 5: How likely is contact between wild waterfowl and infected released mallards?

Captive-reared ducklings in rearing pens may have variable contact with wild bird species depending on the construction of the pens. Once the mallards are released onto ponds, usually from 6 to 8 weeks old, there are likely to be many opportunities for close contact with both wild mallards and other species of waterfowl. Birds prospecting for good habitats are thought to use the presence of closely related species as a positive indicator of habitat suitability: Sebastián-González et al (2010) observed seven species of waterfowl including mallard on 221 artificial irrigation ponds in Spain between 2002 and 2008 and found that the presence of heterospecifics increased the likelihood that a species would be found there. In addition, BASC (2023) reports in guidance that mallard flight ponds regularly attract teal, and historically duck decoys, both artificial and pinioned or wing-clipped ducks, have been used to attract wild ducks to flight ponds to increase shooting opportunities leading to congregations of birds and increased potential for contact between released and free-living birds.

Further, McDuie et al (2022) showed through GPS tracking of free-living adult ducks (n=688) in the USA, including mallards (n=213), that ducks will preferentially select sub-optimal habitat, including small, artificial ponds, over more optimal wetland habitat for both foraging and roosting due to greater food resources or perceived safety from predators. As captive-reared ducks are frequently fed after release in order to keep them on the estate, and predator control is widely deployed, it is very likely that release ponds are similarly attractive to free-living waterfowl.

Large scale releases of ducklings are also reported to attract predatory and scavenging species such as crows and gulls (Boyd and Harrison, 1962). In addition, infected birds are more likely to be predated than healthy individuals (Adelman et al, 2017).

The evidence on post-release movement of captive-reared mallards is scant but most studies suggest that mallards generally show high fidelity to release sites, which is encouraged by post-release feeding (Champagnon et al, 2016; Söderquist et al, 2024). Nevertheless, studies of captive-reared reintroduced mallards suggest that some individuals will disperse over short distances to neighbouring watercourses: Champagnon (2011) reports that 92% of captive-bred mallards (n=87) in a study in France were recovered from the release site and, where birds did disperse, the average range was 6.0 +/- 0.5km. In a larger study (n=975) over 7 years, Boyd and Harrison (1962) found that 19.9% of recoveries were more than 10 miles from the release site and some individuals may travel substantially further: the Westmoreland Wildfowlers Association found a maximum dispersal distance of 15 miles from 300 mallards released in 2010 (WWA, 2023) and one mallard in the study by Champagnon (2011) was recovered 49.9km from the release site.

Infected mallards move around the landscape less than uninfected birds (van Dijk,2014) but may still travel beyond release sites. In the study by van Dijk (2014) the average flight distance from the roost of 22 wild adult mallards infected with LPAIV was found to be 1.3km. However, Teitelbaum et al, 2023) found no differences in total daily distance moved or maximum daily displacement between infected (n=3) and uninfected (n=27) wild mallards in California. Similarly, Bengtsson et al (2016) found no difference in the speed or distance travelled by infected wild mallards (n=20) in Sweden. It is therefore likely that some captive-reared mallard infected with H5N1 will travel beyond release sites with potential to disseminate the virus to waterfowl on neighbouring sites in addition to release ponds.

Conclusion: There is a very high likelihood that captive-reared mallards will be in close contact with other waterfowl both at release sites and on neighbouring watercourses (medium certainty).

Review question 6: How likely is it that wild waterfowl will be infected with H5N1 shed by released mallards?

If exposed to H5N1, birds of most species are likely to become infected because infection has been reported in a wide range of avian species. APHA has reported mortality associated with H5N1 infection in 59 species of wild bird since the current outbreak began (APHA, 2023), including, as noted above, 21 species of waterfowl and five species of gull likely to be found on waterways in association with mallards. In addition, H5N1 has been found in nine species of raptor, probably exposed through ingestion of infected birds, some of which species may predate on ducklings. There is limited evidence of wild birds of some species recovering from apparent infection with HPAI (based on detection of antibodies by serology), but it is widely believed that birds of all taxa can become acutely ill and die following infection with H5N1 due to either species susceptibility or transient immunosuppression following e.g. migration, starvation or concomitant illness in individual birds.

Serology testing to assess previous exposure to, and recovery from, HPAI has not been undertaken at scale to date. However, it is unlikely that there are substantial numbers of susceptible wild birds with immunity to H5N1.

Conclusion: Wild birds of most species are likely to be susceptible to severe disease and mortality following infection with H5N1 resulting from direct or indirect contact with infected released mallards (high certainty).

Review question 7: What is the potential for exposure of wild birds to H5N1 shed by infected released mallards via bridging species?

The role of species such as Charadriiformes and Anseriformes in disseminating both low and high pathogenicity avian influenza viruses over long distances along migratory pathways is widely recognised (Lycett et al, 2019). Evidence for the movement of HPAI over shorter distances via such bridging species is circumstantial and this review found no reports where an individual bird had been shown to have disseminated HPAI shed by an infected mallard to wild birds at a different location. However, it is highly likely that birds which move between sites have potential to act as bridging species, indirectly disseminating pathogens such as HPAIV. For example, many species of gull are known to frequent inland waterways and may be attracted to release ponds by supplementary feeding and the opportunity to predate/scavenge ducklings and sick birds. Infected mallards are very likely to contaminate water and muddy pond margins with virus in their faeces, particularly where birds are at high density. H5N1 may remain viable in wet and dry poultry faeces for four days at 24˚C (Kurmi et al, 2013) and for 19 days at 20˚C in freshwater (Nazir et al, 2010), typical temperatures during late summer and early autumn when and after mallards are released. Gulls and other mobile species on ponds used by released mallards could therefore be exposed to and infected with H5N1 by ingestion of contaminated water or infected mallards, or could act as mechanical vectors to transport virus on the undersurface of their feet or plumage to new locations.

Gulls are reported to forage widely from breeding colonies during the summer with mean maximum foraging ranges noted by Woodward et al (2019) as:

- Herring Gull: 58.8(+/- 26.8) km
- Lesser black-backed Gull: 127(+/- 109) km
- Black-headed Gull: 18.5 km
- Common Gull: 50 km

Gull species in particular could therefore act as bridging species to disseminate H5N1 to sites distant from release ponds.

Susceptible wild birds could be exposed to H5N1 by eating food or drinking water that has been contaminated via faeces on bridging species' feet or plumage or excreted by infected birds. The likelihood of this occurring is increased by the potential for prolonged H5N1 persistence, particularly in water, but will vary from species to species and site to site depending on the density and behaviours of birds present. In addition, predatory or scavenging birds such as raptors, corvids and gulls could be exposed to H5N1 by ingesting the carcases of infected bridging birds.

Conclusion: Extended ranging distances of bridging bird species and prolonged virus survival could result in H5N1 being spread to locations at some distance from mallard release sites (medium certainty).

Review question 8: How likely is it that mammals will be infected with H5N1 via infected released mallards?

The extremely low number of human infections with the currently predominant strain of H5N1 suggest that the current strain does not have particular tropism for mammalian cells. However, infection with this strain of H5N1 has been reported in a wide range of mammals that scavenge or predate on birds, including otters and foxes (APHA, 2023) confirming that mammals can be infected with H5N1 under some circumstances. The viral load of H5N1 in infected birds is likely to be high and consequently mammals that ingest infected ducklings or adult birds are likely to be exposed to very high viral loads increasing their risk of infection with H5N1.

Mammals could also be exposed to H5N1 in drinking water but this risk is likely to be very low due to the likely low viral load when faeces are diluted in water.

Conclusion: Mammals could be exposed to and infected with H5N1 by eating infected mallards (high certainty).

Conclusion

The abundance and high densities of immunologically naïve juvenile released mallards, a species known to be highly susceptible to H5N1 infection and likely to be a substantial contributor to environmental loads of H5N1, combined with widespread intermingling with other waterfowl species and potential bridging species on shared watercourses, means that the evidence is consistent with there being a very high risk to wild birds from H5N1 associated with ongoing releases of captive-reared mallards (high certainty).

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