

# High Pathogenicity Avian Influenza (HPAI) clade 2.3.4.4b incursion risk assessment for Australia

Based on information as of 20 July 2023

ABRIDGED VERSION<sup>1</sup>

## Table of Contents

<b>Executive Summary</b> .....	<b>2</b>
Overall risk question .....	4
Risk definitions .....	4
Event likelihood summary.....	4
Consequence summary.....	5
Risk summary .....	6
<b>Introduction</b> .....	<b>7</b>
<b>Background</b> .....	<b>7</b>
Avian influenza and current global outbreaks .....	7
<b>Hazard identification</b> .....	<b>9</b>
<b>Risk assessment</b> .....	<b>9</b>
Scope.....	9
Assumptions.....	10
<b>Entry Assessment</b> .....	<b>11</b>
Entry and exposure pathways via wild birds.....	11
Risk question 1a: What is the likelihood of a HPAI incursion by long-distance migratory wild birds via movements along the East Asian-Australasian flyway? .....	11
Risk question 1b: What is the likelihood of a HPAI incursion by wild birds via movements within the Australo-Papuan region? .....	11
Overarching considerations .....	12
Summary .....	16
<b>Exposure Assessment</b> .....	<b>17</b>
Overarching considerations .....	17
Risk question 2: What is the likelihood of HPAI exposure and establishment in wild birds in Australia? ...	19
Summary .....	20
Risk question 3: What is the likelihood of HPAI exposure and establishment in poultry? .....	21
Summary .....	23
Risk question 4: What is the risk of HPAI exposure and establishment in mammals? .....	24
Summary .....	24
<b>Estimation of the likelihood of entry and exposure</b> .....	<b>25</b>
Summary .....	25
<b>Consequence analysis</b> .....	<b>26</b>
Summary .....	28
<b>Risk estimation</b> .....	<b>28</b>
Summary .....	29
<b>Uncertainties</b> .....	<b>29</b>
<b>References</b> .....	<b>30</b>

<sup>1</sup> Comprehensive reports prepared by Dr Marcel Klaassen (Deakin University) and Dr Michelle Wille (The University of Melbourne) informed development by Wildlife Health Australia of this abridged risk assessment report which incorporates risk ratings based on likelihood and consequence assessments. Feedback from members of the National Avian Influenza Wild Bird Steering Group was also incorporated.

## Executive Summary

This report was funded by the Australian Government Department of Agriculture, Fisheries and Forestry Office of the Chief Veterinary Officer to provide an updated risk assessment on the likelihood of entry and establishment of HPAI in Australia via wild birds.

Compared with previous risk assessments, the overall risk associated with HPAI in wild birds has increased and is considered **HIGH** with **moderate** uncertainty (see Tables 6 & 7). This is based on a moderate increase in the likelihood of entry and exposure of HPAI with a significant increase in the consequence of HPAI incursions. The overall risk to poultry is considered **MODERATE/HIGH** with **moderate** uncertainty and the overall risk to wild mammals assessed as **LOW** with **high** uncertainty.

These increased risk levels are associated with the following the likelihood of incursions:

- 1) via long-distance migratory birds of the orders Charadriiformes (notably shorebirds) and Procellariiformes (notably shearwaters) considered **MODERATE** with **moderate** uncertainty during the upcoming spring migratory period,  
OR
- 2) via nomadic Anseriformes (waterfowl) within the Australo-Papuan region considered **MODERATE** with **moderate** uncertainty. The risk period being all year-round with frequent yet irregular movements of birds, driven by strong environmental conditions within the region (Ferenczi et al. 2016, Purnell 2022), with no apparent or consistent seasonal patterns in contrast to movements by long-distance migratory birds.

Changes in risk factors compared with previous risk assessments are associated with the current high pathogenicity avian influenza (HPAI) H5N1 clade 2.3.4.4b viruses which significantly differ from previous HPAI H5 viruses in their increased pathogenicity, replication and viral shedding in wild birds, increased avian and mammalian host range, increased persistence of virus in the environment and ability to spread via a wide range of avian species including both poultry and wild birds, in particular the ability of wild birds to directly infect poultry with HPAI viruses<sup>2</sup>.

The number of HPAI H5N1 clade 2.3.4.4b outbreaks amongst wild birds and poultry in the northern hemisphere, Africa and South America over the past one and a half years is unprecedented. In wild birds this has involved an array of species across all major bird orders, resulting in wild bird deaths 2-3 orders of magnitude higher than ever seen before. A wide range of domestic and wild mammal species have also been affected, although in substantially lower numbers than birds.

It is expected that the likelihood and associated risk of incursions into Australia will continue to remain at these levels for some time and potentially increase rather than diminish given continued virus evolution. If entry and establishment of HPAI H5N1 clade 2.3.4.4b occurs within wild birds and poultry, there are likely to be considerable consequences for wild birds and the poultry industry as seen in many currently affected countries. However, the frequency of HPAI incursions into Australia via wild birds may be lower compared with other continents due to multiple factors including the

The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), HPAI emerged in the sub-Antarctic, thousands more wild birds and marine mammals have been infected, and a considerable number of scientific studies have been published addressing the ecology, evolution, virology, pathogenicity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular the risk to marine mammals.

A small number updates are annotated in GREEN FONT throughout the document, mainly as footnotes.

<sup>2</sup> World Organisation for Animal Health (WOAH) infographic: <https://www.woah.org/app/uploads/2023/06/avian-influenza-understanding-new-dynamics-to-better-combat-the-disease.pdf>

species infected and potentially geographically isolated foci of arrival<sup>3</sup>. As a result, management of outbreaks may be more achievable in the Australian context if they are identified early, and appropriate mitigation measures implemented.

This risk assessment may need to be revised on an ongoing basis given the rapidly evolving epidemiology, ecology, and evolution of HPAI H5N1 clade 2.3.4.4b viruses. As such, continued monitoring of the global situation and ongoing surveillance within Australia will be required.

---

<sup>3</sup> Migratory bird movements, in particular waterfowl, into North America are infrequent compared to movements between North America and South America. There were two introductions which subsequently established and spread in north America over a period of several months, whereas there were multiple introductions into South American over a much shorter timeframe (Alkie et al. 2022; Ariyama et al. 2023). Migratory bird connectivity to Australia may present reduced frequency compared to North America scenario. **NOTE: since 20 July 2023, studies have now shown there were multiple introductions to North America (Ramey et al. 2023).**

## Overall risk question

What is the risk (likelihood and consequence) of HPAI H5N1 clade 2.3.4.4b incursions into Australia via wild birds with establishment in wild birds, poultry, and/or wild mammals?

## Risk definitions

**Table 1.** Likelihood Terminology (WHO et al. 2021)

Probability level	Definition
Negligible	Almost certain not to occur except in exceptional circumstances
Low	Unlikely to occur
Moderate	May occur
High	Likely to occur

**Table 2.** Uncertainty Terminology (WHO et al. 2021)

Uncertainty probability level	Definition
Very low	Reliable data and information are available in sufficient quantity with extensive data and/or concrete information
Low	Reliable data and information is available but may be limited in quantity, or be variable; results based on expert consensus
Moderate	Some gaps in availability or reliability of data and information, or conflicting data; results based on limited consensus
High	Limited data or reliable information available; results based on educated guess
Very high	Lack of data or reliable information; results based on crude speculation only

## Event likelihood summary

**Table 3.** HPAI H5N1 clade 2.3.4.4b overarching likelihood summary

Event	Likelihood	Uncertainty
HPAI virus incursions via <b>wild birds</b> :		
via movements along the East Asian-Australasian flyway	Moderate	Moderate
via movements within Australo-Papuan region	Moderate	Moderate
HPAI virus exposure and establishment in resident <b>wild birds</b>	Moderate/High <sup>4</sup>	Moderate
HPAI virus exposure and establishment in <b>poultry</b> via wild birds	Low/Moderate <sup>4</sup>	Moderate
HPAI virus exposure and establishment in <b>wild mammals</b> via wild birds	Low <sup>5</sup>	High

<sup>4</sup> Two likelihood levels are provided given substantially variable risk pathways. For further details see Entry and Exposure Assessments in Tables 8 and 9 below.

<sup>5</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), HPAI emerged in the sub-Antarctic, thousands more wild birds and marine mammals have been infected, and a considerable number of scientific studies have been published addressing the ecology, evolution, virology, pathogenicity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular the risk to marine mammals.

## Consequence summary

**Table 4.** Consequence definitions

Description	Definition
Insignificant	No detectable conservation or welfare effects; effect unlikely to be recognised at any level within Australia.
Very minor	Local short-term population loss or economic impact, no significant ecosystem effect; OR mild animal welfare effects; effect is likely to be minor to directly affected parties
Minor	Some localised, reversible ecosystem impact; OR mild animal welfare effects; effect and significant to directly affected parties.
Moderate	Measurable long-term damage to populations and/or ecosystem, but little spread, no extinction; OR more significant animal welfare effects; effects significant within the region, with economic and social effect highly significant to directly affected parties; recognised on a national level.
High	Long-term irreversible ecosystem change, spreading beyond local area; OR significant animal welfare effects; effects highly significant within the region, with serious economic stability, societal values or social well-being limited to a given region; significant at the national level
Catastrophic	Widespread, long-term population loss affecting several species OR local extinction of a species, serious ecosystem effects; OR severe animal welfare effects; effect highly significant nationally, with economic stability, societal values or social well-being seriously affected; highly significant at the national level.

**Table 5.** Consequence of HPAI H5N1 clade 2.3.4.4b incursions via wild birds\*

Event	Consequence	Uncertainty
Establishment within wild bird populations	Catastrophic	Moderate
Establishment within poultry populations	High	Moderate
Establishment within wild mammal populations	Minor <sup>6</sup>	Moderate

\*Please refer to Table 13 for further consequence analysis

<sup>6</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), HPAI emerged in the sub-Antarctic, thousands more wild birds and marine mammals have been infected, and a considerable number of scientific studies have been published addressing the ecology, evolution, virology, pathogenicity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular the risk to marine mammals.

## Risk summary

**Table 6.** Risk estimation matrix (duplicated from Table 14)

		Consequences of HPAI entry and establishment					
		Insignificant	Very minor	Minor	Moderate	High	Catastrophic
Likelihood of entry and exposure	Negligible	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk
	Low	Negligible risk	Negligible risk	Low risk <sup>#</sup>	Low risk	Moderate risk <sup>*</sup>	High risk
	Moderate	Negligible risk	Very low risk	Low risk	Moderate risk	High risk <sup>*</sup>	High risk <sup>^</sup>
	High	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Extreme risk

<sup>^</sup>Risk for wild birds; <sup>\*</sup>Risk for poultry; <sup>#</sup>Risk for wild mammals

**Table 7.** Overall risk (likelihood and consequence) of HPAI H5N1 clade 2.3.4.4b incursions into Australia via wild birds

Risk	Risk level	Uncertainty
Risk of incursions and establishment in wild birds	High risk	Moderate
Risk of entry and establishment within poultry	Moderate/High risk	Moderate
Risk of entry and establishment with wild mammals	Low risk	High

## Introduction

The objective of this report is to evaluate changes in risk factors for currently circulating strains of high pathogenicity avian influenza (HPAI) worldwide to provide an updated risk assessment on the likelihood of entry, establishment and spread of HPAI in Australia via wild birds. The risk assessment is in response to the accelerating global outbreaks of HPAI H5N1 of clade 2.3.4.4b since October 2021. This panzootic is affecting wild birds, poultry and increasingly also wild mammals across all continents except Antarctica and Australia.

The report reviews and assesses HPAI H5N1 clade 2.3.4.4b viruses to inform the risk (likelihood of incursions and subsequent consequence) to Australia. With respect to previous risk assessments, the review also identifies and discusses changes in the current circulating viruses at the molecular, ecological and host levels in relation to movements of long-distance migratory birds and wild birds within the Australo-Papuan region. Whilst the primary focus of the risk assessment is the role of wild birds in the potential introduction of HPAI H5N1 clade 2.3.4.4b to Australia, the potential consequence to wild birds, poultry and mammals is also assessed.

## Background<sup>7</sup>

### Avian influenza and current global outbreaks

High pathogenicity avian influenza (HPAI; Influenza A virus, Family *Orthomyxoviridae*), or “bird flu”, is an infectious disease that causes severe illness and death in poultry and wild birds. HPAI can also cause disease in mammals, including rare cases in people. Since 2021, a new strain of HPAI, called HPAI H5N1 clade 2.3.4.4b, has caused significant illness and deaths in poultry and wild birds on all continents except Oceania. This strain of HPAI has not been detected in Australia.

Most avian influenza viruses (AIV) are of low pathogenicity, and are commonly found amongst wild birds, notably waterfowl (Anseriformes) and shorebirds, terns and gulls (Charadriiformes). While the first descriptions of outbreaks of HPAI date back to the late 1800s, outbreaks occurred only rarely. Between 1955, when the virus was identified, and 2000, there were only 18 outbreaks reported globally (Swayne and Suarez 2000). The situation changed with the emergence of the goose/Guangdong (gs/GD) HPAI H5 lineage. Since 2005, this lineage has regularly led to outbreaks in both poultry and wild birds, mainly in Eurasia. A step-change evolutionary shift in this lineage in 2014 (Lycett et al. 2019) resulted in more incursions into Africa in 2016 (Fusaro et al. 2019) and a spread to North America. Since October 2021, the intensity, geographic distribution, and number of wild bird species affected has radically changed (Figure 1) with 10489 reported outbreaks (*i.e.* notifications) of HPAI in wild birds and 8203 in poultry (domestic ducks, turkey, chickens etc) (data downloaded from [World Animal Health Information System of the World Organisation for Animal Health](#), updated 17 November 2023)(World Organisation for Animal Health 2022). Outbreaks in wild birds have largely occurred in the Northern Hemisphere, involving over 335 different bird species, in many bird Orders (Figure 2) resulting in at least 70,601 reported wild bird deaths and probably many more (Klaassen and Wille 2023). In the vast majority of cases the outbreaks are caused by HPAI H5N1 with very few outbreaks of H5N8 or other H5Nx subtypes. Where tested, all H5 subtypes appear to belong to HPAI H5 clade 2.3.4.4b, except in Asia. Prior to October 2021, most HPAI cases involving wild birds were discovered in locations in relative proximity to intensive poultry production

---

<sup>7</sup> This background section is a significantly abridged. A comprehensive overview of the current HPAI H5N1 clade 2.3.4.4b global situation is available in the original document and should be consulted for further detailed information.

(see Figure 1, overlap of blue [poultry outbreaks] and red [wild bird outbreaks]). However, recent outbreaks in wild birds have also been observed in areas geographic distant to intensive poultry farming, e.g., the Arctic, Faroe Islands<sup>8</sup>.

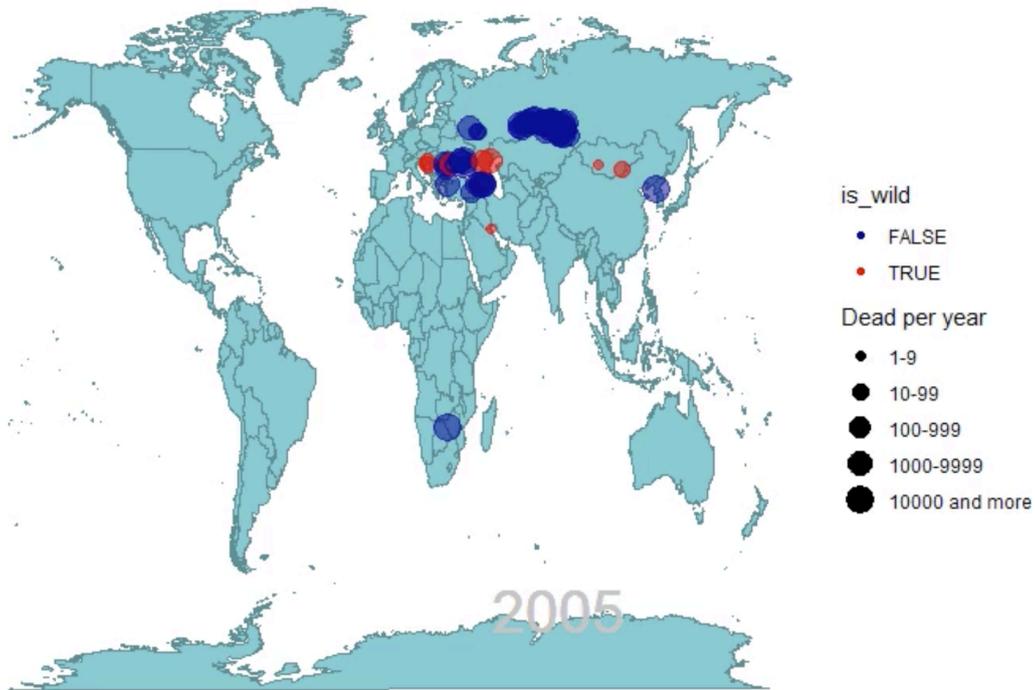


Figure 1. Animation of the annual distribution of number of H5 and H7 HPAI cases (i.e. bird deaths per 1 degree latitude and longitude) in poultry (blue) and wild birds (red) starting 2005, illustrating the considerable increase in incidences **from 2021 to 2023**. Animation can be found at <https://vimeo.com/895709099?share=copy>. Data from World Animal Health Information System. Note that, while very useful in depicting variations over time and space, the WAHIS data incompletely reflects to true scale of the panzootic amongst wild birds (e.g. number dead per year; see text). This figure provides data up to 23 November 2023.

<sup>8</sup> The global avian influenza situation is dynamic and since this report finalised (20 July 2023), HPAI has emerged in the sub-Antarctic. South Georgia and the Sandwich Island HPAI H5N1 detection in a brown skua report to WOA: <https://wahis.woah.org/#/in-review/5313?reportId=163628&fromPage=event-dashboard-url>

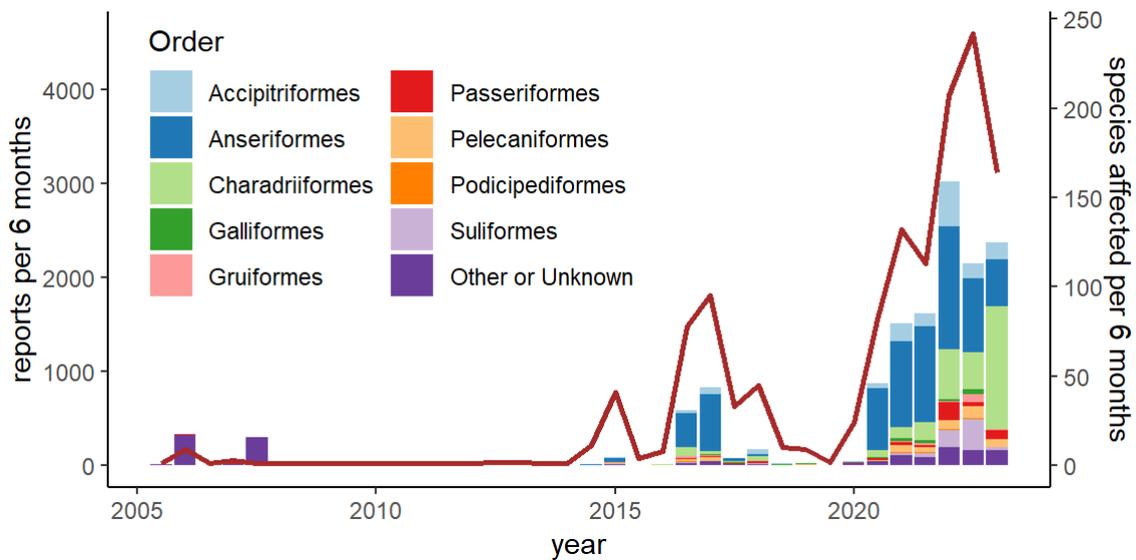


Figure 2. Total number of wild bird cases reported (stacked bars) and number of species involved (brown line) as a function of time (half yearly periods). The different colours denote the order to which the various species of birds belong. Data from World Animal Health Information System. From Klaassen and Wille (2023).

## Hazard identification

For the purposes of the risk assessment the hazard is HPAI H5N1 clade 2.3.4.4b.

The scope has been limited to HPAI H5N1 clade 2.3.4.4b (hereafter referred to as HPAI unless otherwise specified) because it is the dominant, currently circulating clade worldwide causing significant morbidity and mortality in wild birds and poultry. There have also been an increasing number of spillover infections in mammals<sup>9</sup> in addition to sporadic cases in humans.

## Risk assessment

A rapid qualitative risk assessment approach was undertaken according to established guidelines (WHO et al. 2021). The terminology associated with likelihood and uncertainty is defined in Tables 1 and 2.

## Scope

The report uses data available up to 20 July 2023. The risk assessment covers next 12 months until August 2024, noting a highest risk period from August 2023 until December 2023 which includes the annual spring wild bird migratory period.

If the global prevalence of HPAI disease stays the same or increases, the likelihood of HPAI incursions via wild birds into Australia increases (e.g. there is a higher likelihood that the incursion will occur at a point in the future), noting the assumptions detailed below.

<sup>9</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), HPAI emerged in the sub-Antarctic, thousands more wild birds and marine mammals have been infected, and a considerable number of scientific studies have been published addressing the ecology, evolution, virology, pathogenicity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular the risk to marine mammals.

The more widespread and abundant the virus is, the greater the overall exposure and infection pressure is. Therefore, the risk should be regularly re-assessed to incorporate any significant changes in the epidemiology in the region or globally.

Whilst the risk assessment does consider movement of virus via wild birds in terms of entry and establishment (within the area of arrival), spread of the virus within Australia (expansion of the geographical distribution) is not specifically addressed.

The risk of human infection with HPAI viruses derived from wild birds and poultry has been deemed out of scope for this review.

### Assumptions

Throughout the risk assessment process, a number of assumptions have been made including:

- There are no significant changes in the pathogenicity and virulence of the currently circulating clades of HPAI.
- Current biosecurity practices within Australian poultry establishments are maintained, including no vaccination of poultry with influenza vaccines.
- There are no significant weather events (e.g. drought, floods, bushfires) which may alter migration patterns of wild birds.
- There are no significant changes in the geographic distribution, abundance and host range of the currently circulating clades of HPAI.<sup>10</sup>

---

<sup>10</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), HPAI emerged in the sub-Antarctic, and the host range has expanded. A considerable number of scientific studies have been published addressing the ecology, evolution, virology, pathogenicity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular the risk to marine mammals.

## Entry Assessment

### Entry and exposure pathways via wild birds

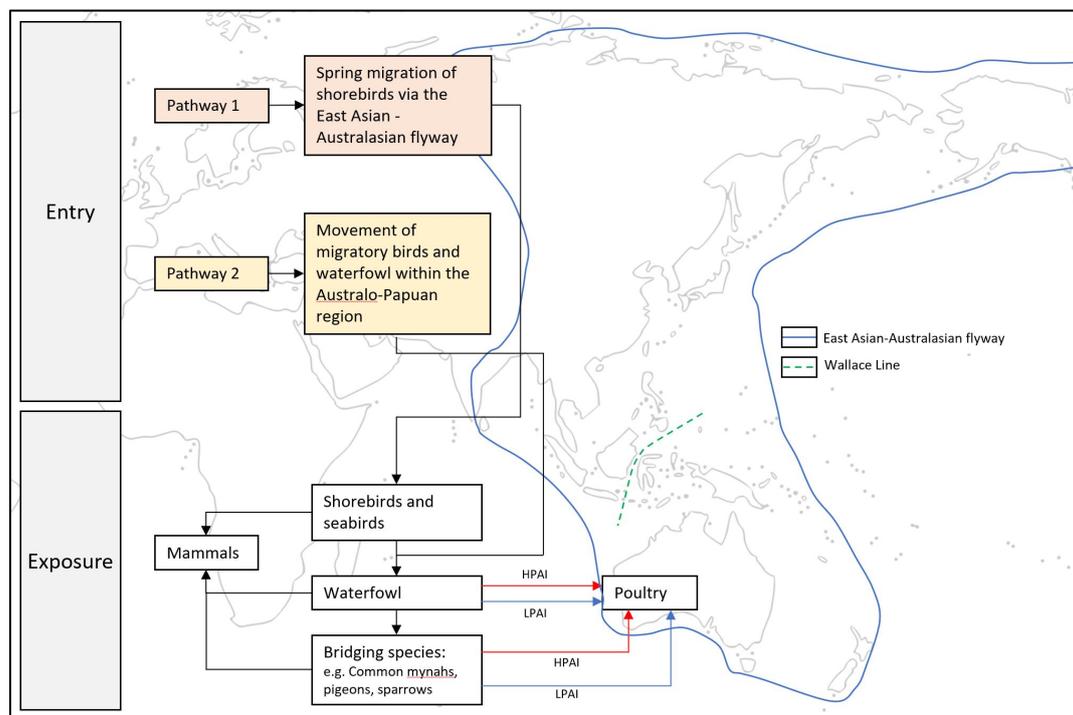


Figure 3. Entry and exposure pathways via wild birds

**Risk question 1a:** What is the likelihood of a HPAI incursion by long-distance migratory wild birds via movements along the East Asian-Australasian flyway?

**Risk question 1b:** What is the likelihood of a HPAI incursion by wild birds via movements within the Australo-Papuan region?

For the purpose of the risk assessment, entry is defined as the biological pathway/s of introduction of HPAI into Australia via wild birds.

Factors considered when assessing the likelihood of entry include:

1. Route of entry via wild birds:
  - a. Detections of HPAI viruses within the East Asian-Australasian flyway outside of the Australo-Papuan region within both wild birds and poultry.
  - b. Detections of HPAI viruses outside of Australia within the Australo-Papuan region in both wild birds and poultry.
2. Exposure and susceptibility of migratory birds to infection with the virus.
  - a. Exposure to HPAI viruses.
  - b. Prior reports of HPAI infection in bird taxa overseas (bird taxa known to migrate to Australia in the same order/family/genus).
  - c. Prior seroconversion of wild birds to other AIVs, including HPAI.
3. Ability of wild birds to migrate whilst infected with the virus.
  - a. The route of migration, including the distance to Australia and ability to 'island hop'.
  - b. The pathogenicity of the virus.

### *Overarching considerations*

HPAI H5N1 clade 2.3.4.4b viruses have an increased capability to infect and disperse with wild birds. Previous to clade 2.3.4.4b, the likelihood for HPAI viral maintenance in wild birds in isolation for a prolonged period of time was low. The ability of clade 2.3.4.4b to infect a greater range of potential wild bird species, not normally susceptible, broadens the sources of onward exposure and infection. This clade's increased viral fitness is evidenced by the (multiple) entries, establishment and spread into North America (Alkie et al. 2022; Bevins et al. 2022; Ramey et al. 2023) and South America (Jimenez-Bluhm et al. 2023).

### **The increased viral abundance, geographic distribution and host range increases the number of wild birds likely to be exposed to and subsequently infected with HPAI H5N1 clade 2.3.4.4b.**

Since October 2021, HPAI outbreaks have been and continue to be reported across the Asia-Pacific region (Figure 1). The likelihood of incursions via wild birds into Australia will be determined by the geographic area where HPAI is present in the Asian-Pacific region. For the purpose of this risk assessment, the biogeographically boundary (the Wallace line, Figure 3) will be used to distinguish entry via long-distance migratory bird movements along the East Asian-Australasian flyway versus via wild bird movements within the Australo-Papuan region. The majority of bird migration within the Australo-Papuan region is nomadic and confined to locations east of the Wallace line. There is minimal waterfowl (Anseriformes) movement across this line which has been thought to limit HPAI virus incursions from South-East Asia to Australia (East et al. 2008b). However, it should be noted that a small number of species have distributions which extend across this line, such as the Pacific Black duck (*Anas superciliosa*) and Spotted Whistling duck (*Dendrocygna guttata*) (Purnell 2022; Roshier et al. 2012).

Although many studies on the factors contributing to successful entry, establishment and spread of pathogens into new environments tend to focus on pathogen traits and environmental conditions, increasing empirical and statistical evidence implicates propagule pressure (i.e., the number of introduction events multiplied by the number of individuals per introduction event) both temporally and spatially to be important (Simberloff 2009; Ogden et al. 2019). Thus, prevalence of outbreaks and virus circulation in neighbouring countries (particularly at key stopover sites for migratory birds) needs to be considered when assessing likelihood of entry into Australia, in addition to wild bird migration pathways and virus pathogenicity in wild birds (notably whether wild birds are able to migrate while infected).

**Table 8.** Likelihood of entry of HPAI via wild birds

Risk factor	Likelihood*	Uncertainty*	Rationale
<b>1a. HPAI virus incursions by long-distance migratory birds via movements along the East Asian-Australasian flyway</b>			<p><b>Risk is highest between August – December, the period during which long-distance migratory shorebirds arrive in Australia.</b></p> <ul style="list-style-type: none"> <li>- Indonesia has recently reported a detection of HPAI H5N1 clade 2.3.4.4b in domestic duck mortality event in South Kalimantan (west of the Wallace line) in April 2022 (<a href="https://wahis.woah.org/#/in-review/5041">https://wahis.woah.org/#/in-review/5041</a>). Further detections reported from the same location in March 2023 (based on a single sequence deposited in <a href="#">GISAID</a><sup>11</sup>).</li> <li>- Previous entry risk assessments for Australia for HPAI clade 2 deemed the likelihood of entry to be low via movements along the East Asian-Australasian flyway, largely because of limited interchange of Anseriformes (waterfowl) species between Australia and Asia and the infrequent detection of AIVs in Charadriiformes (notably shorebirds) and other species that do migrate long distances along the flyway (Curran, 2012; Tracey et al. 2004; McCallum et al. 2008).</li> <li>- Some 40 species of shore-, sea- and land birds migrate from Asia to the Australo-Papuan region (Dingle 2004), comprising millions of individuals, annually migrating from predominantly Asia but also North America to Australia (McCallum et al. 2008). Millions of migratory birds thus use stopover sites in countries where 2.3.4.4b is endemic in poultry (although data on circulation in wild birds in these countries is limited).</li> <li>- The number of migratory shorebirds coming to Australia from outside Australo-Papua has decreased over the past decades (Clemens et al. 2016), however concurrently, more recent and detailed tracking studies have shown shorebirds to fly directly from East Asia to Australia during non-stop flights at speeds of around 1500 km/day (e.g. Lisovski et al. 2021). Thus, the distance between regions where HPAI H5N1 clade 2.3.4.4b is endemic and Australia can potentially be crossed by shorebirds within 1 – 4 days.</li> <li>- LPAI viruses are known to occasionally arrive in Australia via migratory wild birds from overseas (Bhatta et al. 2020; Hoque et al. 2015; Hoye et al. 2021; Hurt et al. 2006; Kishida et al. 2008; Vijaykrishna et al. 2013; Wille et al. 2022), which subsequently circulate and some eventually going extinct. Within Australia, LPAI virus sequences forming distinct Australian lineages (Bulach et al. 2010; Hansbro et al. 2010; Hoye et al. 2021; Wille et al. 2022).</li> <li>- Australian wild bird AIV studies to date demonstrate that LPAI detections in migratory shorebirds occur predominantly in autumn and winter (pre-departure from Australia), as opposed to in the Australian spring in newly arrived birds (Curran 2012; Curran et al. 2014; Hansbro et al. 2010; Hoye et al. 2021, Wille et al. 2023a).</li> <li>- Charadriiformes (notably shorebirds) are known hosts to LPAI viruses globally and within Australia (e.g. Curran et al. 2013; Hansbro et al. 2010; Haynes et al. 2009; Grillo et al. 2015; Olsen et al. 2006; Wille et al. 2022) and have been considered candidates for HPAI entry to Australia (East et al. 2008a).</li> <li>- Spread by migratory Procellariformes (notably seabirds) was previously deemed negligible based on low AIV prevalence typically detected (Tracey et al. 2004, Wille et al. 2023a) and the fact they rarely make landfall. However, Procellariformes have been poorly surveyed for AIV over the last three decades (Lang et al. 2016),</li> </ul>
Exposure & infection of migratory Charadriiformes via East-Asian-Australasian flyway	High	Very low	
Exposure and infection of migratory Procellariformes via East-Asian-Australasian flyway	Moderate	Moderate	
Ability of <b>Charadriiformes</b> to migrate whilst infected with HPAI virus.	Moderate	Moderate	
Ability of <b>Procellariformes</b> to migrate whilst infected with HPAI virus.	Moderate	Moderate	

<sup>11</sup> GISAID, the Global Initiative on Sharing All Influenza Data.

therefore it is not possible to make inferences on their role as reservoirs for LPAI or their putative role in movement of HPAI. Note, the 1<sup>st</sup> detection of LPAI in healthy wild birds was in wedge-tailed shearwaters in Australia (Downie and Laver 1973).

- There is increasing evidence for infection by HPAI H5N1 2.3.4.4b in migratory birds, particularly Charadriiformes (notably shorebirds) and Procellariiformes (notably seabirds) (WAHIS WOA data; Fig. 2), which have also been implicated in long-distance dispersal (Caliendo et al. 2022b; Yang et al. 2023)
- Evidence of HPAI infection in Procellariiformes include Southern (*Macronectes giganteus*) and Northern giant petrels (*Macronectes halli*) and a sooty shearwater (*Ardenna grisea*) in Chile and South Africa (FAO 2023) and short-tailed shearwater (*Puffinus tenuirostris*) in Alaska, USA in September 2023 (Department of Environmental Conservation, Alaska, 2023)
- A number of experimental studies demonstrate some shorebirds are able to tolerate infection with HPAI H5 (Reperant et al. 2011), particularly if previously exposed to LPAI H5 (Hall et al. 2013).
- Migratory shorebirds have also been shown to be exposed and infected with HPAI H5 (including clade 2.3.4.4) while on migration to Australia (Curran et al. 2014; Wille et al. 2019). However, currently no evidence these migratory birds are carrying infectious HPAI H5Nx clade 2.3.4.4 viruses when they arrive in Australia.
- Sampling of recently arrived migratory sea- and shorebirds (250 samples from short-tailed shearwaters (*Puffinus tenuirostris*) taken shortly after arrival from the northern Pacific region in the last week of September 2022); 500 samples from a variety of shorebird species 0-3 months after arrival from East Asia to NW Australia; 75 samples from Ruddy Turnstones (*Arenaria interpres*) caught on King Island, Tasmania in the first half of December), has revealed no evidence of infections with HPAI (Wille and Klaassen 2023). Serological testing also revealed that none of the birds sampled had experienced recent exposure to HPAI 2.3.4.4b (Wille and Klaassen 2023).

Risk factor	Likelihood*	Uncertainty*	Rationale
<b>1b. HPAI incursion by wild birds via movements within Australo-Papuan region</b>			<ul style="list-style-type: none"> <li>- No reports of HPAI H5N1 2.3.4.4b within the Australo-Papuan region to date in poultry nor wild birds.</li> <li>- Indonesia comprises states both within and outside of the Australo-Papuan region (e.g. the Wallace line cuts through Indonesia). Poultry production in Indonesia has increased (Statistica 2023). HPAI H5N1 2.3.4.4b has been detected in South Kalimantan, Indonesia, outside of the Australo-Papuan region.</li> <li>- Poultry are an increasing source of protein in New Guinea (Kohun et al. 2015; Nurhasan et al. 2022).</li> <li>- Long distance migratory wild birds (shorebirds) do stop on the island of New Guinea during migrations (Lisovski et al. 2021). Frequent yet irregular movements of ducks, geese, and other waterbirds movements of migratory and nomadic birds occur within the Australo-Papuan region (Roshier et al; McCallum et al. 2008; East et al 2008b). The range of some populations of Australian waterfowl extends to the archipelagos of SE Asia, including species that are highly dispersive within Australia (Pacific Black Duck: <i>Anas superciliosa</i>, Grey Teal: <i>Anas gracilis</i> and Wandering Whistling Duck: <i>Dendrocygna arcuata</i>). However, significant temporal, spatial and research gaps preclude a full understanding of bird movements between Australia and the islands to the north (Purnell 2022).</li> <li>- Movement and phylogenetic studies show migratory (waterfowl) birds have a role in spread of HPAI H5N8 virus clade 2.3.4.4 across Eurasia (Zhang et al. 2023; Teitelbaum et al., 2023). Recent tracking studies in China show Mallards (<i>Anas platyrhynchos</i>) are capable of flying hundreds of kilometres while infected with HPAI H5N8 clade 2.3.4.4b virus (Lv et al. 2022).</li> <li>- One study on HPAI H5N1 2.3.4.4b pathogenicity in wild birds (Spackman et al. 2023) found 58% of ducks were sub-clinically infected and 65% of Mallard ducks shed virus cloacally for 14 days (considerably longer than what is normally found in ducks infected with other AIVs); suggesting increased potential for superspreading by some individuals (Lloyd-Smith et al. 2005). Other experimental infections studies (as of 20 July 2023) with HPAI H5Nx 2.3.4.4b viruses include: one study 8/8 common teal were infected with H5N6 2.3.4.4b virus, shed viruses for a prolonged period, via the trachea more than the cloaca, without displaying distinctive clinical signs (Tanikawa et al. 2021), and another study using H5N8, in which 6 of 7 mallards, naturally pre-exposed to LPAI viruses, recovered completely after initial mild clinical signs, with virus shedding reduced in the seropositive mallards compared to seronegative mallards (Koethe et al. 2020). However, multiple studies also indicate high pathogenicity and increased waterbird adaption of clade 2.3.4.4b viruses (Banyard et al. 2022; Caliendo et al. 2022a; Grund et al. 2018; James et al. 2023)</li> <li>- Detection of Eurasian HPAI H5N1 in apparently healthy hunter-harvested wild ducks in USA indicates potential for active infection and shedding without obvious clinical signs (Bevins et al. 2022; USDA et al. 2016). Telemetry data from a single HPAI infected wild lesser scaup (<i>Aythya affinis</i>; a diving duck) suggest this bird may have been shedding virus for some period prior to death, with opportunities for direct bird-to-bird or environmental transmission (Prosser et al. 2022).</li> </ul> <p><b>Note: Overarching likelihood changes to HIGH if HPAI H5N1 2.3.4.4b is detected within the Australo-Papuan region, with the risk period being all year-round with frequent yet irregular movements of birds within the region with no seasonal patterns.</b></p>
Exposure & infection of nomadic waterfowl within the Australo-Papuan region	Low	Moderate	
Ability of nomadic waterfowl to 'island-hop' and migrate whilst infected with HPAI virus.	High	Low	

\*See Table 1 for likelihood terminology definitions.

### *Summary*

**Risk question 1a: What is the likelihood of a HPAI incursion by long-distance migratory wild birds via movements along the East Asian-Australasian flyway?**

This question assesses the likelihood of wild migratory birds being infected outside the Australo-Papuan region and arriving in the Australo-Papuan region or Australia still infected and infectious. Overall, the likelihood has been assessed as **MODERATE** with **moderate** uncertainty.

**Risk question 1b: What is the likelihood of a HPAI incursion by wild birds via movements within the Australo-Papuan region?**

This question assesses the likelihood that wild migratory birds are infected in the Australo-Papuan region, outside of Australia but south of the Wallace line and arrive in Australia still infected and infectious with no reports of HPAI H5N1 2.3.4.4b within the region. Overall, the likelihood has been assessed as **MODERATE** with **moderate** uncertainty. Noting that the likelihood will increase to **HIGH** if HPAI H5N1 is reported in the Australo-Papuan region.

Compared with previous risk assessments the likelihood of HPAI incursions into Australia has **increased** as a result of the new clade of H5N1 2.3.4.4b producing significant changes in the ecology of HPAI with respect to wild birds.

## Exposure Assessment

For the purposes of this risk assessment, exposure is defined as the first opportunity for transmission of the virus within Australia, and establishment is defined as subsequent perpetuation of the virus within a resident animal population (e.g., single or multiple poultry flocks or wild bird nesting sites) (COAG, 2019). Exposure may lead to subsequent establishment of the virus and spread within Australia pathways for exposure are shown in Figure 3. Exposure to HPAI could occur via one or multiple migratory wild birds following arrival in Australia or via one or multiple resident wild birds following establishment in resident wild bird populations, noting a key epidemiological feature associated with current outbreaks in poultry overseas, is the ability of wild birds to directly infect poultry with HPAI viruses<sup>12</sup>.

Factors considered when assessing the likelihood of exposure and establishment include:

1. The pathway of introduction.
2. The number of exposure events including contact rates and transmission probabilities between infected and susceptible animals.
3. The species susceptibility to infection.
4. Distribution of susceptible populations (e.g., poultry).
5. Survival in the environment.

### *Overarching considerations*

The number of exposure events may be somewhat informed by sequence analysis of LPAI viruses that indicate that incursions of AIVs into Australia occur, but are infrequent (Kishida et al 2008, Vijaykrishna et al 2013, Wille et al 2022). However, the current 2.3.4.4b clade has the potential to increase the number of incursions given the high viral loads in the countries of origin of the migratory birds.

Both specific mutations as well as gene segment reassortment in AIVs can result in changes to the virus' infectivity, pathogenicity and host immune response, manifested in the tissue tropism of the virus and changes in viral shedding. The end result can be a HPAI virus that is more or less evolutionarily "fit". High rates of reassortment in 2.3.4.4 H5Nx viruses (including 2.3.4.4b H5N1) have been observed (Bi et al. 2016; Kandeil et al. 2022; Xie et al. 2023), with a substantial fitness advantage currently observed with H5N1 2.3.4.4b viruses. Based on a review of the literature, comprehensive profiles to explain the virus' fitness and pathogenicity in domestic and wild birds have yet to be developed<sup>13</sup>. However of the studies of HPAI H5N1 2.3.4.4b virus fitness and pathogenicity that have recently become available (Spackman et al. 2023; Vigeveno et al. 2020; Grund et al. 2018), Grund et al. (2018) and Leyson et al (2021) have revealed increased virulence, pathogenicity and higher viral shedding of H5N8 2.3.4.4b virus in ducks compared to the H5N8 2.3.4.4a virus. Based on experimental data (Kandeil et al. 2022; Scheibner et al. 2022; Vigeveno et al. 2020), there is also evidence that subsequent reassortment will have a substantial impact on the phenotype of these viruses (e.g. virulence and pathology), with further studies still exploring this in both birds and mammal models (Kandeil et al. 2022; Kobasa et al. 2023).

---

<sup>12</sup> World Organisation for Animal Health (WOAH) infographic: <https://www.woah.org/app/uploads/2023/06/avian-influenza-understanding-new-dynamics-to-better-combat-the-disease.pdf>

<sup>13</sup> A considerable number of scientific studies continue to be published addressing the ecology, evolution, virology, pathogenicity, and infectivity of this virus. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course.

Whilst virulence and pathogenicity will influence ability for onward transmission, the current increased ability to infect a wide range of wild bird species, results in more frequent presentation of infection, and therefore greater opportunities for onward transmission. The susceptibility of the wild bird species to infection may also impact exposure and establishment.

Distribution of waterfowl may also impact the likelihood of exposure and establishment. For example, due to extensive rainfall over the past three years, waterfowl are spread out over large parts of the country, resulting in low densities and limited chances for the development of an epizootic in wild birds following entry of HPAI into Australia (cf. Ferenczi et al. 2021).

### Survival in the environment

Whilst there are limited studies examining the persistence of H5N1 clade 2.3.4.4b viruses in the environment, data from the UK indicated from the current HPAI H5N8 clade (2020/21) may persist for 50% longer at 4°C and 40% longer at 20°C than previous H5N8 viruses from 2016/17 (DEFRA 2021). Longer survival of the virus in the environment, particularly in water bodies (Furness et al., 2023) promotes greater exposure for the same level of shedding from each bird, resulting in a greater observed host range. Higher viral shedding by waterbirds and increased numbers of infected carcasses may lead to increased environmental contamination (EPIC 2023; Grund et al., 2018). Studies from Australia suggest decreased temperatures in southern Australia may increase virus survival times compared with northern Australia (Curran 2012; Dalziel et al. 2016; DEFRA 2022).

Risk question 2: What is the likelihood of HPAI exposure and establishment in wild birds in Australia?

The exposure assessment examines the risk pathways associated with infected migratory birds (e.g. long-distance migratory birds or nomadic waterfowl) infecting resident wild birds with subsequent transmission between resident wild birds within Australia.

**Table 9:** Likelihood of HPAI exposure and establishment in resident wild birds in Australia given two pathways of introduction.

Risk Pathway	Likelihood	Uncertainty	Rationale
via long distance migratory birds' movements along the East-Asian-Australasian flyway	Moderate	Moderate	<ul style="list-style-type: none"> <li>- The first landing point for the vast majority of migratory species is in the northern states and territories, in particular around the coastline, particularly in the north and north-west, although some species also land with southern states (East et al. 2008a; <a href="https://vwsg.org.au/waders/geolocator-studies/">https://vwsg.org.au/waders/geolocator-studies/</a>).</li> <li>- RAMSAR wetlands, significant shorebird areas and the Important Wetland Areas for migratory shorebirds (including arrival sites) are areas where resident waterfowl occur (BirdLife Australia 2020; East et al. 2008a; Tracey 2005; Warner et al. 2006).</li> <li>- Whilst the number of long-distance migratory shorebirds coming to Australia from outside Australo-Papua has decreased over the past decades (Clemens et al. 2016), for the 37 listed migratory shorebird species, numbers arriving each year in spring are in the order of 8.5 million (Hansen et al. 2016; Hansen et al. 2022; Runge et al. 2017) and detailed tracking studies have shown shorebirds to fly directly from East Asia to Australia during non-stop flights at speeds of around 1500 km/day (e.g. Lisovski et al. 2021). In 2022, a bar-tailed godwit (shorebird) completed a non-stop 11-day migration of 8,425 miles from Alaska to Tasmania<sup>14</sup>.</li> <li>- The origin of many of these species is the northern hemisphere in which HPAI outbreaks are numerous and ongoing and all species of wild birds are likely to be susceptible to infection.</li> <li>- Phylogenetic data from (Wille et al. 2022) demonstrate that LPAI detection in shorebirds in Australia is followed by lineage extinction in LPAI, however it is unclear whether this will also be the case for HPAI.</li> <li>- Data from (Hicks et al. 2023) show few transition events between shorebirds and ducks, relative to transition events between different duck species.</li> <li>- Based on Australian LPAI studies there is a chance the virus may go extinct following the first detection/introduction (Wille et al. 2022) and/or may not be transmitted from shorebirds to ducks (Hicks et al. 2023).</li> <li>- Previous studies assessed the risk of establishment of H5N1 HPAI clade 2 (via transfer of from migratory shorebirds to native waterfowl) as moderate in the vicinity of Broome in the Kimberley region of Western Australia (East et al. 2008a), noting HPAI H5N1 clade 2.3.4.4b viruses risk factors significantly differ from previous HPAI H5 viruses.</li> </ul>

<sup>14</sup> USGS News 3<sup>rd</sup> November 2023: <https://www.usgs.gov/centers/alaska-science-center/news/juvenile-bar-tailed-godwit-b6-sets-world-record>

			<ul style="list-style-type: none"> <li>- Temperature and environmental conditions may be less suitable for virus survival in the environment in northern Australia, despite limited data suggesting increased survival times for the 2.3.4.4b clade (Curran 2012; Dalziel et al. 2016; DEFRA 2022).</li> </ul>
via nomadic waterfowl movements within Australo-Papuan region	High	Low	<ul style="list-style-type: none"> <li>- The first landing point for nomadic waterfowl species is likely to be in the northern states and territories (<a href="https://vwsg.org.au/waders/geolocator-studies/">https://vwsg.org.au/waders/geolocator-studies/</a>).</li> <li>- Movements of these species within the Australo-Papuan region are frequent yet irregular (Roshier et al; McCallum et al. 2008; East et al 2008b).</li> <li>- Native waterfowl are currently widely dispersed across Australia due to high rainfall, this situation is likely to change. During the imminent El Nino, ephemeral wetlands dry out, when waterfowl and other waterbirds start concentrating in permanent wetlands, including dams on farms, followed by an increased risk of spillovers into poultry (Klaassen et al. 2011; Ferenczi et al. 2021).</li> <li>- Temperature and environmental conditions may be less suitable for virus survival in the environment in northern Australia, despite limited data suggesting increased survival times for the 2.3.4.4b clade (Curran 2012; Dalziel et al. 2016; DEFRA 2022)</li> <li>- Data from (Hicks et al. 2023) show many transition events of LPAI between duck species.</li> <li>- Phylogenetic data from (Wille et al. 2022) do not show any evidence lineage extinction if detected in ducks (compared to extinction of shorebird incursions).</li> </ul>

### Summary

#### Risk question 2: What is the likelihood of HPAI exposure and establishment in wild birds in Australia?

Compared with previous risk assessments, the likelihood of exposure and establishment within wild birds in Australia has **increased** as a result of the potential alternative pathway via nomadic waterfowl movements and the ability of HPAI H5N1 clade 2.3.4.4b to infect a wide range of migratory wild bird species.

Overall, the likelihood of exposure and establishment of resident populations of wild birds in Australia to HPAI H5N1 clade 2.3.4.4b following entry via wild bird pathway is assessed as **MODERATE/HIGH** with **moderate** uncertainty.

### Risk question 3: What is the likelihood of HPAI exposure and establishment in poultry?

**The exposure assessment examines the risk pathways associated with infected migratory birds (e.g. long-distance migratory birds or nomadic waterfowl) infecting single or multiple poultry flocks with subsequent transmission within a poultry system (e.g. single farm).**

A key change in the epidemiology associated with current H5N1 outbreaks in poultry is the ability of wild birds to directly infect poultry with HPAI viruses (<https://www.woah.org/app/uploads/2023/06/avian-influenza-understanding-new-dynamics-to-better-combat-the-disease.pdf>). Evidence using molecular sequence analysis suggests 83 percent of HPAI 2.3.4.4b outbreaks on commercial chicken farms in South Africa were due to wild bird introductions or movement from the contaminated environment into the operations (Abolnik et al. 2023). In the USA, at least 84 percent of analysed HPAI detections in poultry were consistent with independent wild bird introductions and in Sweden sequenced viruses detected in poultry and captive birds clustered phylogenetically with the sequences detected in wild birds (Grant et al. 2022; USDA 2022). Previously, typical infection pathways in Australia involved exposure to wild bird LPAI viruses and subsequent mutation to HPAI within poultry flocks. If HPAI H5N1 clade 2.3.4.4b enters Australia, the direct route of HPAI infection via wild birds increases the risk of exposure and subsequent establishment within poultry systems. In addition, high viral shedding of clade 2.3.4.4b viruses means that there is the potential for greater environmental contamination. Poultry are highly susceptible to clade 2.3.4.4b viruses with high mortalities and variable rates of transmissibility (Kwon et al. 2023).

There is potential for contact between wild birds and poultry in Australia. This is evidenced by camera trapping studies on poultry farms (Scott et al. 2018a). Of consideration is that there have been eight HPAI outbreaks in Australian poultry, and in all instances, viruses evolved from Australian wild bird LPAI viruses, demonstrating contact between poultry and wild birds. However, the frequency of spillover events is probably much higher than the number of HPAI outbreaks suggest; exactly how often, when and where AIV spillovers from wild birds into poultry systems take place, is unknown. Studies considering LPAI viruses in wild birds in Australia, assessed the probability of a first LPAI virus exposure to a chicken in an Australian commercial chicken farms from one wild bird at any point in time is extremely low (Scott et al, 2018b). The contact rates will also be dependent on the production system (e.g. cage, barn, free-range) and poultry type (e.g. duck, chicken, turkey) as well as level of biosecurity applied.

Whilst waterfowl are currently widely dispersed across Australia due to high rainfall, this situation is likely to change. During the imminent El Nino, ephemeral wetlands dry out, when waterfowl and other waterbirds start concentrating in permanent wetlands, including dams on farms, followed by an increased risk of spillovers into poultry (Klaassen et al. 2011; Ferenczi et al. 2021).

However, despite these factors, it is likely that subsequent management decisions (e.g. movement restrictions, housing orders, and rapid depopulation) will significantly mitigate the risk of establishment within the poultry population as has recently been seen in Japan (<https://www.woah.org/app/uploads/2022/07/2022-06-japan-self-d-hpai.pdf>)<sup>15</sup>.

---

<sup>15</sup> HPAI H5N1 has since re-occurred in Japan, with formal notification to WOA in November 2023: Japan - High pathogenicity avian influenza viruses (poultry) (Inf. with) - Immediate notification: <https://wahis.woah.org/#/in-review/5360?reportId=164121&fromPage=event-dashboard-url>

**Table 10.** Likelihood of HPAI exposure and establishment in poultry.

Risk factor	Likelihood	Uncertainty	Rationale
Co-location of wild birds and poultry in northern Australia	Low	Moderate	<ul style="list-style-type: none"> <li>- The first landing point for the vast majority of migratory species is in the northern states and territories, in particular around the coastline, particularly in the north and north-west, although some species also land with southern states (East et al. 2008a; <a href="https://vws.org.au/waders/geolocator-studies/">https://vws.org.au/waders/geolocator-studies/</a>).</li> <li>- There is frequent yet irregular movement of waterfowl driven by strong environmental conditions within the region (Ferenczi et al. 2016), with no apparent or consistent seasonal patterns in contrast to movements by long-distance migratory birds.</li> <li>- There are a limited number of poultry properties in these areas, reducing opportunities for exposure of poultry (OCVO 2010; East et al. 2008a, 2008b).</li> </ul>
Co-location of wild birds and poultry in southern Australia	Moderate	Moderate	<ul style="list-style-type: none"> <li>- Some long-distance migratory birds land directly within southern states and territories from overseas to a lesser extent during the spring migratory period.</li> <li>- Whilst East et al. 2008 noted low risk to southern states via nomadic waterfowl this assessment was based on HPAI H5 clade 2 viruses. Waterfowl can move significant distances. Detailed assessment of this pathway was not assessed for clade 2.3.4.4b viruses, given limited current understanding.</li> <li>- Whilst there are fewer wild bird landing sites within southern states, this risk factor may be countered by the increased poultry and poultry property density in these states. Major chicken meat, chicken layer, duck, turkey, ratite and game bird farms in Australia are based in Southern Australia (OCVO 2010).</li> </ul>

*Summary*

**Risk question 3: What is the likelihood of HPAI exposure and establishment in poultry?**

Compared with previous risk assessments the risk to poultry has increased despite strong poultry biosecurity, as the broad species susceptibility of HPAI H5N1 clade 2.3.4.4b increases the likelihood of an infected wild bird visiting a poultry premises, however uncertainty is high.

Overall, the probability of HPAI H5N1 clade 2.3.4.4b entering Australia via a migratory bird with exposure and establishment in poultry is assessed **LOW/MODERATE** with **moderate** uncertainty dependent on the location of poultry within Australia.

#### Risk question 4: What is the risk of HPAI exposure and establishment in mammals?

**The exposure assessment examines the risk pathways associated with infected migratory birds (e.g. long-distance migratory birds or nomadic waterfowl) infecting single or multiple resident wild mammals with subsequent transmission between wild mammals.**

While risk assessments deem 2.3.4.4 viruses to have low human pandemic potential (WHO 2022), there is concern over the ever-increasing list of mammalian hosts that have been infected with 2.3.4.4b H5N1 viruses (Chestakova et al. 2023). Multiple spillover events into a wide range of mammals from wild birds have been documented overseas, particularly in species that predate or scavenge on infected birds, such as carnivores (FAO 2023; Elsmo et al. 2023).

While wild mammals are considered dead-end hosts, viruses isolated from a large number of mammals had a range of critical mutations facilitating mammalian infection (e.g. PB2 E627K) (Alkie et al. 2023; Bordes et al. 2023; Elsmo et al. 2023; Vreman et al. 2023). Of substantially greater concern are the several mass-mortality events in mammals<sup>16</sup>, with suggestion, although no direct evidence, of mammal-to-mammal transmission (e.g., Agüero et al. 2023; Gamarra-Toledo et al. 2023; Puryear et al. 2023), and subsequent confirmation of direct mammal-to-mammal transmission in experimental challenge studies (Agüero et al. 2023). Obviously, there is great need for ongoing monitoring of H5N1 clade 2.3.4.4b viruses for adaptive mutations in mammals in view of the potential pandemic risk for humans.

Contact rates between wild birds and mammals may be somewhat lower in Australia compared with other continents due to fewer species of predatory and scavenging mammals, in particular in the north of Australia, noting assessment of species abundance, densities, as well as carcass decomposition and inter-species interactions requires further consideration (Feral Scan; Newsome and Barton 2023). The contact rates will also be dependent on the scale of outbreaks in wild birds, which will affect the density of contaminated carcasses in the environment.

#### *Summary*

##### **Risk question 4: What is the risk of HPAI exposure and establishment in mammals?**

Compared with previous risk assessments the risk of HPAI exposure in wild mammals has **increased**, however despite the broad species susceptibility and pathogenicity of HPAI H5N1 clade 2.3.4.4b, sustained mammal-to-mammal transmission within wild populations has not yet been confirmed and establishment has not been observed overseas.

The likelihood of exposure and establishment of HPAI within wild mammal populations is assessed as **LOW** with **high** uncertainty.<sup>17</sup>

<sup>16</sup> This now spanning more than 20 000 individuals, with affected mammals mostly species that predate or scavenge on infected birds or live in close proximity to infected birds (e.g. marine mammals (Breed et al. 2023; Gamarra-Toledo et al. 2023; FAO 2023; Ulloa et al. 2023; Wille et al. 2023). Species include foxes, seals and sea-lions, dolphins, bears, felids, opossums, coatis and mustelids including wild otters and farmed American Mink (Agüero et al., 2023). A list of mammalian species affected by H5Nx HPAI (excluding laboratory animals and humans) is currently maintained by the FAO (2023).

<sup>17</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), thousands more marine mammals have been infected. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular exposure and consequence assessment for marine mammals.

## Estimation of the likelihood of entry and exposure

Table 11 provides a matrix for combining the likelihood of entry of HPAI via wild birds and the likelihood of exposure to give an overall likelihood estimate.

**Table 11: Matrix for combining entry and exposure**

		Likelihood of entry			
		Negligible	Low	Moderate	High
Likelihood of exposure and establishment	Negligible	Negligible	Negligible	Low	Low
	Low	Negligible	Low	Low	Moderate
	Moderate	Low	Low	Moderate	Moderate
	High	Low	Moderate	Moderate	High

### Summary

The overall likelihood of entry, exposure and establishment of HPAI in wild birds is assessed as **MODERATE** (with moderate uncertainty).

The overall likelihood of entry, exposure and establishment of HPAI via wild birds in poultry is assessed as **LOW/MODERATE** (with moderate uncertainty).

The overall likelihood of entry, exposure and establishment of HPAI via wild birds in mammals is assessed as **LOW** (with high uncertainty).<sup>18</sup>

<sup>18</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), thousands more marine mammals have been infected. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular exposure and consequence assessment for marine mammals.

## Consequence analysis

**Table 12.** Consequence definitions

Description	Definition
Insignificant	No detectable conservation or welfare effects; effect unlikely to be recognised at any level within Australia.
Very minor	Local short-term population loss or economic impact, no significant ecosystem effect; OR mild animal welfare effects; effect is likely to be minor to directly affected parties
Minor	Some localised, reversible ecosystem impact; OR mild animal welfare effects; effect and significant to directly affected parties.
Moderate	Measurable long-term damage to populations and/or ecosystem, but little spread, no extinction; OR more significant animal welfare effects; effects significant within the region, with economic and social effect highly significant to directly affected parties; recognised on a national level.
High	Long-term irreversible ecosystem change, spreading beyond local area; OR significant animal welfare effects; effects highly significant within the region, with serious economic stability, societal values or social well-being limited to a given region; significant at the national level
Catastrophic	Widespread, long-term population loss affecting several species OR local extinction of a species, serious ecosystem effects; OR severe animal welfare effects; effect highly significant nationally, with economic stability, societal values or social well-being seriously affected; highly significant at the national level.

**Table 13.** Consequence assessment of HPAI H5N1 incursions via wild birds

Event	Consequence	Uncertainty	Impacts
Establishment of HPAI within wild bird populations	Catastrophic	Moderate	<ul style="list-style-type: none"> <li>- Animal welfare</li> <li>- Species dependent impacts to conservation status (CMS FAO Scientific Taskforce 2023; Pearce-Higgins et al. 2023, NatureScotland 2023, Harvey et al. 2023).</li> <li>- Based on evidence from overseas, there is potential for widespread, long-term population loss affecting several species (e.g. &gt; 2 species) or local extinction of a species.</li> <li>- Indirect ecological effects, for example, mortality of one species may open reproductive or foraging opportunities for others or alter predation rates. Such effects may be positive or negative. In Australia, this may favour invasive species.</li> <li>- Accumulation effect or age-related mortality risk resulting in populations not recovering their numbers fully from outbreaks.</li> <li>- Note: Australia has a number of unique endemic fauna not found elsewhere, therefore impacts may differ. The Australian black swan has recently been determined to be highly susceptible (Karawita et al. 2023).</li> <li>- Environmental impacts associated with increased dead bird carcasses</li> <li>- Social and cultural impacts (including indigenous communities)</li> </ul> <p>From Oct 2021-April 2023, over 335 species wild birds have been impacted in 8403 reported wild bird outbreaks</p>

			<p>reported to WOAH globally (Figure 1 &amp;2), some of them endangered (e.g. <a href="#">endangered Californian condors</a> (National Park Service 2023)).</p> <p>In multiple outbreaks the scale of mortality has been extremely high often involving deaths of 100s, 1,000s or 10,000s of individuals with significant proportions of birds, resulting mortality globally estimated to be in the millions (Klaassen &amp; Wille 2023; CMS FAO Scientific Taskforce 2023). Examples include ~30% UK breeding population of roseate terns, great skua and gannet mortalities of global significance (DEFRA 2023)<sup>19</sup>.</p>
Establishment of HPAI within poultry populations	High	Moderate	<ul style="list-style-type: none"> <li>- Animal welfare</li> <li>- Trade implications</li> <li>- Economic impact</li> <li>- Food supply</li> <li>- Increased risk of human exposure</li> </ul> <p>An outbreak scenario in Australia will be unlike previous eight HPAI outbreaks, due to the changes to the epidemiology of HPAI H5N1 2.3.4.4b and ability of wild birds to directly infect poultry (Swayne et al. 2023).</p>
Establishment of HPAI within wild mammal populations	Minor <sup>20</sup>	Moderate	<ul style="list-style-type: none"> <li>- Animal welfare</li> <li>- Species dependent impacts to conservation status</li> <li>- Environmental impacts associated with increased dead mammal carcasses</li> <li>- Social and cultural impacts</li> </ul> <p>An increasing diversity of mammalian species are being affected by disease (24 carnivore species, four species of marine mammal and some evidence in domestic pigs and wild boar), including mass mortality events in North and South America (Harvey et al. 2023, Swayne et al. 2023, Leguia et al. 2023, Puryear et al. 2023).</p>

<sup>19</sup> The scale of HPAI outbreaks is unprecedented in wild birds, with mass mortality events causing population level effects for several waterbird species (Wille et al. 2023).

<sup>20</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), thousands more marine mammals have been infected. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular exposure and consequence assessment for marine mammals (FAO 2023; Gamarra-Toledo et al. 2023; Ulloa et al. 2023; Wille et al. 2023).

### Summary

Extrapolating from global outbreaks of HPAI H5N1 clade 2.3.4.4b, there are likely to be significant consequences associated with incursion and establishment of HPAI in Australia via wild birds given a moderate likelihood of incursions. However, the frequency of HPAI incursions into Australia via wild birds may be significantly lower compared with other continents and as a result, containment of outbreaks may be more achievable in the Australian context if they are identified early.

If establishment of the disease occurs within Australian wild birds there are likely to be substantial welfare, conservation, social and economic impacts across multiple sectors including the poultry sector. Consequences to wild birds are assessed as **CATASTROPHIC** with **moderate** uncertainty, consequences to poultry are assessed as **HIGH** with **moderate** uncertainty and consequences to wild mammals are assessed as **MINOR** with **moderate** uncertainty.<sup>21</sup>

### Risk estimation

The risk estimation matrix combines the likelihood of entry and establishment of HPAI from Table 12 with the consequences of establishment as outlined in Table 15. This provides an overall estimation of the risk to wild birds, poultry and wild mammals.

**Table 14.** Risk estimation matrix

		Consequences of HPAI entry and establishment					
		Insignificant	Very minor	Minor	Moderate	High	Catastrophic
Likelihood of entry and exposure	Negligible	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk
	Low	Negligible risk	Negligible risk	Low risk <sup>#</sup>	Low risk	Moderate risk <sup>*</sup>	High risk
	Moderate	Negligible risk	Very low risk	Low risk	Moderate risk	High risk <sup>*</sup>	High risk <sup>^</sup>
	High	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Extreme risk

<sup>^</sup>Risk for wild birds; <sup>\*</sup>Risk for poultry; <sup>#</sup>Risk for wild mammals

<sup>21</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), thousands more marine mammals have been infected. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular exposure and consequence assessment for marine mammals.

### Summary

According to the risk estimation matrix, the overall risk estimates indicate that there is a **HIGH** risk associated with HPAI H5N1 clade 2.3.4.4b incursions and establishment into Australia for wild birds (with moderate uncertainty), a **MODERATE/HIGH** risk for poultry (with moderate uncertainty) and a **LOW** risk for wild mammals (with high uncertainty).<sup>22</sup>

### Uncertainties

There are a number of factors which limit interpretation of risk throughout this assessment. In particular, global under-reporting of wild bird cases, delays in reporting and reporting bias associated with increased reporting in areas of high human population density hamper the up-to-date assessment of risk of incursions via wild bird pathways.

There are few detailed animal studies involving the current H5N1 clade 2.3.4.4b virus at this point in time which limits a detailed assessment of some virological factors such as species susceptibility, minimum infective dose, shedding and virus stability. In particular, the role of species in close proximity to poultry farms such as common mynahs, sparrows and pigeons is unclear.

There are also few studies which directly assess the ability of wild bird species to migrate whilst infected with the current HPAI H5N1 clade, in particular long-distance shorebirds and species relevant to the Australian context. In addition, the effect of HPAI on the behaviour and movement of wild birds is unclear but in some seabird cases it is suggested that there may be increased long-distance spread (Jeglinski et al. 2023). We also have limited data on the ability of wild birds to migrate across the Wallace line into the Australo-Papuan region whilst infected with HPAI viruses and the risk posed by illegal poultry movement in this region.

Up to date Australian poultry demographic data is not readily accessible which has limited the ability to undertake spatial analysis of overlapping wild bird and poultry production sites.

It is also worth noting that a number of countries in the Asia-Pacific region rely on vaccines to control HPAI, and HPAI is endemic in many flocks. The use of vaccination may result in large viral loads of HPAI in poultry without evidence of clinical disease (i.e silent spread), leading to the absence of detections and notifications, particularly if adequate surveillance systems are not in place (Gobbo et al. 2022).

---

<sup>22</sup> The global avian influenza situation is dynamic and since this report was finalised (20 July 2023), thousands more marine mammals have been infected. As remaining knowledge gaps and uncertainties are being steadily addressed, sections of the risk assessment will be revised in due course, in particular exposure and consequence assessment for marine mammals.

## References

- Abolnik C, Phiri T, Peyrot B, de Beer R, Snyman A, Roberts D, Ludynia K, Jordaan F, Maartens M, Ismail Z, Strydom C, van der Zel G, Anthony J, Daniell N, De Boni L, Grewar J, Olivier A, Roberts L. (2023) 'The Molecular Epidemiology of Clade 2.3.4.4B H5N1 High Pathogenicity Avian Influenza in Southern Africa, 2021-2022', *Viruses*. 2023 Jun 16;15(6):1383. <https://doi.org/10.3390/v15061383>.
- Agüero M, Monne I, Sanchez A, Zecchin B, Fusaro A, Ruano MJ, Del Valle Arrojo M, Fernandez-Antonio R, Souto AM, Tordable P, Canas J, Bonfante F, Giussani E, Terregino C and Orejas JJ (2023) 'Highly pathogenic avian influenza A(H5N1) virus infection in farmed minks, Spain, October 2022', *Euro Surveill*, 28(3), <https://doi.org/10.2807/1560-7917.ES.2023.28.3.2300001>
- Alkie TN, Cox S, Embury-Hyatt C, Stevens B, Pople N, Pybus MJ, Xu W, Hisanaga T, Suderman M, Koziuk J, Kruczkiewicz P, Nguyen HH, Fisher M, Lung O, Erdelyan CNG, Hochman O, Ojkic D, Yason C, Bravo-Araya M, Bourque L, Bollinger TK, Soos C, Giacinti J, Provencher J, Ogilvie S, Clark A, MacPhee R, Parsons GJ, Eaglesome H, Gilbert S, Saboraki K, Davis R, Jerao A, Ginn M, Jones MEB and Berhane Y (2023) 'Characterization of neurotropic HPAI H5N1 viruses with novel genome constellations and mammalian adaptive mutations in free-living mesocarnivores in Canada', *Emerg Microbes Infect*, 12(1):2186608, <https://doi.org/10.1080/22221751.2023.2186608>
- Alkie TN, Lopes S, Hisanaga T, Xu W, Suderman M, Koziuk J, Fisher M, Redford T, Lung O, Joseph T, Himsworth CG, Brown IH, Bowes V, Lewis NS and Berhane Y (2022) 'A Threat from Both Sides: Multiple Introductions of Genetically Distinct H5 HPAI Viruses into Canada Via both East Asia-Australasia/Pacific and Atlantic Flyways', *Virus Evolution*, <https://doi.org/10.1093/ve/veac077>
- Ariyama N, Pardo-Roa C, Muñoz G, Aguayo C, Ávila C, Mathieu C, Almonacid LI, Medina RA, Brito B, Johow M & Neira V (2023) 'Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b Virus in Wild Birds, Chile.', *Emerging infectious diseases*, 29(9), <https://doi.org/10.3201/eid2909.230067>
- Banyard AC, Lean FZX, Robinson C, Howie F, Tyler G, Nisbet C, Seekings J, Meyer S, Whittard E, Ashpitel HF, Bas M, Byrne AMP, Lewis T, James J, Stephan L, Lewis NS, Brown IH, Hansen RDE & Reid SM (2022) 'Detection of Highly Pathogenic Avian Influenza Virus H5N1 Clade 2.3.4.4b in Great Skuas: A Species of Conservation Concern in Great Britain', *Viruses*, 14(2), <https://doi.org/10.3390/v14020212>
- Bevins S, Shriner S, Cumbee J, Dilione K, Douglass K, Ellis J, Killian ML, Torchetti M and Lenocho J (2022) 'Intercontinental movement of highly pathogenic avian influenza A(H5N1) clade 2.3.4.4 virus to the United States, 2021', *Emerging Infectious Disease journal*, 28(5):1006, <https://doi.org/10.3201/eid2805.220318>
- BirdLife Australia (2020) 'Australian National Directory of Important Migratory Shorebird Habitat', <https://www.eaaflyway.net/australian-national-directory-of-important-migratory-shorebird-habitat/>
- Bi Y, Chen Q, Wang Q, Chen J, Jin T, Wong G, Quan C, Liu J, Wu J, Yin R, Zhao L, Li M, Ding Z, Zou R, Xu W, Li H, Wang H, Tian K, Fu G, Huang Y, Shestopalov A, Li S, Xu B, Yu H, Luo T, Lu L, Xu X, Luo Y, Liu Y, Shi W, Liu D and Gao GF (2016) 'Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China', *Cell Host & Microbe*, 20(6):810-821, <https://doi.org/https://doi.org/10.1016/j.chom.2016.10.022>
- Bordes L, Vreman S, Heutink R, Roose M, Venema S, Pritz-Verschuren SBE, Rijks JM, Gonzales JL, Germeraad EA, Engelsma M and Beerens N (2023) 'Highly Pathogenic Avian Influenza H5N1 Virus Infections in Wild Red Foxes (*Vulpes vulpes*) Show Neurotropism and Adaptive Virus Mutations', *Microbiology Spectrum*, 11(1):e02867-02822, <https://doi.org/doi:10.1128/spectrum.02867-22>

Breed A, Dewar M, Dodyk L, Kuiken T, Matus R, Serafini PS, Uhart M, Vanstreels RET and Wille M (2023) 'Southward expansion of high pathogenicity avian influenza H5 in wildlife in South America: estimated impact on wildlife populations, and risk of incursion into Antarctica', <https://www.offlu.org/wp-content/uploads/2023/11/OFFLU-statement-HPAI-wildlife-South-America-20230823.pdf>

Bulach D, Halpin R, Spiro D, Pomeroy L, Janies D & Boyle DB (2010) 'Molecular Analysis of H7 Avian Influenza Viruses from Australia and New Zealand: Genetic Diversity and Relationships from 1976 to 2007', *Journal of Virology*, 84(19), <https://doi.org/10.1128/jvi.00930-10>

Caliendo V, Leijten L, van de Bildt M, Germeraad E, Fouchier RAM, Beerens N and Kuiken T (2022a) 'Tropism of Highly Pathogenic Avian Influenza H5 Viruses from the 2020/2021 Epizootic in Wild Ducks and Geese', *Viruses*, 14(2), <https://doi.org/10.3390/v14020280>

Caliendo V, Lewis NS, Pohlmann A, Baillie SR, Banyard AC, Beer M, Brown IH, Fouchier RAM, Hansen RDE, Lameris TK, Lang AS, Laurendeau S, Lung O, Robertson G, van der Jeugd H, Alkie TN, Thorup K, van Toor ML, Waldenström J, Yason C, Kuiken T and Berhane Y (2022b) 'Transatlantic spread of highly pathogenic avian influenza H5N1 by wild birds from Europe to North America in 2021', *Sci Rep*, 12(1):11729, <https://doi.org/10.1038/s41598-022-13447-z>

Chestakova, IV, van der Linden, A, Martin, BB, Caliendo, V, Vuong, O, Thewessen, S, Hartung, T, Bestebroer, T, Dekker, J, Poerink, BJ, Gröne, A, Koopmans, M, Fouchier, R, van den Brand, JMA & Sikkema, RS (2023) 'High number of HPAI H5 Virus Infections and Antibodies in Wild Carnivores in the Netherlands, 2020-2022', *bioRxiv*, <https://www.biorxiv.org/content/early/2023/05/12/2023.05.12.540493>.

Clemens R, Rogers DI, Hansen BD, Gosbell K, Minton CDT, Straw P, Bamford M, Woehler EJ, Milton DA, Weston MA, Venables B, Wellet D, Hassell C, Rutherford B, Onton K, Herrod A, Studds CE, Choi C-Y, Dhanjal-Adams KL, Murray NJ, Skilleter GA and Fuller RA (2016) 'Continental-scale decreases in shorebird populations in Australia', *Emu - Austral Ornithology*, 116(2):119-135, <https://doi.org/10.1071/MU15056>

COAG (2019) 'Intergovernmental Agreement on Biosecurity', Council of Australian Governments, Canberra, [https://federation.gov.au/sites/default/files/about/agreements/2019-IGA-biosecurity\\_1.pdf](https://federation.gov.au/sites/default/files/about/agreements/2019-IGA-biosecurity_1.pdf)

CMS FAO Co-convened Scientific Task Force on Avian Influenza and Wild Birds (2023) *Scientific Task Force on Avian Influenza and Wild Birds statement on H5N1 high pathogenicity avian influenza in wild birds - Unprecedented conservation impacts and urgent needs*, <http://www.cms.int/en/publication/h5n1-high-pathogenicity-avian-influenza-wild-birds-unprecedented-conservation-impacts>.

Curran J (2012) 'The surveillance and risk assessment of wild birds in northern Australia for highly pathogenic avian influenza H5N1 virus', PhD thesis, Murdoch University

Curran JM, Ellis TM and Robertson ID (2014) 'Surveillance of charadriiformes in Northern Australia shows species variations in exposure to avian influenza virus and suggests negligible virus prevalence', *Avian Diseases*, 58(2), <https://doi.org/10.1637/10634-080913>

Dalziel AE, Delean S, Heinrich S & Cassey P (2016) 'Persistence of low pathogenic influenza A virus in water: A systematic review and quantitative meta-analysis', *PLoS ONE*, 11(10), <https://doi.org/10.1371/journal.pone.0168789>

Department of Environmental Conservation, Alaska (2023) Highly Pathogenic Avian Influenza (HPAI) outbreaks and biosecurity toolkit from USDA APHIS.  
<https://dec.alaska.gov/eh/vet/announcements/avian-influenza-outbreaks/>

DEFRA (2021) *Risk assessment on the likelihood of spread of highly pathogenic avian influenza (H5Nx) associated with bird fairs, shows, markets, sales and other gatherings*,  
[https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/1032584/qra-gatherings-licensing1121.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1032584/qra-gatherings-licensing1121.pdf) [Note revised version now available DEFRA (2023) *Risk assessment on the likelihood of spread of highly pathogenic avian influenza H5N1 associated with bird fairs, shows, markets, sales and other gatherings*  
[https://assets.publishing.service.gov.uk/media/64e4b0b0bc2b520014a00479/QRA\\_Gatherings\\_for\\_Licensing\\_July\\_2023.pdf](https://assets.publishing.service.gov.uk/media/64e4b0b0bc2b520014a00479/QRA_Gatherings_for_Licensing_July_2023.pdf)]

DEFRA (2022) *Risk Assessment on the spread of High Pathogenicity Avian Influenza (HPAI) H5N1 to wild birds from released, formerly captive gamebirds in Great Britain: Pheasants*,  
[https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/1124975/Risk\\_Assessment\\_on\\_the\\_spread\\_of\\_High\\_Pathogenicity\\_Avian\\_Influenza\\_HPAI\\_H5N1\\_to\\_wild\\_birds\\_from\\_released\\_formerly\\_captive\\_gamebirds\\_in\\_Great\\_Britain\\_Pheasants.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1124975/Risk_Assessment_on_the_spread_of_High_Pathogenicity_Avian_Influenza_HPAI_H5N1_to_wild_birds_from_released_formerly_captive_gamebirds_in_Great_Britain_Pheasants.pdf)

DEFRA (2023) *Highly pathogenic avian influenza in Great Britain : evaluation and future actions*,  
<https://www.gov.uk/government/publications/highly-pathogenic-avian-influenza-in-great-britain-evaluation-and-future-actions/highly-pathogenic-avian-influenza-in-great-britain-evaluation-and-future-actions>.

Dingle H (2004) 'The Australo-Papuan bird migration system: another consequence of Wallace's Line', *Emu - Austral Ornithology*, 104(2):95-108, <https://doi.org/10.1071/MU03026>

Downie JC and Laver WG (1973) 'Isolation of a type A influenza virus from an Australian pelagic bird', *Virology*, 51(2):259–269, [https://doi.org/10.1016/0042-6822\(73\)90426-1](https://doi.org/10.1016/0042-6822(73)90426-1)

East IJ, Hamilton S and Garner G (2008a) 'Identifying areas of Australia at risk of H5N1 avian influenza infection from exposure to migratory birds: a spatial analysis', *Geospatial Health*, 2(2):203-213, <https://doi.org/10.4081/gh.2008.244>

East IJ, Hamilton S, Sharp LA and Garner MG (2008b) 'Identifying areas of Australia at risk for H5N1 avian influenza infection from exposure to nomadic waterfowl moving throughout the Australo-Papuan region', *Geospatial Health*, 3(1):17-27, <https://doi.org/10.4081/gh.2008.228>

Elsmo E, Wünschmann A, Beckmen K, Broughton-Neiswanger L, Buckles E, Ellis J, Fitzgerald S, Gerlach R, Hawkins S, Ip H, Lankton J, Lemley E, Lenocho J, Killian M, Lantz K, Long L, Maes R, Mainenti M, Melotti J, Moriarty M, Nakagun S, Ruden R, Shearn-Bochsler V, Thompson D, Torchetti M, Wettere AV, Wise A and Lim A (2023) 'Pathology of natural infection with highly pathogenic avian influenza virus (H5N1) clade 2.3.4.4b in wild terrestrial mammals in the United States in 2022', *bioRxiv*:2023.2003.2010.532068, <https://doi.org/10.1101/2023.03.10.532068>

EPIC (2023) *Epic Veterinary Risk Assessment: Wild Bird Carcass Collection in the Event of Mass Mortality due to Suspected Highly Pathogenic Avian Influenza (HPAI)*, accessed 19 July 2023  
<https://www.epicscotland.org/resources/publications-by-epic-members/epic-veterinary-risk-assessment-wild-bird-carcass-collection-in-the-event-of-mass-mortality-due-to-suspected-highly-pathogenic-avian-influenza-hpai/>

FAO (2023) *Global Avian Influenza Viruses with Zoonotic Potential situation update: Bird species affected by H5Nx HPAI and Mammalian species affected by H5Nx HPAI, Assessed 14 December 2023*,  
<https://www.fao.org/animal-health/situation-updates/global-aiv-with-zoonotic-potential/bird-species-affected-by-h5nx-hpai/en>

Ferenczi M, Beckmann C and Klaassen M (2021) 'Rainfall driven and wild-bird mediated avian influenza virus outbreaks in Australian poultry', *BMC Veterinary Research*, 17(1):306, <https://doi.org/10.1186/s12917-021-03010-9>

Ferenczi M, Beckmann C, Warner S, Loyn R, O'Riley K, Wang X and Klaassen M (2016) 'Avian influenza infection dynamics under variable climatic conditions, viral prevalence is rainfall driven in waterfowl from temperate, south-east Australia', *Veterinary Research*, 47(1), <https://doi.org/10.1186/s13567-016-0308-2>

Furness RW, Gear SC, Camphuysen KCJ, Tyler G, de Silva D, Warren CJ, James J, Reid SM & Banyard AC (2023) 'Environmental Samples Test Negative for Avian Influenza Virus H5N1 Four Months after Mass Mortality at A Seabird Colony', *Pathogens*, 12(4), <https://doi.org/10.3390/pathogens12040584>.

Fusaro A, Zecchin B, Vrancken B, Abolnik C, Ademun R, Alassane A, Arafa A, Awuni JA, Couacy-Hymann E, Coulibaly M. B, Gaidet N, Go-Maró E, Joannis T, Jumbo SD, Minoungou G, Meseko C, Souley MM, Ndumu DB, Shittu I, Twabela A, Wade A, Wiersma L, Akpeli YP, Zamperin G, Milani A, Lemey P & Monne I (2019) 'Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza', *Nature Communications*, 10(1):5310, <https://doi.org/10.1038/s41467-019-13287-y>.

Gamarra-Toledo V, Plaza PI, Gutiérrez R, Inga-Díaz G, Saravia-Guevara P, Pereyra-Meza O, Coronado-Flores E, Calderón-Cerrón A, Quiroz-Jiménez G, Martínez P and Huamán-Mendoza D (2023) 'Mass Mortality of Sea Lions Caused by Highly Pathogenic Avian Influenza A (H5N1) Virus', *Emerging Infectious Diseases*, 29(12):2553. <https://doi.org/10.3201/eid2912.230192>

Gobbo F, Zanardello C, Bottinelli M, Budai J, Bruno F, De Nardi R, Patregnani T, Catania S and Terregino C (2022) 'Silent Infection of Highly Pathogenic Avian Influenza Virus (H5N1) Clade 2.3.4.4b in a Commercial Chicken Broiler Flock in Italy', *Viruses*, 14(8), <https://doi.org/10.3390/v14081600>

Grant M, Bröjer C, Zohari S, Nöremark M and Uhlhorn H (2022) 'Highly Pathogenic Avian Influenza (HPAI H5Nx, Clade 2.3.4.4.b) in Poultry and Wild Birds in Sweden: Synopsis of the 2020 – 2021 Season', *Veterinary Sciences*, 9(7), 344, <https://doi.org/10.3390/vetsci9070344>

Grund C, Hoffmann D, Ulrich R, Naguib M, Schinköthe J, Hoffmann B, Harder T, Saenger S, Zscheppang K, Tönnies M, Hippenstiel S, Hocke A, Wolff T and Beer M (2018) 'A novel European H5N8 influenza A virus has increased virulence in ducks but low zoonotic potential', *Emerg Microbes Infect*, 7(1):132, <https://doi.org/10.1038/s41426-018-0130-1>

Grillo VL, Arzey KE, Hansbro PM, Hurt AC, Warner S, Bergfeld J, Burgess GW, Cookson B, Dickason CJ, Ferenczi M, Hollingsworth T, Hoque MDA, Jackson RB, Klaassen M, Kirkland PD, Kung NY, Lisovski S, O'Dea MA, O'Riley K, Roshier D, Skerratt LF, Tracey JP, Wang X, Woods R and Post L (2015) 'Avian influenza in Australia: A summary of 5 years of wild bird surveillance', *Australian Veterinary Journal*, 93(11):387–393, <https://doi.org/10.1111/avj.12379>

Guan Y, Peiris JSM, Lipatov AS, Ellis TM, Dyrting KC, Krauss S, Zhang LJ, Webster RG and Shortridge KF (2002) 'Emergence of multiple genotypes of H5N1 avian influenza viruses in Hong Kong SAR', *Proceedings of the National Academy of Sciences*, 99(13):8950-8955, <https://doi.org/doi:10.1073/pnas.132268999>

Hall JS, Krauss S, Franson JC, TeSlaa JL, Nashold SW, Stallknecht DE, Webby RJ and Webster RG (2013) 'Avian influenza in shorebirds: experimental infection of ruddy turnstones (*Arenaria interpres*) with avian influenza virus', *Influenza Other Respir Viruses*, 7(1):85-92, <https://doi.org/10.1111/i.1750-2659.2012.00358.x>

Hansbro PM, Warner S, Tracey JP, Arzey KE, Selleck P, O'Riley K, Beckett EL, Bunn C, Kirkland PD, Vijaykrishna D, Olsen B and Hurt AC (2010) 'Surveillance and analysis of avian influenza viruses, Australia', *Emerging Infectious Diseases*, 16(12), <https://doi.org/10.3201/eid1612.100776>

Hansen BD, Fuller RA, Watkins D, Rogers DI, Clemens RS, Newman M, Woehler EJ and Weller DR (2016) 'Revision of the East Asian-Australasian Flyway Population Estimates for 37 listed Migratory Shorebird Species', Unpublished report for the Department of the Environment, BirdLife Australia, Melbourne, <https://www.dcceew.gov.au/sites/default/files/documents/revision-east-asian-australasian-flyway-population-sept-2016.pdf>

Hansen BD, Rogers DI, Watkins D, Weller DR, Clemens RS, Newman M, Woehler EJ, Mundkur T and Fuller RA (2022) 'Generating population estimates for migratory shorebird species in the world's largest flyway', *Ibis*, 164(3):735–749, <https://doi.org/10.1111/ibi.13042>

Harvey JA, Mullinax JM, Runge MC & Prosser DJ (2023) 'The Changing Dynamics of Highly Pathogenic Avian Influenza H5N1: Next Steps for Management & Science in North America', *Biological Conservation*, 282:1–27. <https://doi.org/10.1016/j.biocon.2023.110041>

Haynes L, Arzey E, Bell C, Buchanan N, Burgess G, Cronan V, Dickason C, Field H, Gibbs S, Hansbro PM, Hollingsworth T, Hurt AC, Kirkland P, McCracken H, O'Connor J, Tracey J, Wallner J, Warner S, Woods R and Bunn C (2009) 'Australian surveillance for avian influenza viruses in wild birds between July 2005 and June 2007', *Australian Veterinary Journal*, 87(7), <https://doi.org/10.1111/j.1751-0813.2009.00446.x>

Hicks JT, Edwards K, Qui X, Kim D-K, Hixson JE, Krauss S, Webby RJ, Webster RG and Bahl J (2023) 'Host diversity and behavior determine patterns of interspecies transmission and geographic diffusion of avian influenza A subtypes among North American wild reservoir species', *PLoS pathogens*, 18:e1009973. <https://doi.org/10.1371/journal.ppat.1009973>.

Hoque MA, Burgess GW, Cheam AL & Skerratt LF (2015) 'Epidemiology of avian influenza in wild aquatic birds in a biosecurity hotspot, North Queensland, Australia', *Preventive Veterinary Medicine*, 118(1), <https://doi.org/10.3390/v13020212>

Hoye BJ, Donato CM, Lisovski S, Deng Y-M, Warner S, Hurt AC, Klaassen M & Vijaykrishna D (2021) 'Reassortment and Persistence of Influenza A Viruses from Diverse Geographic Origins within Australian Wild Birds: Evidence from a Small, Isolated Population of Ruddy Turnstones', *Journal of Virology*, 95(9), <https://doi.org/10.1128/jvi.02193-20>

Hurt AC, Hansbro PM, Selleck P, Olsen B, Minton C, Hampson AW & Barr IG (2006) 'Isolation of avian influenza viruses from two different transhemispheric migratory shorebird species in Australia', *Archives of Virology*, 151(11), <https://doi.org/10.1007/s00705-006-0784-1>

James J, Billington E, Warren CJ, De Sliva D, Genova CD, Airey M, Meyer SM, Lewis T, Peers-Dent J, Thomas SS, Lofts A, Furman N, Slomka MJ, Brown IH and Banyard AC (2023) 'Clade 2.3.4.4b H5N1 high pathogenicity avian influenza virus (HPAIV) from the 2021/22 epizootic is highly duck adapted and poorly adapted to chickens', *J Gen Virol*, 104(5), <https://doi.org/10.1099/jgv.0.001852>

Jimenez-Bluhm P, Siegers JY, Tan S, Sharp B, Freiden P, Orozco K, Ruiz S, Baumberger C, Galdames P, Gonzalez MA, Rojas C, Karlsson EA, Hamilton-West C and Schultz-Cherry S (2023) 'Detection and Phylogenetic Analysis of Highly Pathogenic A/H5N1 Avian Influenza Clade 2.3.4.4b Virus in Chile, 2022', *bioRxiv:2023.2002.2001.526205*, <https://doi.org/10.1101/2023.02.01.526205>

Jeglinski J, Lane J, Votier S, Furness R, Hamer K, Nager R, Sheddan M, Wanless S and Matthiopoulos J (2023) 'HPAIV outbreak triggers long-distance movements in breeding Northern gannets – implications for disease spread', *Authorea*, <https://doi.org/10.22541/2Fau.168173494.41037735%2Fv2>

Kandeil A, Patton C, Jones J, Jeevan T, Harrington W, Trifkovic S, Seiler J, Fabrizio T, Woodard K, Turner J, Crumpton J-C, Miller L, Rubrum A, DeBeauchamp J, Russell C, Govorkova E, Vogel P, Torchetti M, Berhane Y, Stallknecht D, Poulson R, Kercher L and Webby R (2022) *Rapid evolution of A(H5N1) influenza viruses after intercontinental spread to North America* Research Square,

Karawita AC, Cheng Y, Chew KY, Challgula A, Kraus R, Mueller RC, Tong MZW, Hulme KD, Beielefeldt-Ohmann H, Steele LE, Wu M, Sng JDJ, Noye E, Bruxner TJ, Au GG, Lowthe S, Blommaert J, Suh A, McCauley AJ, Kaur P, Olga D, Aiden E, Fedrigo O, Formenti G, Mountcastle J, Chow W, Martin FJ, Ogeh DN, Thiaud-Nissen F, Howe K, Collins J, Tracey A, Smith J, Kuo RI, Renfree M b, Kimura T, Sakoda Y, McDougall M, Spencer HG, Pyne M, Tolf C, Waldenstrom J, Jarvis ED, Baker ML, Burt DW & Short KR (2022) 'The swan genome and transcriptome: its not all black and white', *Genome Biology*, :2022.05.02.490350, <https://doi.org/10.1186/s13059-022-02838-0>

Kishida N, Sakoda Y, Shiromoto M, Bai GR, Isoda N, Takada A, Laver G, Kida H (2008) H2N5 influenza virus isolates from terns in Australia: genetic reassortants between those of the Eurasian and American lineages, *Virus Genes*, 37(1):16-21. <https://doi.org/10.1007/s11262-008-0235-z>

Klaassen M, Hoyer BJ and Roshier DA (2011) 'Identifying crucial gaps in our knowledge of the life-history of avian influenza viruses—an Australian perspective', *Emu - Austral Ornithology*, 111(2):103-112, <https://doi.org/10.1071/MU10042>

Klaassen M and Wille M (2023) 'Wild birds' plight and role in the current bird flu panzootic', *bioRxiv*:2023.2005.2002.539182, <https://doi.org/10.1101/2023.05.02.539182>

Kobasa D, Warner B, Alkie T, Vendramelli R, Moffat E, Taylor N, Audet J, Gunawardena T, Safronetz D, Mubareka S, Moraes T, Lung O, Embury-Hyatt C and Berhane Y (2023) 'Transmission of lethal H5N1 clade 2.3.4.4b avian influenza in ferrets', *Research Square*, <https://doi.org/10.21203/rs.3.rs-2842567/v1>

Koethe S, Ulrich L, Ulrich R, Amler S, Graaf A, Harder TC, Grund C, Mettenleiter TC, Conraths FJ, Beer M & Globig A (2020) 'Modulation of lethal HPAIV H5N8 clade 2.3.4.4B infection in AIV pre-exposed mallards', *Emerging Microbes and Infections*, 9(1):180–193, <https://doi.org/10.1080/22221751.2020.1713706>.

Kohun P, Dom M, Pandi J, Besari F, Sine M, Ayalew W and Glatz P (2015) 'Low-cost feed for chicken farmers in Papua New Guinea', in Francis JA (ed.), *CTA Top 20 Innovations that Benefit Smallholder Farmers*. [https://www.researchgate.net/publication/320196576\\_Low-cost\\_feed\\_for\\_chicken\\_farmers\\_in\\_Papua\\_New\\_Guinea](https://www.researchgate.net/publication/320196576_Low-cost_feed_for_chicken_farmers_in_Papua_New_Guinea)

Kwon J-H, Bertran K, Lee D-H, Criado MF, Killmaster L, Pantin-Jackwood MJ & Swayne DE (2023) 'Diverse infectivity, transmissibility, and pathobiology of clade 2.3.4.4 H5Nx highly pathogenic avian influenza viruses in chickens', *Emerging Microbes & Infections*, 12(1):2218945, <https://doi.org/10.1080/22221751.2023.2218945>.

Lang AS, Lebarbenchon C, Ramey AM, Robertson GJ, Waldenström J and Wille M (2016) 'Assessing the Role of Seabirds in the Ecology of Influenza A Viruses', *Avian Dis*, 60(1 Suppl):378-386, <https://doi.org/10.1637/11135-050815-RegR>

Leyson CM, Youk S, Ferreira HL, Suarez DL and Pantin-Jackwood M (2021) 'Multiple Gene Segments Are Associated with Enhanced Virulence of Clade 2.3.4.4 H5N8 Highly Pathogenic Avian Influenza Virus in Mallards', *J Virol*, 95(18):e0095521, <https://doi.org/10.1128/jvi.00955-21>

Lisovski S, Gosbell K, Minton C and Klaassen M (2021) 'Migration strategy as an indicator of resilience to change in two shorebird species with contrasting population trajectories', *Journal of Animal Ecology*, 90(9):2005-2014, <https://doi.org/https://doi.org/10.1111/1365-2656.13393>

- Lloyd-Smith JO, Schreiber SJ, Kopp PE and Getz WM (2005) 'Superspreading and the effect of individual variation on disease emergence', *Nature*, 438(7066):355-359, <https://doi.org/10.1038/nature04153>
- Lv X, Li X, Sun H, Li Y, Peng P, Qin S, Wang W, Li Y, An Q, Fu T, Qu F, Xu Q, Qin R, Zhao Z, Wang M, Wang Y, Wang Y, Zeng X, Hou Z, Lei C, Chu D, Li Y and Chai H (2022) 'Highly pathogenic avian influenza A (H5N8) clade 2.3.4.4b viruses in satellite-tracked wild ducks, Ningxia, China, 2020', *Emerging Infectious Disease journal*, 28(5):1039, <https://doi.org/10.3201/eid2805.211580>
- Lycett SJ, Duchatel F and Digard P (2019) 'A brief history of bird flu', *Philosophical Transactions of the Royal Society of London B Biological Sciences*, 374(1775):20180257, <https://doi.org/doi:10.1098/rstb.2018.0257>
- McCallum HI, Roshier D, Tracey JP, Joseph L and Heinsohn R (2008) 'Will Wallace's line save Australia from avian influenza?', *Ecology and Society*, 13(2):41. [https://www.academia.edu/3881939/Will\\_Wallace\\_s\\_Line\\_save\\_Australia\\_from\\_avian\\_influenza](https://www.academia.edu/3881939/Will_Wallace_s_Line_save_Australia_from_avian_influenza)
- National Park Service (2023) 'Highly Pathogenic Avian Influenza Confirmed as Cause of Three California Condor Mortalities in Arizona', accessed July 7 2023, <https://www.nps.gov/orgs/1207/highly-pathogenic-avian-influenza-confirmed-as-cause-of-three-california-condor-mortalities-in-arizona.htm>.
- NatureScotland (2023) 'NatureScot Scientific Advisory Committee Sub-Group on Avian Influenza Report on the H5N1 outbreak in wild birds 2020-2023', <https://www.nature.scot/doc/naturescot-scientific-advisory-committee-sub-group-avian-influenza-report-h5n1-outbreak-wild-birds>
- Newsome BT & Barton P (2023) *Carcass Ecology in the Alps : How to minimise carcass loads*, retrieved 20 July 2023, [https://theaustralionalpsnationalparks.org/wp-content/uploads/2023/06/Carcass-Ecology-in-the-Alps\\_ReportFinal.pdf](https://theaustralionalpsnationalparks.org/wp-content/uploads/2023/06/Carcass-Ecology-in-the-Alps_ReportFinal.pdf).
- Nurhasan M, Maulana AM, Ariesta DL, Usfar AA, Napitupulu L, Rouw A, Hurulean F, Hapsari A, Heatubun CD and Ickowitz A (2022) 'Toward a Sustainable Food System in West Papua, Indonesia: Exploring the Links Between Dietary Transition, Food Security, and Forests', *Frontiers in Sustainable Food Systems*, 5. <https://www.frontiersin.org/articles/10.3389/fsufs.2021.789186>
- OCVO (2010) *National Avian Influenza Surveillance Dossier*, Office of the Chief Veterinary Officer, Australian Government Department of Agriculture, Fisheries and Forestry, Canberra, accessed 19 July 2023 <https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/animal-health/livestock-movement/national-avian-influenza-sept-2010.pdf>.
- Ogden NH, Wilson JRU, Richardson DM, Hui C, Davies SJ, Kumschick S, Le Roux JJ, Measey J, Saul WC and Pulliam JRC (2019) 'Emerging infectious diseases and biological invasions: a call for a One Health collaboration in science and management', *R Soc Open Sci*, 6(3):181577, <https://doi.org/10.1098/rsos.181577>
- Olsen B, Munster VJ, Wallensten A, Waldenström J, Osterhaus AD and Fouchier RA (2006) 'Global patterns of influenza a virus in wild birds', *Science*, 312(5772):384-388, <https://doi.org/10.1126/science.1122438>
- Pearce-Higgins JW, Humphreys EM, Burton NHK, Atkinson PW, Pollock C, Gary D, Johnston DT, Hanlon NJO, Balmer DE, Frost TM, Harris SJ & Baker H (2023) *Highly pathogenic avian influenza in wild birds in the United Kingdom in 2022 : impacts , planning for future outbreaks , and conservation and research priorities . Report on virtual workshops held in November 2022*, BTO Research Report, 752.

Prosser DJ, Schley HL, Simmons N, Sullivan JD, Homyack J, Weegman M, Olsen GH, Berlin AM, Poulson RL, Stallknecht DE and Williams CK (2022) 'A lesser scaup (*Aythya affinis*) naturally infected with Eurasian 2.3.4.4 highly pathogenic H5N1 avian influenza virus: Movement ecology and host factors', <https://doi.org/10.1111/tbed.14614>

Puryear W, Sawatzki K, Hill N, Foss A, Stone JJ, Doughty L, Walk D, Gilbert K, Murray M, Cox E, Patel P, Mertz Z, Ellis S, Taylor J, Fauquier D, Smith A, DiGiovanni RA, Jr., van de Guchte A, Gonzalez-Reiche AS, Khalil Z, van Bakel H, Torchetti MK, Lantz K, Lenocho JB and Runstadler J (2023) 'Highly Pathogenic Avian Influenza A(H5N1) Virus Outbreak in New England Seals, United States', *Emerg Infect Dis*, 29(4):786-791, <https://doi.org/10.3201/eid2904.221538>

Purnell C (2022) *The role of waterbirds in Australia's 2022 Japanese Encephalitis outbreak Unpublished - a rapid synthesis*, Carlton, BirdLife Australia, accessed 19 July 2023, [https://wildlifehealthaustralia.com.au/Portals/0/Incidents/Role\\_of\\_waterbirds\\_Aus\\_2022-JEV-outbreak\\_RapidSynthesis\\_BirdLifeAustralia.pdf](https://wildlifehealthaustralia.com.au/Portals/0/Incidents/Role_of_waterbirds_Aus_2022-JEV-outbreak_RapidSynthesis_BirdLifeAustralia.pdf)

Ramey AM, Scott LC, Ahlstrom CA, Buck EJ, Williams AR, Torchetti MK, Stallknecht DE and Poulson RL (2023) 'Molecular detection and characterization of highly pathogenic H5N1 clade 2.3.4.4 b avian influenza viruses among hunter-harvested wild birds provides evidence for three independent introductions into Alaska', *Virology*: 109938, <https://doi.org/10.1016/j.virol.2023.109938>

Reperant LA, van de Bildt MW, van Amerongen G, Buehler DM, Osterhaus AD, Jenni-Eiermann S, Piersma T and Kuiken T (2011) 'Highly pathogenic avian influenza virus H5N1 infection in a long-distance migrant shorebird under migratory and non-migratory states', *PLoS One*, 6(11):e27814, <https://doi.org/10.1371/journal.pone.0027814>

Roshier DA, Heinsohn R, Adcock GJ, Beerli P, Joseph L. (2012) 'Biogeographic models of gene flow in two waterfowl of the Australo-Papuan tropics', *Ecol Evol*, 2(11):2803-14.

<https://doi.org/10.1002/ece3.393> Salaheldin AH, Elbestawy AR, Abdelkader AM, Sultan HA, Ibrahim AA, Abd El-Hamid HS and Abdelwhab EM (2022) 'Isolation of Genetically Diverse H5N8 Avian Influenza Viruses in Poultry in Egypt, 2019-2021', *Viruses*, 14(7), <https://doi.org/10.3390/v14071431>

Runge CA, Gallo-Cajiao E, Carey MJ, Garnett ST, Fuller RA and McCormack PC (2017) 'Coordinating Domestic Legislation and International Agreements to Conserve Migratory Species: A Case Study from Australia', *Conservation Letters*, 10(6):765-772, <https://doi.org/10.1111/conl.12345>

Scott AB, Phalen D, Hernandez-Jover M, Singh M, Groves P, Toribio J-A. (2018a) 'Wildlife Presence and Interactions with Chickens on Australian Commercial Chicken Farms Assessed by Camera Traps', *Avian Diseases*. 62(1):65-72. <https://doi.org/10.1637/11761-101917-Reg.1>

Scott AB, Toribio J-A, Singh M, Groves P, Barnes B, Glass K, Moloney B, Black A and Hernandez-Jover M (2018b) 'Low Pathogenic Avian Influenza Exposure Risk Assessment in Australian Commercial Chicken Farms', *Frontiers in Veterinary Science*, 5, <https://www.frontiersin.org/articles/10.3389/fvets.2018.00068>

Simberloff D (2009) 'The Role of Propagule Pressure in Biological Invasions', *Annual Review of Ecology, Evolution, and Systematics*, 40(1):81-102, <https://doi.org/10.1146/annurev.ecolsys.110308.120304>

Spackman E, Pantin-Jackwood MJ, Lee SA and Prosser D (2023) 'The pathogenesis of a 2022 North American highly pathogenic clade 2.3.4.4b H5N1 avian influenza virus in mallards (*Anas platyrhynchos*)', *Avian Pathology*:1-10, <https://doi.org/10.1080/03079457.2023.2196258>

Statista (2023) *Chicken production in Indonesia from 2012 to 2021*, accessed 19 July 2023, <https://www.statista.com/statistics/659054/indonesia-chicken-production/>

Swayne DE and Suarez DL (2000) 'Highly pathogenic avian influenza', *Rev Sci Tech*, 19(2):463-482, <https://doi.org/10.20506/rst.19.2.1230>

Swayne DE, Sims L, Brown I, Harder T, Stegeman A, Delgado M & Awada L (2023) *Technical Item: Strategic Challenges in the Global Control of High Pathogenicity Avian Influenza*, WOAHP 90<sup>th</sup> General Session, <https://www.woah.org/app/uploads/2023/05/a-90sg-8.pdf>

Tanikawa T, Sakuma S, Yoshida E, Tsunekuni R, Nakayama M & Kobayashi S (2021) 'Comparative susceptibility of the common teal (*Anas crecca*) to infection with high pathogenic avian influenza virus strains isolated in Japan in 2004–2017', *Veterinary Microbiology*, 263:109266, <https://doi.org/10.1016/j.vetmic.2021.109266>.

Teitelbaum CS, Mastro NM, Sullivan JD, Keever AC, Poulson RL, Carter DL, Blake-Bradshaw AG, Highway CJ, Feddersen JC, Hagy HM, Gerhold RW (2023) 'North American wintering mallards infected with highly pathogenic avian influenza show few signs of altered local or migratory movements', *Scientific Reports*, 13(1):14473, <https://doi.org/10.1038/s41598-023-40921-z>

Tracey JP, Woods R, Roshier D, West P and Saunders GR (2004) 'The role of wild birds in the transmission of avian influenza for Australia: an ecological perspective', *Emu - Austral Ornithology*, 104(2):109-124, <https://doi.org/10.1071/MU04017>

Tracey, JP (2005) 'Targeting surveillance for avian influenza in wild birds: a pilot investigation in New South Wales', *Final report to the Department of Agriculture, Fisheries and Forestry, Wildlife and Exotic Disease Preparedness Program*. NSW Department of Primary Industries, Orange, NSW. <https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/emergency/wildlifeexoticdiseaseprogram/08-09/ai-birds-nsw-tracey.pdf>

USDA APHIS, USGS, USFWS, CDC & Council NF (2016) 'Highly Pathogenic Avian Influenza and North American Wild Birds: Frequently Asked Questions', retrieved July 17, 2023, [https://www.aphis.usda.gov/animal\\_health/downloads/animal\\_diseases/ai/faqs.pdf](https://www.aphis.usda.gov/animal_health/downloads/animal_diseases/ai/faqs.pdf).

USDA APHIS (2022) *Epidemiologic and Other Analyses of HPAI Affected Poultry Flocks July 2022 Interim Report*, accessed 17 July 2023, [https://www.aphis.usda.gov/animal\\_health/downloads/animal\\_diseases/ai/epi-analyses-hpai-poultry-july2022.pdf](https://www.aphis.usda.gov/animal_health/downloads/animal_diseases/ai/epi-analyses-hpai-poultry-july2022.pdf).

Vijaykrishna D, Deng YM, Su YC, Fourment M, Iannello P, Arzey GG, Hansbro PM, Arzey KE, Kirkland PD, Warner S, O'Riley K, Barr IG, Smith GJ, Hurt AC (2013) 'The recent establishment of North American H10 lineage influenza viruses in Australian wild waterfowl and the evolution of Australian avian influenza viruses', *J Virol*, 87(18):10182-9, <https://doi.org/10.1128/JVI.03437-12>

Vigevano RM, Poen MJ, Parker E, Holwerda M, de Haan K, van Montfort T, Lewis NS, Russell CA, Fouchier RAM, de Jong MD and Eggink D (2020) 'Outbreak Severity of Highly Pathogenic Avian Influenza A(H5N8) Viruses Is Inversely Correlated to Polymerase Complex Activity and Interferon Induction', *J Virol*, 94(11), <https://doi.org/10.1128/jvi.00375-20>

Vreman S, Kik M, Germeraad E, Heutink R, Harders F, Spierenburg M, Engelsma M, Rijks J, van den Brand J and Beerens N (2023) 'Zoonotic Mutation of Highly Pathogenic Avian Influenza H5N1 Virus Identified in the Brain of Multiple Wild Carnivore Species', *Pathogens*, 12(2):168. <https://www.mdpi.com/2076-0817/12/2/168>

Ulloa M, Fernández A, Ariyama N, Colom-Rivero A, Rivera C, Nuñez P, Sanhueza P, Johow M, Araya H, Torres JC and Gomez P (2023) 'Mass mortality event in South American sea lions (*Otaria flavescens*) correlated to highly pathogenic avian influenza (HPAI) H5N1 outbreak in Chile', *Veterinary Quarterly*, 43(1):1-0. <https://doi.org/10.1080/01652176.2023.2265173>

Warner, S, Welch A, Ainsworth C, Tracey JP, Zikesch F, Saunders GR, & Lukins B (2006) 'Application of rapid diagnostic tests in the targeted surveillance of avian influenza virus within Victorian wild bird populations', Final Report to the Wildlife and Exotic Disease Preparedness Program. Primary Industries Research Victoria, Melbourne.

<https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/emergency/wildlifeexoticdiseaseprogram/08-09/ai-wildbirds-vic-august06.pdf>

WHO (2022) 'Rapid Risk Assessment: Assessment of risk associated with recent influenza A(H5N1) clade 2.3.4.4b viruses' 21 December 2022, <https://cdn.who.int/media/docs/default-source/influenza/avian-and-other-zoonotic-influenza/h5-risk-assessment-dec-2022.pdf>

WHO, FAO and OIE (2021) Joint risk assessment operational tool (JRA OT): an operational tool of the tripartite zoonoses guide: taking a multisectoral, one health approach: a tripartite guide to addressing zoonotic diseases in countries, accessed.

<https://www.who.int/publications/i/item/9789240015142>

Wille M, Grillo V, Ban de Gouvea Pedroso S, Burgess GW, Crawley A, Dickason C, Hansbro PM, Hoque MA, Horwood PF, Kirkland PD, Kung NY-H, Lynch SE, Martin S, McArthur M, O'Riley K, Read AJ, Warner S, Hoyer BJ, Lisovski S, Leen T, Hurt AC, Butler J, Broz I, Davies KR, Mileto P, Neave M, Stevens V, Breed A, Lam TTY, Holmes EC, Klaassen M and Wong FYK (2022) 'Australia as a global sink for the genetic diversity of avian influenza A virus', *PLoS pathogens*, 18(5):e1010150, <https://doi.org/doi.org/10.1371/journal.ppat.1010150>

Wille M and Klaassen M (2023a) 'No evidence for HPAI H5N1 2.3.4.4b incursion into Australia in 2022', *Influenza and Other Respiratory Viruses*, 17(3):e13118, <https://doi.org/https://doi.org/10.1111/irv.13118>

Wille M, Lisovski S, Risely A, Ferenczi M, Roshier D, Wong FYK, Breed AC, Klaassen M and Hurt AC (2019) 'Serologic evidence of exposure to highly pathogenic avian influenza H5 viruses in migratory shorebirds, Australia', *Emerg Infect Dis*, 25(10):1903-1910, <https://doi.org/10.3201/eid2510.190699>

Wille M and Waldenström J (2023b) 'Weathering the Storm of High Pathogenicity Avian Influenza in Waterbirds', *Waterbirds*, 46(1):100-9. <https://doi.org/10.1675/063.046.0113>

World Organisation for Animal Health (2022) *Situation report 09 Jun 2022 - 29 Jun 2022*, Paris, France, accessed. <https://www.woah.org/app/uploads/2022/07/hpai-situation-report-20220707.pdf>

Xie R, Edwards KM, Wille M, Wei X, Wong SS, Zanin M, El-Shesheny R, Ducatez M, Poon LL, Kayali G and Webby RJ (2023) 'The episodic resurgence of highly pathogenic avian influenza H5 virus', *Nature*:1-8, <https://doi.org/10.1038/s41586-023-06631-2>

Yang AQ, Wang B, Lemey P, Dong L & Mu T (2023) 'Synchrony of Bird Migration with Avian Influenza Global Spread; Implications for Vulnerable Bird Orders', *bioRxiv*, <https://doi.org/10.1101/2023.05.22.541648>

Zhang G, Li B, Raghwanji J, Vrancken B, Jia R, Hill SC, Fournié G, Cheng Y, Yang Q, Wang Y, Wang Z, Dong L, Pybus OG & Tian H (2023) 'Bidirectional Movement of Emerging H5N8 Avian Influenza Viruses Between Europe and Asia via Migratory Birds Since Early 2020', *Molecular Biology and Evolution*, 40(2) <https://doi.org/10.1093/molbev/msad019>.