

Technical Update:

Global High Pathogenicity Avian Influenza in Wildlife

Version 4, developed by the National Avian Influenza Wild Bird Steering Group, February 2025

Summary

This document summarises current global high pathogenicity avian influenza (HPAI) events in wildlife and the risks to Australia, with a focus on HPAI H5 clade 2.3.4.4b. Recognising the increased risk to Australia and need for heightened vigilance, this document also summarises activities to reduce and mitigate this risk.

HPAI H5 emerged in 1996 and has been endemic in poultry populations in parts of Asia and Africa for the past two decades. Belonging to the goose/Guangdong (gs/gd) lineage, HPAI H5 is constantly evolving through mutation and reassortment, and has caused HPAI outbreaks in wild birds and poultry in Asia, Africa, Europe, North America and South America.

Since 2021, a new strain from this lineage, HPAI H5Nx clade 2.3.4.4b, has rapidly spread globally and caused HPAI outbreaks in wild birds, poultry and mammals (both wild, domestic, terrestrial and aquatic). These outbreaks are unprecedented in number, frequency and intensity, and have been documented on all continents except Oceania (which includes Australia and New Zealand). Over 500 wild bird and 80 wild mammal species have been affected, which includes the first reports of HPAI in *circa* 300 bird and over 40 mammal species. The impacts of outbreaks associated with this clade of HPAI H5 have ranged from individual deaths to mass mortalities, and marked negative population-level impacts have been reported for numerous wild bird and mammal species across several continents.

The risk of introduction of HPAI H5 to Australia was previously assessed as low ([East et al. 2008](#); [East et al. 2008](#); [Curran 2012](#); [Wille et al. 2019](#))¹. However, a recent risk assessment² indicates that with the emergence of HPAI H5 clade 2.3.4.4b, the overall risk to Australia has increased. This is due to the increased likelihood of HPAI H5 entry into Australia via wild bird movements (resulting from globally increased viral abundance and expansions in geographic distribution and host range²) and anticipated consequences if it were to emerge.

Avian influenza is a nationally notifiable disease.

Anyone who suspects an animal might be infected with avian influenza has a legal responsibility to report it to their jurisdiction's biosecurity agency by phoning the Emergency Animal Disease Hotline on 1800 675 888.

Unusual signs of disease or deaths in wildlife can also be reported to the State or Territory WHA Coordinator.

¹ Note: [East et al. 2008a](#); [East et al. 2008b](#); [Curran 2012](#) assessed the risk of introduction of H5 clade 2.2.1 C viruses to Australia. [Wille et al. 2019](#) explored exposure of the long-distance migratory red-necked stint to H5 including clade 2.3.4.4 viruses.

² [High Pathogenicity Avian Influenza \(HPAI\) clade 2.3.4.4b incursion risk assessment for Australia abridged report.](#)

Avian Influenza

Low pathogenicity avian influenza (LPAI) viruses occur naturally in wild birds without causing disease, most notably in waterfowl (i.e., ducks, geese and swans), seabirds (i.e., gulls) and shorebirds. Wild birds are hosts for a considerable diversity of LPAI virus subtypes, including 17 HA (haemagglutinin, H1-16, H19) and 9 NA (neuraminidase, N1-9) subtypes, the majority of which have been detected in Australian wild birds.

Virus evolution from LPAI to HPAI can take place when LPAI H5 and H7 subtypes spillover from wild bird sources and subsequently circulate and mutate in poultry. To date, all instances of virus evolution from LPAI to HPAI have occurred in poultry; this is not known to occur in wild birds.

Infection with HPAI viruses causes severe disease and high mortality rates (up to 100%) in poultry. Upon spillback from a poultry reservoir, HPAI viruses may also impact other species, including wild birds, humans and other mammals. Further, spillback from poultry into wild birds contributes to the geographic spread of HPAI (see [Current Global Situation](#) below).

Although avian influenza viruses infrequently infect humans, some subtypes have been associated with disease, which can range from mild to severe illness and even death (see [Australian Department of Health and Aged Care](#)).

High Pathogenicity Avian Influenza H5 clade 2.3.4.4b

HPAI H5 belongs to the *gs/gd* lineage, which was first detected in 1996. Viruses of this lineage are endemic in multiple countries in Asia and Africa (e.g., Egypt). Since its emergence, HPAI H5 has continued to evolve, resulting in a large diversity of clades and genotypes that have caused significant disease outbreaks in poultry, particularly in Europe, Africa and Asia.

Of profound concern is HPAI H5 clade 2.3.4.4b, which emerged recently and is now causing a global panzootic ([Wille & Waldenstrom 2023](#)). The emergence of HPAI H5 clade 2.3.4.4b is associated with a significant increase in the frequency and geographic range of HPAI outbreaks in both wild birds and poultry overseas, including in Europe, North and South America and the Antarctic³. This strain is also associated with a significant increase in the range of avian and mammalian species impacted by HPAI, with outbreaks now occurring throughout the year in some locations. These recent epidemiological changes, including increased species and temporal ranges, appear to be due to the strong adaptation of clade 2.3.4.4b to wild birds and ongoing genomic reassortment that has occurred as the virus has spread to new geographic locations ([James et al. 2023](#); [Peacock et al. 2025](#)).

³ [Avian influenza overview September-December 2024 \(European Food Safety Authority\)](#)

Avian Influenza in Australia

HPAI H5 clade 2.3.4.4b has not yet been detected in Oceania, which includes Australia ([NAIWB Surveillance Program](#); [Wille & Klaassen 2023](#); [Wille et al. 2024](#)).

HPAI viruses have not been detected in free-ranging Australian wild birds, whereas LPAI viruses are part of the natural virus community and are routinely detected ([NAIWB Surveillance Newsletter](#)).

Between 1976 and 2024, there were 11 HPAI outbreaks in Australian poultry, all successfully eradicated. All outbreaks were associated with HPAI H7 subtypes resulting from spillover of LPAI H7 viruses from local wild birds (waterfowl) to commercial poultry, with subsequent mutation to HPAI H7 after circulation within commercial poultry: a well-documented occurrence. Worldwide, HPAI H7 viruses are rarely detected in wild birds⁴. At the time of writing (Feb 2025), another HPAI H7 outbreak in Australian poultry is under investigation and response (please see the [WHA Incident Information](#) page for more information).

The [National Avian Influenza Wild Bird Surveillance \(NAIWB\) program](#) collects and screens samples from Australian wild birds to monitor for avian influenza viruses and inform risk assessments and preparedness for poultry, wildlife and human health. Detailed analysis of avian influenza viruses detected in wild birds through the NAIWB program assists in tracking virus evolution and dynamics in Australia; supports maintenance of sampling and testing programs; contributes to a virus sequence library allowing comparison of Australian and overseas strains; and informs the potential risk of spillover into poultry.

Based on sequence analyses to date, it can be concluded that LPAI viruses in Australia tend to occur as distinct Australian lineages ([Bulach et al. 2010](#); [Hansbro et al. 2010](#); [Wille et al. 2022](#)). However, incursions of LPAI viruses into Australia from overseas do occur occasionally ([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](#); [Wille et al. 2024](#); [Wille et al. 2024](#)). Recent research suggests these viruses may subsequently circulate among Australian wild bird populations, with some strains going extinct and a small number persisting ([Wille et al. 2024](#); [Wille et al. 2024](#)).

Current Global High Pathogenicity Avian Influenza Situation

HPAI H5 clade 2.3.4.4b is the predominant HPAI strain circulating overseas, although other clades circulate in Asian poultry (e.g., 2.3.2.1a, 2.3.2.1c).

Between October 2021 and June 2023, there were notifications of 9080 HPAI outbreaks in wild birds and 8203 in poultry to the [World Organisation for Animal Health \(WOAH\)](#)⁵, from all geographical regions except Oceania (including Australia and New Zealand). These HPAI outbreaks have caused significant mortalities in wild birds, poultry and mammals (wild and domestic/livestock), and represent a substantial increase in intensity, frequency and geographic range compared to previous years.

⁴ National Avian Influenza Wild Bird Surveillance Newsletter - Wild Bird News - December 2020

⁵ [WOAH World Animal Health Information System](#)

HPAI H5 clade 2.3.4.4b viruses have infected a much larger range of wild bird species than previous strains, which has likely contributed to rapid global spread and incursion into novel geographic regions.

To date, at least 500 species from more than half of all bird orders have reportedly been affected by HPAI H5 clade 2.3.4.4b. Over 50% of these represent the first report of HPAI infection in these species⁶.

While HPAI H5 clade 2.3.4.4b has been detected in apparently healthy waterfowl, it has also contributed to substantial wild bird mortality events. This includes the mortality of 8000 Eurasian cranes in Israel in December 2021 and January 2022, *circa* 20% of the Svalbard-breeding population of barnacle geese in the United Kingdom in January 2022⁷, and over 500,000 seabirds in South America between October 2022 and December 2023⁸, including almost 40% of Peruvian pelicans in Peru alone.

HPAI H5 clade 2.3.4.4b has also resulted in unprecedented morbidity and mortality events in terrestrial and aquatic mammals. More than 80 mammalian species have been affected since 2021, over 40 of which represent the first reports of HPAI in these species⁶. Species most affected are predators, scavengers and species with high potential for direct or indirect contact with infected wild birds, such as pinnipeds.

Mass mortalities in free-living marine mammals have been recorded, with *circa* 50,000 pinnipeds affected across Peru ([Leguia et al. 2023](#)), Chile ([Azat et al. 2023](#)), Argentina ([Campagna et al. 2023](#)), Uruguay ([Tomás et al. 2024](#)) and Brazil ([de Lima et al. 2024](#)). In terrestrial mammals, a high number of species have been reported with infection in North America⁹ and outbreaks have occurred in captive wild and domestic species, including farmed mink in Spain ([Aguero et al. 2023](#)), farmed fox, American mink and raccoon dog in Finland ([Lindh et al. 2023](#)), and an ongoing outbreak in dairy cows in the USA¹⁰.

In addition to infections with other avian influenza strains, human infections with HPAI H5N1 clade 2.3.4.4b have occurred sporadically. The majority of human HPAI infections have been in poultry workers, people with infected backyard birds, people who work in or visit live poultry markets, and dairy workers (in the USA). The most recent quadripartite risk assessment¹¹ states that the risk is low to the general population, and low to medium with high uncertainty for occupationally exposed workers. Human infections with HPAI, including H5N1 clade 2.3.4.4b, can be asymptomatic or associated with disease ranging from mild to severe illness and even death (see [Australian Department of Health and Aged Care](#)).

⁶ [Bird species affected by H5Nx HPAI \(fao.org\)](#)

⁷ [Convention on Migratory Species, Scientific Task Force on Avian Influenza and Wild Birds statement](#)

⁸ [OFFLU, Wildlife statement](#)

⁹ [USDA Animal and Plant Health Inspection Service, Detections of Highly Pathogenic Avian Influenza in Mammals](#)

¹⁰ [USDA Animal and Plant Health Inspection Service, HPAI in Livestock](#)

¹¹ [Updated joint FAO/WHO/WOAH assessment of recent influenza A \(H5\) virus events in animals and people](#)

The risk of High Pathogenicity Avian Influenza to Australian wild birds and poultry

HPAI could occur in Australia by evolution of endemically circulating LPAI to HPAI in poultry (e.g., [HPAI H7 outbreak in 2024](#)); seasonal migration of HPAI-infected wild birds on established flyways; nomadic movements of HPAI infected wildlife within the Australo-Papuan (year-round) or Antarctic/sub-Antarctic regions (seasonal); or, the importation of HPAI virus-contaminated poultry, poultry products, equipment or other materials (though strict biosecurity controls for importation mitigate this risk). Seasonal migration or nomadic movements of HPAI infected wild birds are the most likely incursion route(s) for HPAI H5N1 clade 2.3.4.4b.

LPAI viruses known to circulate in Australian wild birds remain an ongoing biosecurity threat to Australian poultry through direct or indirect (e.g. contaminated drinking water, fomites) contact. This spillover risk may be enhanced by poultry increasingly being farmed under extensive systems, which involves greater potential for contact between poultry and wild birds.

To date, all HPAI [outbreaks](#) in poultry in Australia have evolved from endemic LPAI H7 viruses circulating in Australian wild bird species, rather than via introduction of an HPAI strain from overseas.

Previous research (prior to the emergence of clade 2.3.4.4b) assessed the overall risk of introduction of HPAI H5 virus to Australia via migratory birds to be low ([East et al. 2008](#); [East et al. 2008](#); [Curran 2012](#)). This is because (1) wild birds are not reservoirs of other HPAI clades, despite the occasional spillover from poultry causing mass mortality events, and (2) waterfowl, the main group of birds associated with virus movement, are not long-distance migrants in Australia, but rather are nomadic within the Australo-Papuan region. In contrast, for clade 2.3.4.4b, (1) wild birds are reservoirs, and (2) a large diversity of avian species are contributing to long distance spread, as evidenced by two separate introductions into (sub-)Antarctica ([Banyard et al. 2024](#)), a region with no native duck species.

Shorebirds (order *Charadriiformes*) regularly migrate between Australia and Asia. Recent research has demonstrated that Australian migratory shorebirds are exposed to HPAI H5 clade 2.3.4.4b viruses along their migratory route between Asia and Australia ([Wille et al. 2019](#)). However, there is currently no evidence that these migratory birds are carrying HPAI H5 clade 2.3.4.4b viruses when they arrive in Australia ([Wille et al. 2019](#)). Sampling of inbound migratory seabirds and shorebirds in both 2022 (September to December) and 2023 (October to December) found no evidence of HPAI H5 clade 2.3.4.4b incursion into Australia ([Wille & Klaassen 2023](#), [Wille et al. 2024](#)).

A formal assessment of the risk to Australia from HPAI H5 clade 2.3.4.4b was undertaken in 2023². The risk assessment focused on the likelihood and consequence of HPAI H5 clade 2.3.4.4b incursions into Australia via wild birds with subsequent establishment in wild birds, poultry or wild mammals. It found that the risk of HPAI virus incursion/s into Australia via wild birds has increased due to changes in the epidemiology and ecology of HPAI H5 clade 2.3.4.4b virus. It also found a likelihood of more severe impacts for wildlife and the poultry sector than previous strains of HPAI.

A report from the joint WOAHA-FAO scientific network on animal influenza ([OFFLU](#)) on the continued expansion of HPAI¹² indicated that introduction of HPAI H5 clade 2.3.4.4b virus into Australia via infected birds from the Antarctic region is plausible. However, given the current unprecedented HPAI situation and limited movement data for birds in this region, there is high uncertainty surrounding this potential route of introduction.

Surveillance for Avian Influenza Viruses in Australia

Australia's [National Avian Influenza Wild Bird Surveillance Program](#) (the Program) includes:

Targeted surveillance

Environmental faecal swabs and cloacal and/or oropharyngeal samples are collected from 'apparently' healthy live and hunter-shot wild birds. Surveillance is undertaken on a risk-based approach and considers mixing between shorebirds and waterfowl, proximity to poultry enterprises and human health risks, with sampling locations distributed broadly across the country and some external territories. Target species for surveillance include waterfowl, shorebirds and seabirds.

Since 2022, targeted surveillance has been enhanced via:

- Increased shorebird sampling. In 2022, 2023 and 2024, sampling of nearly 5000 shorebirds and seabirds from locations around Australia was undertaken with assistance from numerous bird conservation organisations. This enhanced surveillance has been supported by NAIWB surveillance partners, particularly from Deakin University and University of Melbourne, with part funding via the Program.
- Expansion of sampling locations to cover all jurisdictions as part of the Program. This includes collection of samples by the Department of Agriculture, Fisheries and Forestry's [Northern Australia Quarantine Strategy](#) via engagement with First Nations communities and close collaboration with Indigenous rangers who have extensive and invaluable knowledge of Australia's ecosystems.
- Additional contributions to the Program. This includes *ad hoc* testing of samples from wildlife collected by researchers.

General surveillance

Investigation of significant or unexplained morbidity and mortality events in wild birds (with a focus on H5 and H7 virus exclusion testing) and other susceptible wildlife species. General surveillance sensitivity has been increased via revised triggers for investigations and tailored messages and outreach to multiple audiences (see [WHA website](#)).

Detailed analysis of LPAI viruses detected in wild birds through the national program continues to contribute to tracking evolution and dynamics of Australian avian influenza viruses, supports maintenance of fit-for-purpose sampling and testing programs, and contributes to a virus sequence library that enables comparison of Australian (endemic) and overseas (exotic or introduced) strains (see [Wild Bird News](#)).

¹² [OFFLU, Continued expansion of high pathogenicity avian influenza H5 in wildlife in South America](#)

In commercial poultry, surveillance is based around passive and syndromic surveillance activities, with intermittent active surveillance associated with outbreak response, research, or industry/jurisdictional initiatives. These activities are run at the jurisdictional level ([Commonwealth of Australia, 2010](#)). The Australian Government is also working with poultry industries to improve preparedness.

Further Information

Please note: all Australian Jurisdictions require that all avian influenza virus infections be reported to the relevant Chief Veterinary Officer. The national notifiable diseases list includes avian influenza but does not specify strains, see the [national list of notifiable animal diseases](#) for further information.

More information and resources on HPAI and wildlife are available on the [WHA HPAI incident page](#).

Global Situation

- World Organisation for Animal Health (WOAH), [updates on avian influenza in animals \(types H5 and H7\)](#)
- Joint OIE-FAO Scientific Network on Animal Influenza (OFFLU), [situation updates and statements on avian influenza](#)
- Food and Agriculture Organisation of the United Nations (FAO), [Global AIV with Zoonotic Potential situation update](#)
- Convention on the Conservation of Migratory Species of Wild Animals, [Scientific Task Force on Avian Influenza and Wild Birds](#)
- World Organisation for Animal Health & IUCN Wildlife Health Specialist Group, [Avian Influenza and Wildlife: Risk management for people working with wild birds](#)

Regional or country-specific data

- European Union Reference Laboratories, [Avian Flu Data Portal](#)
- IZSve, [Avian influenza in Europe: update](#)
- Canadian Food Inspection Agency National Emergency Operations Center GIS services, [High Pathogenicity Avian Influenza in Wildlife dashboard](#)
- United States Department of Agriculture, [HPAI in wild birds map](#)
- Centers for Disease Control and Prevention, [Information on Bird Flu](#)
- Scientific Committee on Antarctic Research, [Current Suspected and Confirmed Cases in the Region](#)