Emergence, spread, and impact of high pathogenicity avian influenza H5 in wild birds and mammals of South America and Antarctica, October 2022 to March 2024

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Abstract

The currently circulating high pathogenicity avian influenza (HPAI) virus of the subtype H5 causes variable illness and death in wild and domestic birds and mammals, as well as in humans. This virus evolved from the Goose/Guangdong lineage of HPAI H5 virus, which emerged in commercial poultry in China in 1996, spilled over into wild birds, and spread through Asia, Europe, Africa and North America by 2021, causing the deaths of hundreds of millions of poultry and likely millions of wild birds. Our objective was to summarize the spread and impact of HPAI H5 virus in wild birds and mammals in South America, evaluate the risk of its spread and potential impact in Antarctic wildlife, and consider actions to manage the current and future HPAI outbreaks in wildlife. We found in our review that the virus arrived in South America in October 2022, followed by wide and rapid spread throughout the continent, where it infected at least 83 wild bird species and 11 wild mammal species, and is estimated to have killed at least 667,000 wild birds and 52,000 wild mammals. HPAI H5 virus spread to the Antarctic region by October 2023 and to mainland Antarctica by December 2023, associated with multiple mortality events in seabirds and

marine mammals. The high spatial density of colonies of various Antarctic species of birds and mammals provides conditions for potentially devastating outbreaks with severe conservation implications. Ecosystem-level impacts may follow and affected populations may take decades to recover. Although little can be done to stop virus spread in wildlife, it is important to continue targeted surveillance of wildlife populations for HPAI H5 virus incursion, and assessment of the spread and impact of disease, both to provide information for wildlife managers to adapt conservation plans, and to help policymakers mitigate and prevent future HPAI outbreaks.

Introduction

The continued emergence of high pathogenicity avian influenza (HPAI) virus of the H5 subtype is a major hazard for wildlife health and conservation. In contrast to most infectious disease agents, HPAI H5 virus has a broad host range among wild birds and mammals, is highly infectious, and can cause high mortality. HPAI H5 virus therefore represents a novel but poorly understood threat to a broad range of wild animal populations and their ecosystems. This has been exemplified in South America, where HPAI H5 virus had not been reported until 2022 and thus entered into wild bird and mammal populations that presumably had never been exposed to that virus. It spread rapidly across the continent in the following months, causing mass mortality events of unprecedented magnitude in many wildlife species, in particular seabirds and marine mammals (Ariyama et al., 2023; Campagna et al., 2023; Carrazco-Montalvo et al., 2023; Cruz et al., 2023; Leguia et al., 2023; Marandino et al., 2023).

The current epidemic HPAI H5 virus is a descendant of the A/Goose/Guangdong/1/96 (Gs/GD) lineage. The term ‘high pathogenicity’ refers to the high morbidity and mortality rates in infected chickens, not necessarily in other infected species. The term ‘H5’ refers to the number of the hemagglutinin subtype to which this virus belongs; avian influenza viruses are categorized in 16 subtypes based on the antigenic properties of their hemagglutinin (Neumann, Treanor, & Kawaoka, 2021). While mortality from other HPAI viruses is mainly restricted to poultry, the Gs/GD lineage is unusual in also causing mortality in wild birds and mammals. Since its emergence, HPAI H5 has caused mortality in at least 356 species of wild birds (Klaassen & Wille, 2023a), 49 species of wild mammals (European Food Safety Authority et al., 2023) and hundreds of millions of poultry (Shi, Zeng, Cui, Yan, & Chen, 2023). It also has caused mortality in hundreds of people (Lai et al., 2016), with case fatality rates varying between different clades, countries, time periods, and types of exposure. This transmission of infection among a wide variety of species demonstrates the interconnectedness of domestic animals, wildlife, humans, and their shared environment, and highlights the need for a One Health approach to HPAI H5. The consensus definition of the One Health approach was in 2021 formulated by the interdisciplinary One Health High-Level Expert Panel and supported by the Food and Agriculture Organization, the World Organization for Animal Health, the United Nations Environment Programme and the World Health Organization, as “an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems. It recognizes that the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent" (One Health High-Level Expert et al., 2022; World Health Organization, 2021).

The Gs/GD lineage of HPAI H5 virus was first detected in commercially farmed geese in China in 1996 and has circulated and evolved in poultry ever since (Xie et al., 2023). Multiple virus variants within the Gs/GD lineage spread among the rapidly growing poultry populations in Asia. In 2005, there was substantial spillover into migratory wild birds, and subsequent spread to Europe and Africa. The virus caused numerous outbreaks in wild birds in Asia, Europe and Africa in the following years, typically during autumn and winter with spread primarily linked to migratory movements of wild birds. Additional resurgent events occurred in 2014, 2016, and 2020, associated with the emergence of the 2.3.4.4 clade (Xie et al., 2023). Since 2021, however, one clade of HPAI H5 virus (2.3.4.4b) has persisted year-round in wild birds in Europe (Pohlmann et al., 2022). This clade of HPAI H5 virus (further referred to as 'HPAI H5 virus' for the pathogen and 'HPAI H5' for the associated disease) spread across both the Atlantic Ocean (in 2021) and the Pacific Ocean (in 2022) to North America (Alkie et al., 2022; Caliendo et al., 2022), where it spread rapidly across the continent during 2022 and southwards, reaching Central and South America by October 2022 (European Food Safety Authority et al., 2022), South Georgia (Islas Georgia del Sur) by October 2023 (Banyard et al., 2024) and the Antarctic Peninsula by February 2024 (Scientific Committee of Antarctic Research, 2024).

Although national and international surveillance for HPAI H5 provides a relatively accurate overview of the geographic spread of HPAI H5 and its impact on poultry populations, as well as occurrence of human infections, surveillance and mortality estimates are limited in wild birds and mammals (Klaassen & Wille, 2023b). Hence the picture of the spread and impact of HPAI H5 in wildlife is fragmented across numerous reports and notifications, e.g., (Caliendo et al., 2024; Camphuysen & Gear, 2022). We here define impact as a major effect on affected wildlife species, including loss of individual lives, disruption of social structures such as those between parents and offspring, and reduction of population numbers. Also, there is little evidence by which routes HPAI H5 can spread through the Antarctic region as many wildlife species in the region are unique to that continent and their movements through the region are poorly understood (Bestley et al., 2020; Shirihai H, Jarrett B, Cox J, & GM., 2008). Furthermore, the potential impact on Antarctic wildlife populations is unclear as exposure risks and species susceptibility are poorly known. Therefore, the goals of this review were to: 1) synthesize data on spread of HPAI H5 virus and, as a measure of its impact, of associated mortality in wildlife in South America and the Antarctic region; 2) evaluate potential pathways for further introduction and virus spread through the Antarctic region; and 3) review potential concerns for wildlife conservation of HPAI H5 emergence in South America and Antarctica. By focusing on the impact of HPAI H5 on wildlife and ecosystems, which have been relatively neglected compared to the impacts on poultry and people (Klaassen & Wille, 2023b; Kuiken et al., 2005), we support greater equity among the health of ecosystems, wild and domestic animals, and humans, and so emphasize the One Health approach regarding HPAI H5 (One Health High-Level Expert et al., 2022).

Data on HPAI H5 virus detection and reported wildlife deaths for Central America and South America were obtained from reports to the World Organization for Animal Health (WOAH), which are centrally archived on the website of the World Animal Health Information System (WAHIS). These data were supplemented by data from websites of national government websites of Argentina, Brazil, and Chile; newspaper articles (Brazil, Uruguay); and scientific publications (Argentina, Brazil). Data for the Falkland Islands (Islas Malvinas) were obtained from a national government website and a newspaper article. Data for South Georgia (Islas Georgia del Sur) were obtained from a scientific publication and the website of the Agreement on Conservation of Albatrosses and Petrels. Data for the Antarctic Peninsula were obtained from the website of the Scientific Committee for Antarctic Research. Data on numbers of individuals found dead per species and country were summed in Appendix S1. HPAI H5 virus infection was confirmed in all reported species-country associations, with a few specified exceptions.

Spread of HPAI H5 through South America, October 2022 to December 2023

In the year following its introduction into South America, HPAI H5 virus infected at least 83 wild bird species and 11 wild mammal species and was the probable cause of death of at least 667,000 wild birds and 52,000 wild mammals (Figure 1, Appendix S1). (For ease of reading, mortality counts above ten are rounded off to the nearest ten, hundred or thousand, depending on the scale of mortality. Precise counts of dead animals are reported in Appendix S1.) These data are derived from reports of HPAI H5 virus detections in wild animals found ill or dead and mortality counts of wild animals during HPAI H5 outbreaks. Numerical comparisons among countries may be unreliable since countries differ considerably in their approach for surveillance, diagnostic methods and reporting of suspected/confirmed HPAI cases. Also, the correlation between the distribution of wildlife cases reported and human population density strongly suggests the potential for vast underreporting in sparsely populated areas (Klaassen & Wille, 2023a). Therefore, these data need to be interpreted with caution. For most species affected (e.g., pelicans, boobies, cormorants, sea lions) there was robust evidence that the unusual mortality recorded in South America during 2022-2023 was largely attributable to HPAI H5, with evidence including the high frequency of HPAI H5 detection in carcasses, spatiotemporal patterns of morbidity and mortality consistent with the epidemiology of an acute highly transmissible disease and absence of other factors that could explain the mortality events. However, there were a few species (e.g., shearwaters, ibises, parakeets) for which the evidence was less robust, and it is plausible that other causes of mortality may have coincided with HPAI H5 outbreaks. Regarding the scale of mortality events, it is extremely unlikely that all sick or dead animals were found and reported, especially in remote areas where observations and surveillance effort were scarce. For example, collection rates of waterbird carcasses during typical avian botulism outbreaks in the North American prairie are 10%–25% of total mortality (Bollinger et al., 2011). Moreover, as the outbreaks extended over months and then seasons, surveillance, detection and testing effort markedly decreased in the region, with some countries in South America failing to report new wildlife cases since late 2023. Therefore, the actual levels of wildlife mortality from HPAI H5 were undoubtedly much higher than the reported counts.

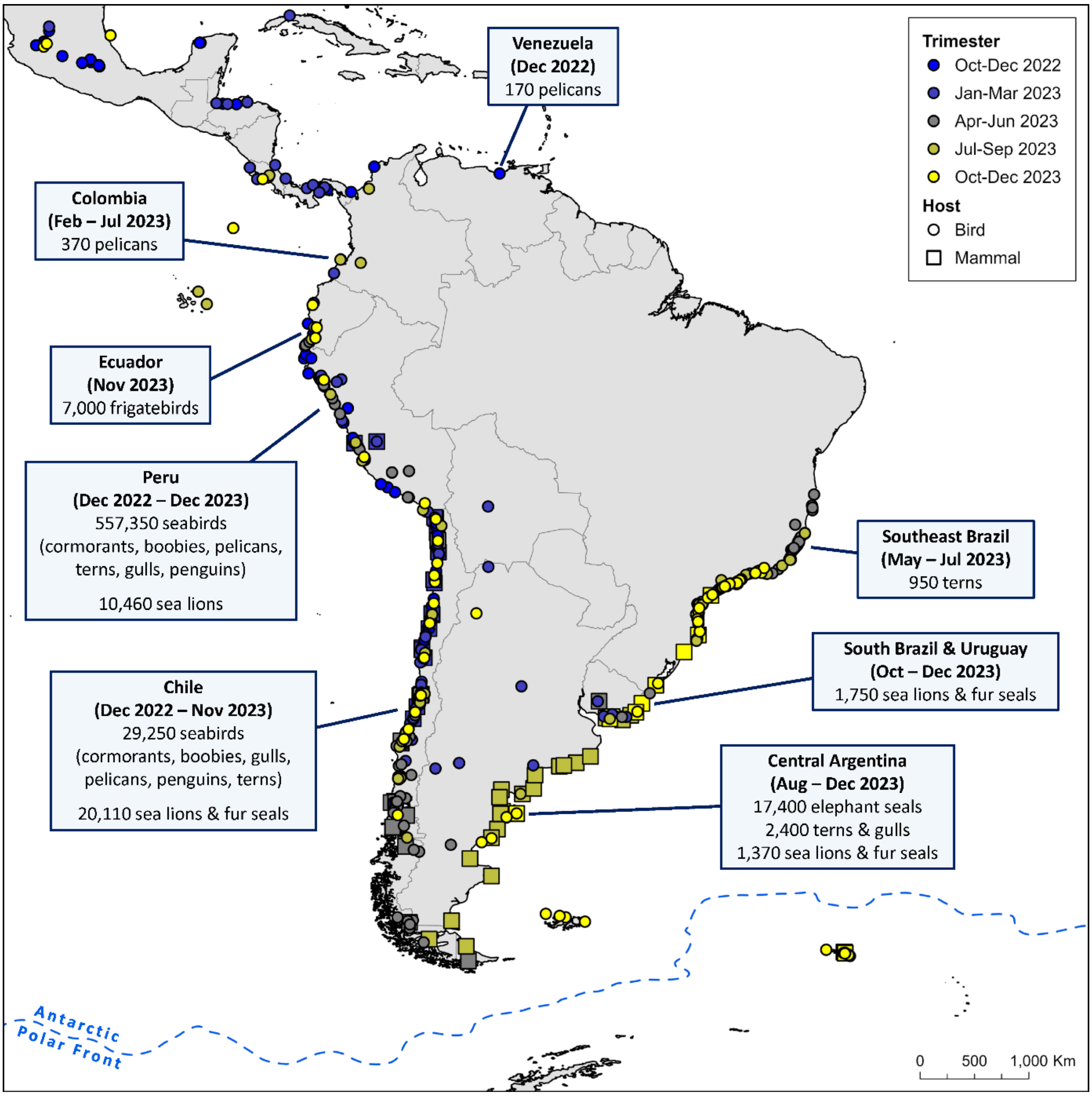

Figure 1: Overall geographical locations of reported incidents of HPAI-H5-associated mortality of wild birds and wild mammals in Central America, South America, and neighbouring islands groups (Galápagos, Falkland/Malvinas, South Georgia/Georgia del Sur) across time between October 2022 and December 2023. Selected major mortality events are indicated in text boxes. For details of mortality reports, see Appendix S1.

The chronology of HPAI H5 virus detections and associated wildlife mortalities, combined with genetic analyses (Banyard et al., 2024; Jimenez-Bluhm et al., 2023; Leguia et al., 2023; Marandino et al., 2023; Pardo-Roa et al., 2023; Reischak et al., 2023; Rimondi et al., 2024) suggests that HPAI H5 virus entered South America in October 2022, and that multiple independent viral introduction events occurred (Cruz et al., 2023; Leguia et al., 2023). Not all introduced viruses spread further through the continent. Following virus introduction, HPAI H5 spread southwards along the west coast of South America (Peru and Chile) from November 2022 to January 2023, and subsequently spread via two separate pathways: a) eastward across the Andes to infect poultry and waterbirds on the La Plata Basin (Bolivia, northern Argentina, Uruguay, and Paraguay) and inland areas of the Southern cone (central and southern Argentina) in February to April 2023 as well as to seabirds on the Atlantic coast (eastern Brazil) from June to October 2023; and b) southward along the southern Pacific coast (Chile) to infect seabirds and marine mammals (Castro-Sanguinetti et al., 2024), eventually reaching the southern tip of the continent and subsequently spreading northwards along the Atlantic coast (Argentina, Uruguay, and southern Brazil) from August to December 2023 (Figure 2). Below we describe events in South America from November 2022 to December 2023.

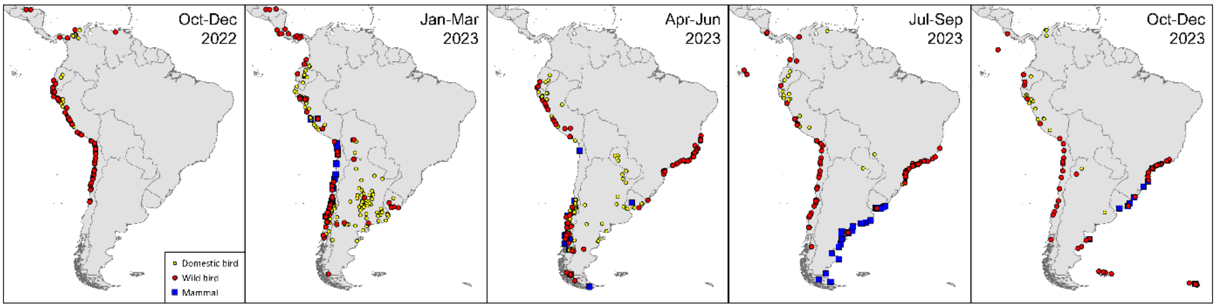

Figure 2: Progression per trimester of reported incidents of HPAI-H5-associated mortality of wild birds, wild mammals and domestic birds in Central America, South America, and neighbouring islands groups (Galápagos, Falkland/Malvinas, South Georgia/Georgia del Sur) from October 2022 to December 2023.

Venezuela (November 2022)

Among the first outbreaks of HPAI H5 in wildlife occurred in Venezuela in November 2022 (WAHIS, 2022c) (Figure 1) affecting 200 brown pelicans (*Pelecanus occidentalis*) (WAHIS, 2022d). This die-off in Venezuela is consistent with the relatively low mortality of wild birds reported in Central America in December 2022 and January 2023, specifically in Panama (Promed mail, 2022), Honduras(WAHIS, 2022b), Costa Rica (WAHIS, 2023f), and Guatemala (WAHIS, 2023h). Overall, numbers of wild birds reported dead in these countries were relatively low (hundreds) and mostly restricted to brown pelicans.

Peru (December 2022 to December 2023)

The largest HPAI-H5-associated mass mortality event occurred along the coast of Peru, affecting large numbers of seabirds and marine mammals that feed on abundant fish populations inhabiting the nutrient-rich Peruvian current upwelling ecosystem (Figure 1) (Peru Ministerio de Salud, 2023). About 558,000 seabirds of at least 14 species were found dead, mainly in the period December 2022 to June 2023 (Appendix S1, Figure 2). This number represents 84% of the total number of wild birds found dead in South America. The most frequently recorded species were cormorants (Phalacrocoracidae spp., n= 255,000), Peruvian boobies (*Sula variegata*, n=236,000), Peruvian pelicans (*Pelecanus thagus*, n=58,000), Inca terns (*Larosterna inca*, n=8,000) and gulls (Larinae spp., n=1,000). In addition, 11,000 South American sea lions (*Otaria byronia*) were found dead, mainly between January to March 2023. A short-beaked common dolphin (*Delphinus delphis*) also was found dead during that period.

Chile (December 2022 to November 2023)

There was HPAI-H5-associated mass mortality of aquatic birds—both sea and freshwater—and marine mammals along the coast of Chile, part of the same Peruvian current upwelling ecosystem as in Peru (Figure 1) (Chile Servicio Agrícola y Ganadero, 2023; Chile Servicio Nacional de Pesca y Acuicultura, 2023). About 97,000 aquatic birds of at least 46 species were found dead, mainly in the period December 2022 to June 2023 (Appendix S1, Figure 2). The main species found dead were guanay cormorants (*Leucocarbo bougainvilliorum*, n=30,000), sooty shearwaters (*Ardenna grisea*, n=24,000), Peruvian boobies (n=13,000), kelp gulls (*Larus dominicanus*, n=6,000), Peruvian pelicans (n=6,000), Humboldt penguins (*Spheniscus humboldti*, n=5,000), grey gulls (*Larus modestus*, n=4,000), neotropical cormorants (*Nannopterum brasilianum,* n=1,000), black-necked swans (*Cygnus melancoryphus*, n=1,000) and elegant terns (*Thalasseus elegans*, n=800). In addition to aquatic birds, HPAI H5 was also detected in nine species of terrestrial birds, with 1,000 individuals found dead, mainly turkey vultures (*Cathartes aura*, n=600).

There also were 22,000 marine mammals of nine species found dead, mainly in the period January to June 2023, starting a month later than reported seabird mortality (Chile Servicio Agrícola y Ganadero, 2023; Chile Servicio Nacional de Pesca y Acuicultura, 2023). This number represents 41% of the total number of wild mammals found dead in South America in association with this HPAI H5 outbreak. The main species affected was the South American sea lion (n=21,000), with more than double the mortality recorded in Peru. Other marine mammal species affected included short-beaked common dolphins (n=60), marine otters (*Lontra felina*) (n=50), Burmeister's porpoises (*Phocoena spinipinnis*, n=40), South American fur seals (*Arctocephalus australis*, n=40), and Chilean dolphins (*Cephalorhynchus eutropia*, n=20).

Bolivia, Argentina, Paraguay, Uruguay and Brazil (January to June 2023)

Starting in January 2023, a number of HPAI H5 outbreaks were recorded in poultry and wild waterbirds along the Rio de la Plata basin across Bolivia (WAHIS, 2023b), Argentina (initially at the north, then spreading southward to the Patagonian steppe) (Argentina Servicio Nacional de Sanidad y Calidad Agroalimentaria, 2023; WAHIS, 2023a), Paraguay (WAHIS, 2023i), Uruguay (WAHIS, 2023j) and Southern Brazil (Brazil Ministério da Agricultura e Pecuária, 2023a, 2023b; Reischak et al., 2023; WAHIS, 2023c). Most detections in wild waterbirds were not accompanied by large-scale mortality, with the exception of isolated clusters of mortality of black-necked swans (*Cygnus melancoryphus*, total n=300) in southern Brazil, Uruguay and Argentina. By early May 2023 most of these outbreaks had resolved and HPAI H5 detections dwindled. In mid-May 2023 a new wave of HPAI H5 detections emerged in seabirds in Espirito Santo, eastern Brazil. Cayenne terns (*Thalasseus acuflavidus eurygnathus*), royal terns (*Thalasseus maximus*) and South American terns (*Sterna hirundinacea*) were most heavily affected, with over 1,000 birds found dead. While most of the seabird mortality occurred in May and June 2023 and was concentrated in Espirito

Santo, HPAI H5 was detected sporadically in various species of seabirds found ashore (ill or dead) throughout the southeastern and southern coast of Brazil over the following months, suggesting continued HPAI H5 circulation in seabirds in the region.

Colombia (February 2023)

In February 2023, a brown pelican die-off in Colombia (Figure 1) occurred, affecting 400 individuals on Gorgona Island, near the country's Pacific coast (WAHIS, 2022a). This is the only mass mortality event reported in Colombia thus far.

Coastal Argentina (August to December 2023)

There was HPAI-H5-associated mass mortality of marine mammals and later of seabirds along the coast of Argentina (Figure 1) at the edge of the Patagonian Shelf, which extends from 35 degrees Southern Latitude south to the tip of Tierra del Fuego, and from the coast to approximately the 1000 m isobath (Falabella, Campagna, & Croxall, 2009; Raya Rey & Huettmann, 2020). Between August and December, there were 19,000 marine mammals of three species found dead along the Atlantic coast of Argentina (Appendix S1, Figure 2). Although small numbers of South American sea lions were found dead in the south of Argentina in August 2023 (Argentina Ministerio de Economía Secretaría de Agricultura Ganadería y Pesca, 2023a, 2023b), mortality soon spread north along the country's entire coast in August to December 2023, with more than 1,000 South American sea lions and South American fur seals found dead at a few monitored sites (Argentina Ministerio de Economía Secretaría de Agricultura Ganadería y Pesca, 2023a, 2023b). In October 2023, there was a mass mortality of southern elephant seal pups (*Mirounga leonina*) attributed to HPAI H5 in Peninsula Valdés, Chubut province. It was estimated that 97% of the pup population died, comprising over 17,000 deaths, the most substantial mortality event recorded for this species (Campagna et al., 2023).

Also, between October to November 2023, 3,000 seabirds of at least 10 species were found dead along the shoreline. Terns were the most heavily affected, with 2,000 individuals found dead across three species—South American terns, Cayenne terns and royal terns—at a few monitored sites along the coast of Patagonia (Argentina Servicio Nacional de Sanidad y Calidad Agroalimentaria, 2023). Because most tern breeding sites in this region were not monitored during this period, the overall mortality was likely higher.

Uruguay and southern Brazil (October to December 2023)

Shortly after the mortality of pinnipeds in Argentina, an HPAI-H5-associated mass mortality of more than 1,000 South American sea lions and South American fur seals (available reports fail to distinguish between the two species) occurred along the coasts of Uruguay (Anonymous, 2023a) and southern Brazil (Figure 1, Figure 2, Appendix S1) (Vara & Mano, 2023), in continuity with the mortality of pinnipeds recorded along the coast of Argentina.

Ecuador (November 2023)

Although HPAI H5 outbreaks were reported in Ecuadorian poultry since December 2022, detections in wildlife were relatively scarce and not associated with large mortalities. In November 2023, however, magnificent frigatebirds (*Fregata magnificens*, n=6,000) and great frigatebirds (*Fregata minor*, n=1,000) were found dead in association with HPAI H5 virus infection in areas of mangrove on the Ecuadorian coast (WAHIS, 2023g). These deaths had been preceded in September 2023 by the detection of HPAI H5 in a small number of great frigatebirds and red-footed boobies (*Sula sula*) on the Galápagos Islands (1,000 km west of mainland Ecuador) (WAHIS, 2023g). Fortunately, these earlier detections at the Galápagos were not associated with large wildlife mortality events.

Risk of further HPAI H5 spread in the Antarctic region

Following the rapid southbound movement of HPAI H5 through South America, its spread through Antarctica is highly plausible. The geographical area of Antarctica is defined differently according to different perspectives. The provisions of the Antarctic Treaty apply to the area south of 60 degrees Southern Latitude (Antarctic Treaty, 2023)(Secretariat of the Antarctic Treaty, 2023). However, biogeographically, the Antarctic region extends north of this line and includes the waters and islands up to the Antarctic polar front, where colder and nutrient-rich southern waters meet warmer northern waters (Figure 3). The Antarctic polar front is also the boundary of the area of the Convention for the Conservation of Antarctic Marine Living Resources (CCAMLR, 2023)(Commission for the Conservation of Antarctic Marine Living Resources, 2023). In this paper, we will use the Antarctic polar front as the boundary of the Antarctic region. This definition excludes the Falkland (Malvinas), Gough, Prince Edward, Crozet, Amsterdam/St Paul, Macquarie, Auckland, Campbell, Bounty and Antipodes islands, which we consider in this paper as part of the Subantarctic region when discussing the spread and impacts of HPAI H5.

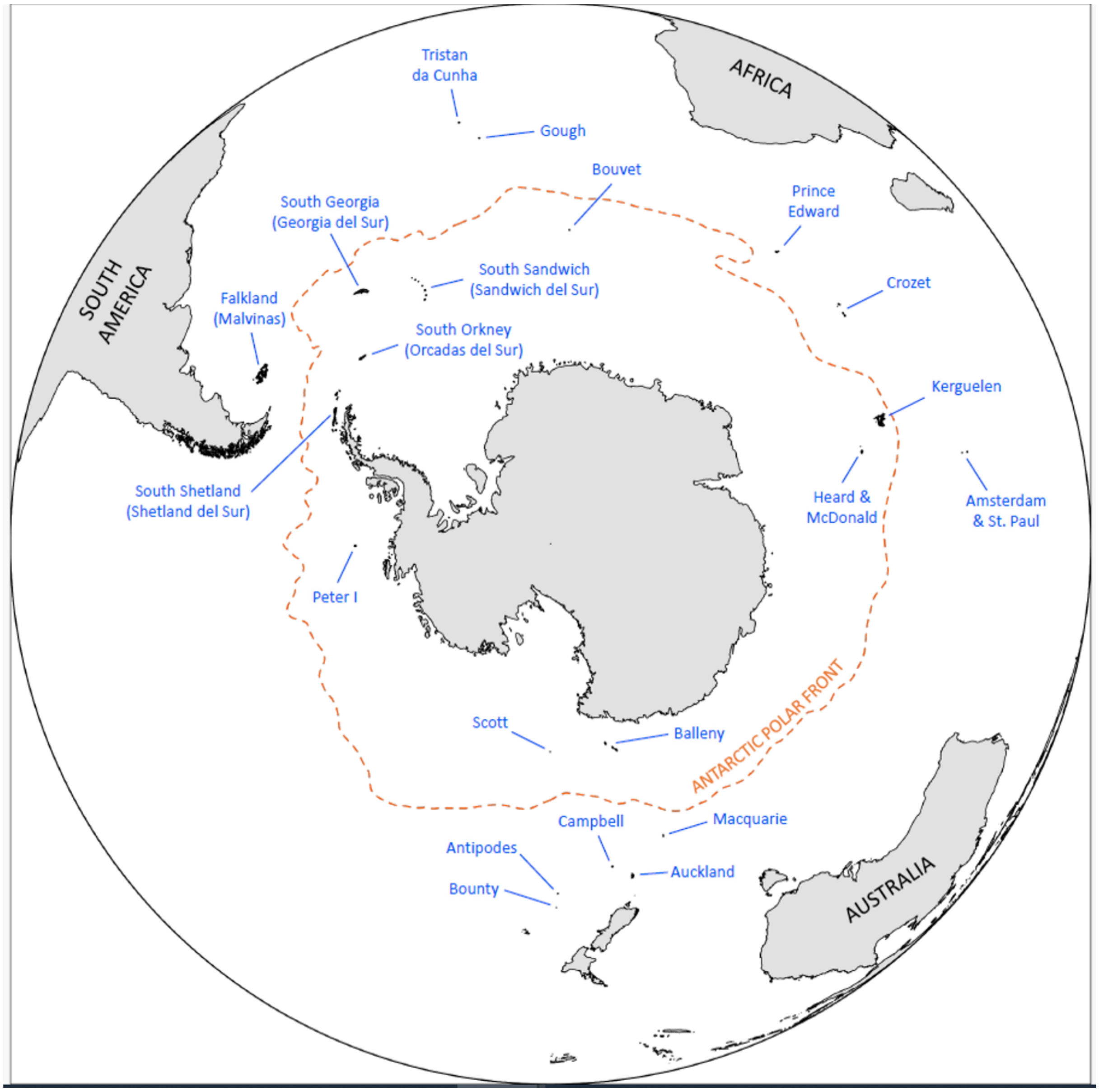

Figure 3: Map of Antarctica, showing the approximate position of the Antarctic Polar Front (dashed blue line, drawn from Moore et al., 1999) and the location of Antarctic and Subantarctic island groups.

Spread of HPAI H5 to the Falkland Islands and South Georgia, October to December 2023

The Falkland Islands (Islas Malvinas) are 1,000 km east of the mainland coast of Argentina and are part of the Patagonian Shelf. In October and November 2023, around the same time as seabird and marine mammal die-offs were reported along the coasts of Argentina and Uruguay (see above), HPAI H5 was detected in two southern fulmars (*Fulmarus glacialoides*) and one black-browed albatross (*Thalassarche melanophris*) found dead on the Falkland Islands (Falkland Islands Department of Agriculture, 2023). In December 2023, there was mortality of approximately 30 black-browed albatrosses attributed to HPAI H5 (Falkland Islands Department of Agriculture, 2023).

South Georgia (Islas Georgia del Sur) is an archipelago within the Antarctic Polar Front and lies 1,000 km southeast of the Falkland (Malvinas) Islands. South Georgia is part of the Scotia Arc, a chain of islands between the southern tip of South America and the Antarctic Peninsula, which also include the South Sandwich Islands (Islas Sándwich del Sur), the South Orkney Islands (Islas Orcadas del Sur), and the South Shetland Islands (Islas Shetland del Sur). In October and November 2023, about 60 brown skuas (*Stercorarius antarcticus*), 20 kelp gulls, 1 Antarctic tern (*Sterna vittata*), and unspecified numbers of southern elephant seals and Antarctic fur seals (*Arctocephalus gazella*) were found dead in association with HPAI H5 at multiple locations on South Georgia (Scientific Committee on Antarctic Research, 2023). Based on a limited number of publicly available virus sequences, genetic analysis showed the HPAI H5 virus from Bird Island to be most closely related to those from Uruguay, Peru and Chile collected between December 2022 and April 2023 (Banyard et al., 2024; Government of South Georgia and the South Sandwich Islands, 2023; Scientific Committee on Antarctic Research, 2023).

Significant recent events in Antarctic region, January to March 2024

HPAI-H5-associated deaths of more than 200 gentoo penguin (*Pygoscelis papua*) chicks and thousands black-browed albatross chicks on the Falkland Islands/Islas Malvinas were recorded in January 2024 (Mercopress, 2024), as well as in brown skuas and a variable hawk (*Geranoaetus polyosoma*) found dead in January and February 2024 (Scientific Committee of Antarctic Research, 2024). Mortality of more than 50 adult wandering albatrosses (*Diomedea exulans*) in South Georgia (Islas Georgia del Sur in February 2024 was attributed to HPAI H5 (ACAP online news article, 2023; Falkland Islands Department of Agriculture, 2023).

Furthermore, HPAI H5 virus was detected in two skuas found dead in February 2024 on Primavera Cape, on the west coast of the Antarctic Peninsula, and in five skuas found dead on James Ross Island, off the north-east coast of the Antarctic Peninsula (Anonymous, 2024; Bennet-Laso et al, 2024); it is unclear whether these were brown skuas or south polar skuas (*Stercorarius maccormicki*). These were the first detections of HPAI H5 on the continent of Antarctica (Scientific Committee of Antarctic Research, 2024).

Potential pathways for further introduction and spread of HPAI H5 in the Antarctic region

There are three main potential pathways through which additional incursion events into the Antarctic region could occur: (a) introduction to the Antarctic Peninsula by migratory species foraging on the Patagonian Shelf, (b) introduction to the Antarctic region by native Antarctic species overwintering throughout the austral temperate zone, and (c) introduction to the Antarctic region by trans-equatorial migratory species.

(a) The Patagonian Shelf may be the most probable and frequent source for spread of HPAI H5 virus to the Antarctic region, with the Falkland (Malvinas) Islands and South Georgia (Islas Georgia del Sur) likely playing a role as stepping stones. Given that more than 60 species of resident and visiting seabirds forage on the Patagonian Shelf (Croxall & Wood, 2002; Falabella et al., 2009; Quintana, 2002; Raya Rey &

Huettmann, 2020; Salyuk et al., 2022; Zamora et al., 2023), there are myriad scenarios by which seabirds may spread the virus further in the Antarctic region. Preliminary evidence from virus genome sequence analysis suggests that seabirds such as southern fulmars and brown skuas in which HPAI H5 was detected on the Falkland (Malvinas) Islands and South Georgia may have been infected on the Patagonian Shelf (Banyard et al., 2024). This is also supported by the numerous detections of HPAI H5 virus in seabirds in Argentina and Uruguay in preceding months (Argentina Servicio Nacional de Sanidad y Calidad Agroalimentaria, 2023; Brazil Ministério da Agricultura e Pecuária, 2023b; WAHIS, 2023c). Seabirds could transport HPAI H5 virus when migrating southwards to their breeding areas in the Scotia Arc, the Antarctic Peninsula, and Antarctic and Subantarctic islands. In addition to seabirds, marine mammals also should be considered as possible vectors of HPAI H5 virus, assuming that some individuals may be infected without showing clinical signs. Marine mammals may swim long distances in the period of infection, which in seals has been shown to be about one week (Webster et al., 1981). For example, southern elephant seals leave their breeding sites after breeding or moulting and migrate south to Antarctica to feed on squid and fish at the edge of the sea-ice (Lewis, Campagna, Marin, & Fernandez, 2006; McGovern et al., 2022; Rodriguez et al., 2017). This implies that, from the Peninsula Valdés or South Georgia (Islas Georgia del Sur), infected southern elephant seals could conceivably transport the virus to the remainder of the Scotia Arc and to the Antarctic Peninsula. Further, marine mammals that have succumbed to HPAI H5 may represent a source of infection for avian species that feed on their carcasses.

(b) Species that are native to the Antarctic region could be exposed to HPAI H5 while foraging at other areas in the austral temperate zone. For instance, Antarctic prions (*Pachyptila desolata*), the most southerly breeding of all prion species, could play a role in virus spread and amplification. HPAI H5 was detected in an individual found dead on the southeast coast of Brazil in September 2023. This species breeds in large numbers on islands of the Scotia Arc, Subantarctic islands in the Indian Ocean near New Zealand, and probably on Scott Island near the Antarctic continent. They congregate in large rafts at sea just before dusk and attend the colonies in huge flocks just after dark, which would provide opportunities for HPAI H5 transmission. After the breeding season, Antarctic prions disperse in a wide geographical range between the Antarctic pack-ice and about 35°S. They are commonly found both on the Patagonian Shelf as well as in the Humboldt Current off South America during the austral winter (Navarro, Cardador, Brown, & Phillips, 2015; Quillfeldt, Masello, Navarro, & Philips, 2013). Similarly, during the austral winter other seabirds such as large numbers of various petrel species may also forage diffusely on open waters and continental shelves of the austral temperate zone, and could be exposed to HPAI H5 through at-sea interactions with other subtropical and temperate species. The susceptibility of petrel species is known from sporadic HPAI H5 detections in southern giant petrels (*Macronectes giganteus*) found ashore in Chile, northern giant petrels (*Macronectes halli*) and great-winged petrels (*Pterodroma macroptera*) in Chile and South Africa and white-chinned petrels (*Procellaria aequinoctialis*) in Brazil (Appendix S1).

(c) HPAI H5 could be introduced to the Antarctic region by trans-equatorial migratory species such as Arctic terns (*Sterna paradisaea*), long-tailed jaegers (*Stercorarius longicaudus*), or south polar skuas. For example, the south polar skua spends the austral winter (boreal summer) in the North Pacific and North Atlantic and breeds in relatively snow-free areas of Antarctica in the austral summer. Although this species is usually reliant on fish, it can also survive exclusively on the predation/scavenging of penguins in some areas (Kopp et al., 2011), which could provide opportunities for transmission of HPAI H5 viruses acquired in the northern hemisphere.

Following introduction to Antarctica, there will likely be numerous opportunities for HPAI H5 virus spread within this region. The Scotia Arc and the Antarctic Peninsula are home to large colonies of seabirds (especially penguins), Antarctic fur seals and southern elephant seals, which are known or likely to be susceptible to HPAI H5 (Appendix S2). Low pathogenicity avian influenza strains (subtypes H4N7, H5N5, H6N8, and H11N2) have been detected in Adélie (*Pygoscelis adeliae*), gentoo and chinstrap penguins (*Pygoscelis antarcticus*), southern giant petrels, snowy sheathbills (*Chionis albus*), and brown skuas, and phylogenetic analysis indicates virus circulation in the Antarctic over several years (Barriga et al., 2016; de Seixas et al., 2022; E. de Souza Petersen et al., 2017; Hurt et al., 2016; Hurt et al., 2014; Ogrzewalska et al., 2022). This indicates that these species are suitable hosts for the transmission and persistence of influenza viruses, and suggests that if introduced, HPAI H5 strains potentially could spread and cause significant impacts on these populations.

Further expansion to other parts of the continent is plausible given that many Antarctic birds and pinnipeds probably are susceptible to infection and have overlapping ranges that form a wide circumpolar band around Antarctica (BirdLife International, 2024; del Hoyo, Elliott, Sargatal, & Collar, 1992-2008; IUCN, 2023) (Figure 4). Several seabirds such as albatrosses are known to perform circumpolar movements in the Southern Ocean, and therefore could support the longitudinal spread of HPAI H5 among Antarctic and Subantarctic islands (e.g. visitors to breeding colonies) or transmission during interactions at sea (e.g. albatrosses and petrels aggregating at foraging sites or near fishing vessels) (Agreement of the Conservation of Albatrosses and Petrels, 2020). This would allow virus expansion along the Antarctic continent and adjacent islands, where dense breeding colonies or other aggregations of susceptible avian or mammalian hosts occur at variable distances of tens to hundreds of kilometres from each other. The success of virus spread depends in part on the distance that infected migrating hosts can travel while actively infected with respect to the distance between colonies (Brown, Stallknecht, & Swayne, 2008; Ramis et al., 2014; Reperant et al., 2011) and the success of virus transmission to hosts and amplification of the virus at uninfected colonies, which likely increases with a higher number and density of susceptible hosts at the colony.

Skuas and giant petrels, through their predatory and scavenging behaviour, visit numerous sites along the southern tip of South America, Antarctic and Subantarctic islands, and the Antarctic Peninsula. These habits and frequent incursions into breeding colonies of other species, suggest these species could also play a significant role in the spread of HPAI H5 among sites in the Antarctic region. Brown skuas, southern fulmars and kelp gulls have repeatedly been affected on the Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur) and thus far have been among the first species affected in new locations.

Predatory and scavenging birds such as great skuas (*Catharacta skua*), gulls, corvids, raptors and vultures have been involved in HPAI H5 outbreaks in the northern hemisphere (Animal and Plant Health Inspection Service U.S. Department Of Agriculture, 2024; Camphuysen & Gear, 2022; Giacinti et al., 2024; van den Brand et al., 2015; Wunschmann et al., 2024).

Conservation implications

The impacts of this HPAI H5 outbreak on wildlife in South America are enormous. Firstly, the immense numbers of lives lost: more than 667,000 wild birds of 83 species and more than 52,000 wild mammals of 11 species reported dead between October 2022 and December 2023, with actual mortality likely many times larger. This has a direct conservation impact on multiple wild bird and mammal species that are already threatened from other causes. This includes species listed by the International Union for Conservation of Nature as being under threat of extinction in the near future (IUCN, 2023). Based on the number of individuals found dead, seabird species that suffered potential conservation impacts included Humboldt penguin (vulnerable), and Peruvian pelican, red-legged cormorant (*Poikilocarbo gaimardi*), sooty shearwater, elegant tern and Inca tern (all near-vulnerable). Mammal species that suffered potential conservation impacts include marine otter and southern river otter (*Lontra provocax*) (both endangered), and Chilean dolphin and Burmeister's porpoise (both near-threatened) (Appendix S1).

If HPAI H5 virus spreads further across the Antarctic region, the negative impact on the region's wild bird and mammalian populations could be immense, both because of their likely susceptibility to mortality from this virus, and their occurrence in dense colonies (Figure 4). Based on mortality events which have occurred elsewhere, bird species found on Antarctica and the Subantarctic islands are likely highly susceptible to HPAI H5. Repeated outbreaks in African penguins (*Spheniscus demersus*) in South Africa and Namibia (Molini et al., 2020; Roberts et al., 2023), outbreaks in Humboldt penguins in Peru and Chile (see above) and outbreaks in gentoo penguins on the Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur) (see above) demonstrate that penguins are susceptible to HPAI H5. The recent mortalities of black-browed albatrosses at the Falkland Islands (Islas Malvinas) and of wandering albatrosses at South Georgia (Islas Georgia del Sur) confirm that Procellariiformes are also highly susceptible, highlighting the potential conservation risk for other endangered populations of these species. Beyond the avian taxa classically associated with Antarctica, it is likely that the many species of endemic teals, cormorants, and parakeets found on Subantarctic Islands are susceptible, too (Rijks et al., 2022; Roberts et al., 2023; WAHIS, 2023d, 2023e). The impacts of HPAI H5 in this region will likely be exacerbated by species endemicity and colonial behaviour such that vast percentages of the world population are concentrated into a few locations. For example, Steeple Jason Island in the Falkland/Malvinas Islands hold 70% of the world population of black-browed albatross. The occurrence of many of these species in dense colonies also likely facilitates rapid virus transmission (Boulinier, 2023). Antarctic and Subantarctic birds already face a myriad of challenges, including declining prey abundance, fisheries bycatch and climate change. We therefore consider HPAI H5 a major conservation threat to all endemic Antarctic and Subantarctic bird species.

Likewise, pinniped populations present in the Subantarctic and Antarctic regions also are probably susceptible to infection and mortality from HPAI H5. All six Antarctic pinniped species belong to the families Otariidae or Phocidae (Appendix S2), both of which have been extensively affected by HPAI H5 in South America (Campagna et al., 2024; Leguia et al., 2023). Given the substantial HPAI-H5-associated mass mortalities of South American fur seals in southern Brazil and Uruguay, it is probable that the fur seals of the Antarctic region would also be highly susceptible such that catastrophic impacts to the species' most significant populations may ensue. For example, 95% of the global population of the Antarctic fur seal is concentrated at South Georgia (Islas Georgia del Sur), (IUCN, 2023) and there has been HPAI-H5-attributed mortality since October 2023. Similarly, approximately 50% of the global population of the southern elephant seal is concentrated at South Georgia (Islas Georgia del Sur) (Boyd et al., 1996), and deaths associated with HPAI H5 have been reported there since October 2023 (Banyard et al., 2024; Government of South Georgia and the South Sandwich Islands, 2023). The most severe HPAI H5 impact in this species so far has been at Peninsula Valdés, Argentina, where 97% of pups died in October and November 2023 (Campagna et al., 2023).

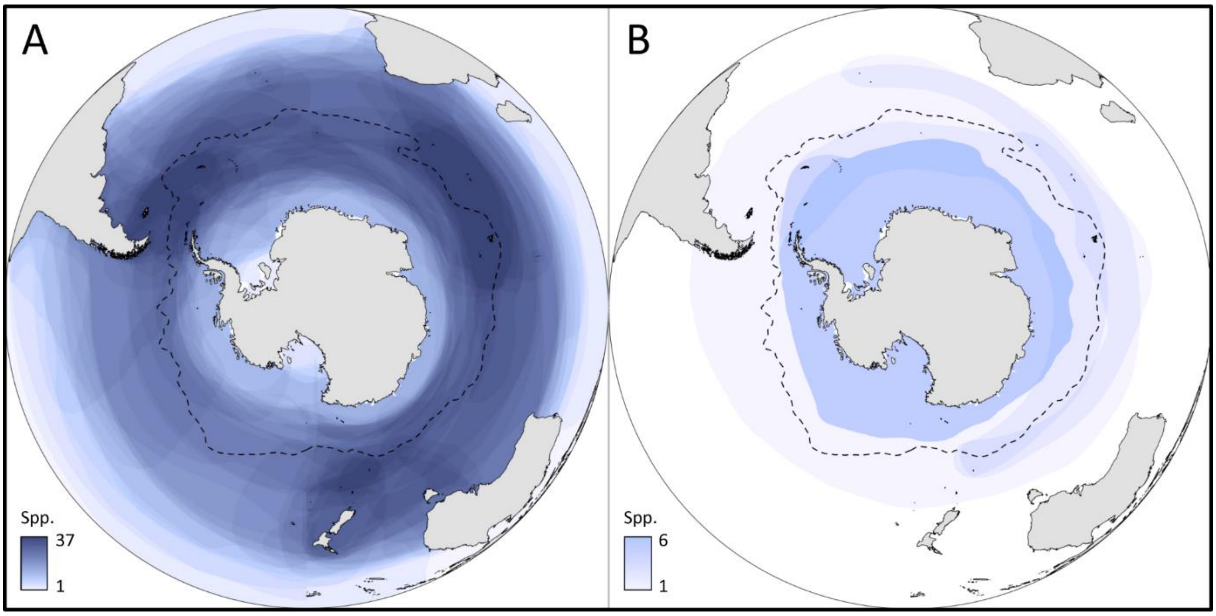

Figure 4: Marine distribution of seabird diversity (A), and pinniped diversity (B). These maps show the number of avian and pinniped species occurring per location, as a measure of the potential for HPAI H5 virus to spread. Avian and pinniped diversity are drawn using the same colour gradient and were derived from publicly available species distribution maps (BirdLife International and Handbook of the Birds of the World, 2019; IUCN, 2023).

Five of 17 Antarctic cetacean species belong to the families Delphinidae or Phocoenidae (Appendix S2), in which HPAI-H5-associated mortality has thus far been detected in Peru and Chile (Chile Servicio Nacional de Pesca y Acuicultura, 2023; Leguia et al., 2023) as well as in the northern hemisphere (Murawski et al., 2023; Thorsson et al., 2023). The mechanisms of transmission of HPAI H5 to cetaceans remain unclear and no mass mortalities of cetaceans have been attributed to the virus. However, it is plausible that at-sea mortalities have gone undetected. Therefore, it would be prudent to consider cetaceans as potentially susceptible to HPAI H5 in Antarctica.

Overall, HPAI H5 is a major conservation concern, not just in the short term, but also in long-term impacts on populations. For example, populations of long-lived species of birds and mammals could take decades to recover, particularly if HPAI outbreaks recur in consecutive years and the disease kills adult females. Moreover, species currently listed as Least Concern (IUCN) could become threatened, with important consequences for conservation priorities.

In addition to conservation challenges for directly affected wildlife species, HPAI H5 may have large ecosystem-level impacts. For example, following Antarctic whaling, the mass removal of animals had substantial ecosystem-level impacts, including species extinction, breakdown of predatory-prey interactions, modification of nutrient cycling, breakdown in carbon sequestration and thus increased CO_2 emissions, negative impacts on global marine productivity and shifts in species compositions (Herr et al., 2022; Roman et al., 2014). If HPAI H5 were to cause mass mortality events in Antarctica to the scale of those reported in South America, this mass "removal" of animals from the landscape could have similar, profound, impacts on Antarctic coastal and marine ecosystems.

Managing the ongoing HPAI H5 outbreak

Now that HPAI H5 virus has spilled over into wildlife and is no longer dependent on poultry for its continued transmission, there is little that can be done to stop the spread of this virus among free-living populations. Nevertheless, there are a few actions that may help to lower the impact of the ongoing HPAI H5 outbreak for wildlife:

1. Surveying wildlife populations for the presence of HPAI H5 virus based on evidence of unusual morbidity and mortality and virological and serological analyses, including timely sharing of disease diagnosis and of viral genome sequences. This will enable prompt detection of new virus introductions and monitoring of virus evolution through phylogenetic analyses, which are relevant for both animal and human health.
2. Recording mortality events in wildlife comprehensively and collecting information and samples to substantiate the cause or causes of mortality. Well-documented descriptions of HPAI H5 outbreaks in wildlife are required to evaluate the impact of this disease on wildlife populations. Due to its relative remoteness, avian influenza surveillance and investigation of unusual wildlife mortality events require careful advance planning and coordination among the scientists from different countries interested in working on avian influenza in Antarctica. This is done through the Antarctic Wildlife Health Network of the Scientific Committee on Antarctic Research (Scientific Committee on Antarctic Research, 2023).
3. Removing infected carcasses as early as possible and repeatedly at wild bird breeding sites that are intensively monitored and managed. While there are studies that suggest that carcass removal is effective to reduce contamination and transmission to other animals (Knief et al., 2024; Reperant, Caliendo, & Kuiken, 2021; Rijks et al., 2022; Yamamoto, Nakamura, & Mase, 2017), efficacy in different scenarios remains uncertain. In Antarctica there are additional challenges associated with carcass removal due to rules preventing carcass burial and the lack of incinerators (Dewar et al., 2023). Also, the

potential benefits of removing carcasses need to be weighed up against the potential adverse effects of repeated disturbance of breeding colonies.

4. Reducing non-essential human activities (e.g. tourism, extraction/exploitation of natural resources) at affected sites, to prevent unintentionally spreading the virus and to minimize the risks of human exposure. Rules for tourism are of particular relevance to Antarctica, where there were 122,072 tourists in the 2023-2024 austral season (International Association of Antarctica Tour Operators, 2024). These measures may also be particularly important at breeding sites of affected birds and mammal species, in order to reduce disturbance and enhance post-outbreak population recovery.
5. Essential human activities (e.g. research, implementation of conservation measures) at affected sites should involve appropriate biosafety measures, such as disinfection of footwear and the use of personal protective equipment. Some measures need to be adapted to the unique circumstances in the sub-Antarctic and Antarctica (Dewar et al., 2023). This aims both to reduce the risk of human-caused spread of virus to other wildlife populations, and to protect people exposed to HPAI H5 virus from infected animals.

Under no circumstance should disease control measures include consideration of killing of wild birds or mammals, spraying toxic products or negatively affecting wetlands and other habitats, nor deterring animals from access to their habitat. This is based on advice of the Food and Agriculture Organization (FAO) and the World Organisation for Animal Health (WOAH), and international obligations under the Convention on Migratory Species (CMS), the Agreement on the Conservation of African-Eurasian Migratory Waterbirds (AEWA) and the Ramsar Convention on Wetlands (CMS & FAO, 2023).

Concluding remarks

A consequence of the Anthropocene with human beings as the dominating factor on Earth is an increase in the rate of emerging infectious disease events. These events include diseases spilling over from farmed or traded animals into free-ranging wildlife populations, such as mycoplasmosis from poultry to North American songbirds (Dhondt et al., 2005), African swine fever from domestic pigs to Eurasian wild boar and Asian wild pigs (Luskin et al., 2020), and HPAI H5 from poultry to multiple species of wild birds and mammals world-wide (Wille & Barr, 2022). This is a paradigm shift where wildlife is not just a source but also a victim of emerging infectious diseases (Kuiken & Cromie, 2022).

A parallel paradigm shift is needed in infectious disease prevention and control to prevent escalation of emerging infectious disease events in wildlife, livestock and humans from happening in the future, as well as to minimize their impacts when they do occur. To this end, we advocate a One Health approach, which aims to optimize health not only of people and livestock, but also of wildlife and ecosystems. Such a One-Health-based paradigm shift includes integrating previously siloed government departments of agriculture, public health and environment; building a One-Health workforce capable of handling these complex wicked problems; and greatly increasing financial support for research, surveillance and management of emerging infectious disease events in wildlife and ecosystems, to similar levels as for livestock and people.

The current HPAI H5 outbreak, which stems from a virus that emerged in a rapidly expanding poultry sector in eastern Asia, has led to catastrophic impacts on seabird and pinniped populations in South America. This highlights that ecosystems are globally connected, that viruses do not recognize political or species barriers, and that once such an adaptable virus spills over into wildlife, it is out of our control. To prevent future HPAI outbreaks in wildlife, reduce risk for humans and protect food security, we need to recognise the links between livestock production, wildlife populations and ecosystem health in disease prevention, preparedness and response. Moreover, we need to be proactive in addressing the drivers of disease emergence, with a renewed focus on biodiversity conservation.

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References

ACAP online news article. (2023). Retrieved from https://www.acap.aq/latest-news/high-pathogenicity-avian-influenza-has-spread-to-wandering-albatrosses-on-subantarctic-islands

Agreement of the Conservation of Albatrosses and Petrels. (2020). Species Assessment. Retrieved from https://www.acap.aq/resources/acap-species

Alkie, T. N., Lopes, S., Hisanaga, T., Xu, W., Suderman, M., Koziuk, J., . . . 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 Evol, 8*(2), veac077.

Animal and Plant Health Inspection Service U.S. Department Of Agriculture. (2024). Wild Bird Avian Influenza Surveillance. Retrieved from https://www.aphis.usda.gov/aphis/maps/animal-health/wild-bird-avian-flu-surveillance

Anonymous. (2023a). Preocupación por 552 lobos marinos muertos a pocos kilómetros del Chuy [Concern over 552 dead sea lions a few kilometers from Chuy]. Retrieved from www.elobservador.com.uy/nota/preocupacion-por-552-lobos-marinos-muertos-a-pocos-kilometros-del-chuy-20231025183255

Anonymous. (2024). Scientists confirm first cases of bird flu on mainland Antarctica. The Guardian. Retrieved from www.theguardian.com/environment/2024/feb/26/scientists-confirm-first-cases-of-bird-flu-on-mainland-antarctica

Argentina Ministerio de Economía Secretaría de Agricultura Ganadería y Pesca. (2023a). Influenza aviar: Se confirmó un caso positivo en mamíferos silvestres en Río Negro. Retrieved from https://www.argentina.gob.ar/noticias/influenza-aviar-se-confirmo-un-caso-positivo-en-mamifero-marino-en-rio-negro

Argentina Ministerio de Economía Secretaría de Agricultura Ganadería y Pesca. (2023b). Influenza aviar: Se confirmó un caso positivo en mamíferos silvestres en Tierra del Fuego. . Retrieved from www.argentina.gob.ar/noticias/influenza-aviar-se-confirmo-un-caso-positivo-en-mamiferos-silvestres-en-tierra-del-fuego

Argentina Servicio Nacional de Sanidad y Calidad Agroalimentaria. (2023). Estado de la situación epidemiológica en la Argentina [State of the epidemiological situation in Argentina]. . Retrieved from www.argentina.gob.ar/senasa/estado-de-la-situacion-epidemiologica-en-la-argentina

Ariyama, N., Pardo-Roa, C., Munoz, G., Aguayo, C., Avila, C., Mathieu, C., . . . Neira, V. (2023). Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b Virus in Wild Birds, Chile. *Emerg Infect Dis, 29*(9), 1842-1845.

Banyard, A., Bennison, A., Byrne, A. M. P., Reid, S. M., Lynton-Jenkins, J. G., Mollett, B., . . . James, J. (2024). Detection and spread of high pathogenicity avian influenza virus H5N1 in the Antarctic Region. *Nat. Commun., 15*(1).

Barriga, G. P., Boric-Bargetto, D., San Martin, M. C., Neira, V., van Bakel, H., Thompsom, M., . . . Medina, R. A. (2016). Avian Influenza Virus H5 Strain with North American and Eurasian Lineage Genes in an Antarctic Penguin. *Emerg Infect Dis, 22*(12), 2221-2223.

Bennett-Laso, B., Berazay, B., Muñoz, G., Ariyama, N., Enciso, N., Braun, C.,... Confirmation of highly pathogenic avian influenza H5N1 in skuas, Antarctica 2024. Front Vet Sci. 2024 Dec 6;11:1423404. doi: 10.3389/fvets.2024.1423404.

Bestley, S., Ropert-Coudert, Y., Bengtson Nash, S., Brooks, C. M., Cotté, C., Dewar, M., . . . Wienecke, B. (2020). Marine Ecosystem Assessment for the Southern Ocean: Birds and Marine Mammals in a Changing Climate. *Frontiers in Ecology and Evolution, 8*. doi:10.3389/fevo.2020.566936

BirdLife International. (2024). Data zone. Retrieved from https://datazone.birdlife.org/species/search

Bollinger, T. K., Evelsizer, D. D., Dufour, K. W., Soos, C., Clark, R. G., Wobeser, G., . . . Pybus, M. J. (2011). *Ecology and management of avian botulism on the Canadian prairies.* . Retrieved from www.phjv.ca/wp-content/uploads/2017/10/BotulismReport_FINAL_FullReport_Aug2011.pdf

Brazil Ministério da Agricultura e Pecuária. (2023a). Panorama da ocorrência da infecção pelo vírus influenza A de alta patogenicidade (H5N1) em aves silvestres e domésticas de subsistência no Brasil - maio a julho de 2023 [Overview of the occurrence of infection by the highly pathogenic influenza A virus (H5N1) in subsistence wild and domestic birds in Brazil - May to July 2023]. . Retrieved from www.gov.br/agricultura/pt-br/assuntos/sanidade-animal-e-vegetal/saude-animal/programas-de-saude-animal/pnsa/panorama_iaap_br_maio_julho2023.pdf

Brazil Ministério da Agricultura e Pecuária. (2023b). Influenza Aviária [Avian influenza]. Retrieved from https://mapa-indicadores.agricultura.gov.br/publico/extensions/SRN/SRN.html

Brown, J. D., Stallknecht, D. E., & Swayne, D. E. (2008). Experimental infections of herring gulls (*Larus argentatus*) with H5N1 highly pathogenic avian influenza viruses by intranasal inoculation of virus and ingestion of virus-infected chicken meat. *Avian Pathol, 37*(4), 393-397.

Caliendo, V., Kleyheeg, E., Beerens, N., Camphuysen, K. C. J., Cazemier, R., Elbers, A. R. W., . . . Rijks, J. M. (2024). Effect of 2020-21 and 2021-22 Highly Pathogenic Avian Influenza H5 Epidemics on Wild Birds, the Netherlands. *Emerg Infect Dis, 30*(1), 50-57.

Caliendo, V., Lewis, N. S., Pohlmann, A., Baillie, S. R., Banyard, A. C., Beer, M., . . . Berhane, Y. (2022). Transatlantic spread of highly pathogenic avian influenza H5N1 by wild birds from Europe to North America in 2021. *Sci Rep, 12*(1), 11729.

Campagna, C., Uhart, M., Falabella, V., Campagna, J., Zavattieri, V., Vanstreels, R. E. T., & Lewis, M. (2023). Catastrophic mortality of southern elephant seals caused by H5N1 avian influenza. . *Marine Mammal Science*. doi:doi.org/10.1111/mms.13101

Camphuysen, K. C. J., & Gear, S. C. (2022). Great Skuas and Northern Gannets on Foula, summer 2022 - an unprecedented, H5N1 related massacre. *NIOZ Report 2022*(02), 312-323.

Carrazco-Montalvo, A., Luje, L., Rodríguez-Pólit, C., Ampuño, A., Patiño, L., Gutiérrez-Pallo, D., . . . De La Torre, D. (2023). Highly pathogenic Avian Influenza A (H5N1) Clade 2.3.4.4b in Wild Birds, Ecuador. *bioRxiv*, 2023.2010.2018.562614.

Castro-Sanguinetti, G. R., Gonzalez-Veliz, R., Callupe-Leyva, A., Apaza-Chiara, A. P., Jara, J., Silva, W., . . . More-Bayona, J. A. (2024). Highly pathogenic avian influenza virus H5N1 clade 2.3.4.4b from Peru forms a monophyletic group with Chilean isolates in South America. *Sci Rep, 14*(1), 3635.

Chile Servicio Agrícola y Ganadero. (2023). Influenza Aviar (IA) [Avian influenza dashboard]. Retrieved from www.sag.gob.cl/ambitos-de-accion/influenza-aviar-ia

Chile Servicio Nacional de Pesca y Acuicultura. (2023). Influenza Aviar [Avian influenza summary]. Retrieved from www.sernapesca.cl/influenza-aviar

CMS & FAO (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. www.cms.int/en/publication/h5n1-high-pathogenicity-avian-influenza-wild-birds-unprecedented-conservation-impacts

Commission for the Conservation of Antarctic Marine Living Resources. (2023, October 2017). Map of the CAMLR Convention Area. Retrieved from www.ccamlr.org/node/86816

Croxall, J. P., & Wood, A. G. (2002). The importance of the Patagonian Shelf for top predator species breeding at South Georgia. *Aquatic Conservation Marine and Freshwater Ecosystems, 12*(1), 101-118.

Cruz, C. D., Icochea, M. E., Espejo, V., Troncos, G., Castro-Sanguinetti, G. R., Schilling, M. A., & Tinoco, Y. (2023). Highly Pathogenic Avian Influenza A(H5N1) from Wild Birds, Poultry, and Mammals, Peru. *Emerg Infect Dis, 29*(12), 2572-2576.

de Seixas, M. M. M., de Araujo, J., Krauss, S., Fabrizio, T., Walker, D., Ometto, T., . . . Durigon, E. L. (2022). H6N8 avian influenza virus in Antarctic seabirds demonstrates connectivity between South America and Antarctica. *Transbound Emerg Dis, 69*(6), e3436-e3446.

del Hoyo, J., Elliott, A., Sargatal, J., & Collar, N. H. (1992-2008). *Handbook of the Birds of the World.* (Vol. 1-14). Barcelona: Lynx Edicions.

Dewar, M., Vanstreels, R. E. T., Boulinier, T., Craig, C., Clessin, A., Gamble, A., . . . Wille, M. (2023). Biological risk assessment of Highly Pathogenic Avian Influenza in the Southern Ocean. 77. Retrieved from https://scar.org/~documents/route%3A/download/5976

Dhondt, A. A., Altizer, S., Cooch, E. G., Davis, A. K., Dobson, A., Driscoll, M. J., . . . Sydenstricker, K. V. (2005). Dynamics of a novel pathogen in an avian host: Mycoplasmal conjunctivitis in house finches. *Acta Trop, 94*(1), 77-93.

E. de Souza Petersen, J. de Araujo, L. Krüger, M. M. Seixas, T. Ometto, L. M. Thomazelli, . . . Petry, M. V. (2017). First detection of avian influenza virus (H4N7) in Giant Petrel monitored by geolocators in the Antarctic region. *Marine Biology, 164, 62*.

European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Adlhoch, C., Fusaro, A., Gonzales, J. L., . . . Kohnle, L. (2023). Avian influenza overview September–December 2023. *efsa journal*. doi:10.2903/j.efsa.2023.8539

European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Cornelia Adlhoch, Alice Fusaro, José L Gonzales, . . . Baldinelli, F. (2022). Avian influenza overview September – December 2022. *efsa journal*. doi:https://doi.org/10.2903/j.efsa.2023.7786

Falabella, V., Campagna, C., & Croxall, J. (2009). *Atlas of the Patagonian Sea. Species and Spaces.* . Buenos Aires, Argentina: Wildlife Conservation Society and BirdLife International.

Giacinti, J. A., Signore, A. V., Jones, M. E. B., Bourque, L., Lair, S., Jardine, C., . . . Soos, C. (2024). Avian influenza viruses in wild birds in Canada following incursions of highly pathogenic H5N1 virus from Eurasia in 2021-2022. *mBio, 15*(8), e0320323.

Government of South Georgia and the South Sandwich Islands. (2023). Biosecurity-Help protect South Georgia. Retrieved from https://gov.gs/biosecurity

Herr, H., Viquerat, S., Devas, F., Lees, A., Wells, L., Gregory, B., . . . Meyer, B. (2022). Return of large fin whale feeding aggregations to historical whaling grounds in the Southern Ocean. *Sci Rep, 12*(1), 9458.

Hurt, A. C., Su, Y. C. F., Aban, M., Peck, H., Lau, H., Baas, C., . . . Gonzalez-Acuna, D. (2016). Evidence for the Introduction, Reassortment, and Persistence of Diverse Influenza A Viruses in Antarctica. *J VIROL, 90*(21), 9674-9682.

Hurt, A. C., Vijaykrishna, D., Butler, J., Baas, C., Maurer-Stroh, S., Silva-de-la-Fuente, M. C., . . . Gonzalez-Acuna, D. (2014). Detection of evolutionarily distinct avian influenza a viruses in antarctica. *mBio, 5*(3), e01098-01014.

International Association of Antarctica Tour Operators. (2024). *Report of the International Association of Antarctica Tour Operators 2023-24.* Retrieved from https://documents.ats.aq/ATCM46/WW/ATCM46_WW018_e.pdf

IUCN. (2023). The IUCN Red List of Threatened Species. Version 2023-1. Retrieved from https:/www.iucnredlist.org

Jimenez-Bluhm, P., Siegers, J. Y., Tan, S., Sharp, B., Freiden, P., Johow, M., . . . Schultz-Cherry, S. (2023). Detection and phylogenetic analysis of highly pathogenic A/H5N1 avian influenza clade 2.3.4.4b virus in Chile, 2022. *Emerg Microbes Infect, 12*(2), 2220569.

Klaassen, M., & Wille, M. (2023a). *Highly Pathogenic Avian Influenza (HPAI) incursion risk assessment for Australia*. Retrieved from https://wildlifehealthaustralia.com.au/Portals/0/ResourceCentre/BiosecurityMgmt/HPAI_incursion_risk_assessment_Australia.pdf

Klaassen, M., & Wille, M. (2023b). The plight and role of wild birds in the current bird flu panzootic. *Nat Ecol Evol, 7*(10), 1541-1542.

Knief, U., Bregnballe, T., Alfarwi, I., Ballmann, M. Z., Brenninkmeijer, A., Bzoma, S., . . . Courtens, W. (2024). Highly pathogenic avian influenza causes mass mortality in Sandwich Tern *Thalasseus sandvicensis* breeding colonies across north-western Europe. *Bird Conservation International., 34*, e6.

Kopp, M., Peter, H., Mustafa, O., Lisovski, S., Ritz, M., Phillips, R., & Hahn, S. (2011). South polar skuas from a single breeding population overwinter in different oceans though show similar migration patterns. *Mar. Ecol.-Prog. Ser., 435*, 263-267.

Kuiken, T., & Cromie, R. (2022). Protect wildlife from livestock diseases. *Science, 378*(6615), 5.

Kuiken, T., Leighton, F. A., Fouchier, R. A., LeDuc, J. W., Peiris, J. S., Schudel, A., . . . Osterhaus, A. D. (2005). Public health. Pathogen surveillance in animals. *Science, 309*(5741), 1680-1681.

Lai, S., Qin, Y., Cowling, B. J., Ren, X., Wardrop, N. A., Gilbert, M., . . . Yu, H. (2016). Global epidemiology of avian influenza A H5N1 virus infection in humans, 1997-2015: a systematic review of individual case data. *Lancet Infect Dis, 16*(7), e108-e118.

Leguia, M., Garcia-Glaessner, A., Munoz-Saavedra, B., Juarez, D., Barrera, P., Calvo-Mac, C., . . . Lescano, J. (2023). Highly pathogenic avian influenza A (H5N1) in marine mammals and seabirds in Peru. *Nat Commun, 14*(1), 5489.

Lewis, M., Campagna, C., Marin, M. R., & Fernandez, T. (2006). Soutern elephant seals north of the Antlantic Polar Front. *Antarctic Science, 18*(2), 213-221.

Luskin, M. S., Meijaard, E., Surya, S., Sheherazade, Walzer, C., & Linkie, M. (2020). African swine fever threatens Southeast Asia’s 11 endemic wild pig species. *Conservation Letters*. doi:doi:10.1111/conl.12784

Marandino, A., Tomas, G., Panzera, Y., Leizagoyen, C., Perez, R., Bassetti, L., . . . Perez, R. (2023). Spreading of the High-Pathogenicity Avian Influenza (H5N1) Virus of Clade 2.3.4.4b into Uruguay. *Viruses, 15*(9). doi:10.3390/v15091906

McGovern, K. A., Rodriguez, D. H., Lewis, M. N., Eder, E. B., Piola, A. R., & Davis, R. W. (2022). Habitat associations of post-breeding female southern elephant seals (*Mirounga leonina*) from Peninsula Valdes, Argentina. *Deep Sea Research Part I: Oceanographic Research Papers, 185*(103789).

Mercopress. (2024). Survey in Falklands' small islands shows avian flu is continues to threaten [online]. Retrieved from https://en.mercopress.com/2024/01/30/survey-in-falklands-small-islands-shows-avian-flu-is-continues-to-threaten

Molini, U., Aikukutu, G., Roux, J. P., Kemper, J., Ntahonshikira, C., Marruchella, G., . . . Dundon, W. G. (2020). Avian Influenza H5N8 Outbreak in African Penguins (Spheniscus demersus), Namibia, 2019. *J Wildl Dis, 56*(1), 214-218. Retrieved from https://www.ncbi.nlm.nih.gov/pubmed/31483707

Murawski, A., Fabrizio, T., Ossiboff, R., Kackos, C., Jeevan, T., Jones, J., . . . Webby, R. (2023). Highly pathogenic avian influenza A(H5N1) virus in a common bottlenose dolphin (Tursiops truncatus) in Florida. In: Research Square.

Navarro, J., Cardador, L., Brown, R., & Phillips, R. A. (2015). Spatial distribution and ecological niches of non-breeding planktivorous petrels. *Sci Rep, 5*, 12164.

Neumann, G., Treanor, J., & Kawaoka, Y. (2021). Orthomyxoviruses. In Howley, P.M., Knipe, D.M., Whelan, S.P. J., (Eds.), *Fields Virology 7th ed Volume 1* (Vol. 1, pp. 596-668). Philadelphia, UK: Wolters Kluwer.

Ogrzewalska, M., Couto Motta, F., Resende, P. C., Fumian, T., Fonseca da Mendonca, A. C., Appolinario Reis, L., . . . Mendonca Siqueira, M. (2022). Influenza A(H11N2) Virus Detection in Fecal Samples from Adelie (Pygoscelis adeliae) and Chinstrap (Pygoscelis antarcticus) Penguins, Penguin Island, Antarctica. *Microbiol Spectr, 10*(5), e0142722.

One Health High-Level Expert, Panel,, Adisasmito, W. B., Almuhairi, S., Behravesh, C. B., Bilivogui, P., Bukachi, S. A., . . . Zhou, L. (2022). One Health: A new definition for a sustainable and healthy future. *PLoS Pathog, 18*(6), e1010537.

Pardo-Roa, C., Nelson, M. I., Ariyama, N., Aguayo, C., Almonacid, L. I., Munoz, G., . . . Neira, V. (2023). Cross-species transmission and PB2 mammalian adaptations of highly pathogenic avian influenza A/H5N1 viruses in Chile. *bioRxiv*. doi:10.1101/2023.06.30.547205

Peru Ministerio de Salud. (2023). Sala de influenza aviar [Avian influenza dashboard]. Retrieved from www.dge.gob.pe/influenza-aviar-ah5/#aves

Pohlmann, A., King, J., Fusaro, A., Zecchin, B., Banyard, A. C., Brown, I. H., . . . Harder, T. (2022). Has Epizootic Become Enzootic? Evidence for a Fundamental Change in the Infection Dynamics of Highly Pathogenic Avian Influenza in Europe, 2021. *mBio, 13*(4), e0060922.

Promed mail. (2022). PRO/AH/EDR>Avian influenza (245): Americas (Panama) wild bird, HPAI H5N1, 1st rep, alert. Archive Number: 20221226.28707471.

Quillfeldt, P., Masello, J. F., Navarro, L., & Philips, R. A. (2013). Year-round distribution suggests spatial segregation of two small petrel species in the South Atlantic. *Journal of Biogeography, 40*(3), 430-441.

Quintana, F. D. A., P.O. (2002). Foraging grounds of southern giant petrels (*Macronectes giganteus*) on the Patagonia shelf *Polar Biology, 25*(2), 159-161.

Ramis, A., van Amerongen, G., van de Bildt, M., Leijten, L., Vanderstichel, R., Osterhaus, A., & Kuiken, T. (2014). Experimental infection of highly pathogenic avian influenza virus H5N1 in black-headed gulls (Chroicocephalus ridibundus). *Vet Res, 45*(1), 84.

Raya Rey, A., & Huettmann, F. (2020). Telecoupling analysis of the Patagonian Shelf: A new approach to study global seabird-fisheries interactions to achieve sustainability. *Journal for Nature Conservation, 53*, 1-13.

Reischak, D., Rivetti, A. V., Jr., Otaka, J. N. P., Domingues, C. S., Freitas, T. L., Cardoso, F. G., . . . Camargos, M. F. (2023). First report and genetic characterization of the highly pathogenic avian influenza A(H5N1) virus in Cabot's tern (Thalasseus acuflavidus), Brazil. *Vet Anim Sci, 22*, 100319.

Reperant, L. A., Caliendo, V., & Kuiken, T. (2021). EWDA Diagnosis Card Avian Influenza. Retrieved from https://ewda.org/wp-content/uploads/2021/05/EWDA_DiagnCard_AvianInfluenza_updated_def.pdf

Reperant, L. A., van de Bildt, M. W., van Amerongen, G., Buehler, D. M., Osterhaus, A. D., Jenni-Eiermann, S., . . . 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.

Rijks, J. M., Leopold, M. F., Kuhn, S., In 't Veld, R., Schenk, F., Brenninkmeijer, A., . . . Beerens, N. (2022). Mass Mortality Caused by Highly Pathogenic Influenza A(H5N1) Virus in Sandwich Terns, the Netherlands, 2022. *Emerg Infect Dis, 28*(12), 2538-2542.

Rimondi, A., Vanstreels, R. E. T., Olivera, V., Donini, A., Lauriente, M. M., & Uhart, M. M. (2024). Highly Pathogenic Avian Influenza A(H5N1) Viruses from Multispecies Outbreak, Argentina, August 2023. *Emerg Infect Dis, 30*(4). doi:10.3201/eid3004.231725

Roberts, L. C., Abolnik, C., Waller, L. J., Shaw, K., Ludynia, K., Roberts, D. G., . . . Abernethy, D. (2023). Descriptive Epidemiology of and Response to the High Pathogenicity Avian Influenza (H5N8) Epidemic in South African Coastal Seabirds, 2018. *Transbound. Emerg. Dis.* doi:https://doi.org/10.1155/2023/2708458

Rodriguez, J. P., Fernandez-Gracia, J., Thums, M., Hindell, M. A., Sequeira, A. M., Meekan, M. G., . . . Eguiluz, V. M. (2017). Big data analyses reveal patterns and drivers of the movements of southern elephant seals. *Sci Rep, 7*(1), 112.

Roman, J., Estes, J. A., L., M., Smith, C., Costa, D., McCarthy, J., . . . Smetacek, V. (2014). Whales as marine ecosystem engineers. . *Frontiers in Ecology and the Environment., 12*(7), 377-385.

Salyuk, P. A., Mosharov, S. A., Frey, D. I., Kasyan, V. V., Ponomarev, V. I., Kalinina, O. Y., . . . Lipinskaya, N. A. (2022). Physical and biological features of the waters in the outer Patagonian shelf and the Malvinas Current. *Water, 28*(14 (23)), 3879.

Scientific Committee on Antarctic Research. (2023). Sub-Antarctic and Antarctic highly pathogenic avian influenza H5N1 monitoring project. Retrieved from https://scar.org/library-data/avian-flu#cases

Secretariat of the Antarctic Treaty. (2023). The Antarctic Treaty. Retrieved from www.ats.aq/e/antarctictreaty.html

Shi, J., Zeng, X., Cui, P., Yan, C., & Chen, H. (2023). Alarming situation of emerging H5 and H7 avian influenza and effective control strategies. *Emerg Microbes Infect, 12*(1), 2155072.

Shirihai H, Jarrett B, Cox J, & GM., K. (2008). *The Complete Guide to Antarctic Wildlife: Birds and Marine Mammals of the Antarctic Continent and the Southern Ocean. 2nd ed.*: Princeton University Press.

Thorsson, E., Zohari, S., Roos, A., Banihashem, F., Brojer, C., & Neimanis, A. (2023). Highly Pathogenic Avian Influenza A(H5N1) Virus in a Harbor Porpoise, Sweden. *Emerg Infect Dis, 29*(4), 852-855.

Uhart, M., Vanstreels, R. E. T., Nelson, M. I., Olivera, V., Campagna, J., Zavattieri, V., . . . Rimondi, A. (2024). Massive outbreak of Influenza A H5N1 in elephant seals at Península Valdés, Argentina: increased evidence for mammal-to-mammal transmission. *bioRxiv*, 2024.2005.2031.596774.

van den Brand, J. M., Krone, O., Wolf, P. U., van de Bildt, M. W., van Amerongen, G., Osterhaus, A. D., & Kuiken, T. (2015). Host-specific exposure and fatal neurologic disease in wild raptors from highly pathogenic avian influenza virus H5N1 during the 2006 outbreak in Germany. *Vet Res, 46*, 24.

Vara, D., & Mano, A. (2023). Bird flu kills over 900 seals, sea lions in south Brazil. Retrieved from www.reuters.com/world/americas/bird-flu-kills-over-900-seals-sea-lions-south-brazil-2023-12-11/

WAHIS, World Organisation for Animal Health (WOAH). (2022a). *Colombia - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-).* Retrieved from https://wahis.woah.org/#/in-event/4668/dashboard

WAHIS, World Organisation for Animal Health (WOAH). (2022b). *Honduras - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 3 [FINAL].* Retrieved from https://wahis.woah.org/#/in-review/4824?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH) (2022c). *Venezuela - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Immediate notification.* Retrieved from https://wahis.woah.org/#/in-review/4760?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2022d). *Venezuela - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Immediate notification.* . Retrieved from https://wahis.woah.org/#/in-review/4760?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023a). *Argentina - High pathogenicity avian influenza viruses (poultry) (Inf. with) - Follow up report 16.* Retrieved from https://wahis.woah.org/#/in-review/4933?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023b). *Bolivia - High pathogenicity avian influenza viruses (poultry) (Inf. with) - Follow up report 4.* Retrieved from https://wahis.woah.org/#/in-review/4870

WAHIS, World Organisation for Animal Health (WOAH). (2023c). *Brazil - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 9.* Retrieved from https://wahis.woah.org/#/in-review/5057

WAHIS, World Organisation for Animal Health (WOAH). (2023d). *Chile - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 5*. (Report date: 2023/03/03). Retrieved from https://wahis.woah.org/#/in-review/4775?reportId=159615&fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023e). *Chile - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 8*. (Report date: 2023/06/02). Retrieved from https://wahis.woah.org/#/in-review/4775?reportId=160965&fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023f). *Costa Rica - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 4.* Retrieved from https://wahis.woah.org/#/in-review/4858?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023g). *Ecuador - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 7*. Retrieved from https://wahis.woah.org/#/in-review/4869

WAHIS, World Organisation for Animal Health (WOAH). (2023h). *Guatemala - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 2 [FINAL].* Retrieved from https://wahis.woah.org/#/in-review/4903?fromPage=event-dashboard-url

WAHIS, World Organisation for Animal Health (WOAH). (2023i). *Paraguay - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 6 [FINAL]*. Retrieved from https://wahis.woah.org/#/in-review/5068

WAHIS, World Organisation for Animal Health (WOAH). (2023j). *Uruguay - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 6.* Retrieved from https://wahis.woah.org/#/in-review/4900

Wille, M., & Barr, I. G. (2022). Resurgence of avian influenza virus. *Science, 376*(6592), 459-460.

World Health Organization. (2021). Tripartite and UNEP support OHHLEP's definition of "One Health.". *2024*(25 October 2024). Retrieved from https://www.who.int/news/item/01-12-2021-tripartite-and-unep-support-ohhlep-s-definition-of-one-health

Wunschmann, A., Franzen-Klein, D., Torchetti, M., Confeld, M., Carstensen, M., & Hall, V. (2024). Lesions and viral antigen distribution in bald eagles, red-tailed hawks, and great horned owls naturally infected with H5N1 clade 2.3.4.4b highly pathogenic avian influenza virus. *Vet Pathol*, 3009858231222227. doi:10.1177/03009858231222227

Xie, R., Edwards, K. M., Wille, M., Wei, X., Wong, S. S., Zanin, M., . . . Dhanasekaran, V. (2023). The episodic resurgence of highly pathogenic avian influenza H5 virus. *Nature, 622*(7984), 810-817.

Yamamoto, Y., Nakamura, K., & Mase, M. (2017). Survival of Highly Pathogenic Avian Influenza H5N1 Virus in Tissues Derived from Experimentally Infected Chickens. *APPL ENVIRON MICROBIOL, 83*(16). doi:10.1128/AEM.00604-17

Zamora, G., Aguilar Pierle, S., Loncopan, J., Araos, L., Verdugo, F., Rojas-Fuentes, C., . . . Barriga, G. P. (2023). Scavengers as Prospective Sentinels of Viral Diversity: the Snowy Sheathbill Virome as a Potential Tool for Monitoring Virus Circulation, Lessons from Two Antarctic Expeditions. *Microbiol Spectr, 11*(3), e0330222.

APPENDICES:

Appendix S1: Number of birds and mammals reported dead from 1 November 2022 to 10th of December 2023 by countries in South America.

Asterisks indicate species-country associations where HPAI H5 virus infection was not confirmed by at least one case. Numerical comparisons among countries may be unreliable since countries differ considerably in their approach for surveillance, diagnostic methods and reporting of suspected/confirmed HPAI cases.

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Birds													
Accipitridae													
Great black hawk	*Buteogallus urubitinga*	Least concern	500,000-4,999,999[3]						1				
Black-chested buzzard-eagle	*Geranoaetus melanoleucus*	Least concern	unknown[1,3]		13	1							
Harris's hawk	*Parabuteo unicinctus*	Least concern	unknown[1,3]			2							
Anatidae													
White-cheeked pintail	*Anas bahamensis*	Least concern	177,000 – 1,080,000[2]		1		3						

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Yellow-billed teal	*Anas flavirostris*	Least concern	1,043,000 – 1,133,000[2]			1							
Yellow-billed pintail	*Anas georgica*	Least concern	100,000 – 1,000,000[2]			1							
Black-necked swan	*Cygnus melancoryphus*	Least concern	25,000 – 100,000[2]			107	21		1	142			
Black-bellied whistling-duck	*Dendrocygna autumnalis*	Least concern	200,000-2,000,000[2]								1		
White-faced whistling-duck	*Dendrocygna viduata*	Least concern	2,100,000 – 2,500,000[2]								1		
Chiloé wigeon	*Mareca sibilatrix*	Least concern	100,000 – 1,000,000[2]			1							
Silver teal	*Spatula versicolor*	Least concern	50,000 – 200,000[2]				1						
Andean goose	*Chloephaga melanoptera*	Least concern	25,000 – 100,000[2]		102		2						

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Coscoroba swan	*Coscoroba coscoroba*	Least concern	10,000 - 25,000[2]			10							
Magellanic steamer duck	*Tachyeres pteneres*	Least concern	10,000 - 100,000[2]			3							
Upland goose	*Chloephaga picta*	Least concern	188,000 – 405,000[2]			5							
Ardeidae													
Great white egret	*Ardea alba*	Least concern	1,625,000-2,410,000[2]			1							
Cattle egret	*Bubulcus ibis*	Least concern	3,030,801 – 9,757,000[2]		1								
Snowy egret	*Egretta thula*	Least concern	713,000 – 2,428,000[2]		1				1				
Black-crowned night-heron	*Nycticorax nycticorax*	Least concern	588,300 – 2,935,000[2]			1							
Cathartidae													

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Turkey vulture	*Cathartes aura*	Least concern	unknown[1,3]			5							
American black vulture	*Coragyps atratus*	Least concern	unknown[1,3]		1	2							
Andean condor	*Vultur gryphus*	Vulnerable	6,700[3]										
Charadriidae													
American golden plover	*Pluvialis dominica*	Least concern	395,000 – 605,000[2]						1				
Southern lapwing	*Vanellus chilensis*	Least concern	2,000,000 – 2,100,000[2]			1							
Diomedeidae													
Waved albatross	*Phoebastria irrorata*	Critically endangered	>35,000[3]		3								
Black-browed albatross	*Thalassarche melanophris*	Least concern	1,400,000[1]			1							1
Falconidae													

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Crested caracara	*Caracara plancus*	Least concern	2,500,000-4,999,999[3]		28								
Peregrine falcon	*Falco peregrinus*	Least concern	100,000-499,999[3]		2	3							
Chimango caracara	*Phalcoboenus chimango*	Least concern	Unknown[1,3]			3							
Fregatidae													
Magnificent frigatebird	*Fregata magnificens*	Least concern	130,000[3]		12			6000	1				
Great frigatebird	*Fregata minor*	Least concern	16,700[2]					1002					
Haematopodidae													
Blackish oystercatcher	*Haematopus ater*	Least concern	32,000 – 134,000[2]			50							
American oystercatcher	*Haematopus palliatus*	Least concern	36,500 – 112,000[2]		2	1							

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]								
				Bolivia	**Peru**	**Chile**	**Argentina**	**Ecuador**	**Brazil**	**Uruguay**	**Colombia**	**Venezuel**
Hirundidinae												
Blue-and-white swallow	*Pygochelidon cyanoleuca*	Least concern	5,000,000-50,000,000[3]	4								
Laridae												
Inca tern	*Larosterna inca*	Near threatened	150,000[2]		7987	239						
Belcher's gull	*Larus belcheri*	Least concern	1 – 10,000[2]			293						
Grey-headed gull	*Larus cirrocephalus*	Least concern	250,000 – 540,000[2]					1	2			
Kelp gull	*Larus dominicanus*	Least concern	3,287,000 – 4,290,000[2]		1063	4594	1					
Brown-hooded gull	*Larus maculipennis*	Least concern	100,000 – 1,000,000[2]			48			1			
Grey gull	*Larus modestus*	Least concern	25,000[2]			1016						

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Franklin's gull	*Larus pipixcan*	Least concern	1,000,000 – 1,490,000[2]			95							
Dolphin gull	*Larus scoresbii*	Least concern	9,000-28,000[2]			2							
Black skimmer	*Rynchops niger*	Least concern	125,000 – 208,000[2]			26							
Royal tern	*Thalasseus maximus*	Least concern	370,000 – 380,000[2]						60	1			
Cabot's/Cayenne tern	*Thalasseus acuflavidus*	Least concern	153,000 - 158,000[2]				2400		858				
South American tern	*Sterna hirundinacea*	Least concern	25,000 – 1,000,000[2]			58				5			
Elegant tern	*Thalasseus elegans*	Near threatened	270,000[2]			135							
Common tern	*Sterna hirundo*	Least concern	2,260,000 – 3,950,300[2]						15				
Passeridae													

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
House sparrow	*Passer domesticus*	Least concern	896,000,000- 1,310,000,000[3]			1							
Pelecanidae													
Brown pelican	*Pelecanus occidentalis*	Least concern	345,000 – 400,000[2]								302	173	
Peruvian pelican	*Pelecanus thagus*	Near threatened	100,000 - 1,000,000[2]		57447	4509							
Phalacrocoracidae													
Imperial shag	*Leucocarbo atriceps*	Least concern	333,000 - 1.360.000[2]			7							
Guanay cormorant	*Leucocarbo bougainvillioru m*	Near threatened	2,500,00 – 5,000,000[2]		254793	6380							
Neotropical cormorant	*Nannopterum brasilianus*	Least concern	2,160,000 – 3,150,000[2]			726			1				

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Red-legged cormorant	*Poikilocarbo gaimardi*	Near threatened	30,000[2]			498							
Rock shag	*Leucocarbo magellanicus*	Least concern	106,000 – 202,000[2]			1							
Phoenicopteridae													
Chilean flamingo	*Phoenicopterus chilensis*	Near threatened	290,000[2]		3								
Puna flamingo	*Phoenicoparrus jamesi*	Near threatened	106,000 – 107,000[2]				237						
Podicipedidae													
Great grebe	*Podiceps major*	Least concern	40,000 – 140,000[2]			3							
Procellariidae													
Sooty shearwater	*Ardenna grisea*	Near threatened	8,800,000[1]		6	304							
Southern fulmar	*Fulmarus glacialoides*	Least concern	4,000,000[1]										2

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Southern giant petrel	*Macronectes giganteus*	Least concern	95,600-108,000[1]			7							
Antarctic prion	*Pachyptila desolata*	Least concern	50,000,000[1]						1				
Peruvian diving petrel	*Pelecanoides garnotii*	Near threatened	100,000[1]			25							
White-chinned petrel	*Procellaria aequinoctialis*	Vulnerable	3,000,000[1]						1				
Manx shearwater	*Puffinus puffinus*	Least concern	680,000-790,000[1]						3				
Psittacidae													
Slender-billed parakeet	*Enicognathus leptorhynchus*	Least concern	Unknown[1,3]			14							
Rallidae													
Red-gartered coot	*Fulica armillata*	Least concern	1,000,000[2]			2							

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Recurvirostridae													
White-backed stilt	*Himantopus melanurus*	not classified	100,000 - 1,000,000[2]			1							
Scolopacidae													
Ruddy turnstone	*Arenaria interpres*	Least concern	460,000-700,000[2]		1								
Sanderling	*Calidris alba*	Least concern	705,000 – 780,000[2]		1	12							
Whimbrel	*Numenius phaeopus*	Least concern	1,800,000 – 2,650,000[2]		1	2							
Lesser yellowlegs	*Tringa flavipes*	Least concern	400,000[2]			1							
Spheniscidae													
Humboldt penguin	*Spheniscus humboldti*	Vulnerable	23,800[1]		371*	3721							
Stercorariidae													

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Brown skua	*Catharacta antarctica*	Least concern	26,000-28,000[1]		25								
Chilean skua	*Catharacta chilensis*	Least concern	2,500-9,999[1]			6							
Strigidae													
Tropical screech-owl	*Megascops choliba*	Least concern	500,000-4,999,999[1]						1				
Sulidae													
Brown booby	*Sula leucogaster*	Least concern	200,000[1]						3				
Blue-footed booby	*Sula nebouxii*	Least concern	90,000[1]		4			3					
Red-footed booby	*Sula sula*	Least concern	1,400,000[1]					6					

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Peruvian booby	*Sula variegata*	Least concern	1,200,000[1]		235643	6506							
Mammals													
Delphinidae													
Chilean dolphin	*Cephalorhynchus eutropia*	Near threatened	unknown			1							
Short-beaked common dolphin	*Delphinus delphis*	Least concern	unknown		1	9*							
Dusky dolphin	*Lagenorhynchus obscurus*	Least concern	unknown			28							
Phocoenidae													
Burmeister's porpoise	*Phocoena spinipinnis*	Near threatened	unknown			36							
Mustelidae													

Family / Common name /Species name		IUCN Red List assessment	Estimated global population size	Number of individuals reported dead per country[4]									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuel	
Marine otter	*Lontra felina*	Endangered	unknown			43							
Southern river otter	*Lontra provocax*	Endangered	unknown			1							
Otariidae													
South American fur seal	*Arctocephalus australis*	Least concern	109,500[3]			27*	13		552	800			
South American sea lion	*Otaria byronia*	Least concern	222,500[3]		10457	20070	1367						
Phocidae													
Southern elephant seal	*Mirounga leonina*	Least concern	325,000[3]			16*	17400						
Procyonidae													
South American coati	*Nasua nasua*	Least concern	unknown							16			

[1]Population estimate (number of mature individuals) based on data from BirdLife International's "IUCN Red List for birds". Downloaded from https://datazone.birdlife.org in March 2024.

[2]Population estimate (total population) based on data from Wetlands International's "Waterbird Populations Portal". Retrieved from wpp.wetlands.org in March 2024.

[3]Population estimate (number of mature individuals) based on data from IUCN's "The IUCN Red List of Threatened Species". Version 2023-1. Retrieved from https://www.iucnredlist.org>lkjd in March 2024.

[4]Numbers of individuals reported dead per country based on data from the following sources:

- Anonymous (2023). Preocupación por 552 lobos marinos muertos a pocos kilómetros del Chuy [Concern over 552 dead sea lions a few kilometers from Chuy] [last accessed 10 December 2023]. Available from: www.elobservador.com.uy/nota/preocupacion-por-552-lobos-marinos-muertos-a-pocos-kilometros-del-chuy-20231025183255
- Argentina Servicio Nacional de Sanidad y Calidad Agroalimentaria (2023). Estado de la situación epidemiológica en la Argentina [State of the epidemiological situation in Argentina] [cited 2023 10 December]. Available from: www.argentina.gob.ar/senasa/estado-de-la-situacion-epidemiologica-en-la-argentina
- Banyard, A. C., Bennison, A., Byrne, A. M. P., Reid, S. M., Lynton-Jenkins, J. G., Mollett, B., De Sliva, D., Peers-Dent, J., Finlayson, K., Hall, R., Blockley, F., Blyth, M., Falchieri, M., Fowler, Z., Fitzcharles, E. M., Brown, I. H., & James, J. (2024). Detection and spread of high pathogenicity avian influenza virus H5N1 in the Antarctic Region. Nat. Commun., 15(1). doi.org/doi.org/10.1038/s41467-024-51490-8
- Brazil Ministério da Agricultura e Pecuária (2023). Influenza Aviária [Avian influenza] [last accessed 10 December 2023]. Available from: https://mapa-indicadores.agricultura.gov.br/publico/extensions/SRN/SRN.html
- Campagna C, Uhart M, Falabella V, Campagna J, Zavattieri V, Vanstreels RET, Lewis M (2024). Catastrophic mortality of southern elephant seals caused by H5N1 avian influenza. Marine Mammal Science, 40: 322.
- Chile Servicio Agrícola y Ganadero (2023). Influenza Aviar (IA) [Avian influenza dashboard] [last accessed 10 December 2023]. Available from: www.sag.gob.cl/ambitos-de-accion/influenza-aviar-ia
- Chile Servicio Nacional de Pesca y Acuicultura (2023). Influenza Aviar [Avian influenza summary] [last accessed 10 December2023]. Available from: www.sernapesca.cl/influenza-aviar
- Falkland Islands Department of Agriculture (2023). Avian influenza information [last accessed December 2023]. Available from: www.falklands.gov.fk/agriculture/avian-influenza
- Peru Ministerio de Salud (2023). Sala de influenza aviar [Avian influenza dashboard] [Last accessed 10 December 2023]. Available from: www.dge.gob.pe/influenza-aviar-ah5/#aves

- Uhart, M., Vanstreels, R. E. T., Nelson, M. I., Olivera, V., Campagna, J., Zavattieri, V., Lemey, P., Campagna, C., Falabella, V., & Rimondi, A. (2024). Massive outbreak of Influenza A H5N1 in elephant seals at Península Valdés, Argentina: increased evidence for mammal-to-mammal transmission. bioRxiv, 2024.2005.2031.596774. https://doi.org/10.1101/2024.05.31.596774
- Vara D, Mano A (2023). Bird flu kills over 900 seals, sea lions in south Brazil [last accessed 14 December 2023]. Available from: www.reuters.com/world/americas/bird-flu-kills-over-900-seals-sea-lions-south-brazil-2023-12-11/
- World Organisation for Animal Health. World Animal Health Information System (2023) [last accessed 15 December 2023]. Available from: wahis.woah.org/

[5]FMI: Falklands (Malvinas) Islands

Appendix S2: List of species of Antarctic and Subantarctic birds and mammals with IUCN Red List assessment and estimated populations

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
Birds				
Anatidae	Southern pintail	*Anas eatoni*	Vulnerable	47,000-62,000[2]
	Yellow-billed pintail	*Anas georgica*	Least concern	1,800–13,000[2]
Chionidae	Snowy sheathbill	*Chionis albus*	Least concern	unknown[1,3]
	Black-faced sheathbill	*Chionis minor*	Least concern	8,700-13,000[1]
Diomedeidae	Wandering albatross	*Diomedea exulans*	Vulnerable	20,100[1]
	Sooty albatross	*Phoebetria fusca*	Endangered	21,234-28,656[1]
	Light-mantled albatross	*Phoebetria palpebrata*	Near threatened	58,000[1]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Indian yellow-nosed albatross	*Thalassarche carteri*	Endangered	82,000[1]
Diomedeidae	Grey-headed albatross	*Thalassarche chrysostoma*	Endangered	250,000
	Black-browed albatross	*Thalassarche melanophris*	Least concern	1,400,000[1]
Laridae	Kelp gull	*Larus dominicanus*	Least concern	3,117,000–3,222,000[2]
	Kerguelen tern	*Sterna virgata*	Near threatened	3,500-6,500[2]
	Antarctic tern	*Sterna vittata*	Least concern	133,000-144,000[2]
Motacillidae	South Georgia pipit	*Anthus antarcticus*	Least concern	6,000-8,000[1]
Oceanitidae	Black-bellied storm petrel	*Fregetta tropica*	Least concern	500,000[1]
	Grey-backed storm petrel	*Garrodia nereis*	Least concern	200,000[1]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Wilson's storm petrel	*Oceanites oceanicus*	Least concern	8,000,000-20,000,000[1]
Phalacrocoracidae	Imperial shag	*Leucocarbo atriceps*	Least concern	333,000 - 1.360.000[2]
	Kerguelen shag	*Leucocarbo verrucosus*	Least concern	unknown[1,3]
Procellariidae	Kerguelen petrel	*Aphrodroma brevirostris*	Least concern	1,000,000[1]
	Cape petrel	*Daption capense*	Least concern	2,000,000[1]
	Southern fulmar	*Fulmarus glacialoides*	Least concern	4,000,000[1]
	Blue petrel	*Halobaena caerulea*	Least concern	3,000,000[1]
Procellariidae	Southern giant petrel	*Macronectes giganteus*	Least concern	95,600-108,000[1]
	Northern giant petrel	*Macronectes halli*	Least concern	23,600[1]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Slender-billed prion	*Pachyptila belcheri*	Least concern	7,000,000[1]
	Fulmar prion	*Pachyptila crassirostris*	Least concern	150,000-300,000[1]
	Antarctic prion	*Pachyptila desolata*	Least concern	50,000,000[1]
	Salvin's prion	*Pachyptila salvini*	Least concern	12,000,000[1]
	Fairy prion	*Pachyptila turtur*	Least concern	5,000,000[1]
	Snow petrel	*Pagodroma nivea*	Least concern	4,000,000[1]
	South Georgia diving petrel	*Pelecanoides georgicus*	Least concern	15,000,000[1]
	Common diving petrel	*Pelecanoides urinatrix*	Least concern	16,000,000[1]
	White-chinned petrel	*Procellaria aequinoctialis*	Vulnerable	3,000,000[1]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Grey petrel	*Procellaria cinerea*	Near threatened	151,500[1]
	White-headed petrel	*Pterodroma lessonii*	Least concern	600,000[1]
	Great-winged petrel	*Pterodroma macroptera*	Least concern	1,500,000[1]
	Soft-plumaged petrel	*Pterodroma mollis*	Least concern	5,000,000[1]
	Antarctic petrel	*Thalassoica antarctica*	Least concern	10,000,000-20,000,000[1]
Spheniscidae	Emperor penguin	*Aptenodytes forsteri*	Near threatened	>550,000[1]
	King penguin	*Aptenodytes patagonicus*	Least concern	>2,200,000[1]
	Southern rockhopper penguin	*Eudyptes chrysocome*	Vulnerable	2,500,000[1]
	Macaroni penguin	*Eudyptes chrysolophus*	Vulnerable	>12,600,000[1]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Adelie penguin	*Pygoscelis adeliae*	Least concern	14,000,000-16,000,000[1]
	Chinstrap penguin	*Pygoscelis antarcticus*	Least concern	8,000,000[1]
	Gentoo penguin	*Pygoscelis papua*	Least concern	774,000[1]
Stercorariidae	Brown skua	*Catharacta antarctica*	Least concern	26,000-28,000[1]
	South polar skua	*Catharacta maccormicki*	Least concern	6,000-15,000[1]
Mammals				
Balaenidae	Southern right whale	*Eubalaena australis*	Least concern	unknown
Balaenopteridae	Sei whale	*Balaenoptera borealis*	Endangered	50,000[3]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Antarctic blue whale	*Balaenoptera musculus intermedia*	Critically endangered	3,000[3]
	Common minke whale	*Balaenoptera acutorostrata*	Least concern	200,000[3]
	Fin whale	*Balaenoptera physalus*	Vulnerable	100,000[3]
	Humpback whale	*Megaptera novaeangliae*	Least concern	84,000[3]
	Antarctic minke whale	*Balaenoptera bonaerensis*	Near threatened	unknown
Delphinidae	Commersons's dolphin	*Cephalorhynchus commersonii*	Least concern	unknown
	Long-finned pilot whale	*Globicephala melas*	Least concern	unknown
	Hourglass dolphin	*Lagenorhynchus cruciger*	Least concern	unknown
	Southern right whale dolphin	*Lissodelphis peronii*	Least concern	unknown

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
	Killer whale	*Orcinus orca*	Data deficient	unknown
Neobalaenidae	Pygmy right whale	*Caperea marginata*	Least concern	unknown
Otariidae	Antarctic fur seal	*Arctocephalus gazella*	Least concern	700,000-1,000,000[3]
	Subantarctic fur seal	*Arctocephalus tropicalis*	Least concern	200,000[3]
	South American sea lion	*Otaria byronia*	Least concern	222,500[3]
Phocidae	Leopard seal	*Hydrurga leptonyx*	Least concern	18,000[3]
	Weddell seal	*Leptonychotes weddellii*	Least concern	300,000[3]
	Crabeater seal	*Lobodon carcinophagus*	Least concern	4,000,000[3]
	Southern elephant seal	*Mirounga leonina*	Least concern	325,000[3]
	Ross seal	*Ommatophoca rossii*	Least concern	40,000[3]

Family	Common name	Species	IUCN Red list assessment	Estimated global population size
Phocoenidae	Spectacled porpoise	*Phocoena dioptrica*	Least concern	unknown
Physeteridae	Sperm whale	*Physeter macrocephalus*	Vulnerable	unknown
Ziphiidae	Gray's beaked whale	*Mesoplodon grayi*	Least concern	unknown
	Southern bottlenose whale	*Hyperoodon planifrons*	Least concern	unknown
	Strap-toothed whale	*Mesoplodon layardii*	Least concern	unknown
	Arnoux's beaked whale	*Berardius arnuxii*	Least concern	unknown

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[2]Population estimate (total population) based on data from Wetlands International’s “Waterbird Populations Portal”. Retrieved from wpp.wetlands.org in March 2024.

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