PHILOSOPHICAL TRANSACTIONS B

royalsocietypublishing.org/journal/rstb

Opinion piece

Cite this article: Ashley E, Vanstreels RET, Barbieri M, Puryear W, Gulland F, Field C, Johnson CK, Uhart M. 2026 High pathogenicity avian influenza in pinniped conservation. *Phil. Trans. R. Soc. B* **381**: 20240320.
https://doi.org/10.1098/rstb.2024.0320

Received: 1 August 2025
Accepted: 8 October 2025

One contribution of 16 to a theme issue 'Managing infectious marine diseases in wild populations'.

Subject Areas:
health and disease and epidemiology, ecosystem, ecology

Keywords:
HPAI, H5N1, panzootic, marine mammal, seabird, seal, sea lion, epidemiology, wildlife health, One Health

Authors for correspondence:
Christine Kreuder Johnson
e-mail: ckjohnson@ucdavis.edu
Marcela Uhart
e-mail: muhart@ucdavis.edu

†Elizabeth Ashley and Ralph Eric Thijl Vanstreels are joint first authors.

†Christine Kreuder Johnson and Marcela Uhart are joint senior authors.

THE ROYAL SOCIETY PUBLISHING

High pathogenicity avian influenza in pinniped conservation

Elizabeth Ashley[1,2,†], Ralph Eric Thijl Vanstreels[1,†], Michelle Barbieri[3], Wendy Puryear[4], Frances Gulland[5], Cara Field[6], Christine Kreuder Johnson[2,†] and Marcela Uhart[1,2,†]

[1]Karen C Drayer Wildlife Health Center, University of California, Davis, Weill School of Veterinary Medicine, Davis, CA 95616, USA
[2]Institute for Pandemic Insights, University of California, Davis, Weill School of Veterinary Medicine, Davis, CA 95616, USA
[3]Hawaiian Monk Seal Research Program, NOAA Fisheries Pacific Islands Fisheries Science Center, Honolulu, HI 96818, USA
[4]Infectious Disease and Global Health, Tufts University Cummings School of Veterinary Medicine, North Grafton, MA 01536, USA
[5]Marine Mammal Commission, Bethesda, MD 20814, USA
[6]The Marine Mammal Center, Sausalito, CA 94965, USA

EA, 0000-0003-3251-9221; CKJ, 0000-0001-6673-8743

Since 2020, H5Nx high pathogenicity avian influenza viruses (HPAIVs) have caused widespread disruptions not only to global agriculture and trade but also to the health of free-ranging wildlife. Pinnipeds have experienced greater mortality from H5Nx HPAIV than any other mammalian taxa. Emergent virus strains, persisting over long time periods and vast geographic distances, have repeatedly triggered large-scale mortality events in pinniped populations. Of particular concern is the spread of H5Nx HPAIV to the Southern Hemisphere—including the emergence of a marine mammal-adapted clade in South America and detections in the sub-Antarctic and Antarctic—and to other remote locations such as the Hawaiian Islands. These developments elevate concern for the world's endangered, isolated and endemic pinnipeds. While managing HPAIV in any animal population is a formidable task, working with free-ranging marine mammals poses unique challenges. In this review and perspective piece, we attempt to synthesize complexities at this intersection. We describe lessons learned from HPAIV investigations in marine wildlife, highlight gaps in knowledge and capacity, and discuss the incorporation of outbreak risk assessment and countermeasures into pinniped conservation. Finally, we propose ways in which pinnipeds—and marine wildlife broadly—could be better integrated into existing systems for HPAIV intelligence, control and prevention.

This article is part of the theme issue 'Managing infectious marine diseases in wild populations'.

1. Introduction

Avian influenza is not widely considered a marine disease. High pathogenicity avian influenza (HPAI), colloquially known as 'bird flu', causes periodic outbreaks in poultry and wild birds, with drastic economic consequences for agriculture and trade sectors. In the past decade, HPAI viruses (HPAIVs) of the H5Nx subtype have traversed oceans and continents, claiming millions of animal lives and threatening economies, food security and public health [1–3]. Although these viruses are avian in origin, they can also cause disease in a range of mammalian species. At the time of this publication, the wild mammals that have been most severely impacted by H5Nx HPAIVs

are pinnipeds: the marine mammal group comprising seals, sea lions, fur seals and the walrus [2,4]. The recent dramatic shift in the epidemiological landscape—and seascape—of HPAIV cements its status as an ecologically significant marine pathogen.

Since 2020, H5Nx HPAIVs have caused an array of sporadic deaths, localized outbreaks and expansive mass mortality events in seabirds and pinnipeds (figure 1A). Although avian influenza viruses (AIVs) have long affected marine mammals, the magnitude of this panzootic surpasses those caused by earlier AIV strains. In the southern hemisphere, where the largest outbreaks in pinnipeds have occurred, H5Nx HPAIVs have caused near-total losses of demographic cohorts. Widespread reproductive failures and deaths of adult females can have outsized and persistent effects on long-lived vertebrate populations [32,33]. The implications of H5Nx HPAIV infections for conservation of the world's pinnipeds are profound, especially for small, declining or geographically limited populations.

In the H5Nx HPAIV global health discourse, concerns for biodiversity can be overshadowed by conversations surrounding agriculture, trade and public health. Governmental systems for AIV surveillance and testing tend to reflect these priorities. In many countries, wildlife surveillance is primarily passive and focused on waterfowl, if practised at all. National and state diagnostic laboratories are mandated to protect animal production systems and may lack the capacity for high-volume wildlife testing, especially with respect to current H5Nx strains more nimble and far-reaching than any prior HPAIV. Disparities between the scale of outbreaks and the resources available for response and research in wildlife, combined with regulatory complexities, can hinder efforts to investigate HPAIVs in pinnipeds. These challenges are further compounded by the inherent difficulties of working with free-ranging marine animals.

At the same time, the cross-sector visibility and urgency of H5Nx HPAIVs provides a window for pinniped scientists and managers to advance disease research, prevention and mitigation in marine systems. Such momentum is, unfortunately, not always available for marine disease agents that may be destructive to biodiversity but less directly linked to human systems. Recent publications by the Food and Agriculture Organization of the United Nations (FAO) and the World Organization for Animal Health (WOAH) cite wildlife as essential components of a global HPAIV surveillance system, motivated in part by the imperative to protect biodiversity [34]. Avian influenza outbreaks are unlikely to abate naturally, making now the opportune time to evaluate disease management systems for the benefit of vulnerable wildlife species.

In this review and perspective piece, we discuss challenges and recommendations for HPAIV surveillance and testing in pinnipeds. We propose strategies for outbreak response, synthesizing lessons learnt from recent mass mortality events in South America, and suggest research directions to improve evidence-based management. We also assess options for HPAIV prevention and mitigation in free-ranging populations. We hope to inform the development and evaluation of comprehensive pinniped management strategies, which we argue should acknowledge H5Nx HPAIV risks and options for prevention, detection, mitigation and recovery planning.

2. Emergence of the current H5Nx HPAIV panzootic

Influenza A viruses (*Alphainfluenzavirus influenzae*) are common pathogens of birds and mammals. Influenza A virus strains are classified according to two surface proteins, haemagglutinin (HA) and neuraminidase (NA), which can be combined into a multitude of subtypes (e.g. H1N1, H7N9). Waterfowl, shorebirds and gulls are natural reservoir hosts of avian influenza A viruses, or AIVs [35–37]. There is evidence that seabirds such as terns, murres, shearwaters, skuas and penguins also play important roles in AIV ecology [38–40]. Avian influenza virus particles shed in the faeces of infected birds can persist in water and can remain infective for as long as 200 days in low salinities and cool/cold temperatures [41–43]. As a result, birds are susceptible to faecal–oral AIV transmission via contaminated water or sediment [35,36]. Respiratory transmission probably also plays an important role in AIV spread among aquatic birds congregating at rookeries or migratory stopover sites [44,45], and predation and scavenging play a significant role in transmission of HPAIV [46].

Avian influenza viruses of the H5 and H7 subtypes are designated as high pathogenicity (HPAIV) or low pathogenicity (LPAIV) based on their lethality to poultry [36,47,48]. The key feature distinguishing LPAIV from HPAIV in birds is a multi-basic cleavage site that allows HPAIV to infect a broad range of cells and tissues [36]. While LPAIVs seldom cause significant illness in wild birds, HPAIVs that spill 'back' into wild birds from poultry cause disease of varying severity depending on the wild bird's species, age and immunity [49]. Both LPAIVs and HPAIVs can also infect mammals [47,48]. In mammalian hosts, the presence of a multi-basic HA cleavage site has no direct bearing on pathogenicity. In some cases, HPAIV infections cause swift and lethal illness, such as that observed in pinnipeds, and in other cases cause only mild disease, as in dairy cattle [50]. Since 2020, the world has seen a drastic increase in the geographic and host taxonomic range of H5Nx HPAIVs. Particularly concerning is their spread to South America, Antarctica and the sub-Antarctic—regions previously considered naive to H5Nx HPAIV [1–3]. The specific H5Nx HPAIV strains at play descend from the Goose/Guandong lineage (Gs/Gd), which can be traced back to a 1996 outbreak among farmed geese in Guangdong province, southeast China [48,51]. Key resurgence events of Gs/Gd H5Nx HPAIV occurred in Eurasia and Africa in 2016–2017 and 2020–2021, and included major outbreaks in seabirds [52,53]. In 2021–2023, Gs/Gd H5N1 HPAI viruses of the clade 2.3.4.4b continued to evolve in wild birds in Europe, broadening in host range and reassorting with LPAIV strains in wild and domestic birds during new waves of global dissemination [54,55]. Following multiple introductions to North America in Nov–Dec 2021 and extensive reassortment with North American LPAIV strains [56,57], H5Nx HPAIVs moved southward, reaching South America in Oct 2022 [2,9,58], the sub-Antarctic islands in the South Atlantic Ocean (Falkland/Malvinas and South Georgia) in Oct 2023 [15,16] and Antarctica by Jan 2024 [59]. During the following austral spring/summer, these viruses spread eastward across the sub-Antarctic region, reaching Gough Island on the South Atlantic Ocean (Sep 2024) and Crozet (Oct 2024), Prince Edward (Nov 2024) and Kerguelen Islands (Dec 2024) in the Southern Indian Ocean [24,30,60]. During this period of global expansion, H5Nx HPAIVs increasingly infected mammals,

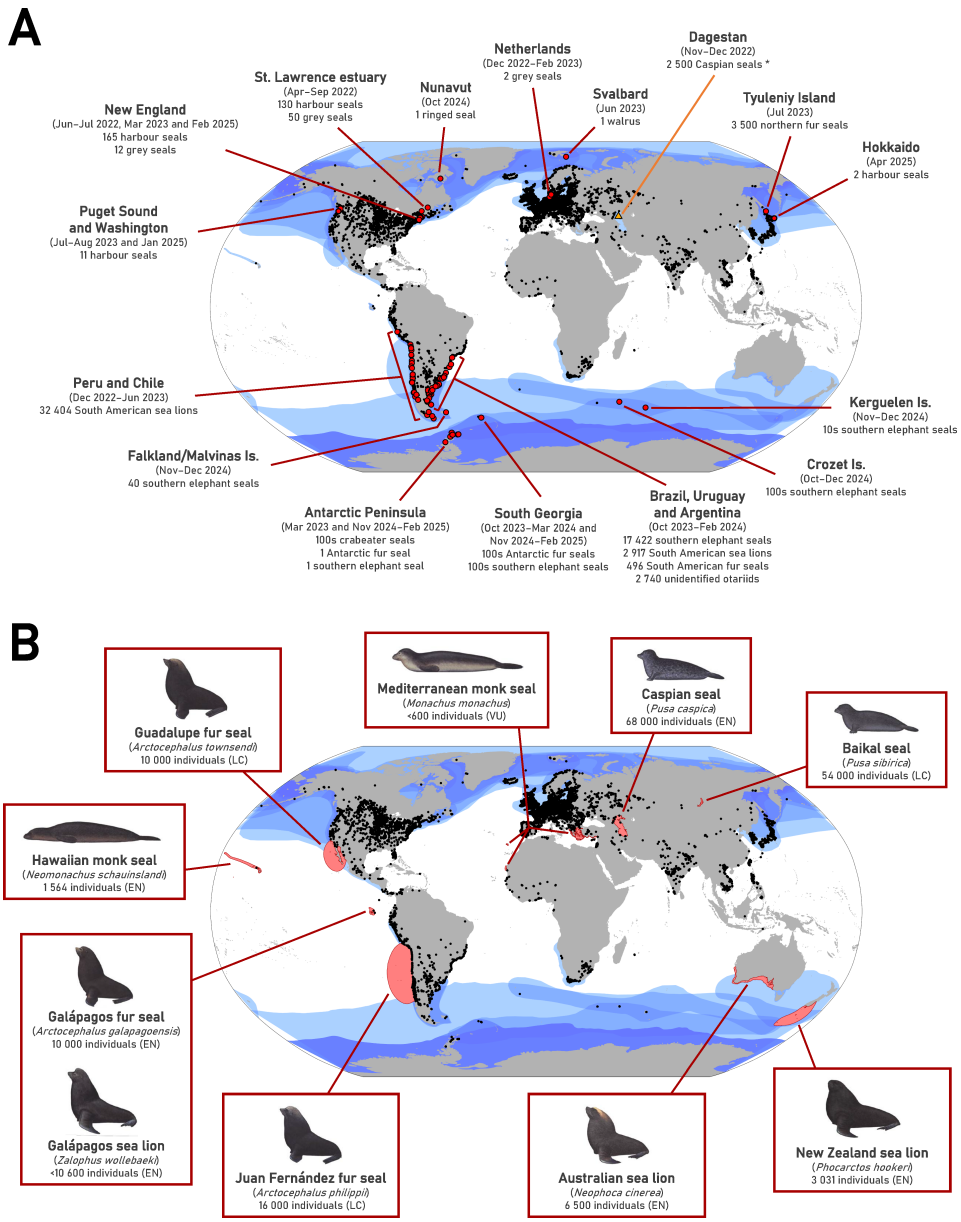

Figure 1. The global impact of H5Nx HPAIVs on wild pinnipeds. (A) Geographic distribution of H5Nx HPAIV confirmed cases (red dots) and suspected cases (orange triangles), with summaries of the location, time period, species and number of individuals affected. (B) Distribution of 10 pinniped species with highly restricted geographic distributions (red areas), with summaries of adult population size and conservation status [5]. Black dots represent H5Nx HPAIV detections in poultry, wild birds and wild mammals from January 2021 to July 2025, inclusive [6]. Shaded blue areas represent distributions of the world's pinniped species (darker shades represent overlapping species distributions) [5]. Notes: Asterisk indicates H5Nx HPAIV mortality was suspected, but laboratory confirmation is pending as of September 2025; LC = Least Concern; VU = Vulnerable; EN = Endangered. Artwork adapted from Jefferson *et al.* [7]. H5Nx HPAIV records compiled from [8–31].

including farmed mustelids, dairy cattle, domestic cats, other terrestrial wild mammals (especially carnivores), aquatic wild mammals and humans [3,4]. As of September 2025, H5Nx HPAIVs have been detected in wildlife on all continents except Oceania [30], not for lack of surveillance in this region [61–63].

3. Pinnipeds as hosts of influenza A viruses

Pinnipeds have a suite of ecological, behavioural, genetic and physiological characteristics that render them susceptible to AIV infections. Pinnipeds stand out among mammals in the diversity of influenza A viruses they host, with variation in their responses to infections [12,64–72]. Evidence suggests that North Atlantic grey seals (*Halichoerus grypus*) serve as natural reservoirs of LPAIV because multiple strains circulate in this population without discernable morbidity or mortality [68,73]. By contrast, sympatric Atlantic harbour seals (*Phoca vitulina vitulina*) are very susceptible and experience recurrent LPAIV mortality events [74–76]. Thus, the HA multi-basic cleavage site characteristic of HPAIV is not necessarily required to produce fatal outcomes in pinnipeds. Variation in innate immune function and in genetic diversity at the major histocompatibility complex (MHC) may contribute to species-specific differences in disease resistance [77]. Grey seals have high MHC-I sequence variation and allelic richness compared with other pinniped species, including northern elephant seals (*Mirounga angustirostris*) and Hawaiian monk seals (*Neomonachus schauinslandi*) [78,79]. Further, grey seal pups naturally exposed to influenza A viruses

exhibit dynamic up- and downregulation of certain immune-related genes, including the antiviral *Mx1* gene [80]. The authors hypothesized this could be an adaptive mechanism by which grey seals resist influenza A virus morbidity and mortality, but described their findings as preliminary [80].

Sporadic deaths and small, localized AIV mortality events in pinnipeds are frequently attributed to independent bird-to-mammal spillover events (e.g. [12,18]). Pinnipeds are amphibious and can be exposed to AIVs from aquatic birds ashore or at sea. AIV infections could be indirectly acquired via inadvertent consumption of faeces or feathers from infected birds, ingestion of contaminated water, or inhalation of aerosols or fomites [19]. Pinnipeds could also become infected via direct interactions with birds, such as during predatory and non-predatory attacks on seabirds by pinnipeds [81–85], multi-species foraging assemblages [86,87], fishery depredation [88], harassment of pinnipeds by seabirds (e.g. gulls scavenging placental and umbilical tissues of pups) or simple habitat sharing [82,83]. On developed coastlines, pinnipeds could become exposed to HPAIVs via contaminated runoff from poultry farms or dairies, or through direct interactions with infected domestic animals. These are currently not confirmed pathways by which pinnipeds have acquired H5Nx HPAIV. However, it is well-known that pinnipeds are vulnerable to terrestrial disease agents transported from land to sea (e.g. *Morbillivirus canis* (canine distemper), *Neospora caninum* (neosporosis), *Toxoplasma gondii* (toxoplasmosis) [89–91]). Moreover, human pandemic H1N1 has been detected in free-ranging pinnipeds [65,71,92].

Many pinnipeds are gregarious [7], and close interactions during breeding, resting or moulting could facilitate mammal-to-mammal transmission of influenza A viruses. Indeed, there is evidence that LPAIV can be transmitted between pinnipeds [64, 66]. The upper respiratory epithelium of harbour seals expresses sialic acid receptors (SA-2,3) permissive to AIV attachment, while the lung parenchyma has abundant mammalian sialic acid receptors (SA-2,6), supporting AIV transmission among seals [68,76,93]. Experimental studies suggest that the pinniped respiratory tract is highly susceptible to infection by clade 2.3.4.4b H5Nx HPAIVs [94]. During H5Nx HPAIV outbreaks, however, it has been difficult to prove the occurrence of direct mammal-to-mammal transmission, as this requires abundant sequencing data from pinnipeds and wild birds involved in local transmission chains [4]. Epidemiological and genomic evidence from H5Nx HPAIV outbreaks in South America increasingly supports the occurrence of propagated, pinniped-to-pinniped virus transmission, not only between elephant seals but also among elephant seals, sea lions and fur seals [21,23,28]. Maternal transmission is another potentially important mechanism; sea lion abortions were observed at several locations in South America, with high concentrations of viral RNA recovered from the mother, placenta and fetus [9,21,95]. It is also plausible that infected mothers shed HPAIV through their milk, infecting nursing pups, given that this phenomenon occurs in dairy cattle [23,96]. These topics merit continued research (table 1).

Pinnipeds infected with H5Nx HPAIV have primarily exhibited neurological and respiratory signs, including tremors, repetitive head or flipper movements, seizures, nasal discharge and laboured respiration, as well as nonspecific signs such as lethargy. In pinnipeds that died and were sampled during H5Nx HPAIV outbreaks, brain and lung tissues have been the most sensitive for molecular detection of the virus compared with nasal, oral or rectal swabs [11,14,19,21,23]. Pinnipeds generally succumb to infections rapidly, within a few days of developing clinical signs [14,22,23]. However, a viral incubation period has not been established. There have been instances during H5Nx HPAIV outbreaks in South America during which sea lions with neurological signs were observed alive for several days. This led to speculation that infected sea lions were travelling to nearby pinniped communities and contributing to intra- and interspecific transmission of H5N1 HPAIV via aggression and sexual interactions [23,95,97]. Some outbreaks have produced disproportionate mortality in young animals (especially pups) and females (especially peri-parturient females) [19,22,23,29]. While this could reflect age- or sex-related differences in disease presentation or severity, missing data on adults, potentially related to differences in behaviour or rates of carcass detection, could be a significant confounder. The mechanisms allowing certain animals to survive infections or to avoid exposure remain unclear, but they could be relevant to how H5Nx HPAIVs disseminate geographically. To investigate these questions, prospective molecular and serological surveillance of asymptomatic and symptomatic pinnipeds is underway in the Americas, Southern Ocean and elsewhere.

4. Impacts of the H5Nx HPAIV panzootic on pinniped populations

At least 17 H5Nx HPAIV mortality events have occurred in free-ranging pinnipeds in Eurasia and the Americas (figure 1A). Significant pinniped mortalities in the northern hemisphere in 2022–2023 include approximately 3500 northern fur seals (*Callorhinus ursinus*) and a Steller sea lion (*Eumetopias jubatus*) in eastern Russia (H5N1 [22]), and potentially 2500 Caspian seals (*Pusa caspica*) in Dagestan, Russia [17,98]. Since 2020, there have been multiple, discrete clusters of harbour seal and grey seal mortality in Europe and on the Pacific and Atlantic coasts of North America, each affecting a few to hundreds of animals [11–13,18,19]. The first-ever detection of HPAIV in a walrus (*Odobenus rosmarus;* H5N5) occurred in Svalbard, Norway, in 2023 [99]. In 2024, an H5N5 HPAIV infection was confirmed in an Arctic ringed seal (*Pusa hispida*) in Nunavut, Canada [30,100]. In the spring of 2025, H5N1 HPAIV was detected in two harbour seal carcasses found among numerous dead seals, sea otters and seabirds in Hokkaido, Japan [101].

Pinnipeds in the southern hemisphere have been hit hardest by the panzootic. Throughout Peru, Chile, Brazil, Uruguay and Argentina, H5N1 HPAIV outbreaks killed a minimum of 36 000 South American sea lions (*Otaria byronia*), 17 400 southern elephant seals (*Mirounga leonina*) and 1000 South American fur seals (*Arctocephalus australis*) [8–10,14,20,21,23,28,29,102,103]. The subsequent spread of H5N1 HPAIV to sub-Antarctic islands and to Antarctica triggered various mass mortality events affecting southern elephant seals, Antarctic fur seals (*Arctocephalus gazella*) and crabeater seals (*Lobodon carcinophagus*). These outbreaks are still being investigated, but preliminary reports indicate that several hundred pinnipeds died [16,24–27,30].

Table 1. Knowledge gaps and research directions regarding H5Nx HPAIV in pinnipeds.

topic	research questions
transmission dynamics and epidemiology	— What are the main transmission routes by which wild pinnipeds become naturally infected? (e.g. aerosol, respiratory droplets, faeces, saliva) — How long do virus particles remain infective under various realistic conditions? (e.g. in decomposing carcasses, sand, seawater, surfaces in rehabilitation facilities) — Which LPAIV strains naturally circulate in pinniped populations, and how does their epidemiology differ from that of HPAIV? — Which pathways of virus transmission contribute to outbreaks with high pup mortality? (e.g. transplacental, milk, saliva, etc.) — How can emerging tools help us investigate contact rates and transmission routes in wild pinniped populations? (e.g. proximity-sensing collars, fixed-point cameras coupled with automated image analysis) — What behavioural or ecological factors could lead to differences in virus exposure by pinniped species, age class or sex?
pathobiology and immunology	— Do pinniped species exhibit variation in sialic acid receptor distribution within the body? Other than the presence of sialic acid receptors in different tissues, what factors determine HPAIV tissue tropism? — Are there species- or age-specific differences in innate or adaptive immune responses to HPAIV infections? — Are certain species or age classes more or less likely to develop severe disease while shedding HPAIV? If so, how does this affect disease spread? — How do HPAIV infections progress in pinnipeds? (e.g. incubation period, viral shedding routes, chronology of lesions and clinical signs) — Do individuals that survive HPAIV infections develop a protective immune response, and how long does this protection last? — Do individuals exposed to other influenza A viruses have cross-protective immunity to HPAIV, and how long does this protection last?
molecular biology and viral evolution	— Do different HPAIV strains and subtypes circulating in pinnipeds exhibit significant differences in transmissibility and pathogenicity? — How do mutations associated with mammalian adaptation influence the transmission, pathogenicity and virulence of HPAIV in pinnipeds? — Are there genomic predictors of zoonotic potential in virus strains found in pinnipeds? — How likely is it that pinnipeds would allow reassortment between HPAIV and other influenza strains (LPAIVs or human influenza viruses)?
animal behaviour and ecology	— How do HPAIV outbreaks affect pinniped movements, migration, social behaviours and intra- and interspecific interactions? — How do maternal abandonment and insemination failures during outbreaks affect social and population dynamics in colony-forming pinnipeds?
detection and diagnostics	— How can we apply novel or existing technologies to enhance detection and monitoring before, during and after HPAIV outbreaks? — How can citizen scientists, park rangers and other groups safely contribute to the early detection and communication of outbreaks? — Can non-invasive technologies be used to detect HPAIV and/or quantify sick or deceased pinnipeds? (e.g. thermal imaging, pathogen sensors) — Are there suitable point-of-care tests that are sensitive and specific for the detection of influenza A in pinnipeds? If so, how can we ensure these tools are used in compliance with official testing and reporting requirements?
population impacts, prevention and mitigation	— How can we apply novel or existing technologies to perform population monitoring more consistently and with minimal disturbance? — What are the immediate and long-term impacts of HPAIV outbreaks on non-breeding individuals (e.g. juveniles, subadults, subordinate males)? What epidemiological roles do these individuals play during outbreaks? — Are there safe, practical and effective approaches to prevent or mitigate outbreaks in pinnipeds? (e.g. vaccination, treatment, carcass removal) — What are the social and economic costs of HPAIV outbreaks in marine wildlife? — What are the costs of expanding HPAIV surveillance, testing, prevention, response and/or mitigation activities in marine wildlife? — What strategies can alleviate other pressures on pinnipeds, increase their resilience to outbreaks and accelerate their recovery after mortality events? — What are the ecological implications of pinniped mass mortalities? (e.g. effects on seabirds, predators, terrestrial scavengers, environmental quality)

Interpreting the demographic and ecological implications of these outbreaks is challenging. Mortality is probably underestimated owing to carcasses being inaccessible, lost at sea [104] or removed by predators and scavengers. Large segments of known pinniped habitats (e.g. vast extents of Antarctic sea-ice) have not been surveyed for morbidity and mortality since the

onset of the panzootic. As such, absolute carcass counts may be only partially informative. For example, an estimated 17 400 southern elephant seal pups (and an unknown number of adults) died in Argentina in 2023 [8,23], which corresponds to a modest fraction of the species' global population (approx. 325 000 mature individuals [105]). However, because the outbreak caused mortality in >95% of pups born that year and disrupted breeding harems, local population recovery could take decades, even in the best possible scenarios (i.e. limited adult female mortality [8,23,106]). Although there are no archipelago-wide estimates for the mortality of southern elephant seals in the Crozet Islands, that only eight live pups were counted on a beach where over 270 pups had been counted weeks earlier was abnormal and suggests mortality could have exceeded 97% [24]. These data indicate that the demographic impacts of H5Nx HPAIVs on southern elephant seal populations may be greater than would be appreciated solely from a carcass count. For some species, especially those difficult to survey, estimating mortality rates is challenging owing to high levels of uncertainty in population abundance estimates. For instance, the estimated global population size of the ice-dependent crabeater seal ranges from <7 million to 30–40 million individuals [107].

Several pinniped species have small populations and/or narrow geographic distributions (figure 1B). An example is the Hawaiian monk seal, a species endemic to the Hawaiian Islands that is classified as endangered, with an estimated total population of 1564 individuals [108]. The sudden loss of a few hundred Hawaiian monk seals could cause a significant population bottleneck and jeopardize the viability of this species. Other pinnipeds have relatively large populations but exhibit highly clustered distributions, potentially increasing their vulnerability to a highly transmissible pathogen like H5Nx HPAIV. For instance, although the Antarctic fur seal is currently classified as Least Concern, with an estimated global population of more than 700 000 mature individuals, 95% of the population is concentrated in South Georgia [105]. In this context, the South Georgia H5Nx HPAIV outbreaks causing mass mortality of Antarctic fur seals in 2023/2024 and 2024/2025 raise concerns that recurrent HPAIV outbreaks could weaken population health and resilience [15,16,27]. Even if the long-term viability of a species is considered secure, HPAIV can cause reductions in evolutionarily unique sub-populations. Such is the case of Antarctic fur seals that breed in the South Shetland Islands. This small, ecologically and genetically distinct population has sharply declined in recent decades and is now threatened with the arrival of HPAIV to the archipelago [59,109,110].

In addition to the loss of individuals, HPAIV outbreaks can shift population demographics by disrupting social dynamics. H5Nx HPAIV outbreaks in southern elephant seals in Argentina in 2023/2024 led to a breakdown of harem structures, with a progressive replacement of mature alpha males by subadult males. With fewer mature alpha males guarding harems, a greater number of South American sea lions intermingled with elephant seals, providing opportunities for interspecific virus exchange and agonistic interactions, including sexual harassment of elephant seal pups by sea lions [23]. Further, because females are typically inseminated at the end of the nursing period [111], the premature abandonment of breeding colonies during the outbreak probably reduced conception rates, resulting in fewer births in the following year [23,106]. Moreover, low recruitment stemming from the loss of nearly an entire cohort of pups will affect future population age structure and sexual competition dynamics [106].

The circulation of H5Nx HPAIV within pinniped populations offers new opportunities for virus evolution and the emergence of novel strains in poorly surveyed ecosystems. This was illustrated by the formation of the 'marine mammal clade' of H5N1 HPAIVs in South America, which possessed multiple mammalian adaptation mutations and probably transmitted effectively between pinnipeds [4,23,28,112]. Virus strains from the marine mammal clade were isolated from a severe human case with no known animal exposures [113] and from a sanderling (*Calidris alba*), a southern fulmar (*Fulmarus glacialoides*) and terns (multiple species), suggesting spillback from marine mammals into coastal birds [23,28]. This strain was also shown experimentally to cause severe disease and death in ferrets, with suspected airborne mammal-to-mammal transmission [114]. There is concern that pinniped populations could support the emergence of zoonotic virus strains that transmit effectively among mammals. Because pinnipeds are known to host human-adapted influenza viruses in addition to LPAIVs [64,65,71,80,92], they could be a suitable vessel for the reassortment of multiple influenza A virus strains, possibly leading to novel genotypes with pandemic potential.

Lastly, H5Nx HPAIV outbreaks in pinnipeds do not occur in a vacuum. The marine mammal clade of H5N1 HPAIV in South America retained the ability to infect and kill wild birds [21,23]. Numerous species predate or scavenge on pinnipeds, including orcas, polar bears, leopard seals, foxes, coyotes, hyenas, wolverines, gulls, giant petrels, ravens, bald eagles and vultures [115,116]. These species could be exposed to HPAIV by consuming pinnipeds. Furthermore, in the long term, they could be at risk of cascading ecosystem effects owing to pinniped population declines (e.g. [117–119]).

5. Surveillance and early detection systems: outstanding challenges and potential solutions

Only a small fraction of the world's pinnipeds is visible at any given time. Elephant seals are at sea and solitary for 10 months of the year, only coming ashore briefly to breed and moult. Hawaiian monk seals in the Northwestern Hawaiian Islands and ice-dependent Antarctic seals are glimpsed by researchers for only a few weeks each year. Other species, while not quite so far from human populations, occupy rugged, offshore habitats difficult for us to access (e.g. Arctic seals, walrus, Guadalupe fur seals, Juan Fernández fur seals, Caspian seals, Baikal seals, Steller sea lions in the Aleutian Islands). Even in populated coastal areas with active marine mammal stranding networks, many pinniped haul-outs are rarely monitored owing to their remoteness, navigational hazards or access restrictions.

Approaching pinnipeds for sampling or close observation requires special permissions in most countries, along with strategic consideration of animal welfare and personnel safety. Field-based approaches can cause flushing, stampedes, pup abandonment, overheating and other stress-related issues in these animals, especially during vulnerable life stages. When a live pinniped appears symptomatic for HPAIV, diagnosis is challenging; there are numerous common aetiologies with similar

clinical presentations (e.g. neurological signs caused by domoic acid toxicosis). Currently, no rapid diagnostic tests for influenza A or H5N1 have been validated for use in marine mammals, though efforts are underway to evaluate potential candidates.

A common pitfall of wildlife disease investigations is that detailed data collection begins in reaction to a morbidity or mortality event. For pinnipeds, this typically requires a sufficiently large mass stranding event to be noticed by park rangers, members of the public or stranding networks. By the time personnel, supplies and appropriate permissions are acquired for an investigation, days to weeks may have passed since the inciting event of the outbreak. Thus, it is common for time series data to be largely incomplete. With rapidly spreading HPAIVs, even a modest time delay could result in missing the infection peak. Although end-epidemic data can be used to generate useful epidemiologic parameters, capturing the initial and exponential phases of outbreaks informs downstream analysis and inference. Early case incidence data allow us to reconcile initial population estimates and final carcass counts. If there are missing individuals at the end of a mortality event, detailed observations from early stages of the outbreak could help elucidate whether animals died elsewhere, survived infections or potentially avoided exposure.

With all these obstacles, how do we successfully capture the early stages of marine H5Nx HPAIV epizootics, particularly during the pre-emergence and emergence phases? Moreover, how should we improve our knowledge of HPAIV epidemiology when outbreaks are *not* occurring? Strategizing effective risk-based surveillance is difficult for a virus that continually evolves, spreads via multiple hosts and transmission pathways, and is increasingly unpredictable in seasonality and geography. Should surveillance focus on periods when migratory birds are moving through the area? Or during the breeding and moulting seasons, when animal densities are highest and physiological vulnerability is increased? Should a response be triggered after disease has already been detected in nearby wildlife? And what constitutes 'nearby,' when it is possible that some seabirds or pinnipeds can still travel long distances while infected [15,24]? A surveillance plan incorporating all potential risk factors would inevitably become a year-round undertaking. Limitations in funding and resources—combined with the challenge of consistently observing pinnipeds—render such an approach impractical. However, there are tangible ways to modify existing surveillance systems that could both support pinniped populations and strengthen global HPAIV intelligence.

(a) Improve allocation of funding and resources to expand surveillance

Cooperatively leveraging resources and expertise across government and non-government sectors can aid in developing and maintaining robust active and passive surveillance functions before, during and after outbreaks [120]. Such collaborations might involve the sharing of expertise, capacity and resources across agencies, academic institutions and nonprofit organizations. Multi-national cooperatives and treaties such as WOAH, the International Union for the Conservation of Nature (IUCN), the International Whaling Commission (IWC) and the United Nations Convention on Migratory Species (CMS) could be well-poised to address a fast-moving, transboundary disease and ensure HPAIV detection systems are distributed equitably across borders. Steady funding streams would strengthen our ability to coordinate systematic sample and data collection (as opposed to opportunistic collection alone) and gather inference on population-level disease factors including infection prevalence and seroprevalence, risk factors of infection and exposure, and virus evolution (e.g. [121]). It is important to note that the specific goals of an expanded surveillance programme would vary by species and location, given some pinnipeds are inherently more difficult to monitor than others.

(b) Build stronger networks of communication

The wide host range of H5Nx HPAIV renders taxon-specific communication networks inadequate. Groups overseeing the detection of HPAIV in wildlife generally face similar financial constraints, and open lines of communication and information sharing between mammalian and avian researchers can leverage limited resources. Integrating expertise from veterinary medicine, epidemiology, ecology and molecular biology can maximize survey data collection and interpretation across taxa, providing more comprehensive insights needed to guide decision-making for pinniped disease management. Ideally, surveillance efforts will be consistent in basic methodology across agencies and conservation organizations equipped to conduct investigations and response. Accessible wildlife mortality alert systems could be initiated (or expanded where these already exist) such that a local HPAIV detection triggers network participants to heighten surveillance efforts, review contingency plans and assess current risks not only to wildlife but also to staff, volunteers and/or the public.

(c) Incorporate health surveillance into routine biological research and management activities

The staff of stranding networks, parks and refuges should be supported and encouraged to increase surveys of pinniped morbidity and mortality if HPAIV is detected in nearby waterbirds or other wildlife. Long-term population assessment and monitoring are the primary scientific foundations informing natural resource management and decision-making for many species. Health surveillance is not always incorporated into core research activities, but can be appended to existing efforts as part of a robust biological monitoring programme. Providing field biologists, rangers and managers with training and equipment for observational data collection and basic biomedical sampling is a cost-effective way to monitor and characterize baseline health and establish an early warning system for emerging threats [122]. For example, field biologists routinely deployed to the remote Northwestern Hawaiian Islands to conduct Hawaiian monk seal population surveys are also trained to identify signs of disease, conduct basic necropsies and collect samples from live and dead animals. Field kits and protocols can be modified to safeguard personnel health, limit the need for advanced veterinary skills or expertise, and accommodate

field conditions (e.g. using viral inactivation media unless culture-based media is explicitly necessary; cutting 'windows' into carcasses to collect tissue swabs instead of performing complete necropsies) [123]. Relevant protocols and guidelines from the Global Stranding Network are freely available (globalstrandingnetwork.com).

(d) Engage the public

Stranding networks, refuges, conservation organizations and rehabilitation centres often rely on community volunteers to carry out their operations. Ideally, all volunteers will be informed of zoonotic disease risks and trained in biosecurity and biosafety fundamentals. A qualified subset could receive additional training to perform limited field duties during times of elevated HPAIV risk (e.g. when HPAIV is being detected sporadically in local wild birds). For example, specialized volunteers could record detailed observations, take photographs and videos and relay information to the appropriate supervisor or authority, but should be instructed to forgo hands-on tasks (e.g. measuring carcasses). As for the general public, HPAIV outreach could be readily paired with existing educational activities (e.g. park programmes, visitor centre displays, 'Share the Shore' campaigns). Framing avian influenza through a marine disease lens can bridge issues close to home, such as impacts on poultry and risks to pets, with broader threats to ocean conservation, emphasizing connections between human, wildlife and ecosystem health.

(e) Improve technologies for non-invasive disease monitoring

Innovations in technology offer promising avenues to overcome long-standing limitations in wildlife surveillance, particularly for elusive, remote and mobile species like pinnipeds. Remotely operated cameras, unmanned aerial vehicles (i.e. drones), satellite imagery and pathogen sensors to detect health indexes can be deployed to limited-access sites, reducing the need for close contact while improving the ability to monitor population health and detect abnormal events across a wider geographic range. Marine mammal ecologists have long employed cutting-edge technologies, and these same projects yield valuable longitudinal and large-scale data on movement, life history, contact networks and individual health metrics [124]. There is ample opportunity for applying these technologies and data to enhance HPAIV surveillance at population and ecosystem scales. These data streams, when integrated with health and demographic data, will facilitate epidemiological modelling efforts and inform targeted management strategies.

(f) Streamline laboratory testing pipelines

Timely HPAIV diagnostic testing has been difficult to achieve for pinnipeds. This is true for both prospective surveillance efforts and testing of suspect cases. Conservation groups and authorities—such as reserve managers, park services, researchers, rehabilitation centres and stranding networks—frequently face financial constraints that reduce access to proper sampling supplies, infrastructure for sample storage, personal protective equipment (PPE) and diagnostic testing. Although HPAIV is a mandatory notifiable disease and its surveillance technically falls under veterinary services, these laboratory systems generally serve the agricultural sector. They are not designed for continuous wildlife health monitoring or outbreak response in wild species, with some exceptions (e.g. US Geological Survey laboratories). Pinniped samples are not always accepted or prioritized by diagnostic laboratories, particularly when they are strained during concurrent outbreaks in poultry or livestock. If submission is possible, testing expenses usually become the responsibility of the submitter, whereas food animal testing is often subsidized by governments. Moreover, expertise and diagnostic capacity are not always well-matched; authorities responsible for HPAIV surveillance are not necessarily knowledgeable about pinnipeds, while experts in pinnipeds may not be trained, authorized or equipped to collect and submit diagnostic samples.

To address these challenges at a systems level, diagnostic testing pipelines for high-impact zoonotic diseases would ideally place environmental and wildlife health surveillance on an equal footing with agriculture and public health. This echoes One Health paradigms that have been advocated by international health organizations for years (e.g. [125]). If the diagnosis and reporting of HPAIV in all species remain under the sole purview of governments, many official laboratories will need expanded capacities—budgets, personnel, facilities, equipment—to handle wildlife submissions. Alternatively, or additionally, permissions could be expanded to allow qualified outside networks, such as academic laboratories, to conduct testing. Initiating or expanding existing collaborations with universities can alleviate the burden placed on overstretched government laboratories, especially during outbreaks. Further, as we mention above, there is a need for rapid influenza A diagnostic tests validated for use in wildlife. Point-of-care tests could be used in field camps, research stations, vessels and rehabilitation centres to improve diagnostic capacity and the timeliness of interventions. However, positive results would still require confirmatory testing by a sanctioned diagnostic laboratory for reporting and virus characterization. Thus, improving the accessibility and affordability of official diagnostic testing could help to encourage the responsible use of point-of-care tests in the future.

6. Outbreak investigation and response

HPAIV outbreaks can be sudden and overwhelming in scope. Obtaining the appropriate scientific and regulatory permits in advance can dramatically improve the speed and quality of a response. Additionally, having a pre-established action plan and response kits containing data sheets, sampling protocols and supplies can streamline the process. Protocols should describe the full lifespan of a sample, from collection and transport to testing and communicating results.

Optimal investigation procedures will vary depending on the team, available resources, regulations and field site, and may evolve as new knowledge is gained. In general, it is crucial to record detailed observational data and collect as many high-quality samples as is feasible (for HPAIV detection and sequencing, as well as for serology, pathology and other analyses). Photographs and videos at multiple scales can also be valuable (e.g. [18]). Specific sample and data collection guidelines for marine mammal HPAIV outbreak response are available from WOAH [123].

The top priorities of any outbreak response must be protecting the health of responders and preventing the unintentional spread of HPAIV. In addition, sample and data collection during and following outbreaks must be responsibly designed to avoid imposing additional stressors on live animals. Before deployment, response teams should be informed of potential disturbances (e.g. accidentally collapsing seabird burrows while surveying on foot) and trained on tactics to avoid or mitigate them. It may also be necessary to limit access by tourists and the general public (which also protects public health), or to pause or adapt non-essential research activities.

That said, the complete suspension of research and monitoring activities is not always warranted and could even be counterproductive in the long-term. In some regions, this approach has caused 'information blackout' and a paucity of data on affected populations. Such knowledge gaps can undermine the development of evidence-based strategies for future outbreak management. When feasible, investigating broader research questions related to disease ecology, pathobiology, population biology and other fields can provide powerful insights (table 1). For example, a series of GPS-tracking studies conducted in northern gannets (*Morus bassanus*) after HPAIV mass mortality events revealed alterations in their movement and foraging behaviours following outbreaks [126]. This may have contributed to the regional dissemination of the virus among colonies in Europe and North America [126–128]. Informed planning and careful execution of outbreak management and research activities are imperative to maximize knowledge gained while minimizing risk.

7. Knowledge gaps and research needs

Investigating multi-species HPAIV outbreaks requires comprehensive epidemiological analyses to disentangle multiple potential transmission pathways. A critical step in understanding outbreak dynamics is identifying the source of infection and the ecological, behavioural and environmental factors that enabled the virus to reach and spread through populations and meta-populations. Advancing our knowledge will require casting a wide surveillance net, as well as hypothesis-driven studies on HPAIV ecology and management, response and care in pinnipeds. A selection of research directions is presented in table 1.

Even in apparently unaffected populations, investigating AIV exposure and infection patterns is valuable. Surveillance of at-risk populations between outbreaks, regardless of their prior history with HPAIV, can help capture the full spectrum of disease in pinnipeds and their roles in AIV ecology. To date, much of the biological information available for pinnipeds has disproportionately focused on easily accessible life stages, such as breeding, nursing and post-weaning. By contrast, less is known about non-breeding and subadult females, juvenile and subordinate males, and animals during moult. Animals in these underrepresented categories could exhibit variation in spatial distribution, social interaction or susceptibility that affects virus transmission and maintenance. More consistent surveillance throughout the year (where possible) would facilitate spatiotemporal analyses of virus isolates across avian, mammalian and environmental sources, aiding our ability to track and forecast transmission patterns.

Collaboration between wildlife and public health sectors is needed to understand risks of disease in humans who interact closely with pinnipeds, such as scientists and veterinarians. In addition, cultural and subsistence harvesting of pinnipeds is practised in regions around the world [129,130]. Investigating HPAIV epidemiology in these communities, and in the pinniped populations on which they depend, is an important research direction considering that some H5Nx HPAIV strains have significant zoonotic potential and can cause illness or fatality in humans [47,98,131].

8. Recommendations to incorporate HPAIV into pinniped conservation planning

(a) Consider targeted prevention programmes

Vaccination can be an effective strategy to prevent HPAIV outbreaks in animal populations. Unlike in poultry, vaccinating wildlife for conservation purposes does not raise concerns about interference with sero-surveillance programmes or trade policies—issues that hinder HPAIV vaccination campaigns in some countries [132]. To date, HPAIV vaccination programmes or trials exist for a small number of free-ranging wildlife species: California condors (*Gymnogyps californianus*) in the US [133]), king penguins (*Aptenodytes patagonicus*) at Crozet Island [134] and endangered seabirds in New Zealand [62]. In the condors, US agencies conditionally authorized use of an inactivated H5N1 poultry vaccine because (i) it proved safe and moderately efficacious in a related 'surrogate' species (*Coragyps atratus*), and (ii) California condors are critically endangered, with a small, closely monitored population [6,56,133].

A similar rationale can be applied to pinnipeds. Although economic and logistical constraints will preclude widespread vaccination for most populations, certain pinnipeds meet criteria to be strong candidates for HPAIV vaccination. The endangered Hawaiian monk seal is a notable example; free-ranging Hawaiian monk seals have been vaccinated against morbillivirus since 2016 [132,135]. To inform the potential for HPAIV vaccination in this species, a conditionally approved, inactivated H5N1 cattle vaccine was recently administered to three juvenile northern elephant seals in a California rehabilitation centre [136]. The vaccinated elephant seals were released back into the wild in August 2025, and additional surrogate pinniped studies are

pending. This pilot study—analogous to the condor trial described above—was an important first step to determine whether there is a safe, effective HPAIV vaccine that elicits lasting immunity against variant strains of the virus in pinnipeds.

If a safe, efficacious vaccine is available, mathematical models can be used to estimate the minimum number of animals requiring vaccination to reach an estimated herd immunity threshold (e.g. [137]). The accuracy of these models depends on high-quality data (epidemiological, immunological, behavioural, etc.) for the species, population, pathogen and vaccine of interest. Since much of this information is limited for H5Nx HPAIV in pinnipeds, addressing knowledge gaps will improve our ability to design effective, sustainable vaccination programmes (table 1). Ongoing research aims to estimate HPAIV vaccination thresholds for pinnipeds with differing life histories and social behaviours, with the goal of informing potential intervention strategies.

(b) Establish plans for outbreak control and mitigation

Options for HPAIV outbreak control in free-ranging pinnipeds are limited. The ability to perform mitigation activities will depend on accessibility, resources and environmental features, as well as the species and numbers of animals affected. Strategies include carcass manipulation and treatment or euthanasia of infected animals. With specialized skills and appropriate regulatory permissions, these approaches can be considered on a case-by-case basis to limit the extent of an outbreak. This could be particularly impactful for rare or endangered species.

Treatment approaches for wild pinnipeds affected by HPAIV are not well established. For the vast majority of pinnipeds worldwide, marine mammal rehabilitation centres are not readily available. For these reasons, antiviral therapy and supportive care will not be a cornerstone of HPAIV management in pinnipeds. However, if a suitable facility is available, it may be possible to treat a small number of animals early in the course of disease. Strict measures to safeguard patients, staff, facilities and the environment from infection or contamination would be of paramount importance in this scenario [138]. The option of antiviral therapy should be weighed against the potential for selection of antiviral resistance mutations, which could have downstream implications for human health [96,139]. In most cases, euthanasia is the most humane option for HPAIV-infected pinnipeds in care. It ends suffering in symptomatic animals and can protect those nearby from propagated virus spread [123,140].

There is some evidence that removal of carcasses or infected animals—either for isolation or quarantine, if facilities exist, or by euthanasia—could reduce viral transmission to healthy individuals. Morbillivirus outbreak simulations in endangered Hawaiian monk seals showed that removing infectious individuals early-on reduced the severity of epizootics [137]. Although HPAIV and morbillivirus differ, this suggests that (if resources are abundant) a strategy of rapid diagnosis and removal of infectious individuals could prevent devastating population outcomes. Seabird carcasses have been systematically removed during some H5Nx HPAIV outbreaks, but whether carcass removal significantly affected case incidence is unclear and may be species-dependent [18,141]. Handling potentially infectious animals (if legally permitted) or carcasses should not be considered unless biosafety and biosecurity can be confidently maintained throughout every stage of the process. Plans must also limit disturbances to living animals. Frequent or sustained disturbance of mother–pup pairs or seabird nests could cause young to be abandoned or increase their vulnerability to predation. Finally, the removal and disposal of carcasses are especially difficult for outbreaks that are expansive, remote or involve large-bodied animals. For all these reasons, removing infected animals or carcasses is often impractical, and sometimes even inadvisable.

Deep burial of carcasses in place is an option to reduce the amount of virus easily accessible to other wildlife, domestic animals and humans. However, burial could also disturb sensitive wildlife or habitats, does not prevent persistence of the virus in sediment or groundwater, and might be ill-suited for expansive events. More studies of HPAIV survival in the natural environment and in carcasses would be beneficial to weigh the risks of carcass manipulation against the potential benefits (table 1). Leaving carcasses in place, paired with closure of the area to deter people, domestic animals and scavengers (to the degree this is possible), may be the most appropriate option in many cases.

(c) Prioritize long-term monitoring

H5Nx HPAIV outbreaks can lead to generational losses, particularly in colonial breeders. Long-term monitoring is essential to understand population-level consequences of disease outbreaks. Combining outbreak data with pre- and post-outbreak demographic data can enhance the rigour and utility of epidemiological models that forecast disease emergence or simulate transmission dynamics. These mathematical tools can, in turn, be used to devise targeted intervention strategies (e.g. [135]). Furthermore, predicted or actual HPAIV mortality outcomes can inform population viability assessments for threatened and endangered species to evaluate risks of decline or extinction.

Unfortunately, limitations in pre-outbreak data for wildlife often hamper the ability to understand long-term ramifications of HPAIV mass mortality events. An exception is the southern elephant seal population at Península Valdés, Argentina, which has been intensively studied for decades. Detailed data on annual recruitment, demographics and growth trajectories [111,142,143], combined with data from epidemiological investigations and population monitoring during HPAIV outbreaks in 2023, enabled these researchers to project possible long-term demographic consequences [8,23]. They estimated that the Península Valdés southern elephant seal population will take multiple decades to recover, potentially attributable to multiple factors: losses of adult females, decreased recruitment owing to pup mortality and reduced insemination rates owing to atypical harem dynamics [106]. This example highlights the value of longitudinal population data for detecting and tracking changes in abundance triggered by disease. Of course, not all pinnipeds can be easily monitored on a large scale. Harbour seals, for example, are typically censused via sporadic aerial surveys. In these cases, statistical methods can be employed to account for variable or scarce historical data (e.g. [144]).

(d) Quantify the socioeconomic impacts of outbreaks

Recurrent, large-scale HPAIV mortality events in coastal areas have the potential to generate significant economic impacts, particularly through the loss of ecosystem services provided by marine mammals and seabirds [145,146]. Tourism and recreation could be negatively affected by declines in wildlife populations, as well as by public access restrictions that must be instituted during outbreaks. Public awareness of illness and death in charismatic fauna—either through firsthand observation or media coverage—could harm social wellbeing, especially when threatened or endangered species are involved [147,148].

A cost–benefit analysis that quantifies socioeconomic incentives for protecting marine wildlife from panzootics, and juxtaposes them with the costs of HPAIV prevention and mitigation steps, could inform policy decision-making processes [149]. For example, in the USA, an economic analysis of proposed protections for Southern resident killer whales (*Orcinus orca*) was pivotal in a recent decision to expand critical habitat designations for this endangered marine mammal [150]. Marine wildlife scientists should collaborate with resource economists to generate an economic analysis of HPAIV surveillance and management actions, potentially through existing initiatives such as the Socioeconomic Working Group of the WOAH/FAO Network of Expertise on Animal Influenza (OFFLU) [151]. It is important to note that in communities where marine animals are vital to cultural identity and food security, an economic analysis may not only be insufficient but inappropriate to describe the effects of HPAIV-induced species declines on societal wellbeing [152].

(e) Pursue high-level policy changes

National agencies responsible for managing pinnipeds, along with international conservation organizations, should recognize that H5Nx HPAIVs pose a demonstrable threat to pinniped populations. There are actionable strategies to improve detection and mitigation of HPAIVs in marine environments, and implementing these measures would also support the protection of other vulnerable taxa (e.g. migratory waterbirds). National and international animal and human health organizations incorporating wildlife into HPAIV countermeasures should include pinnipeds as a priority group, to improve our overall scientific understanding of HPAIV panzootics and their prevention.

Our recommendations are synergistic with many goals outlined in existing HPAIV action plans and resolutions, such as those passed by FAO and WOAH [34], FAO and CMS [153], and CMS and the United Nations Environment Programme (UNEP) [154]. Including marine mammal experts in these policy processes would help ensure that pinnipeds are appropriately represented in relevant guidance and recommendations. In parallel, international organizations working to conserve marine mammals (e.g. IUCN, IWC, Global Stranding Network, Rare Pinniped Conservation Network, the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR)) could compose HPAIV preparedness, research and response strategies tailored to pinnipeds. International coalitions such as the Agreement on the Conservation of Albatrosses and Petrels (ACAP) [155], the Scientific Committee on Antarctic Research (SCAR) [156] and CCAMLR [157] produce numerous HPAIV resources, including databases, risk assessments and professional guidelines, and could serve as models for pinniped-focused efforts.

(f) Address concurrent conservation threats

Resilience to HPAIV outbreaks can be fostered through regulations and actions that reduce other pressures to pinnipeds. These pressures include anthropogenic interactions, climate-influenced changes to prey availability and quality, harmful algal blooms and pathogens other than HPAIV. While preventing exposure to HPAIVs will be extremely difficult, we can endeavour to reduce the likelihood that an outbreak pushes a population past its ability to recover. This is especially crucial for rare and endangered pinnipeds (figure 1B). However, it is important to recognize that even stable or increasing populations are not immune to catastrophic impacts or sudden reversals in trajectory [106]. It is easy to forget that many robust pinniped populations were nearly extirpated just a century ago, but flourish today owing to decades of enforced legal protections [158]. Any designation of population status, even Least Concern, carries a degree of precarity. The recovery of species such as California sea lions (*Zalophus californianus*), northern elephant seals, and Pacific harbour seals (*Phoca vitulina richardii*) from historical depletion offers some reassurance in the face of HPAIV panzootics. At the same time, the extinctions of other species such as the Caribbean monk seal (*Neomonachus tropicalis*) and the Japanese sea lion (*Zalophus japonicus*) in the 20th century are a sobering reminder that recovery is not guaranteed. Considering the multiple threats that pinnipeds face today—especially the worsening effects of climate change [159]—concerted efforts should be made to ensure that HPAIV does not precipitate further losses in pinniped diversity.

9. Conclusion

The expanding impact of H5Nx HPAIVs on marine mammal and seabird health constitutes a marine disease emergency [160]. While it will be incredibly challenging to safeguard pinnipeds from HPAIV exposure in the natural environment, we can take actions to characterize risk and bolster population resilience. Allocating resources to surveillance and response for pinnipeds will improve our chances of early detection, enabling us to mobilize interventions and alert local, national and global networks quickly in the event of an outbreak. Integrating epidemiological and ecological knowledge bases through collaboration can expand the management planning toolkit with better technologies for holistic monitoring, as well as with mathematical tools

such as outbreak simulation models [135,161] and integrated population models [162]. Involvement from social scientists and public health practitioners can help to ensure that research and management practices inform, engage and protect communities at risk of disease exposure. The principles of One Health are highly compatible with those of ecosystem-based marine resource management [163], with both frameworks invoking the interdependency of societal and ecological wellbeing.

Notably, every documented outbreak in pinnipeds has involved a significant, often greater, degree of mortality in sympatric birds. Seabirds are among the most threatened avian groups [164], and serious concerns for local extirpation and extinction have led to new or updated HPAIV management actions for many species [153,165]. Moreover, pinnipeds are not the only marine mammals affected by this panzootic. H5Nx HPAIVs have caused mortality in cetaceans [9,166], polar bears (*Ursus maritimus*) [167] and aquatic mustelids [28,101,168]. While these cases have been associated with isolated bird–mammal spillover events, by contrast to the mass mortality observed in some pinnipeds, it is possible that some mortalities have gone unnoticed given the limited visibility of many of these species. With their continually broadening host range, H5Nx HPAIVs merit consideration in conservation planning for any marine bird or marine mammal population.

High-level policy changes and international agreements are ultimately necessary to address the root causes of HPAIV outbreaks. If we are truly committed to combatting HPAIV panzootics within a One Health framework [34,112], the support and attention given to wildlife must be elevated to match that of other sectors [120]. Considering the magnitude of HPAIV's threat to biodiversity, commensurate efforts to invest and redistribute resources are justified. Adapting regulatory frameworks to better serve wildlife health will only strengthen our overall capacity to respond to this far-reaching crisis.

Ethics. This work did not require ethical approval from a human subject or animal welfare committee.

Data accessibility. This article has no additional data.

Declaration of AI use. We have not used AI-assisted technologies in creating this article.

Authors' contributions. E.A.: conceptualization, writing—original draft, writing—review and editing; R.E.T.V.: conceptualization, data curation, writing—original draft, writing—review and editing; M.B.: conceptualization, writing—original draft, writing—review and editing; W.P.: conceptualization, writing—original draft, writing—review and editing; F.G.: writing—original draft, writing—review and editing; C.F.: writing—original draft, writing—review and editing; C.K.J.: conceptualization, supervision, writing—original draft, writing—review and editing; M.U.: conceptualization, supervision, writing—original draft, writing—review and editing.

All authors gave final approval for publication and agreed to be held accountable for the work performed therein.

Conflict of interest declaration. We declare we have no competing interests.

Funding. This work was supported by the US National Science Foundation Center for Pandemic Insights (NSF CPI) Award #2412522. E.A. was supported by a NMFS-Sea Grant Fellowship through NOAA's National Sea Grant College Program (NOAA Grant #NA24OARX417C0176-T1-01) and California Sea Grant (Project #R/Ashley_PED). The statements, findings, conclusions and recommendations are those of the authors and do not necessarily reflect the views of California Sea Grant or the US Government.

Acknowledgements. We thank the anonymous peer reviewers and our colleagues Joseph Gaydos, Deborah Fauquier, Katia Shinkle and Jennifer Paige for providing thoughtful feedback on the manuscript. We are grateful to the guest editors for the opportunity to contribute to this special issue.

References

1. Wille M, Barr IG. 2022 Resurgence of avian influenza virus. *Science* **376**, 459–460. (doi:10.1126/science.abo1232)
2. Kuiken T *et al*. 2025 Emergence, spread, and impact of high-pathogenicity avian influenza H5 in wild birds and mammals of South America and Antarctica. *Conserv. Biol*. **e70052**, e70052. (doi:10.1111/cobi.70052)
3. Krammer F, Hermann E, Rasmussen AL. 2025 Highly pathogenic avian influenza H5N1: history, current situation, and outlook. *J. Virol*. **99**, e02209-24. (doi:10.1128/jvi.02209-24)
4. Peacock TP, Moncla L, Dudas G, VanInsberghe D, Sukhova K, Lloyd-Smith JO, Worobey M, Lowen AC, Nelson MI. 2025 The global H5N1 influenza panzootic in mammals. *Nature* **637**, 304–313. (doi:10.1038/s41586-024-08054-z)
5. IUCN. 2024 The IUCN Red List of Threatened Species. *Version 2024-1* https://www.iucnredlist.org
6. World Organisation for Animal Health (WOAH). 2024 Considerations for emergency vaccination of wild birds against high pathogenicity avian influenza in specific situations. See https://www.woah.org/app/uploads/2024/01/vaccination-wild-birds-hpai-outbreak-dec2023.pdf.
7. Jefferson TA, Webber MA, Pitman RL. 2007 *Marine mammals of the world: a comprehensive guide to their identification*. London, UK: Academic Press.
8. Campagna C, Uhart M, Falabella V, Campagna J, Zavattieri V, Vanstreels RET, Lewis MN. 2024 Catastrophic mortality of southern elephant seals caused by H5N1 avian influenza. *Mar. Mammal Sci*. **40**, 322–325. (doi:10.1111/mms.13101)
9. Leguia M *et al*. 2023 Highly pathogenic avian influenza A (H5N1) in marine mammals and seabirds in Peru. *Nat. Commun*. **14**, 5489. (doi:10.1038/s41467-023-41182-0)
10. Marandino A, Tomás G, Panzera Y, Leizagoyen C, Pérez R, Bassetti L, Negro R, Rodríguez S, Pérez R. 2023 Spreading of the high-pathogenicity avian influenza (H5N1) virus of clade 2.3.4.4b into Uruguay. *Viruses* **15**, 1906. (doi:10.3390/v15091906)
11. Mirolo M *et al*. 2023 Highly pathogenic avian influenza A virus (HPAIV) H5N1 infection in two European grey seals (*Halichoerus grypus*) with encephalitis. *Emerg. Microbes Infect*. **12**, e2257810. (doi:10.1080/22221751.2023.2257810)
12. Puryear W *et al*. 2023 Highly pathogenic avian influenza A(H5N1) virus outbreak in New England Seals, United States. *Emerg. Infect. Dis*. **29**, 786–791. (doi:10.3201/eid2904.221538)
13. Thorsson E, Zohari S, Roos A, Banihashem F, Bröjer C, Neimanis A. 2023 Highly pathogenic avian influenza A(H5N1) virus in a Harbor Porpoise, Sweden. *Emerg. Infect. Dis*. **29**, 852–855. (doi:10.3201/eid2904.221426)
14. Ulloa M *et al*. 2023 Mass mortality event in South American sea lions (*Otaria flavescens*) correlated to highly pathogenic avian influenza (HPAI) H5N1 outbreak in Chile. *Vet. Q*. **43**, 1–10. (doi:10.1080/01652176.2023.2265173)
15. Banyard AC *et al*. 2024 Detection and spread of high pathogenicity avian influenza virus H5N1 in the Antarctic Region. *Nat. Commun*. **15**, 7433. (doi:10.1038/s41467-024-51490-8)

16. Bennison A *et al*. 2024 A case study of highly pathogenic avian influenza (HPAI) H5N1 at Bird Island, South Georgia: the first documented outbreak in the subantarctic region. *Bird Study* **71**, 380–391. (doi:10.1080/00063657.2024.2396563)
17. Coston M. 2023 *Russia: Mass Mortality Event (Seals) In Caspian Sea Linked to Avian Flu*. Avian Flu Diary. See https://afludiary.blogspot.com/2023/01/russia-mass-mortality-event-seals-in.html.
18. Haman KH *et al*. 2024 A comprehensive epidemiological approach documenting an outbreak of H5N1 highly pathogenic avian influenza virus clade 2.3.4.4b among gulls, terns, and harbor seals in the Northeastern Pacific. *Front. Vet. Sci*. **11**, 1483922. (doi:10.3389/fvets.2024.1483922)
19. Lair S *et al*. 2024 Outbreak of highly pathogenic avian influenza A(H5N1) virus in seals, St. Lawrence Estuary, Quebec, Canada. *Emerg. Infect. Dis*. **30**, 1133. (doi:10.3201/eid3006.231033)
20. Rivetti AV Jr *et al*. 2024 Phylodynamics of avian influenza A(H5N1) viruses from outbreaks in Brazil. *Virus Res*. **347**, 199415. (doi:10.1016/j.virusres.2024.199415)
21. Rimondi A, Vanstreels RET, Olivera V, Donini A, Lauriente MM, Uhart MM. 2024 Highly pathogenic avian influenza A(H5N1) viruses from multispecies outbreak, Argentina, August 2023. *Emerging Infect. Dis*. **30**, 812–814. (doi:10.3201/eid3004.231725)
22. Sobolev I *et al*. 2024 Highly pathogenic avian influenza A(H5N1) virus clade 2.3.4.4b infections in Seals, Russia, 2023. *Emerging Infect. Dis*. **30**, 2160–2164. (doi:10.3201/eid3010.231728)
23. Uhart MM *et al*. 2024 Epidemiological data of an influenza A/H5N1 outbreak in elephant seals in Argentina indicates mammal-to-mammal transmission. *Nat. Commun*. **15**, 9516. (doi:10.1038/s41467-024-53766-5)
24. Clessin A *et al*. 2025 Mass mortality events in the sub-Antarctic Indian Ocean caused by long-distance circumpolar spread of highly pathogenic avian influenza H5N1 clade 2.3.4.4b. *bioRxiv* 2025.02.25.640068. (doi:10.1101/2025.02.25.640068)
25. Consejo Superior de Investigaciones Científicas (CSIC). 2025 El virus de la gripe aviar en la Antártida: cerca de 200 animales infectados en 24 localizaciones de la península antártica. See https://www.csic.es/es/actualidad-del-csic/el-virus-de-la-gripe-aviar-en-la-antartida-cerca-de-200-animales-infectados-en-24-localizaciones-de-la-peninsula-antartica.
26. Falkland Islands Deparment of Agriculture (FIDA). 2025 Avian influenza information. See https://www.falklands.gov.fk/agriculture/avian-influenza.
27. Government of South Georgia and the South Sandwich Islands (GSGSSI). 2025 Biosecurity. See https://gov.gs/biosecurity/.
28. Pardo-Roa C *et al*. 2025 Cross-species and mammal-to-mammal transmission of clade 2.3.4.4b highly pathogenic avian influenza A/H5N1 with PB2 adaptations. *Nat. Commun*. **16**, 2232. (doi:10.1038/s41467-025-57338-z)
29. Romero MA, Bartés SN, Grandi MF, Brogger M, Svendsen G, González R, Crespo EA. 2025 Impact of the avian influenza outbreak on the population dynamics of South American Sea Lions *Otaria byronia* in Northern Patagonia. *Mar. Mammal Sci*. **41**, e70031. (doi:10.1111/mms.70031)
30. World Organisation for Animal Health (WOAH). 2025 World Animal Health Information System (WAHIS). See https://wahis.woah.org.
31. Ministerio de Ciencia, Innovación y Universidades. 2024 Investigadores españoles encuentran el virus de la gripe aviar altamente patogénica en un mamífero marino por primera vez en la Antártida. See https://www.ciencia.gob.es/Noticias/2024/Julio/gripe-aviar-antartida.html.
32. Trillmich F. 1993 Influence of rare ecological events on pinniped social structure and population dynamics. In *Marine Mammals: Advances in Behavioural and Population Biology*, The Zoological Society of London, 9–10 April 1992 (ed. IL Boyd), pp. 95–114. Oxford, UK: Oxford University Press. (doi:10.1093/oso/9780198540694.003.0006)
33. Eberhardt LL. 2002 A paradigm for population analysis of long-lived vertebrates. *Ecology* **83**, 2841–2854. (doi:10.1890/0012-9658(2002)083[2841:APFPAO]2.0.CO;2)
34. Food and Agriculture Organization of the United Nations (FAO) & World Organisation for Animal Health (WOAH). 2025 *Global strategy for the prevention and control of high pathogenicity avian influenza (2024–2033) – achieving sustainable, resilient poultry production systems*. (doi:10.4060/cd3840en)
35. Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y. 1992 Evolution and ecology of influenza A viruses. *Microbiol. Rev*. **56**, 152–179. (doi:10.1128/mr.56.1.152-179.1992)
36. Stallknecht DE, Nagy E, Hunter DB, Slemons RD. 2007 Avian influenza. In *Infectious diseases of wild birds* (eds NJ Thomas, DB Hunter, CT Atkinson), pp. 108–130. Ames, IA: Blackwell Publishing. (doi:10.1002/9780470344668)
37. Wille M, Holmes EC. 2020 The ecology and evolution of influenza viruses. *Cold Spring Harb. Perspect. Med*. **10**, a038489. (doi:10.1101/cshperspect.a038489)
38. Hurt AC *et al*. 2016 Evidence for the introduction, reassortment, and persistence of diverse influenza A viruses in Antarctica. *J. Virol*. **90**, 9674–9682. (doi:10.1128/JVI.01404-16)
39. Lang AS, Lebarbenchon C, Ramey AM, Robertson GJ, Waldenström J, Wille M. 2016 Assessing the role of seabirds in the ecology of influenza A viruses. *Avian Dis*. **60**, 378–386. (doi:10.1637/11135-050815-RegR)
40. de Seixas MMM *et al*. 2022 H6N8 avian influenza virus in Antarctic seabirds demonstrates connectivity between South America and Antarctica. *Transbound. Emerg. Dis*. **69**, e3436–e3446. (doi:10.1111/tbed.14728)
41. Stallknecht DE, Shane SM, Kearney MT, Zwank PJ. 1990 Persistence of avian influenza viruses in water. *Avian Dis*. **34**, 406–411. (doi:10.2307/1591428)
42. Brown J, Stallknecht D, Lebarbenchon C, Swayne D. 2014 Survivability of Eurasian H5N1 highly pathogenic avian influenza viruses in water varies between strains. *Avian Dis*. **58**, 453–457. (doi:10.1637/10741-120513-ResNote.1)
43. Martin G, Becker DJ, Plowright RK. 2018 Environmental persistence of influenza H5N1 is driven by temperature and salinity: insights from a Bayesian meta-analysis. *Front. Ecol. Evol*. **6**, 131. (doi:10.3389/fevo.2018.00131)
44. Feare C. J. 2010 Role of wild birds in the spread of highly pathogenic avian influenza virus H5N1 and implications for global surveillance. *Avian Dis.* **54**, 201–212. https://doi.org/10.1637/8766-033109-ResNote.1
45. Bertran K, Balzli C, Kwon YK, Tumpey TM, Clark A, Swayne DE. 2017 Airborne Transmission of Highly Pathogenic Influenza Virus during Processing of Infected Poultry. *Emerging Infect. Dis.* **23**, 1806–1814. https://doi.org/10.3201/eid2311.170672
46. Ringenberg JM *et al*. 2024 Prevalence of avian influenza virus in atypical wild birds host groups during an outbreak of highly pathogenic strain EA/AM H5N1. *Transbound. Emerg. Dis*. **2024**, 4009552. (doi:10.1155/2024/4009552)
47. Swayne DE, Suarez DL, Sims LD. 2020 Influenza. In *Diseases of poultry* (ed. DE Swayne), pp. 210–256. Ames, IA: John Wiley & Sons, Inc. (doi:10.1002/9781119371199)
48. Lee DH, Criado MF, Swayne DE. 2021 Pathobiological origins and evolutionary history of highly pathogenic avian influenza viruses. *Cold Spring Harb. Perspect. Med*. **11**, a038679. (doi:10.1101/cshperspect.a038679)
49. Ramey AM. Avian influenza in wild birds. In *Wildlife disease and health in conservation* (eds DA Jessup, RW Radcliffe), pp. 309–325. Baltimore, MD: Johns Hopkins University Press. (doi:10.56021/9781421446745)
50. American Veterinary Medical Association (AVMA). 2025 Avian influenza virus type A (H5N1) in U.S. dairy cattle. See https://www.avma.org/resources-tools/animal-health-and-welfare/animal-health/avian-influenza/avian-influenza-virus-type-h5n1-us-dairy-cattle.
51. Sims LD, Brown IH. 2016 Multi-continental panzootic of H5 highly pathogenic avian influenza (1996–2015). In *Animal influenza* (ed. DE Swayne), pp. 202–247. Ames, IA: John Wiley & Sons. (doi:10.1002/9781118924341)

52. Molini U, Aikukutu G, Roux JP, Kemper J, Ntahonshikira C, Marruchella G, Khaiseb S, Cattoli G, Dundon WG. 2019 Avian influenza H5N8 outbreak in African Penguins (*Spheniscus demersus*), Namibia, 2019. *J. Wildl. Dis*. **56**, 214–218. (doi:10.7589/2019-03-067)
53. Roberts LC *et al*. 2023 Descriptive epidemiology of and response to the high pathogenicity avian influenza (H5N8) epidemic in South African coastal seabirds, 2018. *Transbound. Emerg. Dis*. **2023**, 2708458. (doi:10.1155/2023/2708458)
54. Xie R *et al*. 2023 The episodic resurgence of highly pathogenic avian influenza H5 virus. *Nature* **622**, 810–817. (doi:10.1038/s41586-023-06631-2)
55. Van Borm S *et al*. 2025 Genesis and spread of novel highly pathogenic avian influenza A(H5N1) clade 2.3.4.4b virus genotype EA-2023-DG reassortant, Western Europe. *Emerg. Infect. Dis*. **31** 1100–1108. . (doi:10.3201/eid3106.241870)
56. Spackman E, Suarez DL, Lee CW, Pantin-Jackwood MJ, Lee SA, Youk S, Ibrahim S. 2023 Efficacy of inactivated and RNA particle vaccines against a North American Clade 2.3.4.4b H5 highly pathogenic avian influenza virus in chickens. *Vaccine* **41**, 7369–7376. (doi:10.1016/j.vaccine.2023.10.070)
57. Signore AV *et al*. 2025 Spatiotemporal reconstruction of the North American A(H5N1) outbreak reveals successive lineage replacements by descendant reassortants. *Sci. Adv*. **11**, eadu4909. (doi:10.1126/sciadv.adu4909)
58. Castro-Sanguinetti GR, González-Veliz R, Callupe-Leyva A, Apaza-Chiara AP, Jara J, Silva W, Icochea E, More-Bayona JA. 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**, 3635. (doi:10.1038/s41598-024-54072-2)
59. Ogrzewalska M *et al*. 2025 Genomic analysis of high pathogenicity avian influenza viruses from Antarctica reveals multiple introductions from South America. *Res. Sq*. rs-6727501. (doi:10.21203/rs.3.rs-6727501/v1)
60. Duvenage E. 2024 *Avian flu suspected on South Africa's remote Marion Island*. Nature Africa. See https://www.nature.com/articles/d44148-024-00345-x#ref-CR2.
61. Wille M *et al*. 2024 Long-distance avian migrants fail to bring 2.3.4.4b HPAI H5N1 into Australia for a second year in a row. *Influenza Other Respir. Viruses* **18**, e13281. (doi:10.1111/irv.13281)
62. New Zealand Department of Conservation (NZDC). 2025 Avian influenza. See https://www.doc.govt.nz/our-work/wildlife-health/avian-influenza/#doc-work.
63. Wildlife Health Australia. 2025 H5 Bird Flu. See https://wildlifehealthaustralia.com.au/Resource-Centre/H5-bird-flu.
64. Bodewes R *et al*. 2015 Avian Influenza A(H10N7) virus-associated mass deaths among harbor seals. *Emerg. Infect. Dis*. **21**, 720–722. (doi:10.3201/eid2104.141675)
65. Boyce WM, Mena I, Yochem PK, Gulland FM, García-Sastre A, Moreno N, Perez DR, Gonzalez-Reiche AS, Stewart BS. 2013 Influenza A(H1N1)pdm09 virus infection in marine mammals in California. *Emerg. Microbes Infect*. **2**, e40. (doi:10.1038/emi.2013.40)
66. Krog JS *et al*. 2015 Influenza A(H10N7) virus in dead harbor seals, Denmark. *Emerging Infect. Dis*. **21**, 684–687. (doi:10.3201/eid2104.141484)
67. Fereidouni S, Munoz O, Von Dobschuetz S, De Nardi M. 2016 Influenza virus infection of marine mammals. *Ecohealth* **13**, 161–170. (doi:10.1007/s10393-014-0968-1)
68. Puryear WB *et al*. 2016 Prevalence of influenza A virus in live-captured North Atlantic gray seals: a possible wild reservoir. *Emerg. Microbes Infect*. **5**, 1–9. (doi:10.1038/emi.2016.77)
69. van den Brand JMA *et al*. 2016 Influenza A (H10N7) virus causes respiratory tract disease in harbor seals and ferrets. *PLoS One* **11**, e0159625. (doi:10.1371/journal.pone.0159625)
70. Gass JD, Kellogg HK, Hill NJ, Puryear WB, Nutter FB, Runstadler JA. 2022 Epidemiology and ecology of influenza A viruses among wildlife in the Arctic. *Viruses* **14**, 1531. (doi:10.3390/v14071531)
71. Plancarte M *et al*. 2023 Human influenza A virus H1N1 in marine mammals in California, 2019. *PLoS One* **18**, e0283049. (doi:10.1371/journal.pone.0283049)
72. Chrzastek K, Kapczynski DR. 2024 In silico genomic analysis of avian influenza viruses isolated from marine seal colonies. *Pathogens* **13**, 1009. (doi:10.3390/pathogens13111009)
73. McCosker CM, Levin M, Puryear WB, Runstadler JA, Murray KT, Cammen KM. 2025 Gray seal (*Halichoerus grypus*) pups fail to mount an inflammatory cytokine response to influenza A virus. *J. Wildl. Dis*. **61**, 628–641. (doi:10.7589/JWD-D-24-00166)
74. Webster RG, Hinshaw VS, Bean WJ, Van Wyke KL, Geraci JR, St. Aubin DJ, Petursson G. 1981 Characterization of an influenza A virus from seals. *Virology* **113**, 712–724. (doi:10.1016/0042-6822(81)90200-2)
75. Hinshaw VS, Bean WJ, Webster RG, Rehg JE, Fiorelli P, Early G, Geraci JR, St Aubin DJ. 1984 Are seals frequently infected with avian influenza viruses? *J. Virol*. **51**, 863–865. (doi:10.1128/JVI.51.3.863-865.1984)
76. Anthony SJ *et al*. 2012 Emergence of fatal avian influenza in New England harbor seals. *MBio* **3**, e00166-12. (doi:10.1128/mBio.00166-12)
77. Slade RW. 1992 Limited MHC polymorphism in the southern elephant seal: implications for MHC evolution and marine mammal population biology. *Proc. R. Soc. Lond. B* **249**, 163–171. (doi:10.1098/rspb.1992.0099)
78. Aldridge BM, Bowen L, Smith BR, Antonelis GA, Gulland F, Stott JL. 2006 Paucity of class I MHC gene heterogeneity between individuals in the endangered Hawaiian monk seal population. *Immunogenetics* **58**, 203–215. (doi:10.1007/s00251-005-0069-y)
79. Gigliotti AK, Bowen WD, Hammill MO, Puryear WB, Runstadler J, Wenzel FW, Cammen KM. 2022 Sequence diversity and differences at the highly duplicated MHC-I gene reflect viral susceptibility in sympatric pinniped species. *J. Hered*. **113**, 525–537. (doi:10.1093/jhered/esac030)
80. McCosker CM, Unal E, Gigliotti A, Puryear WB, Runstadler JA, Murray KT, King BL, Cammen KM. 2025 Molecular mechanisms underlying response to influenza in grey seals (*Halichoerus grypus*), a potential wild reservoir. *Mol. Ecol*. **34**, e70012. (doi:10.1111/mec.70012)
81. Riedman M. 1990 *The pinnipeds: seals, sea lions, and walruses*. Berkeley, CA: University of California Press. (doi:10.2307/jj.8501146)
82. Haddad WA, Reisinger RR, Scott T, Bester MN, de Bruyn PJN. 2015 Multiple occurrences of king penguin (*Aptenodytes patagonicus*) sexual harassment by Antarctic fur seals (*Arctocephalus gazella*). *Polar Biol*. **38**, 741–746. (doi:10.1007/s00300-014-1618-3)
83. Giljov A, Karenina K, Kochnev A. 2017 Prey or play: interactions between walruses and seabirds. *Acta Ethologica* **20**, 47–57. (doi:10.1007/s10211-016-0248-x)
84. Swan GJF, Silva-Rodríguez EA, Osman LP, Jaramillo E. 2020 Pinniped predation of birds: a cause for conservation concern? *Condor* **122**, duz068. (doi:10.1093/condor/duz068)
85. Ainley DG, Ballard G, Karl BJ, Dugger KM. 2005 Leopard seal predation rates at penguin colonies of different size. *Antarct. Sci.* **17**, 335–340. (doi:10.1017/S0954102005002750)
86. Thiebot JB, Weimerskirch H. 2013 Contrasted associations between seabirds and marine mammals across four biomes of the southern Indian Ocean. *J. Ornithol*. **154**, 441–453. (doi:10.1007/s10336-012-0909-0)
87. Veit RR, Harrison NM. 2017 Positive interactions among foraging seabirds, marine mammals and fishes and implications for their conservation. *Front. Ecol. Evol*. **5**, 121. (doi:10.3389/fevo.2017.00121)
88. Jackson J, Arlidge WNS, Oyanedel R, Davis KJ. 2024 The global extent and severity of operational interactions between conflicting pinnipeds and fisheries. *Nat. Commun*. **15**, 7449. (doi:10.1038/s41467-024-51298-6)
89. Dubey JP *et al*. 2003 *Toxoplasma gondii*, *Neospora caninum*, *Sarcocystis neurona*, and *Sarcocystis canis*-like infections in marine mammals. *Vet. Parasitol*. **116**, 275–296. (doi:10.1016/s0304-4017(03)00263-2)
90. Kuiken T *et al*. 2006 The 2000 canine distemper epidemic in Caspian seals (*Phoca caspica*): pathology and analysis of contributory factors. *Vet. Pathol*. **43**, 321–338. (doi:10.1354/vp.43-3-321)

91. Greig D *et al*. 2014 Surveillance for zoonotic and selected pathogens in harbor seals *Phoca vitulina* from central California. *Dis. Aquat. Org*. **111**, 93–106. (doi:10.3354/dao02762)
92. Goldstein T *et al*. 2013 Pandemic H1N1 influenza isolated from free-ranging northern elephant seals in 2010 off the Central California Coast. *PLoS One* **8**, e62259. (doi:10.1371/journal.pone.0062259)
93. Ramis AJ, van Riel D, van de Bildt MWG, Osterhaus A, Kuiken T. 2012 Influenza A and B virus attachment to respiratory tract in marine mammals. *Emerg. Infect. Dis*. **18**, 817–820. (doi:10.3201/eid1805.111828)
94. Shin DL, Siebert U, Haas L, Valentin-Weigand P, Herrler G, Wu NH. 2022 Primary harbour seal (*Phoca vitulina*) airway epithelial cells show high susceptibility to infection by a seal-derived influenza A virus (H5N8). *Transbound. Emerg. Dis*. **69**, e2378–e2388. (doi:10.1111/tbed.14580)
95. Fiorito C, Colom A, Fernández A, Alonso-Almorox P, Andrada M, Lombardo D, Sierra E. 2025 Pathology of influenza A (H5N1) infection in pinnipeds reveals novel tissue tropism and vertical transmission. *bioRxiv* 2025.02.07.636856. (doi:10.1101/2025.02.07.636856)
96. Nguyen HT *et al*. 2023 Antiviral susceptibility of clade 2.3.4.4b highly pathogenic avian influenza A(H5N1) viruses isolated from birds and mammals in the United States, 2022. *Antivir. Res*. **217**, 105679. (doi:10.1016/j.antiviral.2023.105679)
97. Grandi MF, Sosa Drouville A, Fiorito C. 2024 Abortions and sexual behaviour alterations associated with highly pathogenic avian influenza H5N1 outbreak in South American Sea Lion from Patagonia. (doi:10.2139/ssrn.4675610)
98. Gadzhiev A *et al*. 2024 Pinnipeds and avian influenza: a global timeline and review of research on the impact of highly pathogenic avian influenza on pinniped populations with particular reference to the endangered Caspian seal (*Pusa caspica*). *Front. Cell. Infect. Microbiol*. **14**, 1325977. (doi:10.3389/fcimb.2024.1325977)
99. Postel A, Gremmel N, Lydersen C, Kovacs KM, Schick LA, Siebert U, Nymo IH, Becher P. 2025 Highly pathogenic avian influenza virus (H5N5) detected in an Atlantic walrus (*Odobenus rosmarus rosmarus*) in the Svalbard Archipelago, Norway, 2023. *Emerg. Microbes Infect*. **14**, 2456146. (doi:10.1080/22221751.2025.2456146)
100. Canadian Wildlife Health Cooperative (CWHC). 2025 High pathogenicity avian influenza in wildlife. See https://cfia-ncr.maps.arcgis.com/apps/dashboards/89c779e98cdf492c899df23e1c38fdbc.
101. Homma H. 2025 *Bird flu suspected in mass deaths of sea animals in eastern Hokkaido*. The Mainichi. See https://mainichi.jp/english/articles/20250507/p2a/00m/0li/020000c.
102. Szteren D, Franco-Trecu V. 2024 Incidence of highly pathogenic avian influenza H5N1 in pinnipeds in Uruguay. *Dis. Aquat. Org*. **160**, 65–74. (doi:10.3354/dao03827)
103. De Lima RC, Estima SC, Tavares M, Canabarro PL, Botta S, Dias LA, da Silva AP, de Amorim DB, de Oliveira LR. 2025 Impacts and lessons learned from the first highly pathogenic avian influenza (H5N1) outbreak in South American pinnipeds along the southern Brazilian coast. *Mar. Mammal Sci*. **41**, e13163. (doi:10.1111/mms.13163)
104. Harting AL, Barbieri MM, Baker JD, Mercer TA, Johanos TC, Robinson SJ, Littnan CL, Colegrove KM, Rotstein DS. 2021 Population-level impacts of natural and anthropogenic causes-of-death for Hawaiian monk seals in the main Hawaiian Islands. *Mar. Mammal Sci*. **37**, 235–250. (doi:10.1111/mms.12742)
105. Hofmeyr GJG. 2015 *Mirounga leonina*. The IUCN Red List of threatened species 2015: e.T13583A45227247. See https://doi.org/10.2305/IUCN.UK.2015-4.RLTS.T13583A45227247.en.
106. Campagna C, Condit R, Ferrari M, Campagna J, Eder E, Uhart M, Vanstreels RET, Falabella V, Lewis MN. 2025 Predicting population consequences of an epidemic of high pathogenicity avian influenza on Southern Elephant seals. *Mar. Mammal Sci*. **41**, e70009. (doi:10.1111/mms.70009)
107. Southwell C, Bengston J, Bester M, Blix AS, Bornemann H, Boveng P, Trathan P. 2012 A review of data on abundance, trends in abundance, habitat use and diet of ice-breeding seals in the Southern Ocean. *CCAMLR Sci*. **19**, 49–74. https://www.ccamlr.org/en/system/files/science_journal_papers/Southwell-et-al.pdf
108. Carretta JV, Oleson EM, Forney KA. 2023 *U.S. Pacific marine mammal stock assessments: 2023*. U.S. Department of Commerce, NOAA Technical Memorandum NMFS-SWFSC-704.2024. (doi:10.25923/aqdn-f357)
109. Krause DJ, Bonin CA, Goebel ME, Reiss CS, Woodman SM, Watters GM. 2022 The rapid population collapse of a key marine predator in the Northern Antarctic Peninsula endangers genetic diversity and resilience to climate change. *Front. Mar. Sci*. **8**, 796488. (doi:10.3389/fmars.2021.796488)
110. Brownell RL Jr, Krause DJ, Baylis AMM, Bonin CA, Oliveira LR, Uhart MM, Ulloa M, Watters GM. 2024 Avian influenza H5N1 threatens imperiled krill-dependent predators in Antarctica. *Front. Mar. Sci*. **11**, 1453737. (doi:10.3389/fmars.2024.1453737)
111. Campagna C, Lewis M. 1992 Growth and distribution of a southern elephant seal colony. *Mar. Mammal Sci*. **8**, 387–396. (doi:10.1111/j.1748-7692.1992.tb00053.x)
112. Bellido-Martín B, Rijnink WF, Iervolino M, Kuiken T, Richard M, Fouchier RAM. 2025 Evolution, spread and impact of highly pathogenic H5 avian influenza A viruses. *Nat. Rev. Microbiol*. **24**, 45–60. (doi:10.1038/s41579-025-01189-4)
113. Castillo A *et al*. 2023 The first case of human infection with H5N1 avian Influenza A virus in Chile. *J. Travel Med*. **30**, taad083. (doi:10.1093/jtm/taad083)
114. Pulit-Penaloza JA *et al*. 2024 Highly pathogenic avian influenza A(H5N1) virus of clade 2.3.4.4b isolated from a human case in Chile causes fatal disease and transmits between co-housed ferrets. *Emerg. Microbes Infect*. **13**. (doi:10.1080/22221751.2024.2332667)
115. Weller DW. 2018 Predation on marine mammals. In *Encyclopedia of marine mammals* (eds B Würsig, JGM Thewissen, KM Kovacs), pp. 923–932. London, UK: Academic Press. (doi:10.1016/B978-0-12-373553-9.00210-8)
116. Nagel R, Coleman J, Stainfield C, Forcada J, Hoffman JI. 2022 Observations of giant petrels (*Macronectes* sp.) attacking and killing antarctic fur seal (*Arctocephalus gazella*) pups. *Aquat. Mamm*. **48**, 509–512. (doi:10.1578/am.48.6.2022.509)
117. Kuhn BF, Wiesel I, Skinner JD. 2008 Diet of brown hyaenas (*Parahyaena brunnea*) on the Namibian coast. *Trans. R. Soc. South Afr*. **63**, 150–159. (doi:10.1080/00359190809519219)
118. Wiesel I. 2010 Killing of cape fur seal (*Arctocephalus pusillus pusillus*) pups by brown hyenas (*Parahyaena brunnea*) at mainland breeding colonies along the coastal Namib Desert. *Acta Ethol*. **13**, 93–100. (doi:10.1007/s10211-010-0078-1)
119. Lemerle MA, Wiesel I, Somers MJ. 2024 Recommendations for the development of a carnivore viewing site at a colony of cape fur seals (*Arctocephalus pusillus pusillus*) in southern Namibia. *J. Ecotourism* **23**, 685–702. (doi:10.1080/14724049.2024.2307363)
120. Uhart MM, Sleeman JM. 2024 New approaches to wildlife health: Scientific and Technical Review. ***Special Edition*** 145–151. (doi:10.20506/rst.SE.3569)
121. Pepin KM *et al*. 2025 Expanding national-scale wildlife disease surveillance systems with research networks. *Ecol. Evol*. **15**, e71492. (doi:10.1002/ece3.71492)
122. Montecino-Latorre D *et al*. 2024 *Rangers as an essential One Health workforce: strengthening the preservation of biodiversity and One Health in practice*. Wildlife Conservation Society. (doi:10.2139/ssrn.4997409)
123. World Organisation for Animal Health (WOAH). 2024 Practical guide for authorised field responders to HPAI outbreaks in marine mammals, with a focus on biosecurity, sample collection for virus detection and carcass disposal. See https://www.woah.org/app/uploads/2024/02/woah-practicalguide-forauthorisedfieldresponders-hpaimarinemammals-feb24.pdf.
124. Trego ML. 2025 *Report of the NOAA fisheries cetacean species in the spotlight health assessment workshop: Seattle, Washington, 25–26 June 2024*. (doi:10.25923/4mh0-ez19)
125. World Organisation for Animal Health (WOAH). 2020 OIE wildlife health framework. See https://www.woah.org/fileadmin/Home/eng/Internationa_Standard_Setting/docs/pdf/WGWildlife/A_Wildlifehealth_conceptnote.pdf.
126. Jeglinski JWE *et al*. 2024 HPAIV outbreak triggers short-term colony connectivity in a seabird metapopulation. *Sci. Rep*. **14**, 3126. (doi:10.1038/s41598-024-53550-x)

127. Grémillet D *et al*. 2023 Strong breeding colony fidelity in northern gannets following high pathogenicity avian influenza virus (HPAIV) outbreak. *Biol. Conserv*. **286**, 110269. (doi:10.1016/j.biocon.2023.110269)
128. Careen NG, Collins SM, D'Entremont KJN, Wight J, Rahman I, Hargan KE, Lang AS, Montevecchi WA. 2024 Highly pathogenic avian influenza resulted in unprecedented reproductive failure and movement behaviour by northern gannets. *Mar. Ornithol*. **52**, 121–128. (doi:10.5038/2074-1235.52.1.1566)
129. Hovelsrud GK, McKenna M, Huntington HP. 2008 Marine mammal harvests and other interactions with humans. *Ecol. Appl*. **18**, S135–S147. (doi:10.1890/06-0843.1)
130. De Klerk S. 2013 Seal harvesting in Namibia: a critical analysis. Doctoral dissertation, University of Namibia. https://www.harpseals.org/about_the_hunt/s.de_klerk-namibia_seal_harvesting_analysis-dissertation_2013.pdf.
131. Garg S *et al*. 2025 Highly pathogenic avian influenza A(H5N1) virus infections in humans. *N. Engl. J. Med*. **392**, 843–854. (doi:10.1056/nejmoa2414610)
132. Gulland FMD, Barbieri M, Cleaveland S, Gilbert M, Hall AJ, Rocke TE. 2024 Vaccination of endangered wildlife as a conservation tool: hindsights and new horizons in the pandemic era. *Biol. Conserv*. **300**, 110842. (doi:10.1016/j.biocon.2024.110842)
133. Katzner TE *et al*. 2025 Safety and immunogenicity of poultry vaccine for protecting critically endangered avian species against highly pathogenic avian influenza virus, United States. *Emerging Infect. Dis*. **31**, 1131–1139. (doi:10.3201/eid3106.241558)
134. Lejeune M, Tornos J, Bralet T, De Pasquale C, Marçon E, Massin P, Grasland B, Stier A, Boulinier T. 2025 Vaccination against H5 HP influenza virus leads to persistent immune response in wild king penguins. *bioRxiv* 2025.09.06.674613. (doi:10.1101/2025.09.06.674613)
135. Robinson SJ, Barbieri MM, Murphy S, Baker JD, Harting AL, Craft ME, Littnan CL. 2018 Model recommendations meet management reality: implementation and evaluation of a network-informed vaccination effort for endangered Hawaiian monk seals. *Proc. R. Soc. B* **285**, 20171899. (doi:10.1098/rspb.2017.1899)
136. Anthes E. 2025 *Scientists Begin Testing Bird Flu Vaccine in Seals*. The New York Times. See https://www.nytimes.com/2025/09/09/science/bird-flu-seals-vaccine.html.
137. Baker JD, Harting AL, Barbieri MM, Robinson SJ, Gulland FMD, Littnan CL. 2017 Modeling a morbillivirus outbreak in Hawaiian monk seals (*Neomonachus schauinslandi*) to aid in the design of mitigation programs. *J. Wildl. Dis*. **53**, 736–748. (doi:10.7589/2016-10-238)
138. Floyd T *et al*. 2021 Encephalitis and death in wild mammals at a rehabilitation center after infection with highly pathogenic avian influenza A(H5N8) Virus, United Kingdom. *Emerg. Infect. Dis*. **27**, 2856–2863. (doi:10.3201/eid2711.211225)
139. Zhang G, Shi Y, Ge H, Wang Y, Lu L, Jiang S, Wang Q. 2025 Genomic signatures and host adaptation of H5N1 clade 2.3.4.4b: a call for global surveillance and multi-target antiviral strategies. *Curr. Res. Microb. Sci*. **8**, 100377. (doi:10.1016/j.crmicr.2025.100377)
140. World Organisation for Animal Health (WOAH). 2023 Terrestrial Animal Health Code, 31st edition. See https://www.woah.org/en/what-we-do/standards/codes-and-manuals/.
141. Knief U *et al*. 2024 Highly pathogenic avian influenza causes mass mortality in Sandwich Tern *Thalasseus sandvicensis* breeding colonies across north-western Europe. *Bird Conserv. Int*. **34**, e6. (doi:10.1101/2023.05.12.540367)
142. Lewis M, Campagna C, Zavatti J. 2004 Annual cycle and inter-annual variation in the haul-out pattern of an increasing southern elephant seal colony. *Antarct. Sci*. **16**, 219–226. (doi:10.1017/s0954102004002020)
143. Ferrari MA, Campagna C, Condit R, Lewis MN. 2013 The founding of a southern elephant seal colony. *Mar. Mammal Sci*. **29**, 407–423. (doi:10.1111/j.1748-7692.2012.00585.x)
144. Thompson D, Lonergan M, Duck C. 2005 Population dynamics of harbour seals *Phoca vitulina* in England: monitoring growth and catastrophic declines. *J. Appl. Ecol*. **42**, 638–648. (doi:10.1111/j.1365-2664.2005.01025.x)
145. Green AJ, Elmberg J. 2014 Ecosystem services provided by waterbirds. *Biol. Rev*. **89**, 105–122. (doi:10.1111/brv.12045)
146. Gregr EJ *et al*. 2020 Cascading social–ecological costs and benefits triggered by a recovering keystone predator. *Science* **368**, 1243–1247. (doi:10.1126/science.aay5342)
147. Wallmo K, Lew DK. 2012 Public Willingness to Pay for Recovering and Downlisting Threatened and Endangered Marine Species. *Conserv. Biol.* **26**, 830–839. (doi:10.1111/j.1523-1739.2012.01899.x)
148. Richardson L, Loomis J. 2009 The total economic value of threatened, endangered and rare species: an updated meta-analysis. *Ecol. Econ*. **68**, 1535–1548. (doi:10.1016/j.ecolecon.2008.10.016)
149. Lent RJ. 2015 Conservation benefits of an interdisciplinary approach to marine mammal science. *Front. Mar. Sci*. **2**, 67. (doi:10.3389/fmars.2015.00067)
150. Earth Economics. 2021 *Economic impacts associated with the expansion of critical habitat designation for the Southern Resident population of killer whales*. Prepared for the US National Marine Fisheries Service, West Coast Region. See https://media.fisheries.noaa.gov/2021-07/iec-srkw-ch-final-economic-report-19july2021.pdf.
151. OFFLU. 2025 Terms of Reference for the OFFLU Socioeconomics Working Group. See https://offlu.org/socioeconomic/.
152. Marine Mammal Commission. 2023 The Value of Marine Mammals. See https://www.mmc.gov/priority-topics/value-marine-mammals/.
153. Convention on Migratory Species (CMS) and Food and Agriculture Organization of the United Nations (FAO). 2023 *H5N1 High pathogenicity avian influenza in wild birds - Unprecedented conservation impacts and urgent needs*. Scientific Task Force on Avian Influenza and Wild Birds. See https://www.cms.int/sites/default/files/publication/avian_influenza_2023_aug.pdf.
154. Convention on Migratory Species (CMS) and United Nations Environment Programme. See https://www.cms.int/sites/default/files/document/cms_cop14_res.14.18_avian-influenza_e.pdf.
155. Agreement on the Conservation of Albatrosses and Petrels. 2025 Avian Flu. See https://www.acap.aq/resources/disease-threats/avian-flu.
156. Scientific Committee on Antarctic Research. 2025 Sub-Antarctic and Antarctic Highly Pathogenic Avian Influenza H5N1 Monitoring Project. See https://scar.org/library-data/avian-flu.
157. Commission for the Conservation of Antarctic Marine Living Resources. 2025 High Pathogenicity Avian Influenza (HPAI) resources. See https://www.ccamlr.org/en/science/high-pathogenicity-avian-influenza-hpai-resources.
158. Magera AM, Mills Flemming JE, Kaschner K, Christensen LB, Lotze HK. 2013 Recovery Trends in Marine Mammal Populations. *PLoS One* **8**, e77908. (doi:10.1371/journal.pone.0077908)
159. Gulland FMD, Baker JD, Howe M, LaBrecque E, Leach L, Moore SE, Reeves RR, Thomas PO. 2022 A review of climate change effects on marine mammals in United States waters: Past predictions, observed impacts, current research and conservation imperatives. *Clim. Change Ecol*. **3**, 100054. (doi:10.1016/j.ecochg.2022.100054)
160. Groner ML *et al*. 2016 Managing marine disease emergencies in an era of rapid change. *Phil. Trans. R. Soc. B* **371**, 20150364. (doi:10.1098/rstb.2015.0364)
161. Weiss MN, Franks DW, Balcomb KC, Ellifrit DK, Silk MJ, Cant MA, Croft DP. 2020 Modelling cetacean morbillivirus outbreaks in an endangered killer whale population. *Biol. Conserv*. **242**, 108398. (doi:10.1016/j.biocon.2019.108398)
162. Tinker MT *et al*. 2021 *An integrated population model for southern sea otters*. Reston, VA: US Geological Survey. (doi:10.3133/ofr20211076)
163. Pikitch EK *et al*. 2004 Ecosystem-based fishery management. *Science* **305**, 346–347. (doi:10.1126/science.1098222)
164. Phillips RA *et al*. 2023 Conservation status and overview of threats to seabirds. In *Conservation of marine birds* (eds L Young, E VanderWerf), pp. 33–56. Academic Press. (doi:10.1016/B978-0-323-88539-3.00015-7)

165. Serafini PP, Vanstreels RET, Uhart M, Dewar M, Wille M, Roberts L, Work T. 2023 *Guidelines for working with albatrosses and petrels during the high pathogenicity avian influenza (HPAI) H5N1 panzootic*. Hobart, Australia: Agreement for the Conservation of Albatrosses and Petrels. See https://acap.aq/resources/acap-conservation-guidelines/4084-guidelines-for-working-with-albatrosses-and-petrels-during-h5n1-avian-influenza-outbreak/file.
166. Murawski A *et al*. 2024 Highly pathogenic avian influenza A(H5N1) virus in a common bottlenose dolphin (*Tursiops truncatus*) in Florida. *Commun. Biol*. **7**, 476. (doi:10.1038/s42003-024-06173-x)
167. Stimmelmayr R, Rotstein D, Torchetti MK, Gerlach R. 2024 Highly pathogenic avian influenza virus A(H5N1) clade 2.3.4.4b infection in free-ranging Polar Bear, Alaska, USA. *Emerging Infect. Dis*. **30**, 1660–1663. (doi:10.3201/eid3008.240481)
168. Vreman S *et al*. 2023 Zoonotic mutation of highly pathogenic avian influenza H5N1 virus identified in the brain of multiple wild carnivore species. *Pathogens* **12**, 168. (doi:10.3390/pathogens12020168)