

High Pathogenicity Avian Influenza in Pinniped Conservation

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Abstract

Since 2020, H5Nx highly pathogenic 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 ecosystems 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 that pinnipeds—and marine wildlife broadly—could be better integrated into existing systems for HPAIV intelligence, control, and prevention.

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 last 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 (Wille & Barr 2022; Kuiken et al. 2025; Krammer et al. 2025). Though 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 (Kuiken et al. 2025; Peacock et al. 2025). 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 far 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 (Trillmich 1993; Eberhardt 2002). 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 are often 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 practiced 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 previously documented 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 HPAIV 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 HPAIV provides a window for pinniped scientists and managers to advance 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 Organisation for Animal Health (WOAH) cite wildlife as essential components of a global HPAIV surveillance system, motivated in part by the imperative to protect biodiversity (FAO and WOAH 2025). 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 learned 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, hemagglutinin (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 (Webster et al. 1992; Stallknecht et al. 2007; Wille & Holmes 2020). There is evidence that seabirds such as terns, murrelets, shearwaters, skuas, and penguins also play important roles in AIV ecology (Hurt et al. 2016; Lang et al. 2016; Seixas et al. 2022). Avian influenza virus particles shed in the feces of infected birds can persist in water and can remain infective for as long as 200 days in low salinities and cool/cold temperatures (Stallknecht et al. 1990; Brown et al. 2014; Martin et al. 2018). As a result, birds are susceptible to fecal-oral AIV transmission via contaminated water or sediment (Webster et al. 1992; Stallknecht et al. 2007). Respiratory transmission likely also plays an important role in AIV spread among aquatic birds congregating at rookeries or migratory stopover sites (Feare 2010; Filarie et al. 2024), and predation and scavenging play a significant role in transmission of HPAIV (Ringenberg et al. 2024).

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 (Stallknecht et al. 2007; Swayne et al. 2020; Lee et al. 2021). 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 (Stallknecht et al. 2007). 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 (Ramey 2023). Both LPAIVs and HPAIVs can also infect mammals (Swayne et al. 2020; Lee et al. 2021). 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 (AVMA 2025). 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 naïve to H5Nx HPAIV (Wille & Barr 2022; Kuiken et al. 2025; Krammer et al. 2025). The specific H5Nx HPAIV strains at play descend from the Goose/Guangdong lineage (Gs/Gd), which can be traced back to a 1996 outbreak among farmed geese in Guangdong province, southeast China (Sims and Brown 2016; Lee et al. 2021). 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 (Molini et al. 2020; Roberts et al. 2023). 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 (Xie et al. 2023; Van Borm et al. 2025). Following multiple introductions to North America in Nov–Dec 2021 and extensive reassortment with North American LPAIV strains (Youk et al. 2023; Signore et al. 2025), H5Nx HPAIVs moved southward, reaching South America in Oct 2022 (Leguia et al. 2023; Castro-Sanguinetti et al. 2024; Kuiken et al. 2025), the sub-Antarctic islands in the South Atlantic Ocean (Falkland/Malvinas and South Georgia) in Oct 2023 (Banyard et al. 2023; Bennison et al. 2024) and Antarctica by Jan 2024 (Ogrzewalska et al. 2024). In 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 (Clessin et al. 2025; Duvenage 2024; WOA 2025). During this period of global expansion, H5Nx HPAIVs increasingly infected mammals, including farmed mustelids, dairy cattle, domestic cats, other terrestrial wild mammals (especially carnivores), aquatic wild mammals, and humans (Krammer et al. 2025; Peacock et al. 2025). As of September 2025, H5Nx HPAIVs have been detected in wildlife on all continents except Oceania (WOAH 2025), not for lack of surveillance in this region (Wille et al. 2024; New Zealand Department of Conservation 2025; Wildlife Health Australia 2025).

3. Pinnipeds as hosts of influenza A viruses

Pinnipeds have a suite of ecological, behavioral, 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 (Bodewes et al. 2013; Boyce et al. 2013; Krog et al. 2015; Fereidouni et al. 2016; Puryear et al. 2016; van den Brand et al. 2016; Gass Jr et al. 2022; Plancarte et al. 2023; Chrzastek & Kapczynski 2024; Puryear et al. 2025). Evidence suggests North Atlantic gray seals (*Halichoerus grypus*) serve as natural reservoirs of LPAIV, as multiple strains circulate in this population without discernable morbidity or mortality (Puryear et al. 2016; McCosker et al. 2025a). In contrast, sympatric Atlantic harbor seals (*Phoca vitulina*) are very susceptible and experience recurrent LPAIV mortality events (Webster et al. 1981a; Hinshaw et al. 1984; Anthony et al. 2012). 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 (Slade 1992). Gray seals have high MHC-I sequence variation and allelic richness compared to other pinniped species, including northern elephant seals (*Mirounga angustirostris*) and Hawaiian monk seals (*Neomonachus schauinslandi*) (Aldridge et al. 2006; Gigliotti et al. 2022). Further, gray seal pups naturally exposed to influenza A viruses exhibit dynamic up- and down-regulation of certain immune-related genes, including the antiviral Mx1 gene (McCosker et al. 2025b). The authors hypothesized this could be an adaptive mechanism by which gray seals resist influenza A virus morbidity and mortality, but described their findings as preliminary (McCosker et al. 2025b).

Sporadic deaths and small, localized AIV mortality events in pinnipeds are frequently attributed to independent bird-to-mammal spillover events (e.g., Puryear et al. 2023; Haman et al. 2024). 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 feces or feathers from infected birds, ingestion of contaminated water, or inhalation of aerosols or fomites (Lair et al. 2024). Pinnipeds could also become infected via direct interactions with birds, such as during predatory and non-predatory attacks of seabirds by pinnipeds (Riedman 1990; Ainley et al. 2005; Haddad et al. 2015; Giljov et al. 2016; Swan et al. 2020), multi-species foraging assemblages (Thiebot et al. 2013; Veit and Harrison 2017), fishery depredation

(Jackson et al. 2024), harassment of pinnipeds by seabirds (e.g., gulls scavenging placental and umbilical tissues of pups), or simple habitat sharing (Haddad et al. 2015; Giljov et al. 2017). 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) (Dubey et al. 2003; Kuiken et al. 2006; Greig et al. 2014). Moreover, human pandemic H1N1 has been detected in free-ranging pinnipeds (Boyce et al. 2013; Goldstein et al. 2013; Plancarte et al. 2023).

Many pinnipeds are gregarious (Jefferson et al. 2007), and close interactions during breeding, resting, or molting could facilitate mammal-to-mammal transmission of influenza A viruses. Indeed, there is evidence that LPAIV can be transmitted between pinnipeds (Krog et al. 2015; Bodewes et al. 2016). The upper respiratory epithelium of harbor 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 (Anthony et al. 2012, Ramis et al. 2012; Puryear et al. 2016). Experimental studies suggest the pinniped respiratory tract is highly susceptible to infection by clade 2.3.4.4b H5Nx HPAIVs (Shin et al. 2022). 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 (Peacock et al. 2025). 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 (Rimondi et al. 2024; Uhart et al. 2024; Pardo-Roa et al. 2025). 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 (Leguia et al. 2023; Rimondi et al. 2024; Fiorito et al. 2025). It is also plausible that infected mothers shed HPAIV through their milk, infecting nursing pups, given this phenomenon occurs in dairy cattle (Uhart et al. 2024; Nguyen et al. 2025). These topics merit continued research (Table 1).

Pinnipeds infected with H5Nx HPAIV have primarily exhibited neurologic and respiratory signs, including tremors, repetitive head or flipper movements, seizures, nasal discharge, and labored 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 to nasal, oral, or rectal swabs (Mirolo et al. 2023; Ulloa et al. 2023; Rimondi et al. 2024; Lair et al. 2024; Uhart et al. 2024). Pinnipeds generally succumb to infections rapidly, within a few days of developing clinical signs (Ulloa et al. 2023; Sobolev et al. 2024; Uhart et al. 2024). However, a viral incubation period has not been established. There have been instances during H5Nx HPAIV outbreaks in South America in which sea lions with neurological signs were observed alive for several days. This led to speculation that infected sea lions were traveling to nearby pinniped communities and contributing to intra- and interspecific transmission of H5N1 HPAIV via aggression and sexual interactions (Grandi et al. 2024; Uhart et al. 2024; Fiorito et al. 2025). Some outbreaks have produced disproportionate mortality in young animals (especially pups) and females (especially peri-parturient females) (Lair et al. 2024; Sobolev et al. 2024; Uhart et al. 2024; Romero et al. 2025). While this could reflect age- or sex-related differences in disease presentation or severity, missing data on adults, potentially related to differences in behavior or rates of carcass detection, could be a significant confounder. The mechanisms allowing certain animals to survive infections or 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 to 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

~3,500 northern fur seals (*Callorhinus ursinus*) and a Steller sea lion (*Eumetopias jubatus*) in eastern Russia (H5N1; Sobolev et al. 2024), and potentially 2,500 Caspian seals (*Pusa capsica*) in Dagestan, Russia (Coston 2023; Gadzhiev et al. 2024). Since 2020, there have been multiple, discrete clusters of harbor seal and gray seal mortality in Europe and on the Pacific and Atlantic coasts of North America, each affecting a few to hundreds of animals (Mirolo et al. 2023; Puryear et al. 2023; Thorsson et al. 2023; Haman et al. 2024; Lair et al. 2024). The first-ever detection of HPAIV in a walrus (H5N5; *Odobenus rosmarus*) occurred in Svalbard, Norway, in 2023 (Postel et al. 2025). In 2024, an H5N5 HPAIV infection was confirmed in an Arctic ringed seal (*Pusa hispida*) in Nunavut, Canada (CWHC 2025; WOA 2025). In the spring of 2025, H5N1 HPAIV was detected in two harbor seal carcasses found among numerous dead seals, sea otters, and seabirds in Hokkaido, Japan (Homma 2025).

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 1,000 South American fur seals (*Arctocephalus australis*) (Campagna et al. 2023; Leguia et al. 2023; Marandino et al. 2023; Ulloa et al. 2023; Lima et al. 2024; Rimondi et al. 2024; Rivetti Jr et al. 2024; Uhart et al. 2024; Szteren & Franco-Trecu 2024; Pardo-Roa et al. 2025; Romero et al. 2025). 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 (Bennison et al. 2024; Clessin et al. 2025; CSIC 2025; FIDA 2025; GSGSSI 2025; WOA 2025).

Interpreting the demographic and ecological implications of these outbreaks is challenging. Mortality is likely underestimated due to carcasses being inaccessible, lost at sea (Harting et al. 2021), 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 (Campagna et al. 2023; Uhart et al. 2024), which corresponds to a modest fraction of the species' global population (~325,000 mature individuals; Hofmyer 2015). However, because the outbreak caused mortality in >95% of pups born that year, and disrupted the breeding harems, it could take decades for the population in Argentina to recover, even in the best possible scenarios (e.g., limited adult female mortality; Campagna et al. 2023, 2025; Uhart et al. 2024). 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% (Clessin et al. 2025). These data indicate that the demographic impacts of H5Nx HPAIVs on southern elephant seal populations may be far greater than would be appreciated solely from an absolute carcass count. For many species, unknown total population size precludes accurate estimation of mortality rates. For instance, the global population of crabeater seals is estimated at 7 to 75 million individuals (Southwell et al. 2012; Hückstädt 2015); such a wide range would introduce considerable uncertainty to any assessment of demographic impact.

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 1,564 individuals (Caretta et al. 2023). The abrupt death 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 (Hofmeyr 2016). 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 (Banyard et al. 2024; Bennison et al. 2024; GSGSSI 2025). 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 experienced sharp declines in recent decades and is now threatened with the arrival of HPAIV to the archipelago (Krause et al. 2022; Brownell et al. 2024; Ogrzewalska et al. 2025).

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 (Uhart et al. 2024). Further, because females are typically inseminated at the end of the nursing period (Campagna et al. 1993), the premature abandonment of breeding colonies during the outbreak likely reduced conception rates, resulting in fewer births in the following year (Uhart et al. 2024; Campagna et al. 2025). Moreover, low recruitment stemming from the loss of nearly an entire cohort of pups will affect future population age structure and sexual competition dynamics (Campagna et al. 2025).

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 likely transmitted effectively between pinnipeds (Uhart et al. 2024; Pardo-Roa et al. 2025). These mutations are described in Uhart et al. (2024), Pardo-Roa et al. (2025), Peacock et al. (2025), and Bellido-Martín et al. (2025). Virus strains from the marine mammal clade were isolated from a severe human case with no known animal exposures (Castillo et al. 2023) and from a sanderling, a southern fulmar, and multiple terns, suggesting spillback from marine mammals into coastal birds (Uhart et al. 2024; Pardo-Roa et al. 2025). This strain was also shown experimentally to cause severe disease and death in ferrets, with suspected airborne mammal-to-mammal transmission (Pulit-Penaloza et al. 2024). 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 (Boyce et al. 2013; Goldstein et al. 2013; Plancarte et al. 2023), 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 (Rimondi et al. 2024, Uhart et al. 2024). Numerous species predate or scavenge on pinnipeds, including orcas, polar bears, leopard seals, foxes, hyenas, wolverines, gulls, giant petrels, ravens, bald eagles, and vultures (Weller 2008; Nagel et al. 2022). These species could be exposed to HPAIV by consuming pinnipeds. Furthermore, in the long term, they could be at risk of cascading ecosystem effects due to pinniped population declines (e.g., Kuhn et al. 2008; Wiesel 2010; Lemerle et al. 2024).

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 molt. Hawaiian monk seals in the Northwestern Hawaiian Islands and ice-dependent Antarctic seals are glimpsed by researchers for 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 due to 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 etiologies with similar clinical presentations (e.g., neurologic 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 molting 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 (Banyard et al. 2024; Clessin et al. 2025)? 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 and accessing pinnipeds—render such an approach impractical. However, there are tangible ways to modify existing surveillance systems that could support pinniped populations while also strengthening 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 (Uhart and Sleeman 2024). 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 WOAHP, 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, consistent sampling (as opposed to just opportunistic sampling) and gather inference on population-level disease factors including infection prevalence and seroprevalence, risk factors of infection and exposure, and virus evolution (e.g., Pepin et al. 2025). It is important to note the specific goals of an expanded surveillance program would vary by species and location, given some pinnipeds are inherently more difficult to access 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 program. 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 (Montecino-Latorre et al. 2024). 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) (WOAH 2024b). 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 centers 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., 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 programs, visitor center 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 (Trego et al. 2025). 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 modeling 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 centers, and stranding networks—frequently face financial constraints reducing 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 equal footing with agriculture and public health. This echoes One Health paradigms that have been advocated by international health organizations for years (e.g., WOA 2020). If the diagnosis and reporting of HPAIV in all species remains under the sole purview of governments, many official laboratories will need expanded capacities—budget, personnel, facilities, equipment—to handle wildlife submissions. Alternatively, or in addition, 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 pinnipeds. Point-of-care tests could be used in field camps, research stations, vessels, and rehabilitation centers 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 encourage the responsible use of rapid tests for wildlife 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., Haman et al. 2024). Specific sample and data collection guidelines for marine mammal HPAIV outbreak response are available from WOA (WOA 2024b).

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 behaviors following outbreaks. This may have contributed to the regional dissemination of the virus among colonies in Europe and North America (Grémillet et al. 2023; Jeglinski et al. 2023; Careen et al. 2024). 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, behavioral, 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. In contrast, less is known about non-breeding and subadult females, juvenile and subordinate males, and animals during molt. 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 practiced in regions around the world (Hovelsrud et al. 2008; De Klerk 2013). Investigating HPAIV epidemiology in these communities, and in the pinniped populations on which they depend, is an important research direction considering some H5Nx HPAIV strains have significant zoonotic potential and can cause illness or fatality in humans (Swayne et al. 2020; Garg et al. 2024; WHO 2024).

8. Recommendations to incorporate HPAIV into pinniped conservation planning.

i. Consider targeted prevention programs.

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 programs or trade policies—issues that hinder HPAIV vaccination campaigns in some countries (Gulland et al. 2024). To date, HPAIV vaccination programs or trials exist for a small number of free-ranging wildlife species: California condors (*Gymnogyps californianus*) in the US (Katzner et al. 2025)), king penguins (*Aptenodytes patagonicus*) at Crozet Island (Lejeune et al. 2025), and endangered seabirds in New Zealand (New Zealand Department of Conservation 2025). In the condors, US agencies conditionally authorized use of an inactivated H5N1 poultry vaccine because 1) it proved safe and moderately efficacious in a related “surrogate” species (*Coragyps atratus*), and 2) California condors

are critically endangered with a small, closely monitored population (Spackman et al. 2023; WOA 2024; Katzman et al. 2025).

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 (Robinson et al. 2018; Gulland et al. 2024). 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 center (Anthes 2025). 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., Baker et al. 2017). The accuracy of these models depends on high-quality data (epidemiological, immunological, behavioral, etc.) for the species, population, pathogen, and vaccine of interest. As much of this information is limited for H5Nx HPAIV in pinnipeds, addressing knowledge gaps will improve our ability to design effective, sustainable vaccination programs (Table 1). Ongoing research aims to estimate HPAIV vaccination thresholds for pinnipeds with differing life histories and social behaviors, with the goal of informing potential intervention strategies.

ii. 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 centers 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 (Floyd et al. 2021). 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 (Nguyen et al. 2023; Zhang et al. 2025). 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 (WOAH 2024b).

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 (Baker et al. 2017). Though 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 (Haman et al. 2024; Knief et al. 2024). 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 is 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.

iii. 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 rigor 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., Robinson et al. 2018). 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 (Campagna and Lewis 1992; Campagna et al. 1993; Lewis et al. 2004; Ferrari et al. 2013), combined with data from epidemiological investigations and population monitoring during HPAIV outbreaks in 2023, enabled these researchers to project possible long-term demographic consequences (Campagna et al. 2023; Uhart et al. 2024). They estimated the Península Valdés southern elephant seal population will take multiple decades to recover, potentially attributable to multiple factors: losses of adult females, decreased recruitment due to pup mortality, and reduced insemination rates due to atypical harem dynamics (as described above) (Campagna et al. 2025). 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. Harbor 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., Thompson et al. 2005).

iv. 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 (Bossart 2011; Green and Elmberg 2014; Gregr et al. 2020). 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 well-being, especially when threatened or endangered species are involved (Richardson and Loomis 2009; Wallmo and Lew 2012).

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 (Lent 2015). For example, in the US, an economic analysis of proposed protections for Southern Resident Killer Whales was pivotal in a recent decision to expand critical habitat designations for this endangered marine mammal (Earth Economics 2021; NOAA 2021).

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 OFFLU (FAO-WOAH joint network of animal influenza experts) (OFFLU 2025). 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 well-being (Marine Mammal Commission 2023).

v. 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 HPAIV in marine environments, and implementing these measures would also support the protection of other vulnerable taxa (e.g., migratory waterbirds). National and multi-national animal and human health organizations incorporating wildlife into HPAIV countermeasures should include pinnipeds as a priority group to improve 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 WOA (FAO and WOA 2025), FAO and CMS (CMS and FAO 2023), and CMS and the United Nations Environment Programme (UNEP) (CMS and UNEP 2024). 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) (ACAP 2025), the Scientific Committee on Antarctic Research (SCAR) (SCAR 2025), and CCAMLR (CCAMLR 2025) produce numerous HPAIV resources, including databases, risk assessments, and professional guidelines, and could serve as models for pinniped-focused efforts.

vi. 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 endeavor to reduce the likelihood 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 (Campagna et al. 2025). It is easy to forget that many robust pinniped populations were nearly extirpated just a century ago, and flourish today due to decades of enforced legal protections (Magera et al. 2013). 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 harbor seals from historical depletion offers some reassurance in the face of HPAIV panzootics. At the same time, the extinction 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 pinnipeds face today—especially the worsening effects of climate change (Gulland et al. 2022)—concerted efforts should be made to ensure HPAIV does not precipitate further losses in pinniped diversity.

9. Conclusions

The expanding impact of H5Nx HPAIVs on marine mammal and seabird health constitutes a marine disease emergency (Groner et al., 2016). 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 (Robinson et al. 2018, Weiss et al. 2020) and integrated population models (Tinker et al. 2021). Involvement from social scientists and public health practitioners can help ensure 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 (Pikitch et al. 2004), with both frameworks invoking the interdependency of societal and ecological well-being.

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 (Phillips et al. 2023), and serious concerns for local extirpation and extinction have led to new or updated HPAIV management actions for many species (CMS and FAO 2023; Lamb et al. 2024; Serafini et al. 2024). Moreover, pinnipeds are not the only marine mammals affected by this panzootic. H5Nx HPAIVs have killed cetaceans (Leguia et al. 2023; Murawski et al. 2024), polar bears (Stimmelmayer et al. 2024), and aquatic mustelids (Vreman et al. 2023; Pardo-Roa et al. 2025; Homma 2025). While these have been associated with isolated bird-mammal spillover events, in 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 (Bellido-Martín et al. 2025; FAO and WOA 2025), the support and attention given to wildlife must be elevated to match that of other sectors (Uhart & Sleeman, 2024). 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.

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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 (IUCN 2024). Black dots represent H5Nx HPAIV detections in poultry, wild birds, and wild mammals from January 2021 to July 2025, inclusive; WOAH 2024). Shaded blue areas represent distributions of the world's pinniped species (darker shades represent overlapping species distributions) (IUCN 2024). Notes: a) Outbreak in *ex-situ* setting (rehabilitation center or zoo); b) Mortality suspected to be due to H5Nx HPAIV, but without laboratory confirmation as of September 2025; LC = Least Concern; VU = Vulnerable; EN = Endangered. Artwork adapted from Jefferson et al. (2007). H5Nx HPAIV records compiled from Campagna et al. 2023; Leguia et al. 2023; Marandino et al. 2023; Mirolo et al. 2023; Puryear et al. 2023; Thorsson et al. 2023; Ulloa et al. 2023; Banyard et al. 2024; Bennison et al. 2024; Coston 2024; Haman et al. 2024; Lair et al. 2024; Lima et al. 2024; MCIU 2024; Rimondi et al. 2024; Rivetti Jr et al. 2024; Sobolev et al. 2024; Uhart et al. 2024; Clessin et al. 2025; CSIC 2025; FIDA 2025; GSGSSI 2025; Pardo-Roa et al. 2025; Romero et al. 2025; WOAH 2025.

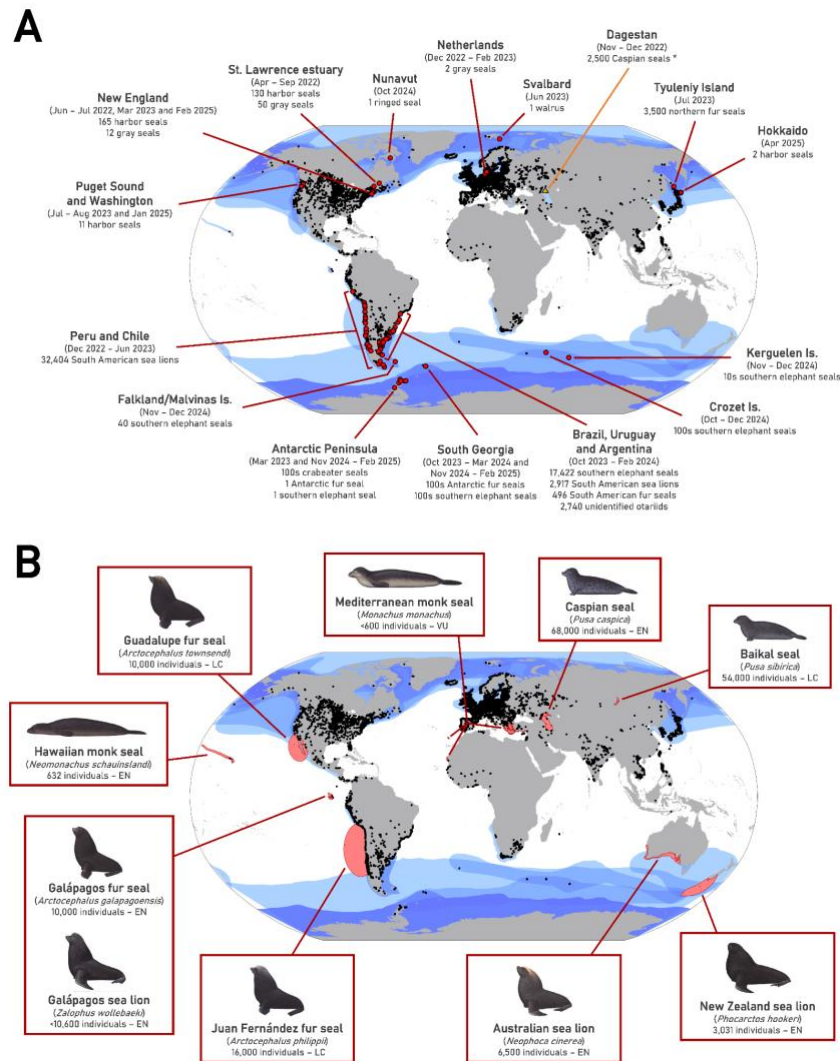


Table 1. A selection of knowledge gaps and potential research directions related to H5Nx HPAIV in pinnipeds.

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, feces, 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 behavioral 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 who 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 behavior and ecology	• How do HPAIV outbreaks affect pinniped movements, migration, social behaviors, 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 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)

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