Marine Mammal Science

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ARTICLE

Predicting Population Consequences of an Epidemic of High Pathogenicity Avian Influenza on Southern Elephant Seals

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ABSTRACT

The colony of southern elephant seals (*Mirounga leonina*) at Península Valdés (Argentina) grew by 0.9% from 2000 to 2022, reaching a population of 18,000 reproductive females. In 2023, an epidemic of the High Pathogenicity Avian Influenza H5N1 virus led to the death of almost all pups and an unknown number of adults. We tested five scenarios that included complete pup mortality along with varying levels of adult mortality and reduced fertility. Newborn mortality had the smallest impact on the future population due to high natural mortality. Consequences of pup deaths will not appear until 2027, when those lost pups would have first reproduced. Scenarios including mature female mortality had more severe and immediate consequences, with a reduction in the breeding population in 2024 predicted to match the flu death rate. It took about 10 years for the population to readjust to the 2022 age distribution. In scenarios including adult mortality, it will take decades for the population to return to the 2022 level. The 2023 epidemic may thus reverse the conservation status of a population previously having no threats to continued growth.

1 | INTRODUCTION

Epidemics can have catastrophic effects on wildlife, causing acute population declines and localized extinctions (Cunningham et al. 2017; Gulland 1995; Smith et al. 2009). Estimating wildlife death during epidemics is difficult due to detection biases—for example, scavenging of carcasses, inability to diagnose the cause of death, carcasses in inaccessible locations (Ward et al. 2006; Williams et al. 2011). Evaluating the long-term demographic impacts of disease outbreaks is further complicated by poor baseline demographic data for many wild populations so that predictions about the population impact of epidemics are subject to high uncertainty (Agostini et al. 2014; McCallum 2016; Moreno et al. 2015; see also Grimaudo et al. 2024). Here, we present a case study for which we have solid demographic knowledge, including observed mortality.

The Patagonian colony of southern elephant seal, *Mirounga leonina*, centered at Península Valdés and nearby areas (Argentina, Figure 1) was recently infected by the High Pathogenicity Avian Influenza (HPAI) H5N1 virus. Because we have been monitoring the population for over 40 years, we were able to demonstrate massive mortality of newborn pups (Campagna et al. 2024a; Uhart et al. 2024). Moreover, given data collected since the 1980s, we have a firm basis for understanding the potential impact of the outbreak. During the past half a century,

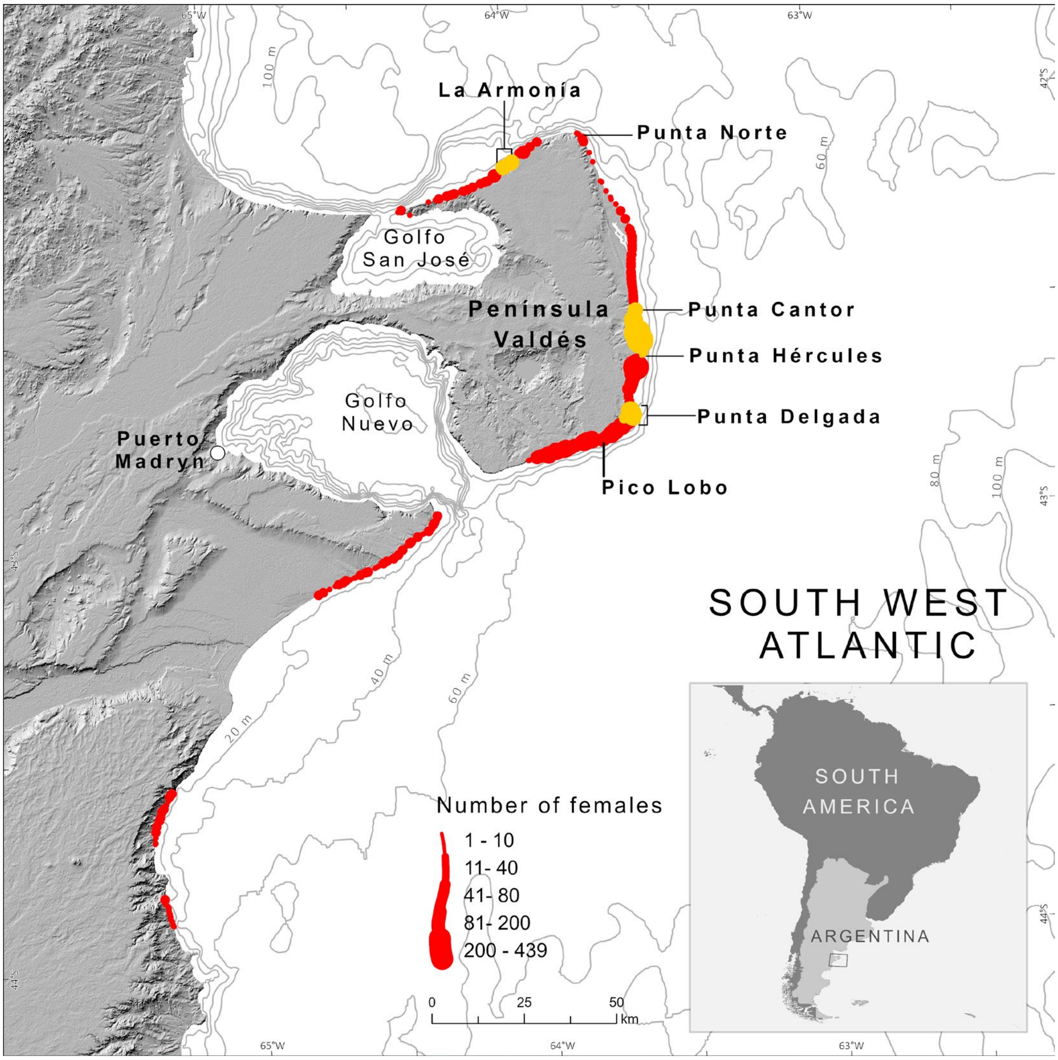

FIGURE 1 | Geographic distribution of southern elephant seals, *Mirounga leonina*, along the Argentine Patagonian coast. The areas sampled in 2023 are highlighted in yellow.

the number of females at Península Valdés expanded at a rate of 1%–3% per year (Ferrari et al. 2013), and predictions for the continuous growth of the population were optimistic. A regional IUCN Red List categorization of marine vertebrates for the Southern Cone designated the southern elephant seal as Least Concern (Campagna et al. 2024b), the category assigned to abundant species that may be exposed to threats that would not affect their abundance. This was based in part on the last census of the Península Valdés population in 2022, when 18,000 reproductive females were recorded, and pre-weaning mortality was only 2%–3%, as in previous years. Viral outbreaks, such as the 2023 HPAI epidemic that affected the southern elephant seals and many other species of marine birds and mammals (Uhart et al. 2024; Kuiken et al. Early View), are predicted to occur more frequently under current forced climate change (Sanderson and Alexander 2020; Paniw et al. 2022), so predicting their impact on wildlife populations is critical for understanding the potential conservation consequences.

Elephant seal females are onshore twice each year, once to reproduce and once to molt, in dense concentrations at consistent breeding colonies (Le Boeuf and Laws 1994). They disperse on solitary foraging migrations for the rest of the year, and time on the coast is minimized. At Península Valdés, Patagonia, breeding takes place in September and October, when females give birth, nurse, and wean their pups, mate, and depart the colony after less than a month. They then return to molt in December to January, and gestation lasts the rest of the cycle until the following September (Ferrari et al. 2009, 2013; Lewis et al. 2004; Lewis and Eder 2021). The population of Península Valdés grew in size steadily over the past 60 years, and breeding groups spread along the coast, now covering 300 km of coastline (Ferrari et al. 2013; Figure 1). Growth of the colony depends on local recruitment because other colonies are so distant that migration is rare (Lewis et al. 2006). In contrast to the expanding Patagonia colony, many southern elephant seal colonies on subantarctic islands are declining (Campagna and Lewis 1992; Hindell et al. 2017; Lewis et al. 2004, 2006; McMahon et al. 2005).

The 2023 outbreak of HPAI H5N1 in the Patagonian elephant seal colony happened in the midst of the breeding season and caused unprecedented mortality of 97% of the pups born (Campagna et al. 2024a; Uhart et al. 2024). A number of adults of both sexes also died, and more might have perished at sea after departing the colony. Some surviving females may have departed without being inseminated, as breeding groups dissolved faster than usual, and some female groups had no males nearby to fertilize them. Could these catastrophic impacts on the colony force us to revise the conservation status of this population, considered strong and healthy before 2023?

The aim of this study is to model population recovery scenarios following the influenza-caused mortality in Patagonian elephant

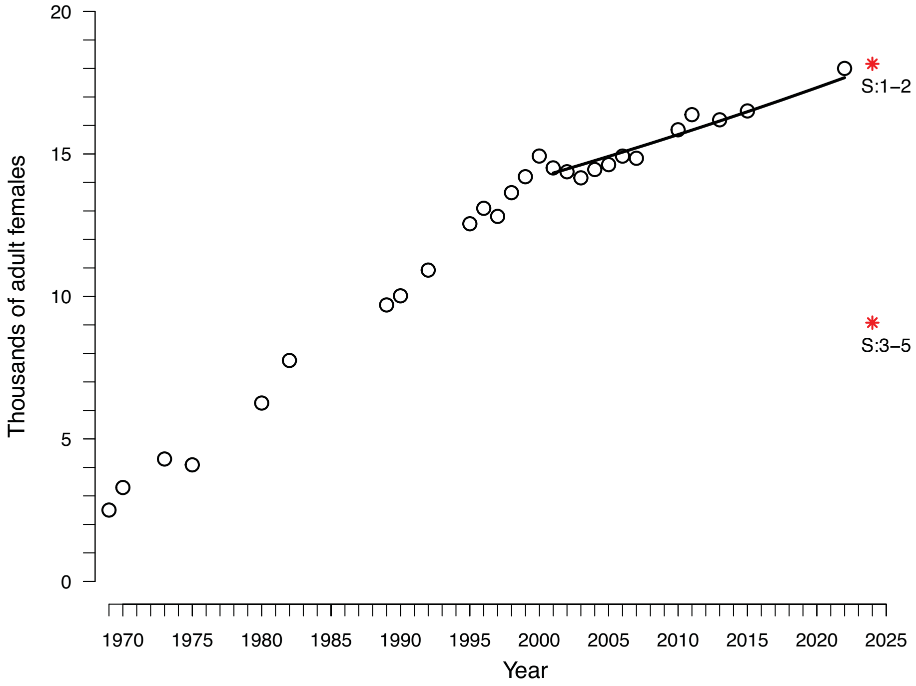

FIGURE 2 | Growth of the female population of the southern elephant seal colony of Península Valdés and nearby areas. The solid line indicates the period of growth of 0.9% per year, the trend used to project scenarios. Asterisks indicate expected female numbers according to the projected scenarios (see Table 1).

TABLE 1 | Parameters describing simulated scenarios predicting the impact of deaths caused by High Pathogenicity H5N1 Avian Influenza in the southern elephant seal colony of Peninsula Valdés.

Scenarios	Adult female mortality	Female fecundity	Minimum number of females (credibility intervals) [year projected]	Percent projected of 2022 females	Recovery year
S1. Baseline, no unusual mortality	12.6%	90%	18,000 [2022]	100	2022
S2. 100% pup mortality in 2023	Same as S1	Same as S1	16,160 (15,053–17,393) [2027]	89.8 (83.6–96.7)	2035 (2029–2051)
S3. S2 + 50% adult female mortality in 2023	50% in 2023	Same as S1	9081 (8718–9458) [2024]	50.5 (48.4–52.5)	2091 (2068–2118)
S4. Same as S3 + 0% of the surviving adult females inseminated in 2023	Same as S3	0% in 2023	8825 (8167–9573) [2028]	49.0 (45.4–53.2)	2101 (2076–2129)
S5. Same as S4 + 20% adult mortality in 2024	50% in 2023 20% in 2024	Same as S4	7438 (6890–8063) [2028]	41.3 (38.3–44.8)	2120 (2091–2151)

Note: Parameters for S1 were derived from Ferrari et al. (2013). Female mortality in S3–S5 was added on top of typical mortality, as females that survived the epidemic and departed the colony were still affected by typical mortality at sea (see Section 2). S4 implies no pups born in 2024. Recovery gives the predicted year when the adult population returns to the 2022 level, assuming no HPAI impact after 2024, with population growth returning to 1.009 per year, the rate estimated over the previous 10 years. Values in parentheses are 50% credibility intervals.

seals. Supported by substantial background knowledge of demographic parameters, we applied hypothetical flu-impacted mortality and fecundity rates to our existing life table and projected the population of breeding females up to 100 years ahead (ca. 10 generations; Hofmeyr 2015). We began with a minimum impact scenario, assuming all pups lost for 1 year, as observed in 2023, but with no excess female mortality nor any impact beyond 2023. We extended this with three more scenarios with increasing impacts, adding adult female mortality for one or for two additional years, and we also reduced insemination of females in 2023 that would lead to fewer births in 2024. The scenarios are intended to reveal the range of possible impacts of an epidemic that would result from observed impacts of the flu outbreak in 2023.

2 | Methods

2.1 | Death rates in 2023

Campagna et al. (2024a) reported observations of flu-related deaths in the Península Valdés elephant seal colony during the 2023 breeding season, and we summarized those here as a basis for modeling their population impact. Three breeding sites, covering 20 km of coastline, were monitored in 2023: two beaches that had high-density groups of breeding females in previous years (Punta Cantor Wildlife Reserve and Punta Delgada Lighthouse) and a third that had lower density groups (La Armonía beach; Figure 1). The entire northern and northeastern coasts of the Peninsula also had low-density groups (Campagna and Lewis 1992; Ferrari et al. 2009). Assuming the rate of pup mortality at all high-density beaches matched that at Caleta Valdés and Punta Delgada, and that all low-density beaches matched mortality at La Armonía, Campagna et al. (2024a) estimated pup mortality of 97% and that 17,500 pups died of 18,000 born.

2.2 | Demographic Parameters

We have conducted full breeding counts of the Península Valdés elephant seal colony regularly since 1982 (Ferrari et al. 2009, 2013; Figure 2). Based on these data, Ferrari et al. (2013) modeled the growth of the population. The model was a simplified life table with two rate parameters (mortality and recruitment) and a single population category, adult females, that was updated annually. The two parameters were estimated using observed counts of females over several decades. These parameters allowed projections of future population size and could also incorporate changes in the mortality rate owing to disease outbreaks.

To include additional disease mortality, we adapted a Leslie matrix to the Ferrari et al. (2013) model. To specify pup mortality and adult mortality separately, we used four age categories: pups (up to age 1 year), juveniles (ages 2 and 3), and adults (age 4 and above). We assumed females give birth for the first time at age 4, as observed in stable breeding colonies (Le Boeuf and Laws 1994; McMahon et al. 2003). As in the Ferrari et al. (2013) model, two parameters sufficed to describe population growth: recruitment rate, q, and annual adult survival, p. But here recruitment included additional pup mortality (m) so it was defined as the product of pup survival ($1-m$), fecundity, f, and juvenile survival from age 1 until age 4, j, so $q=(1-m)\,fj$. We ignored senescence, known to start at age 17 in northern elephant seals, *M. angustirostris* (Condit et al. 2014), and variation in the age of first reproduction, which may range from 3 to 5 years of age (Reiter and Le Boeuf 1991).

The model described the female population as a vector of four, the number of females alive in each age category. Males were not included, except that we assume there were enough of them to inseminate females. The Leslie matrix projected the population through time from any specified starting point. The two juvenile classes were necessary to delay recruitment for 4 years, but we only made use of the number of pups (category 1) and adults (category 4). As in any Leslie matrix (Caswell 2001), the population achieved a stable age distribution given constant p and q, and once it did, it grew at a constant rate λ, with λ defined as the ratio of population size in successive years. For the baseline population projection, we assumed the annual adult female survival estimated in Ferrari et al. 2013, $p=0.874$, and we set the recruitment $q=0.139$ to obtain population growth $\lambda=0.009$. To achieve this, we set fecundity $f=0.45$ and juvenile survival $j=0.3082$. The fecundity term arises from the assumption that 90% of adult females give birth each year (see Hückstädt et al. 2018 in northern elephant seals), with half of those being female. Juvenile survival covers birth to age 4, and the value we use falls well within the range of published values reviewed in Ferrari et al. (2013). Details of the model and its implementation are provided in the Supporting Information.

Based on the above background, we developed predictive models that incorporated mortality caused by HPAI H5N1 above the normal or expected mortality described by parameters p and q. Female mortality caused by the disease was added to typical mortality; that is: females that survived the disease still suffered natural mortality at sea. This meant the adult category was reduced by a flu mortality factor, 50% in year 2023 or 20% in 2024, then multiplied by adult survival p. In all our scenarios, pup mortality was assumed to be 100% in 2023, meaning that we reset the population size of the age-1 category in year 2024 to zero; the other juvenile categories were projected forward normally using the Leslie matrix. Finally, failure to inseminate females in year 2023 was simulated by setting the age-1 category to zero again in 2025, meaning two straight years without pup production.

2.3 | Flu impact Scenarios

We modeled five scenarios, four of which included HPAI H5N1-related mortality. For each scenario, we projected population size forward, starting with the observed pre-epidemic size in 2022 (Table 1, Figure 2).

Scenario 1: Baseline projection. We started with an adult female population of 18,000, based on the 2022 count conducted at Península Valdés and nearby areas (for methodological details see: Campagna and Lewis 1992; Ferrari et al. 2013) and inserted juvenile categories to match the known stable age distribution (see Supporting Information). We called this population *N2022*, and it was the basis for all projections. In the baseline scenario, we simply continued population growth using the Leslie matrix based on p and q that led to population growth of 0.9% per year, as observed over recent years (Figure 2).

Scenario 2: 100% pup mortality in 2023. Starting with the same *N2022*, we projected forward 1 year, then set the pup population (category 1) to zero and projected forward, as under Scenario 1.

Scenario 3: 100% pup mortality, plus 50% adult mortality in 2023. Starting with *N2022*, we projected 1 year, set the pup population to zero, and reduced the adult population by half before projecting the following years.

Scenario 4: 100% pup mortality, 50% adult mortality, plus failed insemination in 2023. Without insemination, no pups would be born in 2024. This means starting as in Scenario 3, but also setting the pup class to zero in a second year.

Scenario 5: 100% pup mortality, 50% adult mortality, and failed insemination in 2023, plus 20% adult mortality in 2024. This proceeded as in scenario 4, with the adult population size reduced a second time by 20% due to a recurrent epidemic.

For each of the five scenarios, the adult female population, age class 4 in the model, was represented in Figure 3. We calculated the year in which the adult female population returned to N2022, as defined in Scenario 1. We assumed in all scenarios that juvenile mortality (ages 1–3) was unaffected by the disease.

2.4 | Uncertainty in Model Forecasts

To incorporate process errors into the model projections, we considered log-normal errors associated with the predicted adult female counts. This was consistent with the modeling approach proposed by Ferrari et al. (2013), where a log-normal process error variance was estimated as $\sigma^2 = 0.0035$. With this error variance, 10,000 simulations were drawn for each scenario, and 50% credible intervals were obtained from the simulated distribution quartiles in each year. For further details, see Supporting Information.

3 | Results

When free of HPAI H5N1-related mortality, the population continued to grow (Table 1, Figure 3). If demographic parameters were kept at the 2022 pre-outbreak levels, the population increased at 0.9% per year and approached 20,000 reproductive females in 2035 (Scenario 1). All scenarios, including flu-related mortality, predicted a decrease in population size.

When the impact of HPAI H5N1 was 100% pup mortality, with no additional mortality (Scenario 2), the predicted adult female population was not affected until 2027, when it declined by 10% compared to the undisturbed scenario. The delay was due to setting the initial breeding age of females at 4. If the rate of increase continued as in 2022 (0.9% per year), the population returned to the pre-epidemic level in 2035, but it remained lower than the baseline projection (Scenario 1).

Scenario 3 simulated mass mortality of adult females (50%), in addition to 100% death of pups born in 2023. The predicted impact was much more severe, as the death of adult females led to a proportionate decrease in the female population size in 2024 (Table 1; Figure 3). The female population partially recovered in 2025 and 2026, due to the recruitment of juveniles born prior to 2023. In 2027–2028, a second decline occurred, due to the failed recruitment of the pups born and dead in 2023.

Scenarios 4 and 5 were more severe. Reduced fertility in 2023 that followed failed insemination during the 2023 epidemic would lead to no births in 2024, on top of the pup mortality of 2023. Again, pup deaths had less of an impact than adult deaths, and the predicted population of Scenario 4 (Figure 3) did not differ substantially from Scenario 3. The worst case was Scenario 5, incorporating all impacts of scenarios 2–4 plus an additional 20% adult female mortality in 2024, which led to a decline in

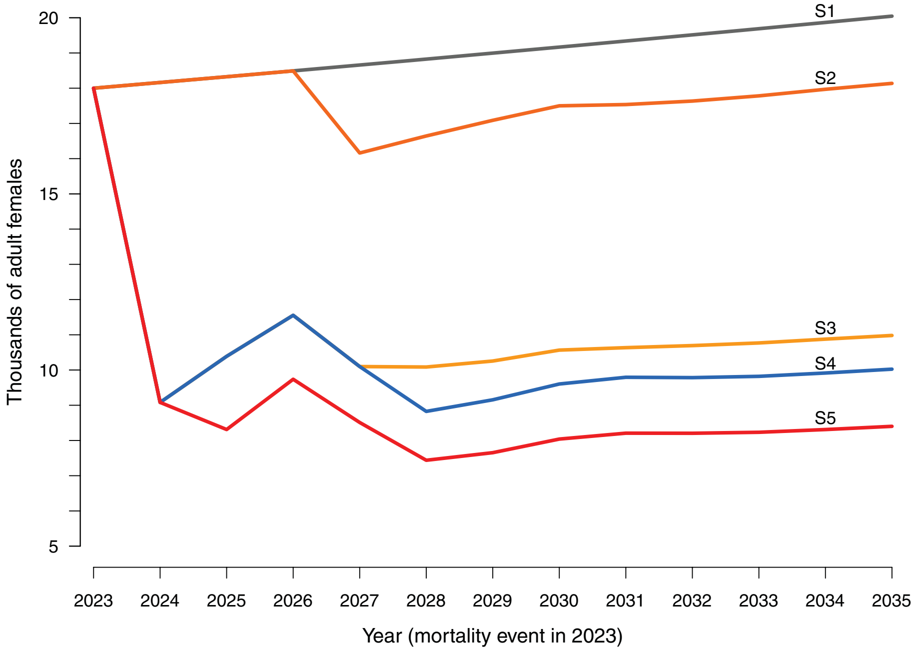

FIGURE 3 | Comparative scenarios of population trajectories following parameters described in Table 1. Projections were extended up to 2035 as population growth for all scenarios readjusts to the pre-2022 annual growth rate of 0.9% per year in about a decade.

the adult population in two straight years, falling below half the pre-endemic level.

Substantial loss in one or two age classes disrupted the stable age distribution. In all four modeled scenarios, it took about 10 years, until 2033, for the population to readjust to the 2022 age distribution. At that time, a population growth of 0.9% per year resumed. The population eventually returned to the 2022 level in every scenario. With pup loss only in 1 year (Scenario 2), the population was restored by 2035 (Figure 3). In the other three scenarios, all involving pup and adult deaths, recovery was much delayed, until 2091, 2101, or 2120, respectively (Table 1).

4 | Discussion

The simulations lead to one important conclusion: If mortality caused by one disease outbreak is limited to newborns, the impact is relatively small. This is due to the high natural mortality of elephant seals in normal years. An estimated 60%–75% of the pups born in 1 year die before reproducing at age 4 (Ferrari et al. 2013). Thus, mortality due to the virus is attenuated. This is a generalization across many long-lived species, where young suffer high mortality, whereas adults can persist for years without successful reproduction (Scoppettone et al. 2015; Taylor et al. 2006; Veblen et al. 1981). In contrast, the loss of adult females has immediate consequences and can be catastrophic, and excessive hunting offers conspicuous examples, particularly the overexploitation of marine mammals in the 19th and 20th centuries (McClenachan and Cooper 2008; Turvey and Risley 2005). Thus, highly transmissible, emerging diseases that impact adults of reproductive age in several episodes are the most concerning. Regardless of which age classes are killed, diseases that recur over several years will have the greatest impact. Occasional outbreaks followed by acquired disease resistance would be routine over evolutionary time scales and unlikely to affect populations.

Our modeled scenarios were intended to include maximum effects so that the real impact of the 2023 event would fall within our range of predictions. Some model parameters, such as 100% pup mortality, were close to what was actually recorded. As virtually all females that come ashore during the reproductive season give birth to a pup, the loss of all 18,000 pups would lead to a loss of 2700 adult females 4 years later. This is because half of the pups affected were males and, as said, ca. 70% of the pups born typically die before age 4 (Ferrari et al. 2013). Conversely, the impact is important and immediate when females 4 years and older die at a significantly higher rate than the typical baseline mortality.

Actual female mortality could not be estimated in 2023. Only a 20-km stretch of coast was monitored weekly, although the sampled areas included beaches where animals had been gathering at high density in all previous seasons. Several adult carcasses were recorded in 2023, where none were usually found (Uhart et al. 2024). This result already suggests unusual mortality since adult carcasses are seldom observed in a typical breeding season. More important, females may also have died at sea. The impact of the epidemic on adult females will be apparent during the 2024 breeding season, when our counts will be compared with theoretical scenarios (see Addendum). A decline in the number of females in 2024 would probably be due to adult female deaths. However, females not inseminated in 2023 would spend less time on the coast during the 2024 breeding season, possibly leading to lower breeding counts. Yet, all females molt in early summer, and a lower number of molting females would suggest mortality. Monitoring beyond 2024 will further test our predictions, since models predict impact related to pup mortality in 2027 and 2028. Moreover, continued monitoring will be necessary to detect unexpected social disruptions at the colony caused by changing behavior of breeding females and males.

When compared with a typical reproductive season, as we have observed and described for many years, the social context of the 2023 breeding season was deeply altered. For example, the number of breeding females at the peak of reproduction was about half to one-third of a typical year. The high-density extension of about 13 km to the south of Punta Cantor (Figure 1) congregated 3306 females in 2022 and 989 in 2023. Beaches were relatively empty of males too, even in places where high-density aggregations had been the norm. Many pups were abandoned to eventually die from disease, dehydration, or starvation because mothers abandoned the colony before weaning their pups. A number of these females may not have been inseminated, considering the low number or even lack of males in some areas. We assumed that males were not a limiting factor in the breeding success of female elephant seals because, besides the dominant male, there are peripheral ones ready to mate. But, because males typically spend 3 months ashore, and females only 1 month, males were exposed for longer to the Influenza virus and may have suffered higher mortality than females.

Recovery time of the Península Valdés colony will depend on the future rate of population growth. In our model, we assumed continued growth at 0.9% per year, as observed over the past decade. The status of food resources and any impact of climate change on those resources are undoubtedly important to continued population growth, but our knowledge of productivity on elephant seals' foraging grounds is limited. We also have little understanding of density dependence in the population (Bradshaw et al. 2002). In Ferrari et al. (2013), we found evidence that population growth has slowed since the 1970s, as it has in the northern elephant seal (Lowry et al. 2014). If density dependence is important, the impact of epidemic mortality would be ameliorated, as the lower population density would lead to increased population growth and faster recovery.

4.1 | Influenza in Other Marine Mammals

Although marine mammals were previously known to be susceptible to influenza A viruses, the outbreaks had been uncommon, with limited demographic impact (Ferreidouni et al. 2016). However, the 2022–2023 HPAI H5N1 outbreak caused mass mortality of pinnipeds and also seabirds in South America, though population-level consequences are unknown (Uhart et al. 2024; Kuiken et al. 2025). The 2022–2023 viruses belong to the clade 2.3.4.4b of the Goose/Guangdong lineage (Gs/Gd) (Leguía et al. 2023; Rimondi et al. 2024; Uhart et al. 2024; Ulloa et al. 2023). This lineage of viruses originated in 1996 in farmed geese in Southeast Asia and slowly developed mutations until it spread globally (Lee et al. 2021; Pohlmann et al. 2023). The global spread prompted an unprecedented wave of marine mammal mortality, particularly since the virus reached South America in late 2022. The virus has acquired novel mammal-adaptation mutations that likely played a role in its deadly, rapid spread among pinnipeds across multiple countries (Leguía et al. 2023; Pardo-Roa et al. 2023; Peacock et al. 2025; Rimondi et al. 2024; Uhart et al. 2024).

In addition to the near complete mortality of southern elephant seal pups at Península Valdés, plus the loss of an undetermined number of adults, over 30,000 South American sea lions (*Otaria byronia*; also referred to as *O. flavescens*) died along the Pacific coast of South America (Peru and Chile) (Leguía et al. 2023, Ulloa et al. 2023, Chile Servicio Nacional de Pesca y Acuicultura 2024, Peru Ministerio de Salud 2024, World Organization for Animal Health 2024). The few available estimates for the mortality of sea lions and South American fur seals (*Arctocephalus australis*) on the Atlantic coast of the continent (Argentina, Uruguay and Brazil) suggest that the death toll exceeded 3500 animals (Rimondi et al. 2024; Szteren and Franco-Trecu 2024; World Organization for Animal Health 2024). The uncertainties regarding the mortality of many marine mammals and birds contrast with our relatively detailed estimate of the impact of an epidemic on elephant seals.

In South Georgia, clusters of mortality of hundreds of animals were observed, including elephant seals and Antarctic fur seals (*Arctocephalus gazella*; Banyard et al. 2024; Scientific Committee on Antarctic Research 2024). The 2020–2023 global wave of HPAI H5N1 also affected other pinniped and cetacean species, including harbor seals (*Phoca vitulina*), gray seals (*Halichoerus grypus*), Northern fur seals (*Callorhinus ursinus*), Atlantic white-sided dolphins (*Lagenorhynchus acutus*), Burmeister's porpoises (*Phocoena spinipinnis*), harbor porpoises (*Phocoena phocoena*), common bottlenose dolphins (*Tursiops truncatus*), Chilean dolphins (*Cephalorhynchus eutropia*), common dolphins (*Delphinus delphis*), dusky dolphins (*Lagenorhynchus obscurus*), marine otters (*Lontra felina*), southern river otters (*Lontra provocax*), and polar bears (*Ursus maritimus*) (Chile Servicio Nacional de Pesca y Acuicultura 2024; Lair et al. 2024; Murawski et al. 2024; Puryear et al. 2023; Rimondi et al. 2024; Sobolev et al. 2024; Thorsson et al. 2023; United States Department of Agriculture 2024).

The global spread of HPAI H5N1 viruses, which began in 2020, forces a revision of the conservation scenarios for marine mammals worldwide, particularly for the southern hemisphere (Brownell Jr et al. 2024; Kuiken et al. 2025; Szteren and Franco-Trecu 2024; Uhart et al. 2024). Influenza A viruses, which were previously a relatively minor threat to wildlife, should now be considered a significant problem for all marine mammals, especially pinnipeds, but also for cetaceans. Thus far, the bulk of the mortality of marine mammals, particularly pinnipeds, occurred in South America. However, it is possible that other populations worldwide will experience similar impacts if these novel mammal-adapted viruses spread to other continents. It is remarkable that the virus that is now decimating marine mammals in the Americas emerged in a poultry setting on the other side of the world, more than two decades earlier. This highlights the interconnected nature of global health and how unpredictable the impacts of emerging pathogens can be (Grimaudo et al. 2024; Pfenning-Butterworth et al. 2024). An integrated, global approach to health issues that threaten the viability of populations for many species should therefore be paramount for disease risk management in all aspects of human activity, especially food production (Gilbert et al. 2017; Kuiken et al. 2025).

In summary, the episode of High Pathogenicity Avian Influenza that affected the elephant seals of Península Valdés suggests that pinniped populations hitherto stable or increasing (i.e., Least Concern in IUCN Red List terms) may rapidly become regionally/globally endangered by infectious disease outbreaks. It is expected that outbreaks of this kind may become more frequent or severe under forced climate conditions (Gulland et al. 2022; Sanderson and Alexander 2020) and may combine with other threats, potentially pushing small or genetically impoverished populations toward extinction (Brownell Jr et al. 2024). The continued monitoring of affected populations in South America and the expansion of disease surveillance in pinnipeds worldwide will be of paramount relevance. Thus, for many key susceptible taxa, strategies for prioritizing resources may need to change in many countries. Preliminary data from the 2024 breeding season (see Section 4.2) strongly suggest that High Pathogenicity Avian Influenza has the ability to cause disastrous impacts, even on populations previously thought to be "safe" from collapse.

4.2 | Addendum

The 2024 reproductive season of elephant seals at Península Valdés took place while this paper was in the review process. Preliminary results from 2024 counts of the highest density areas (Figure 1) suggested that, in addition to pup mortality, the mortality of adults was also important in 2023. In 2024, we recorded 67% fewer reproductive females at beaches that had typically been the most densely populated of the entire colony (6938 females in 2022 vs. 2256 in 2024). Differences could be attributed to mortality, a delay in the arrival of animals, animals that skipped a season, or a redistribution and colonization of new places. So far, evidence suggests that the viral episode significantly impacted adult individuals. Therefore, scenarios 3 and 4 of this paper would apply best to the projected trajectory of the population (see Figure 2).

Author Contributions

Claudio Campagna: conceptualization, data curation, investigation, supervision, writing – original draft. **Richard Condit:** data curation, formal analysis, investigation, methodology, writing – original draft. **Mariano Ferrari:** data curation, formal analysis, investigation, methodology, validation. **Julieta Campagna:** investigation, data curation, validation. **Elena Eder:** investigation, data curation, writing – original draft. **Marcela Uhart:** investigation, validation, writing – original draft. **Ralph E. T. Vanstreels:** investigation, validation, writing – original draft. **Valeria Falabella:** data curation, investigation, validation. **Mirtha N. Lewis:** data curation, investigation, validation. [Correction added on April 26, 2025, after first online publication: Author contribution details for Richard Condit, Julieta Campagna, Elena Eder, Marcela Uhart, and Valeria Falabella have been included.]

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Conflicts of Interest

The authors declare no conflicts of interest.

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Supporting Information

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