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Pacific and Atlantic sea lion mortality caused by highly pathogenic Avian Influenza A(H5N1) in South America

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ABSTRACT

We describe the evolution of the outbreak of Highly Pathogenic Avian Influenza (HPAI) A(H5N1) in sea lions (*Otaria flavescens*) of South America. At least 24,000 sea lions died in Peru, Chile, Argentina, Uruguay, and Brazil between January–October 2023. The most plausible route of infection is cohabiting with or foraging on infected birds. However, we urge a detailed evaluation of the sea lions actual source of infection given that the concomitant massive wild bird mortalities registered in the Pacific Ocean did not occur in the Atlantic Ocean.

Since the beginning of the current panzootic (2020–2024) caused by Highly Pathogenic Avian Influenza (HPAI) A(H5N1), many severe outbreaks have been reported around the world [1]. This is, in fact, the largest panzootic to be associated with this pathogen since its emergence in Chinese farmed geese production in 1996 [1,2]. Current evidence suggests that this virus strain is changing its epidemiological behavior; it is now affecting a massive number of wild birds and other unusual hosts such as wild mammals [3]. This has raised concern not only for wildlife conservation but also for public health, due to the putative zoonotic characteristics of this pathogen.

A wide variety of wild mammalian species, especially mesocarnivores and marine mammals, have been infected by HPAI A (H5N1), producing mortality events in different parts of the world particularly since 2020 [4]. Infected mammals generally display a severe acute disease characterized by neurological and respiratory signs that ultimately result in death; the main findings of necropsies reveal pneumonia and encephalitis as the cause of death [4,5]. The first mass mortality of sea lions (*Otaria flavescens*) affected by this virus was described in Peru [5]. The virus then continued infecting this species throughout South America, so here we report the evolution of sea lion mortality from the Pacific to the Atlantic Ocean during the 10 months following the first outbreak in Peru. For this we used data produced by the World Organization for Animal Health (WAHIS) [2,6], scientific publications [e.g., 7–9], and field observations in Peru [5].

1. The arrival of H5N1 in South America

The (HPAI) A(H5N1) virus was detected in birds for the first time in South America, initially in October 2022 in Colombia and then in November in Peru [2,6,7]. Phylogenetic analysis suggests that the virus reached South America through multiple introductions from North America, especially along the Pacific Migratory Flyway [7,8]. The H5N1 virus arrived at the end of 2021 in North America, where high mortalities (hundreds of individuals) were reported in at least 10 wild bird species; more than 20 species of wild mammals were also affected by this pathogen in this region [3,4].

After the introductions of (HPAI) A(H5N1) into Colombia and Peru, the virus spread between birds throughout South America in a short period of time (e.g., Venezuela and Ecuador in November 2022, Chile in December 2022, Bolivia in January 2023, Argentina and Uruguay in February 2023 and Brazil in May 2023) [6]. In South America, particularly in Peru, the H5N1 virus produced alarming mortality levels in poultry, wild birds, but also in marine mammals [5,6,9]. For instance, more than 100,000 wild birds were reported to have been killed by this pathogen in Peruvian protected areas alone [9].

2. Unusual mortality of sea lions

In January 2023, concomitantly with the deaths of wild birds and

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poultry due to H5N1, several dead or dying sea lions were detected on Peruvian beaches [5] (Fig. 1A and B). The clinical signs in dying individuals were mainly neurological (e.g., convulsions and tremors) and respiratory (e.g., dyspnea, tachypnea), including pathological lesions compatible with encephalitis and pneumonia [5]. Given the surrounding epidemiologic context, the first presumptive diagnosis was acute disease due to HPAI [5]. Laboratory analysis confirmed that HPAI A(H5N1) was the etiologic agent responsible for this mortality [8]. More than 5000 sea lions died as a result of this outbreak only in Peru during the summer of 2023 [5]. In addition, a common dolphin (*Delphinus delphis*) and several seabirds were reported as infected and killed by this virus [8,9].

During the massive mortality event in Peru, in January–February 2023 Chile began to report sick and dead sea lions with clinical signs compatible with HPAI [6,10] (Fig. 1A and B). The number of dead sea lions associated with the (HPAI) A(H5N1) virus in this country reached more than 14,000, plus thousands of wild birds [2,6,10]. Moreover, other mammals, such as the marine otter (*Lontra felina*), southern river otter (*Lontra provocax*), Chilean dolphin (*Cephalorhynchus eutropia*), and a spiny porpoise (*Phocoena spinipinnis*) were reported to have been infected by H5N1 in this country [2,4]. Genome sequences of the virus present in Chilean sea lions suggest that this (HPAI) A(H5N1) cluster monophyletically with the virus affecting the Peruvian populations [11]. Therefore, the Chilean outbreak could be considered an extension of the Peruvian one.

Sea lion mortality due to H5N1 started in Argentina in August 2023 (Fig. 1A); all gene segments of infected individuals showed a close relationship with sequences from Peruvian and Chilean sea lions [6,12]. Several cases were reported along the Atlantic coast in the following provinces: Tierra del Fuego, Santa Cruz, Chubut, Rio Negro and Buenos Aires [6,12] (Fig. 1A and B). Highly Pathogenic Avian Influenza H5N1 has killed at least 1300 sea lions, but this figure is preliminary, considering the outbreak may still be in progress [6]. Similar to what was observed for this species in Peru and Chile, affected individuals showed neurological signs before dying [6,12]. The first detection in Argentina (in Rio Grande, Tierra del Fuego Province, Argentina; −53.71557, −67.80045) occurred in August 2023, after Chile reported

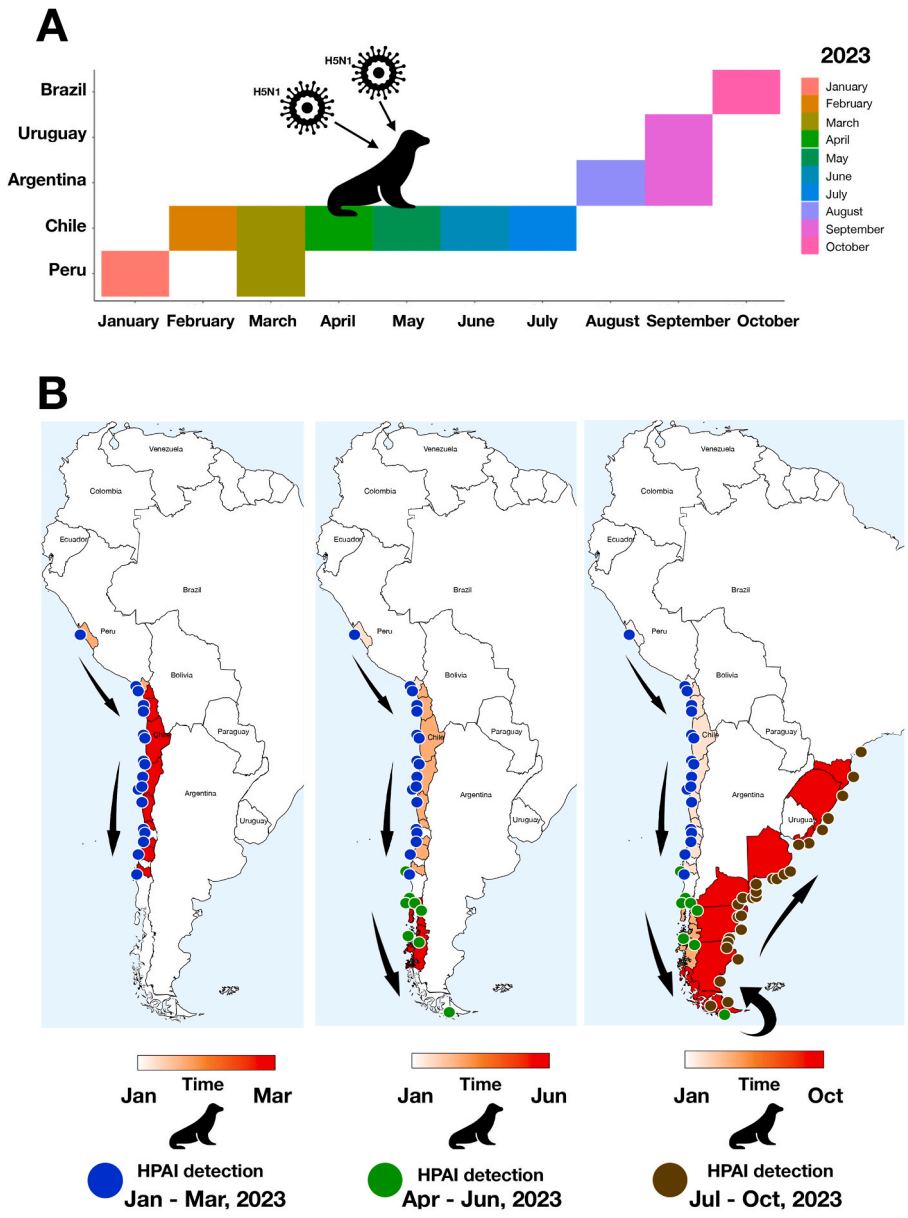

Fig. 1. (A) Scheme showing progression of the outbreak in sea lions, by date and country. (B) Map showing the progression of HPAI A(H5N1) infections in sea lions. The geographical areas depicted correspond to political boundaries (departments or provinces) where the virus infected sea lions.

infected sea lion individuals in the vicinity at the end of June 2023 (in Puerto Williams, Tierra del Fuego, Chile; −54.927686, −67.621811) [6] (Fig. 1A and B). Then, Uruguay began reporting sea lions infected by H5N1 near Montevideo (Cerro beach) in September 2023 and lastly Brazil in Santa Catarina in October 2023 [6,13]. It would therefore be reasonable to assume that the Argentinean outbreak was a continuation of the Chilean event, and the Uruguayan and Brazilian a continuation of the Argentine one (Fig. 1); the Uruguayan and Brazilian viruses detected in sea lions, in fact, clustered with the Peruvian, and Chilean viruses [13,14].

The HPAI A(H5N1) virus traveled approximately 5000 km from Peru to Tierra del Fuego (by way of the Pacific Ocean), and approximately 2800 km from Tierra del Fuego to Uruguay and Brazil (by way of the Atlantic Ocean), infecting sea lions along the way. During this time, H5N1 killed approximately 5% and 12% of the Peruvian and Chilean sea lion populations, respectively [5,10]. The spread of the virus progressed from north to south in the Pacific Ocean between January 2023 and August 2023, and in the Atlantic Ocean, it has progressed very rapidly from south to north between August and October 2023 (Fig. 1). This wave of infection has already produced cases throughout almost the entire distribution range of sea lions, except in the south of the continent [6] (Fig. 1). This region should be alert and prepared for the early detection of sea lions affected by (HPAI) A(H5N1), especially because in this geographical area there is a large population of this and similar pinniped species that are at risk, many in islands and the Antarctic continent [2]. In fact, this outbreak expansion recently affected also Southern elephant seals (*Mirounga leonina*) in the Atlantic Ocean resulting in huge mortalities, with more than 17,000 pups died during this outbreak [6,15].

3. Epidemiologic behavior and transmission

The most likely source of infection for sea lions in South America is associated with HPAI-infected birds: a spillover from wild birds to mammals seems to be the main cause of infection [5,8]. In fact, sea lions in Peru were in close contact with infected birds and have even been reported ingesting dead and dying birds [5]. However, it is important to consider and evaluate potential direct transmission among sea lions due to their gregarious behavior, the large number of affected individuals and the clustering of deaths in groups [5,14]. Most importantly, sea lion mortality seems not always associated with wild or domestic bird mortality (e.g., in Argentina there are no official reports of large bird mortalities on the coasts where sea lions are dying) (Table A.1), but this requires further research because it could be due to underreporting of cases by this country.

Under the current panzootic scenario, potential mammal-to-mammal transmission of (HPAI) A(H5N1) has already been suggested for both terrestrial and marine mammals [4]. Genetic analysis of virus samples obtained from sea lions in Peru, Chile, Argentina, Uruguay and Brazil shows several mutations that suggest a potential adaptation to mammals; the mutations PB2-Q591K and PB2-D701N were present in the viral genomes of infected sea lions of all these countries [8,11–14]. The evaluation of (HPAI) A(H5N1) as a virus that has adapted to replicate in mammalian species is key to assessing the likelihood of a future adaptation to humans, which could potentially lead to a pandemic event.

4. Further suggestions

We call on authorities and researchers in South America to share rapidly any information gathered regarding (HPAI) A(H5N1) infections in mammals (e.g., species, number of individuals affected, and genetic characteristics of isolated H5N1); this is especially important for pinniped species, which are suffering alarming mortalities, but also to detect virus spread to other unusual hosts. This is not only essential for mitigation of the impact of the virus on biodiversity, but also for the public health sector, since (HPAI) A(H5N1) has zoonotic propensity. To address this problem in an integral way, it is necessary to establish interdisciplinary groups, including international reference laboratories that could assist with diagnosis and/or full genome sequencing. The severity of the Highly Pathogenic Avian Influenza issue demands a coordinated response that involves diverse disciplines (e.g., veterinarians, biologists, conservationists, and public health authorities).

Current evidence suggests that the virus affecting sea lions in Chile, Argentina, Uruguay and Brazil probably came from Peru [8,11–14]. There is a need for a cross-border cooperation effort to address genetic changes in the HPAI A(H5N1) virus that could indicate adaptation to viral transmission among sea lions. It is therefore essential to obtain rapid sequencing of the isolated virus across the entire route of infection.

Finally, mitigation measures are important in reducing the spread and amplification of this pathogen. Carcasses of infected animals should be removed from the environment as quickly as possible to prevent their contact with people, especially in tourist areas. It is also important to prevent the contact of infected carcasses with other animals, such as scavenging birds and free ranging dogs, which are susceptible to this virus and likely to spread it to diverse sites [4,6], including urban sites when dogs interact with people. The consequences of this for the health of humans and domestic animals are difficult to predict.

Once an emerging pathogen reaches wildlife the consequences are difficult to foresee, and actions to mitigate its spread are hard to implement [9]: this is the case of H5N1. It is therefore essential to prevent the emergence of dangerous microorganisms, which are generally the result of human impact on the environment. The Highly Pathogenic Avian Influenza A(H5N1) originated in farmed animals [2]; governments and authorities should therefore be extremly careful when evaluating intensive food production systems, to ensure the protection of the ecosystem and of human health from pathogens generated in these circumstances.

CRediT authorship contribution statement

Pablo I. Plaza: Conceptualization, Data curation, Investigation, Methodology, Writing – original draft, Writing – review & editing. **Víctor Gamarra-Toledo:** Conceptualization, Investigation, Methodology, Writing – original draft, Writing – review & editing. **Juan Rodríguez Euguí:** Conceptualization, Writing – original draft, Writing – review & editing. **Natalia Rosciano:** Conceptualization, Investigation, Writing – original draft, Writing – review & editing. **Sergio A. Lambertucci:** Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Writing – original draft, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this commentary.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.tmaid.2024.102712.

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