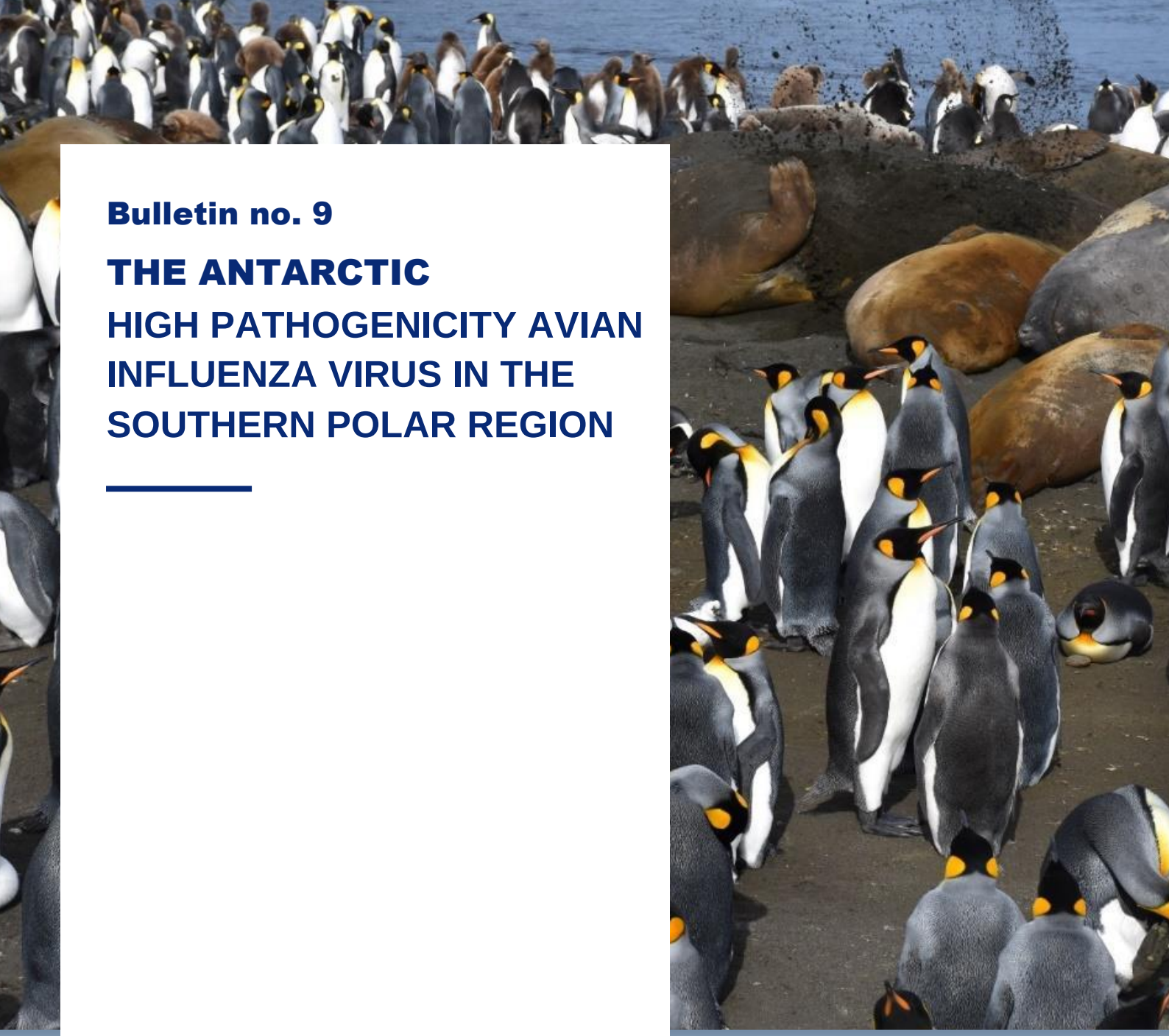

Bulletin no. 9

THE ANTARCTIC
HIGH PATHOGENICITY AVIAN INFLUENZA VIRUS IN THE SOUTHERN POLAR REGION

DECEMBER 2025

POLAR WATCH

Polar Regions Monitoring and Forecasting

LE CERCLE POLAIRE

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GRAPHIC DESIGN AND LAYOUT: Stéphane Hergueta, Pacha Cartographie
PUBLISHED BY: le Cercle Polaire – December 2025
PUBLICATION MANAGER: Stéphane Hergueta
COVER CREDIT: Thierry Boulinier
PRINTER: *Abon'copies*

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Wildlife under Threat as HPAI is Spreading in the Southern Polar Region

The arrival of High Pathogenicity Avian Influenza (HPAI) Virus in sub-Antarctic and Antarctic regions is a major event for these isolated ecosystems, which are extremely vulnerable to infectious diseases.

Polar environments are known for their unique fauna and their high sensitivity to global change. The populations of birds and marine mammals that breed there congregate in a limited number of sites. They are highly vulnerable to climate change, pressure from the exploitation of marine resources, accidental entanglement in fishing gear and, in some of the southern islands, interaction with introduced mammal species (rats, cats), as well as, in South Georgia and the Antarctic Peninsula, increasing pressure from tourism. Added to this is the recent emergence of high pathogenicity avian influenza (HPAI) virus H5N1 clade 2.3.4.4b, whose effects on wild bird populations since 2021 have been dramatic on a global scale. What are the concerns for the sub-Antarctic and Antarctic regions with the emergence of this virus, which originated in intensive poultry farming in Asia?

Southern elephant seals and king penguins on Possession Island, Crozet Archipelago, French Southern Territories. The arrival of HPAI virus in the southern Indian Ocean islands in 2024 was responsible for high mortality rates among these animal populations. *Copyright: Thierry Boulinier/CNRS/IPEV.*

'The health and ecological threat posed by this infectious agent can no longer be ignored and requires increased vigilance.'

The continued spread of HPAI virus poses a major threat to wildlife, livestock and, due to its *zoonotic* potential (the ability of a pathogen to be transmitted from animals to humans and vice versa), to public health. Since its emergence in poultry in China in 1996, the A/goose/Guangdong/1/96 (GsGd) lineage of HPAI H5Nx virus has evolved to spread efficiently among a wide range of bird species worldwide, causing unprecedented mass mortality. It has been responsible for the deaths of millions of individuals among both domestic poultry species and more than 200 wild species that had never been affected by this type of virus before. It has also caused the deaths of hundreds of people, with fatality rates varying according to virus clades, countries, periods and types of exposure. However, no cases of human-to-human transmission have yet been reported.

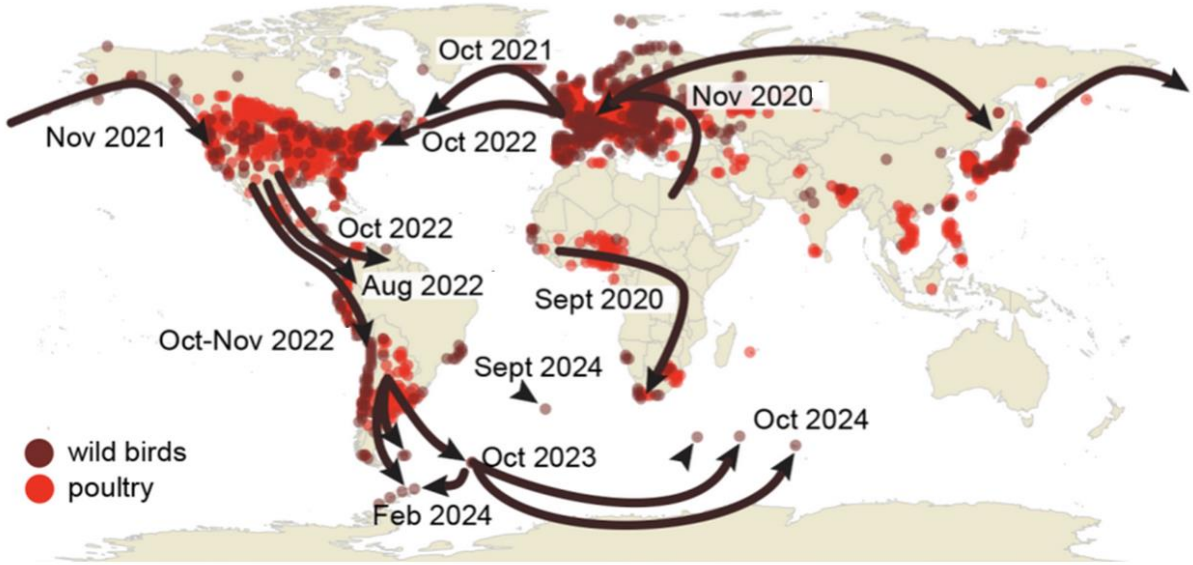

Figure 1: Timeline of the global spread of high pathogenicity avian influenza. The virus infected domestic animals and also a large number of wild species and individuals on every continent except Australia. The arrival of the virus was detected in the sub-Antarctic and Antarctic regions during the southern hemisphere summer of 2023, then in the southern Indian Ocean islands at the beginning of the southern hemisphere summer of 2024, in October 2024 in Crozet and in November 2024 in Kerguelen. *Source: www.michellewille.com*.

HPAI virus reached North America via the transatlantic migratory route after spreading throughout Europe, but also across the Pacific Ocean. It spread rapidly across the North American continent and, by October 2022, had spread throughout South America, with devastating effects on seabird and pinniped populations (Figure 1). In the southern spring of 2023, HPAI virus reached the sub-Antarctic islands and Antarctica, where it was first detected in brown skuas (*Stercorarius antarcticus*) on Bird Island, South Georgia. Shortly afterwards, cases were reported in southern fulmars (*Fulmarus glacialoides*) and black-browed albatrosses (*Thalassarche melanophris*) in the Falkland Islands/Islas Malvinas, as well as in several species on the Antarctic Peninsula.

Between 2023 and 2024, a major geographical expansion of the virus was observed, notably its emergence in the southern Indian Ocean, particularly on Crozet and Kerguelen archipelagos in the *Terres Australes et Antarctiques Françaises* (TAAF). In these archipelagos, the virus was responsible for high mortality rates among southern elephant seals (*Mirounga leonina*), particularly young seals born that year (Figure 2), but also among seabirds such as king penguins (*Aptenodytes patagonicus*) and wandering albatrosses (*Diomedea exulans*). Phylogenetic analyses of virus sequences collected from elephant seal and seabird carcasses in Crozet and Kerguelen archipelagos have shown that the closest viruses were those sequenced the previous year, in South Georgia, south of South America (Figure 3). This jump of nearly 6,000 km in one year shows that at these latitudes, the virus can spread rapidly and over long distances. Its expansion through the sub-Antarctic now threatens Australia and New Zealand, which have not yet been affected by this virus[1]. However, the fact that virus sequences are only available for a small number of sampling points, limits the ability to identify the precise routes taken by the virus. Cases of skua mortality have been detected in several locations on the Antarctic Peninsula, but to date, mortality has not had a massive impact on penguin colonies on the Antarctic continent.

At the end of the southern hemisphere summer of 2024, signs of the disease on the sub-Antarctic islands of the Indian Ocean faded. During the southern summer of 2025, the virus re-emerged on Kerguelen. In South Georgia, very high mortality rates were observed again among marine mammals during the southern summer of 2024, one year after the initial deaths were detected in the same area. The virus could therefore persist and re-emerge via dispersal at these high latitudes. During the southern summer of 2025, in addition to continuing work on these islands, expeditions were planned for the Heard and McDonald Islands (Australia), located southeast of Kerguelen, in order to obtain additional information. The detection of elephant seal deaths on Heard Island revealed the presence of the virus there as well. In the vast oceanic spaces of the Southern Ocean, it is particularly important to monitor the situation on the few islands that are home to vast breeding populations of birds and marine mammals. Yet information is lacking for Bouvet Island, located halfway between South Georgia and the islands of the southern Indian Ocean, and for the East and Cochon Islands in the Crozet Archipelago.

[1] Whilst expansion through the sub-Antarctic is certainly one risk for Australia and New Zealand (Australasia), both are also on important flyways for avian migrants from the northern hemisphere and across the Pacific. So the inevitable arrival in Australasia may occur through multiple routes.

Various hypotheses can be put forward to explain how the virus is dispersed in sub-Antarctic and Antarctic landscapes. The role of species that feed on carcasses is highlighted, as these are likely to be highly exposed to the virus when feeding (Figures 2, 3 and 4A) and then to disperse it during their subsequent movements.

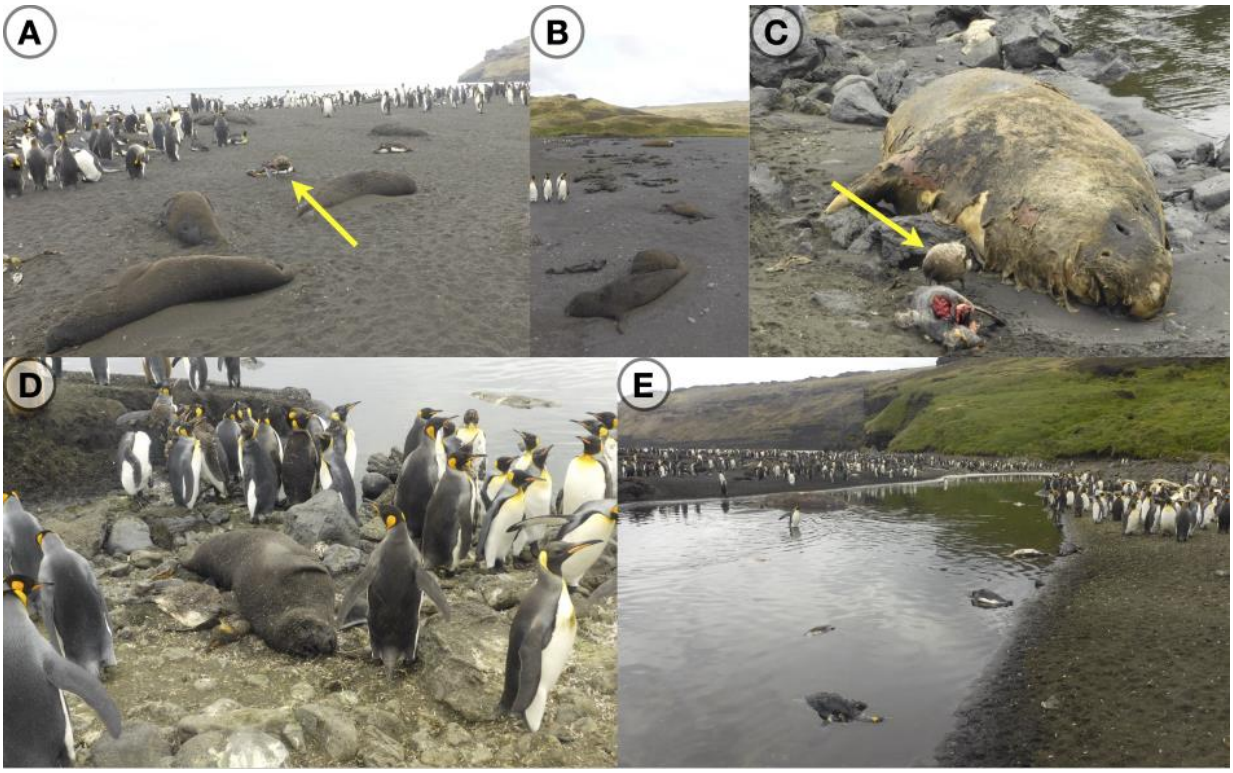

Figure 2: Dead elephant seals and king penguins carcasses on Possession Island in Crozet Archipelago, where abnormal mortality was detected in October 2024. The yellow arrow indicates the presence of a brown skua (Stercorarius antarcticus) feeding on a king penguin carcass. *Source: Clessin et al. 2025, Nature Communications. Copyright: Jérémy Tornos/CNRS/IPEV.*

Transmission could occur on land, at or near the colonies of other species, or at sea, particularly through floating carcasses. Work is underway to explore these different hypotheses. Some species may be much less likely to die when exposed to the virus, which could make them good candidates for contributing to dispersal events. Several questions arise: do certain species in these ecosystems excrete especially strongly the virus when individuals are infected? Do infected individuals change their movements? The virus is excreted for a limited time by an infected individual, so transmission must occur fairly quickly. A large proportion of species in the sub-Antarctic and Antarctic islands undertake long migrations, covering several thousand kilometres each year, but movements that occur during the breeding season, during the incubation period of the egg or the rearing of the chick, are also likely to play an important role in the regional dispersal of the virus. In these marine vertebrate species, movements during breeding and winter have been studied in detail for more than twenty years now, using micro-electronic devices that can be temporarily attached to individuals. The deployment of

these devices and the use of data that can be retrieved by various means (satellite transmission, radio, or by recovering the device when the individual is recaptured a few days, weeks or years after deployment) require specific competences, in particular a detailed knowledge of the ecology of the species. The use of this type of knowledge must be combined with the acquisition of epidemiological data also collected in the field, from samples taken from carcasses or living individuals (Figure 4B). The collection of samples for virus detection and sequencing requires special technical skills and, of course, precautions to avoid any risk of exposure to the virus or contributing to its spread. In this regard, stringent recommendations have been made by expert groups on HPAI in wildlife from various international bodies, such as the Antarctic Wildlife Health Working Group (AWHWG) managed by the Scientific Committee on Antarctic Research (SCAR) or the HPAI H5N1 Group of the Agreement on the Conservation of Albatrosses and Petrels (ACAP)[2]. The recommendations concern in particular the measures to be taken in terms of biosecurity: wearing personal protective equipment, prohibiting access to areas likely to be contaminated, except by trained personnel taking strict precautions in terms of disinfection. Given the types of movements made by different species and what has been observed in recent years, it is expected that the virus will continue to spread to other sites not yet affected, which is a source of great concern for the Australian and New Zealand sub-Antarctic islands, particularly Macquarie Island and the Snares, Bounty, Antipodes, Auckland and Campbell archipelagos. Like the French Southern Territories, these islands are listed as UNESCO World Heritage sites. It is important that eco-epidemiological surveillance be carried out in these territories.

Assessing the effects of HPAI on populations, communities and ecosystems is complex. Carcass counts and breeding monitoring in colonies provide an indication of the short-term impact on populations, particularly during periods of high mortality. However, these counts are subject to sources of uncertainty that can be significant. To surmount this uncertainty, animal demography studies typically use monitoring of live individuals to estimate annual adult survival rates, to which the growth rates of long-lived species such as seabirds and pinnipeds are especially sensitive. The methods used, known as capture-mark-recapture, require the handling of individuals, at least initially, and are carried out

[2] The Council of Managers of National Antarctic Programs (COMNAP) has established a project 'HPAI Preparedness, Monitoring and Response' to assist engagement across the full range of states active in Antarctica. Given the now limited actual contact with the Russian scientific community, this may be particularly important in keeping channels open on HPAI risk management.

at specific sites, where monitoring must be maintained over the long term. As a reference, a wandering albatross can live for more than 50 years and most seabird species live for several decades. In sub-Antarctic and Antarctic areas, many available data series date back several decades. They have been acquired through long-term projects supported by organisations such as the French Polar Institute Paul-Émile Victor (IPEV). They are generally used to assess population response to environmental changes, such as climate change or food resource availability. They are now also essential to assess the possible long-term effects of a *panzootic disease* ('an epizootic disease that can spread across all continents and affect several or all animal species') such as HPAI.

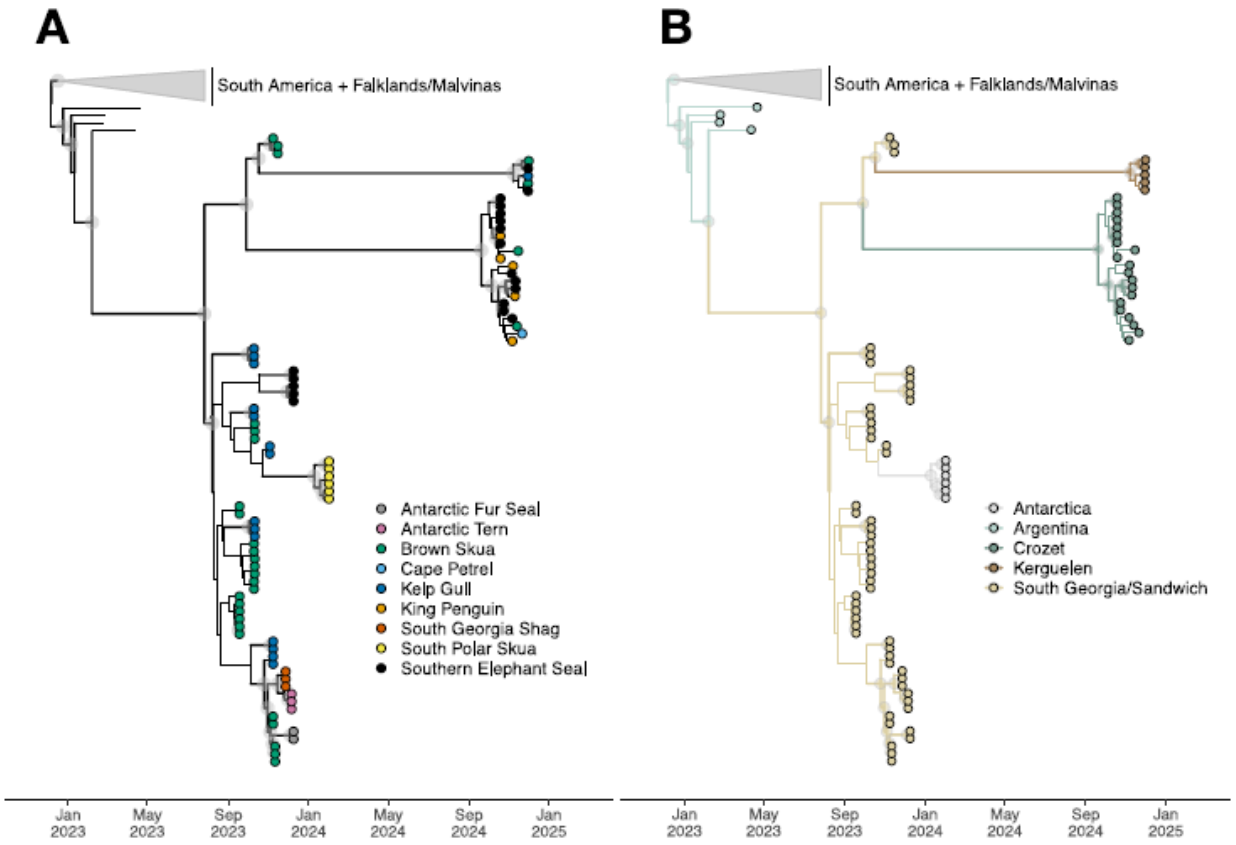

Figure 3: Phylogenetic trees reconstructed from viral RNA sequences obtained from tissue samples taken from the carcasses of seabirds and pinnipeds, collected in particular on Crozet and Kerguelen in 2024. The species and sampling locations are indicated on trees A and B, respectively. Work carried out in collaboration with the ANSES (*Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail*) enabled us to isolate and sequence the H5N1 HP clade 2.3.4.4b virus in the Indian Ocean for the first time and to perform phylogenetic analyses based on virus sequences obtained from different species. The results show (A) that the virus is shared between mammal and bird species at the same sites and that (B) the virus is genetically closest to viruses sequenced the previous year in South Georgia, more than 5,000 km from the French Southern Territories. This highlights the speed at which the virus is spreading and shows that Australia and New Zealand are at high risk of the virus arriving in the near future. *Source: Clessin et al. 2025, Nature Communications.*

Field monitoring will need to include the collection of specific data, in particular to ascertain, as far as possible, whether the HPAI virus was involved in the deaths observed.

Similarly, it will be crucial to use serological data to determine which individuals or populations were exposed to the virus but survived. On Possession Island, in Crozet Archipelago, such data is already available for the years preceding the emergence of HPAI. For Crozet and Kerguelen archipelagos, an inter-project on the impact of HPAI has been set up to coordinate the involvement of IPEV project teams working on different aspects of the ecology of seabirds and marine mammals and teams from the TAAF administration's Environment Department. In addition to this long-term work, it would be important to explore the situation at sites that have not been studied since the emergence of HPAI.

Figure 4A: Species of scavengers around the remains of a king penguin carcass: from left to right, a lesser sheathbill (*Chionis minor*), a brown skua, a northern giant petrel (*Macronectes halli*) and a kelp gull (*Larus dominicanus*). *Copyright: Thierry Boulinier/CNRS/IPEV.*

Figure 4B: Member of the IPEV-ECOPATH research programme team at the Centre for Functional and Evolutionary Ecology (CNRS-University of Montpellier-EPHE-IRD) performing an antigen test in the field wearing personal protective equipment. *Copyright: Mathilde Lejeune/CNRS/IPEV.*

The ecology and evolution of the virus is studied in relation to the ecology of the affected species in order to clarify the risks of spread to other areas, local re-emergence and *endemicity* ('the process of making a disease or phenomenon permanent in a given region') in sub-Antarctic and Antarctic areas, which requires a concerted research effort to enable integrated monitoring of the dynamics at play. The ecology of the movement of different species is particularly important to consider, as is the detailed evolution of the virus through the collection of samples from multiple sites and multiple species, during the austral summer, but also at other times of the year. This work must be based on international collaboration, which requires ensuring that the means to support research are available in the field, as well as in laboratories. Until recently, relatively little effort had been made in terms of surveillance and research on infectious diseases in the southern polar region, but it is clear that a '*One Health*' *approach* ('an integrated, unifying approach that aims to sustainably balance and optimise the health of people, animals, and ecosystems') is important to develop. It will need to be based on internationally

supported programmes, in conjunction with the initiatives already undertaken by various teams and countries.

In addition to the need to document impacts and understand eco-epidemiological processes in order to predict future developments, it is also vital to consider possible means of mitigating the effects of transmission risks. In particular, it is essential to follow strict biosecurity measures to prevent exposure of personnel to the virus, but also to prevent the spread of the virus. This recommendation is becoming increasingly important in the context of expanding tourism[3] and human activities in the Southern Polar Region. HPAI vaccine trials have also been set up, although their possible use could only be considered under very distinct conditions, particularly for highly threatened populations[4].

In summary, the arrival of HPAI virus in sub-Antarctic and Antarctic regions is a major event for these ecosystems, and it is essential to continue documenting the interactions between birds, marine mammals and the virus, taking into account virological and veterinary aspects, but also in relation to the ecology of the species involved, particularly scavenging seabirds and species that are more or less threatened. The health and ecological threat posed by such infectious agents can no longer be ignored and requires increased vigilance on these issues, proactive biosecurity measures, and continued integrated monitoring and research at different spatial scales, not only in Antarctica but also in sub-Antarctic islands. The processes at play are a stark reminder of the vulnerability of isolated ecosystems to infectious diseases and the need to mitigate the already persistent pressures on globally important seabird and marine mammal populations, including overexploitation of the marine environment, climate change, habitat degradation and disturbance, and invasive species, in order to strengthen their resilience.

Thierry BOULINIER[5] for POLAR WATCH[6]

[3] In consultation with the SCAR (AWHWG), additional protocols regarding Avian Influenza have been introduced to IAATO's (International Association of Antarctic Tour Operators) standard biosecurity procedures.

[4] Lejeune et al. 2026, *Nature Communications*.

[5] Director of Research at CNRS in Evolutionary Ecology and Disease Ecology, Centre for Functional and Evolutionary Ecology, Université de Montpellier, France.

[6] The views expressed in this article are those of the author. They do not reflect the official policy or position of any entities of which the author is or was a member.

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