No evidence for highly pathogenic avian influenza virus H5N1 (clade 2.3.4.4b) in the Antarctic region during the austral summer 2022/23

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Abstract

The current highly pathogenic avian influenza H5N1 panzootic has profound impacts on wild birds. Herein, we compiled H5N1 surveillance from Antarctica and Sub-Antarctic Islands to ascertain whether HPAI was present in this region. Observations and HPAI testing indicated no incursion of the virus during the austral summer 2022/23.

Main text

The increasing intensity of highly pathogenic avian influenza virus (HPAIV) H5N1 clade 2.3.4.4b outbreaks have had a profound impact on poultry and wildlife (1). Wild bird movements have underpinned the rapid spread of this virus that swept across most continents within two years (2). Compared to previous HPAIV subtypes and clades, H5N1 2.3.4.4b has significantly improved replication in wild birds (3), and increased fitness through continuous reassortments (4). Also, the virus is able to infect an unusually broad variety of wild bird species (3), which has likely facilitated this spread. In addition to their role as viral spreaders, wild birds are suffering huge losses following mass mortality events, and the scale of mortality amongst wild birds is likely in the millions rather than tens of thousands reported (5). Thus, the recent panzootic is a serious conservation concern for a large range of wild bird species.

Due to the absence of waterfowl species that migrate to the Antarctic and sub-Antarctic islands, the incursion risk of HPAI in notably these southernmost regions had previously been considered low. Still, waterfowl are present in northern fringes of the Southern Ocean.

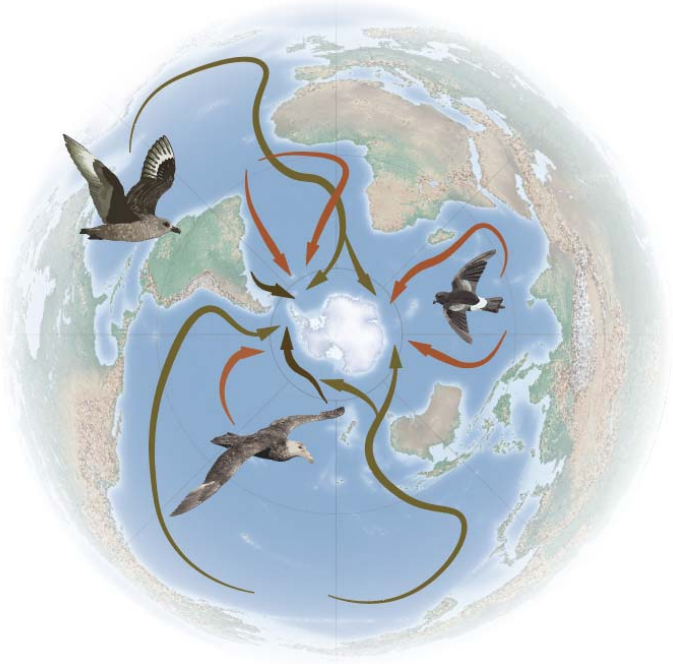

Figure 1: Seabird migration routes connect the world's oceans with Antarctic and sub-Antarctic breeding sites. The south polar skua (Catharacta maccormicki) provides an example of trans-hemispheric migrations (brown arrows, top left image). Brown skuas (Catharacta antarcticus), Giant Petrels (Macronectes giganteus & halli, dark arrows, bottom image) and a whole range of albatross species remain south but can be seen in waters of South America, southern Africa, New Zealand, and Australia. Map made with Natural Earth.

Moreover, the millions of seabirds that breed in the Antarctic region, and known migration and post-breeding dispersal routes establish links and thereby substantial global connectivity (Figure 1), including with regions of recent HPAIV H5N1 outbreaks. And despite the perceived remoteness, LPAIV viruses and antibodies against these viruses have previously been detected in various seabird species nesting at sites along the Antarctic Peninsula and South Shetland Islands, with viral genomes illustrating high phylogenetic relationships to viruses circulating on other continents (6, 7). As a result, experts have considered the risk of incursion of the recent panzootic HPAI H5 viruses into the Antarctic region in 2022/23 summer season to be high (8).

To identify a possible incursion of H5N1 into in Antarctic region during the summer season 2022/23, we sampled migratory seabirds at different locations across Antarctica and in sub-Antarctic areas (Figure 2), and collated observation data from researchers working in and around seabird colonies. In particular, we aimed to collect information pertaining to suspicious signs of unusual mortality and known clinical signs of HPAIV infection including loss of coordination and balance, trembling head and body, lethargy, respiratory distress, and conjunctivitis (8). Across all locations, sample collection was done in accordance with institutional animal ethics approval and sample testing was performed with national frameworks, with details available in the technical annex.

Overall, sampling and observational efforts span from early November to late March, comprising the entire austral breeding season in 2022/23, and include a large range of species (i.e., penguins, gulls, skuas, and petrels; see technical annex for more information) and locations. All swab samples collected were tested negative for avian influence virus and thus for HPAI. Several suspicious observations of dead wild birds were recorded on the Falkland Islands (Gentoo penguin *Pygoscelis papua*, Cattle egret *Bubulcus ibis*), and South Georgia (Wandering albatrosses *Diomedea exulans)* and confirmed negative for HPAI based on qPCR testing. Taken together, and with the general lack of suspicious signs of HPAIV, we conclude that there is no evidence of HPAIV H5N1 clade 2.3.4.4b incursion into the Antarctic region during the austral summer 2022/23.

Obviously, incursion risk of HPAIV is contingent on a combination of factors. Most importantly, that (i) host species get in contact with HPAIV before travelling into the Antarctic regions, (ii) can migrate with an infection, and (iii) have contact with further susceptible species which could be the starting point of a new epizootic. While HPAIV (including H5N1) activity has occurred in South African seabirds since 2017, HPAIV did

not reach South America until ~Oct 2022, and Patagonia and Tierra del Fuego until early 2023 (2, 9, 10). Furthermore, while mainly ducks were previously central to HPAIV outbreaks, the global panzootic includes a large range of bird species, and increasingly novel species groups like seabirds (11). Notably in breeding colonies of seabirds, there have been extensive outbreaks in Europe in 2022 and 2023, and the southward expansion of HPAIV H5N1 in South America was largely driven through outbreaks in coastal seabirds, including pelicans and cormorants, as well as spill-overs to coastal marine mammals with the deaths of >20,000 South American sea lions (3, 9, 12, 13). Millions of seabirds and marine mammals will again return to the Antarctic region during the austral summer (Oct 2023 - Mar 2024), and with H5N1 outbreaks now occurring very close to the Falkland Island and the Antarctic peninsula. Thus, the risk of viral incursion will be even higher compared to 2022 (14).

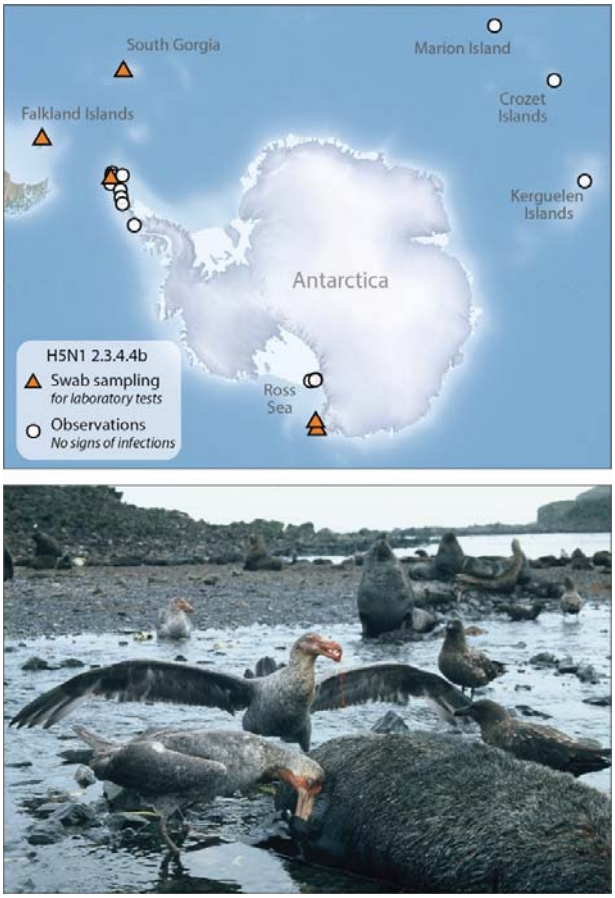

Figure 2: (top) Sampling locations for qPCR analysis and the detection of H5N1 2.3.4.4b, as well as locations with intensive observational efforts to identify signs of HPAIV infections within breeding bird communities. (bottom) Northern giant petrels and Brown skuas scavenging on an Antarctic fur seal carcass, showing inter-species interactions with the potential for HPAI virus transmission (photo taken on South Georgia by Paulo Catry).

The consequences of viral incursion(s) into Southern Ocean wildlife are unclear but based on observations from other regions, will likely have devastating effects. Critically, densities of seabird colonies are very, facilitating the transmissions between individuals (15). Further prospecting movements of potential recruits, predator-prey interactions between bird species (e.g., skuas, penguins, and sheathbills), as well as species scavenging on dead seabirds and mammals, may promote rapid spread of the virus between colonies. The interaction between seabirds and marine mammals in the Antarctic region may also result in further transmissions to mammals and facilitate the adaptation of the virus in mammalian species. Finally, most animals of the Southern Ocean are endemic to the region, such that mass mortality events in Antarctica due to HPAI H5 will cause a very real conservation concern for many species.

Detecting H5N1 incursion(s) into the Antarctic region is highly relevant and surveys for mortality and sampling should therefore be prioritized during the austral summer 2023/24. These activities should be undertaken with consideration of the potentially zoonotic risks of (emerging) HPAIV H5 risks (see details in 8). Importantly, activities should not promote virus transmission within colonies nor the spatial spread between colonies and species. Nevertheless, sampling, and detailed analysis of lineages and virus phenotype will provide crucial information needed to assess risks and respond to future wild bird outbreaks.

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