

1 Unexpected delayed incursion of highly 2 pathogenic avian influenza H5N1 (clade 3 2.3.4.4b) in the Antarctic region

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17 Abstract

18 The current highly pathogenic avian influenza H5N1 panzootic has substantial impacts
19 on wild birds and marine mammals. Although major outbreaks occurred in South
20 America, incursion to Antarctica emerged late in the breeding season of 2023/2024 and
21 was confined the wider region of the Antarctic Peninsula. To infer potential underlying
22 processes, we compiled H5N1 surveillance from Antarctica and Sub-Antarctic Islands
23 prior to the first confirmed cases.

24 Main text

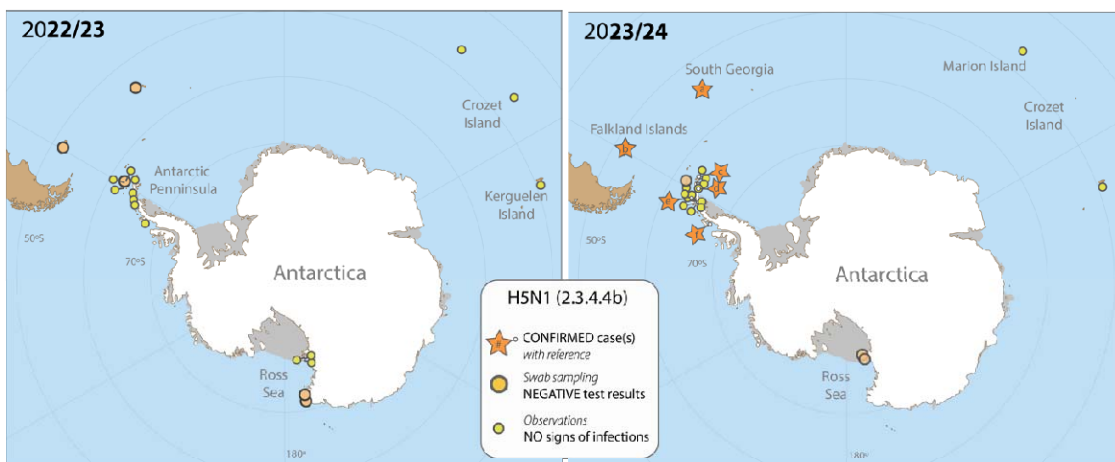
25 The increasing intensity of highly pathogenic avian influenza virus (HPAIV) H5N1
26 clade 2.3.4.4b outbreaks have had a substantial impact on poultry and wildlife ¹. Wild
27 bird movements have underpinned the rapid spread of this virus that swept across most
28 continents, except for Australia and Antarctica, within two years ². Compared to previous
29 HPAIV subtypes and clades, H5N1 2.3.4.4b has significantly improved replication in wild
30 birds ³, and increased fitness through continuous reassortments ⁴ which has likely
31 contributed to a shift in infection dynamics leading to the infection of a broader range of
32 avian species ¹. In addition to their role as viral spreaders, wild birds are suffering huge
33 losses following mass mortality events, and the scale of mortality amongst wild birds is
34 likely in the millions rather than tens of thousands reported ⁵. Thus, the recent panzootic
35 is a serious conservation concern for a large range of wild bird species.

36 Due to the absence of waterfowl species that migrate to the Antarctic and sub-
37 Antarctic islands, the incursion risk of HPAIV in these southernmost regions had been
38 considered low prior to 2021. However, waterfowl are present in northern fringes of the
39 Southern Ocean, and millions of known migration and post-breeding dispersal routes
40 establish links and thereby substantial global connectivity, including with regions of
41 recent HPAI H5N1 outbreaks involving seabirds and marine mammals ². Despite the
42 perceived remoteness, low pathogenicity avian influenza viruses and antibodies against
43 these viruses have previously been detected in various seabird species nesting at sites
44 along the Antarctic Peninsula and South Shetland Islands, with viral genomes illustrating
45 phylogenetic connectivity to viruses circulating on other continents ^{6,7}. As a result, the
46 Scientific Committee on Antarctic Research (SCAR) Antarctic Wildlife Health Network
47 (AWHN) had considered the risk of incursion of the recent panzootic HPAIV H5 into the
48 Antarctic region in 2022/23 summer season to be high ⁸, and considerably higher in
49 2023/24 following virus spread to the southernmost regions of South America ⁹, infecting

50 seabirds including Magellanic penguins (*Spheniscus magellanicus*) and Humboldt
51 penguins (*Spheniscus humboldti*), and several species of marine mammals (9).

52 To identify possible incursions of H5N1 into the Antarctic region during the
53 summer season 2022/23 and the early season 2023/24, we sampled migratory seabirds
54 at different locations across Antarctica and in sub-Antarctic areas (Figure 1), and
55 collated a range of observation data. Here, we define Antarctica as the region south of
56 the Antarctic Convergence and sub-Antarctic areas include adjacent Islands within the
57 Southern Ocean. In particular, we aimed to collect information pertaining to suspicious
58 signs of unusual mortality and known clinical signs of HPAIV infection including loss of
59 coordination and balance, trembling head and body, lethargy, respiratory distress, and
60 conjunctivitis⁸. Across all locations, sample collection was done in accordance with
61 institutional animal ethics approval and sample testing was performed with national
62 frameworks, with details available in the technical annex.

63



64

65 *Figure 1: Sampling locations for qPCR analysis and the detection of H5N1 2.3.4.4b, as well as*
66 *locations with intensive observational efforts to identify signs of HPAI infections within breeding bird*
67 *communities for the breeding season 2022/23 (left) and 2023/24 (right). In addition, locations of*
68 *confirmed cases of infection in 2023/24 (left) are included. Numbers refer to the following references,*
69 *(a) technical annex, (b)¹⁰, (c, e)¹¹, (d, f)¹². Maps created with Natural Earth.*

70

71 Overall, sampling and observational efforts were conducted from early November
72 2022 to late March 2023, and from October 2023 onwards until the end of February in
73 2024. Surveillance efforts included a large range of species (*i.e.*, penguins, gulls, skuas,
74 and petrels; see technical annex for more information) and locations. In 2022/23,
75 samples for HPAIV testing were collected from apparently healthy birds from 20
76 locations in the sub-Antarctic and Antarctic Region. There were several suspicious
77 observations of dead wild birds on the Falkland Islands (Gentoo penguin *Pygoscelis*

78 *papua*, Cattle egret *Bubulcus ibis*), and South Georgia (Wandering albatrosses
79 *Diomedea exulans*). However, all swab samples collected from these animals, in
80 addition to apparently healthy wild birds in other locations were negative for HPAI (see
81 technical annex for details on location and species). Together, this strongly suggests
82 that HPAIV H5N1 clade 2.3.4.4b did not enter the Antarctic region during the austral
83 summer 2022/23, and that the lack of detection was unlikely due to lack of surveillance,
84 testing or disease investigations. This is in contrast to the seabird breeding season
85 2023/24. In October 2023 the first confirmed H5N1 cases were detected on the Falkland
86 (Malvinas) Islands, and in November on South Georgia Island in the sub-Antarctic ^{10,12}
87 (Figure 1). Given the overlap of species breeding and migrating via the Falkland Island
88 and South Georgia towards the Antarctic Peninsula and its offshore Islands (e.g., the
89 South Shetland Islands), researchers in the region and the tourist industry have been
90 very diligent in identifying unusual bird behaviour and mortality events. Despite active
91 cases in the Falkland Islands and South Georgia Island, sample collection and
92 observations from 16 locations between November 2023 – early February 2024 in the
93 Antarctic Peninsula and related island were negative for HPAIV. Data from the SCAR
94 monitoring project did, however, report suspected cases in the Antarctic region starting
95 in December 2023 ¹². These include Brown Skuas on the South Orkney Islands in
96 December 2023 (no samples collected), a mortality in Brown Skuas on Heronia Island in
97 December 2023 (samples collected, HPAIV negative). Since mid-February several
98 positive cases were reported from the Antarctic Peninsula (see Figure 1). This suggests
99 that H5N1 was spread among colonies in the later breeding season, however, so far
100 there is no evidence for large outbreaks on the Antarctic Peninsula. Further, based on
101 observation data, the strain did not appear to have reached the Indian Ocean sub-
102 Antarctic islands as of February 2024 (see technical annex).

103 Obviously, incursion risk, and successful establishment of HPAIV is contingent on
104 a combination of factors. Most importantly, that (i) host species get in contact with
105 HPAIV before travelling into the Antarctic regions, (ii) can migrate with an infection, and
106 (iii) have contact and transmit the virus to susceptible species which could be the
107 starting point of a new epizootic. Most species occupying the Antarctic region are
108 pelagic seabirds with little to no contact with terrestrial birds such as waterfowl,
109 significantly reducing their exposure to outbreaks on land (e.g. South America).
110 However, some species like the Brown skua (*Stercorarius antarcticus*) and the giant
111 petrel species (*Macronectes sp.*) are known scavengers (Figure 2), leading to high risks
112 of exposure to HPAIV via the consumption of infected carcasses. It is thus no surprise

113 that Brown skuas were often among the first confirmed cases both on South Georgia
114 and the Antarctic Peninsula¹⁰. This species, which can be observed at shorelines of
115 South America, the Falkland Islands and South Georgia¹³, is likely to be an important
116 player in spreading the virus. Yet, it seems that the connectivity established by the
117 animals' movements from South America and South Georgia over the Drake Passage to
118 Antarctica is rather limited during the breeding season but might increase again towards
119 the end when the breeding activities terminate, and the movement range of both adults
120 and first juveniles are becoming larger again. Together with the increasing number of
121 naïve juveniles and concomitant changes in densities, this may explain the delay
122 between initial outbreaks in the Falklands/South Georgia and the first confirmed cases
123 on the Antarctic peninsula.
124



125
126
127 *Figure 2: Northern giant petrels and Brown skuas scavenging on an Antarctic fur seal carcass,*
128 *showing inter-species interactions with the potential for HPAI virus transmission (photo taken on*
129 *South Georgia by Paulo Catry).*

130
131 Still, the consequences of viral incursion(s) into Southern Ocean wildlife are
132 unclear but based on observations from other regions, will likely have devastating
133 effects. Critically, densities of seabird colonies are very high, facilitating the
134 transmissions between individuals¹⁴. Further prospecting movements of potential
135 recruits, predator-prey interactions between bird species (e.g., skuas, penguins, and
136 sheathbills), as well as species scavenging on dead seabirds and mammals, may
137 promote rapid spread of the virus between colonies¹⁵. Once the virus has been
138 established in the region, interaction between seabirds and marine mammals may also
139 result in further transmissions and facilitate the adaptation of the virus in mammalian

140 species¹⁴. Finally, most animals of the Southern Ocean are endemic to the region, such
141 that mass mortality events in Antarctica due to HPAIV H5 will cause a very real
142 conservation concern for many species.

143 Detecting H5N1 incursion(s) and describing the infection dynamics into and
144 within the sub-Antarctic and Antarctic regions is highly relevant and standardized
145 surveys for mortality and sampling should therefore be prioritized. These activities
146 should be undertaken with consideration of the potentially zoonotic risks of (emerging)
147 HPAIV H5⁸ and require strict hygiene measures to prevent the spread of the virus
148 through human activities. Sampling and detailed analysis of lineages and virus
149 phenotype will provide crucial information needed to assess risks and respond to future
150 wild bird outbreaks.

151

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