

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

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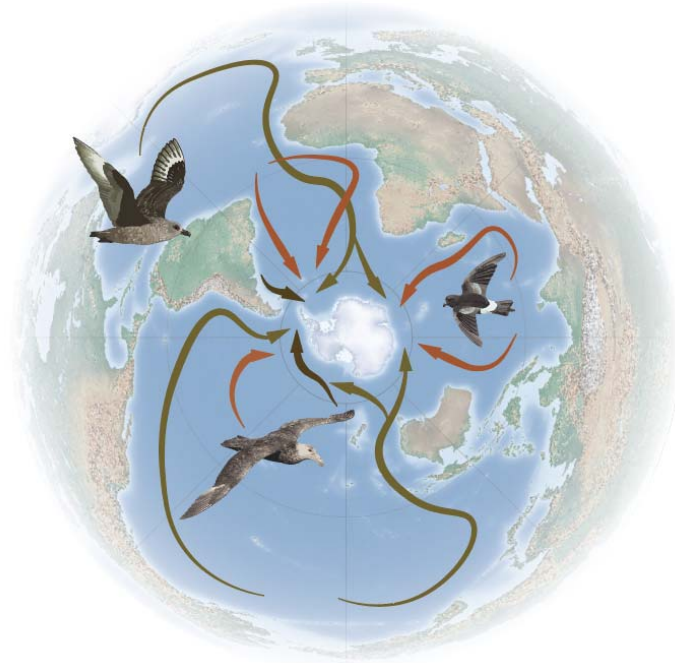
54 **Abstract**

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

59 Main text

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

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



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

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

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

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

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

116 not reach South America until ~Oct 2022, and Patagonia and Tierra del Fuego until early
117 2023 (2, 9, 10). Furthermore, while mainly ducks were previously central to HPAIV
118 outbreaks, the global panzootic includes a large range of bird species, and increasingly
119 novel species groups like seabirds (11). Notably in breeding colonies of seabirds, there
120 have been extensive outbreaks in Europe in 2022 and 2023, and the southward
121 expansion of HPAIV H5N1 in South America was largely driven through outbreaks in
122 coastal seabirds, including pelicans and cormorants, as well as spill-overs to coastal
123 marine mammals with the deaths of >20,000 South American sea lions (3, 9, 12, 13).
124 Millions of seabirds and marine mammals will again return to the Antarctic region during
125 the austral summer (Oct 2023 - Mar 2024), and with H5N1 outbreaks now occurring very
126 close to the Falkland Island and the Antarctic peninsula. Thus, the risk of viral incursion
127 will be even higher compared to 2022 (14).
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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).

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137 The consequences of viral incursion(s) into Southern Ocean wildlife are unclear
138 but based on observations from other regions, will likely have devastating effects.

139 Critically, densities of seabird colonies are very, facilitating the transmissions between
140 individuals (15). Further prospecting movements of potential recruits, predator-prey
141 interactions between bird species (e.g., skuas, penguins, and sheathbills), as well as
142 species scavenging on dead seabirds and mammals, may promote rapid spread of the
143 virus between colonies. The interaction between seabirds and marine mammals in the
144 Antarctic region may also result in further transmissions to mammals and facilitate the
145 adaptation of the virus in mammalian species. Finally, most animals of the Southern
146 Ocean are endemic to the region, such that mass mortality events in Antarctica due to
147 HPAI H5 will cause a very real conservation concern for many species.

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

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