

A summary of Avian Influenza Virus in Antarctic penguins

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Penguins on the Antarctic Peninsula are a vital part of polar ecology and the marine food chain, making them useful biological indicators and worthy of protection. Despite this, little is known about the viral threats facing the eight penguin species on the continent. Avian influenza viruses (AIVs) are of particular interest due to their global distribution and prevalence in migratory birds. Investigation into the possible AIV pathways into Antarctica is necessary to understand and predict future viral outbreaks.

Whilst research into AIVs in Antarctic penguins is limited due to the cost and difficulty of polar research a number of studies have provided pioneering insights. Prior to 2013, the only evidence of AIV in penguins came from serological studies, in which the presence of antibodies for the H1, H3, H7 and H9 influenza A subtypes were described in multiple species of penguins, including Adélie penguins (*Pygoscelis adeliae*) and chinstrap penguins (*Pygoscelis antarcticus*) (Morgan & Westbury, 1981; Baumeister *et al.*, 2004). In 2013, the RNA of four highly homologous H11N2 influenza A viruses were isolated from Adélie penguins in Admiralty Bay, King George Island and Rada Covadonga (Hurt *et al.*, 2014). In 2015, H5N5 influenza virus RNA was isolated from chinstrap and gentoo penguins (*Pygoscelis papua*) on Aitcho Island (Barriga *et al.*, 2016), and one chinstrap penguin on King George Island (Hurt *et al.*, 2016). Figure 1 displays the locations of each viral discovery.

Phylogenetic analysis of each of the three strains demonstrated a strong evolutionary relationship with North American AIVs. For the H11N2 virus, Hurt *et al.*, (2014) suggest a possible oral-faecal transmission route into penguin colonies via south polar skuas (*Stercorarius maccormicki*) and southern giant petrels (*Macronectes giganteus*), due to their notoriety for carrying H11 viruses, their close integration with penguin colonies, and their Antarctic migration coinciding with penguin nesting season. Barriga *et al.*, (2016) specify the Pacific-American flyway as a potential route for the H5N5 virus, theorising that shorebirds like the ruddy turnstone (*Arenaria interpres*) could act as vectors for AIVs. This is supported by the H5N5 neuraminidase segment clustering with a Eurasian clade and ruddy turnstones have previously been found to carry AIVs with Eurasian N5 segments (Kraus *et al.*, 2010). Additionally, there is a small amount of evidence for transmission via South America. One of the H5N5 viruses clustered with a strain found in Chilean kelp gulls (*Larus dominicanus*) in 2008, a species found on the Antarctic Peninsula, with two out of eight gene segments also showing South American linkage (Barriga *et al.*, 2016). However, Hurt *et al.*, (2014) notes that H11 viruses

are unreported in South American wild birds; this implies that they are not direct vectors, or that they represent one of multiple transmission routes. In summary, the virus strains found thus far implicate North American shorebirds and seabirds as a viral entryway to Antarctica, with potential input from South American gulls. However, until more penguin AIVs are analysed, routes of entry to Antarctica are uncertain.

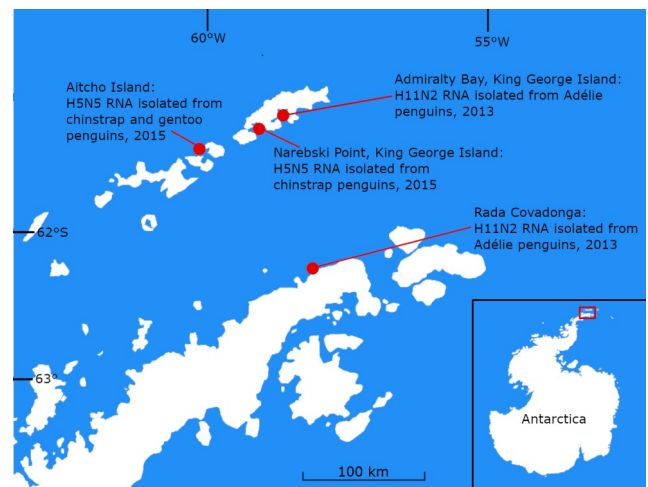


Figure 1. A map showing the four locations where viral RNA was discovered on the Antarctic Peninsula. Labels include the year of discovery, subtype of virus, and species of penguin that each virus was isolated from. The corresponding research for each location is as follows: Hurt *et al.*, (2014) for Rada Covadonga and Admiralty Bay, King George Island; Barriga *et al.*, (2016) for Aitcho Island; Hurt *et al.*, (2016) for Narebski Point, King George Island. Drawn using GNU Image Manipulation Program software (GIMP) 2.10.

At present, there is little evidence to suggest that the presence of AIVs in Antarctic penguins causes significant harm or mortality. Morgan and Westbury (1981) surveyed locations and linked an increase in Adélie chick death to a high serological AIV presence, and Barriga *et al.*, (2016) noted that the H5N5 virus samples were taken from juvenile chinstrap penguins that were “weak, depressed, and possibly ill”. These accounts are based on small samples and therefore are inconclusive, but they do demonstrate a need to thoroughly explore both the effect of AIVs on penguin species, and the likelihood of a more pathogenic virus infecting the continent. Out of the eight Antarctic penguin species, the International Union for Conservation of Nature (IUCN) list two as vulnerable, two as near-threatened, and the remaining four in least-concern category (IUCN, 2020). Despite this being a relatively mild assessment, the prognosis for penguins

may be far more serious due to their behaviour and the global threats facing their habitat. Each of these species congregate in dense breeding colonies, increasing the likelihood of airborne or faecal transmission between individuals. Consequently, if a deadly AIV strain appeared in a colony, the spread could quickly decrease population numbers. In addition, climate change is predicted to alter the populations of certain Antarctic penguin species; whilst some species appear to initially favour warmer temperatures, there is evidence to suggest that this is limited by a decline in krill quantity (Trivelpiece *et al.*, 2011). Furthermore, species that rely on sea ice for their habitat such as emperor penguins (*Aptenodytes forsteri*) and king penguins (*Aptenodytes patagonicus*) may see population decreases as global temperatures rise (Cristofari *et al.*, 2018; Barbraud & Weimerskirch, 2001). When taking these pressures into account, the vulnerability of Antarctic penguins to future disease may be significantly greater than anticipated.

To prevent a potentially devastating virus reaching Antarctic penguin colonies, it is vital to monitor AIVs and other viruses in migratory seabirds. If a highly virulent AIV strain is detected, a quick response could intercept its spread and safeguard vulnerable avian species. There should be a particular focus on avian viruses found in North and South America, as the current evidence implicates transmission via American flyways. It would also be beneficial to conduct longitudinal studies to evaluate the immune response to AIVs in Antarctic penguins, allowing a better assessment of the risk posed by viral threats. As Antarctic wildlife responds to climate change, protecting penguins from preventable disease will provide a greater understanding of Antarctic ecology whilst allowing them to remain as biological indicators for an unpredictable future.

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