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Research Article

Emergence of HPAI H5N1 Clade 2.3.4.4b in Australia's Sub-Antarctic Territory: Implications for National Preparedness and Biosecurity

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Abstract

The Australia mainland has thus far remained free from incursions of highly pathogenic avian influenza (HPAI) H5N1 clade 2.3.4.4b; however, the threat is escalating, particularly considering detections of the virus in Antarctica and Sub-Antarctic regions. While the East Asian-Australasian Flyway (EAAF) has been the primary hypothesised route for potential introduction, the emergence of cases in southern polar regions also highlights the need to consider the Southern Ocean Flyway as a credible transmission pathway.

Keywords: Heard Island, HPAI H5N1, Clade 2.3.4.4b, Australia

Introduction

Confirmation of HPAI H5N1 clade 2.3.4.4b in samples from Heard Island

Recently, Australian researchers have reported unusual mortality among southern elephant seals (Mirounga leonina) on Heard Island, a remote Sub-Antarctic territory of Australia. The clinical presentation of the affected elephant seals strongly resembled that of HPAI, and subsequent pathology results confirmed the presence of the globally circulating HPAI H5N1 clade 2.3.4.4b virus (Tracy, 2025). No mortality events have been observed among other species on Heard Island as of December 2025 (Tracy, 2025). This detection raises significant concern regarding its potential incursion of the virus into mainland Australia. Heard Island and McDonald Islands (HIMI), located in the Southern Ocean approximately 4,100 km south-west of Perth and 1,700 km north of Antarctica (Australian Antarctic Program, 2025), support a diverse array of seabirds, including several penguin species, as well as marine mammals such as elephant seals. Of particular concern is the proximity of the Crozet and Kerguelen Islands—about 460 km away from Heard Island, where detections of HPAI H5N1 clade 2.3.4.4b were reported in October 2024 (Clessin et al., 2025).

Emerging concerns of HPAI H5N1 outbreaks based on Southern Ocean observations

The spread of the virus to Sub-Antarctic islands and continental Antarctica represents an unprecedented geographic spread, facilitated by migratory flyways. Since 2023, notable detections have been reported from South Georgia, the Falkland Islands, King Edward Point, and the Primavera Base on the Antarctic Peninsula (Lisovski et al., 2024). Affected species include a range of avian and pinniped populations, such as penguins, skuas, fulmars, albatrosses, and elephant seals. The detections on the Falkland Islands are likely attributable to avian migration from South America, where the virus has had catastrophic impacts on marine wildlife (Bruno et al., 2025). The confirmation of HPAI H5N1 clade 2.3.4.4b among elephant seals on Heard Island represents a significant epidemiological development, underscoring the urgent need for heightened vigilance, preparedness, and strengthened biosecurity measures to mitigate the risk of HPAI H5N1 clade 2.3.4.4b introduction into mainland Australia.

A significant threat to Australia's animal health arising from the virus's accelerated mutation and adaptive capacity

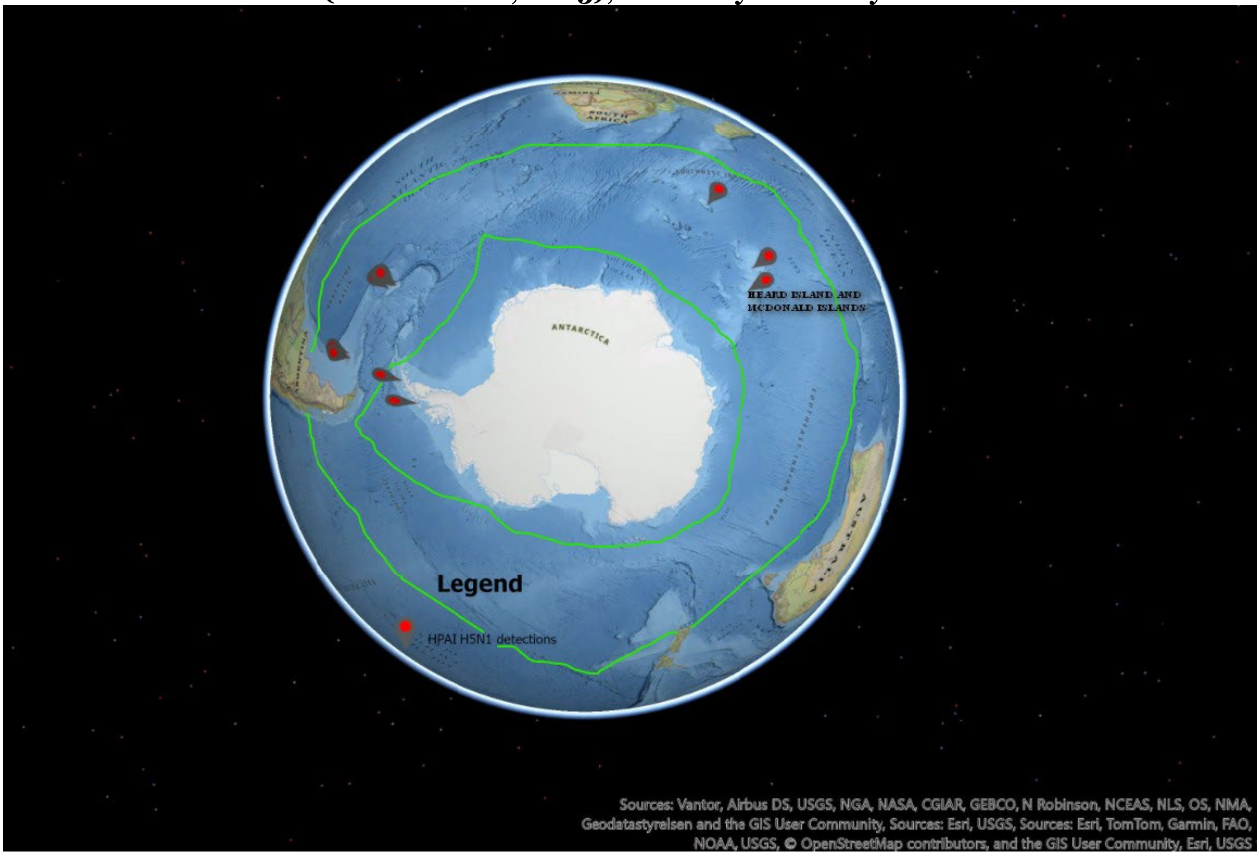
HPAI H5N1 clade 2.3.4.4b could pose an enormous threat to Australia's poultry and endemic wildlife, given its demonstrated capacity for rapid genomic mutation and adaptation to new hosts. The current HPAI H5N1 strain was first identified in poultry in Guangdong Province, China, in 1996. Since then, it has diversified into multiple clades, with clade 2.3.4.4b emerging in 2020 as a globally dominant lineage (Bruno et al., 2025). Initially detected in Europe, it has since spread to nearly all continents, excluding mainland Australia, resulting in the largest recorded panzootic of HPAI. The impact on animal health has been substantial, underscoring the seriousness of the threat (Hunter, 2022). The virus has exhibited a strong ability to reassort with locally circulating low-pathogenic avian influenza (LPAI) viruses, leading to the emergence of novel genotypes with expanded host range, altered pathogenicity, and potentially increased zoonotic potential. In North America, reassortment between Eurasian-origin H5N1 and endemic LPAI strains in wild birds and poultry has produced over 100 genotypes (Tawidian et al., 2024). In addition, HPAI H5N1 infections have been reported across a broad range of mammalian species (US Department of Agriculture, 2025). Notably, the United States has reported the largest known outbreaks of H5N1 in dairy cattle, marking the first widespread detections of HPAI in this species. These cases are likely linked to key genomic mutations that facilitate viral adaptation to mammalian hosts, particularly in the hemagglutinin (HA), neuraminidase (NA), and polymerase basic protein 2 (PB2) genes. Clade 2.3.4.4b H5N1 viruses have been found to possess a distinctive long-stalk NA structure (Hermann & Krammer, 2025), which may enhance viral fitness and facilitate extended transmission in mammals. In bovine isolates, HA may have demonstrated dual-receptor binding specificity to both avian-like α2,3-linked and human-like α2,6-linked sialic acid receptors, potentially enabling zoonotic transmission (Eisfeld et al., 2024). Furthermore, mutations such as PB2-E627K and PB2-D701N, frequently identified in mammalian isolates—particularly in the Americas—are known to augment replication efficiency in mammalian cells (Uhart et al., 2024). Significantly, in addition to spillover events, spillback transmissions, whereby infected mammals transmit H5N1 back to avian species, have been documented in farm and coastal environments, involving transmission from cattle to wild birds (Peacock et al., 2025), and from marine mammals to coastal birds and a human case in Argentina and Chile (Uhart et al., 2024), illustrating the complexity of the virus's transmission dynamics.

Australia, which has historically harboured a variety of LPAI viruses within wild avian populations (Wille et al., 2022), remains vulnerable. In the event of the introduction of HPAI H5N1 clade 2.3.4.4b, reassortment with local LPAI strains is probable, potentially leading to the emergence of novel genotypes with unpredictable pathogenicity and host range. The consequences of such developments could be significant, underscoring the imperative for proactive surveillance, preparedness, and biosecurity measures.

Surveillance imperatives across Sub-Antarctic and Southern Australian regions for national preparedness and biosecurity

Enhanced surveillance of marine wildlife on Australia's Sub-Antarctic islands, particularly Macquarie Island, is essential to prepare against potential incursion of HPAI H5N1 clade 2.3.4.4b into mainland Australia. Notably, Macquarie Island, located in the Southern Ocean approximately 1,500 km southeast of Tasmania, lies along migratory flyways that connect Sub-Antarctic ecosystems with the southern coast of Australia. It is approximately 5,283 km from Heard Island (Australian Antarctic Program, 2022). Many marine species, including elephant seals and some seabirds, migrate between Sub-Antarctic islands and regions of Australia such as South Australia, Tasmania, and Victoria, creating ecological connectivity that may facilitate viral spread (Serafini & de Contaminação Aquática, 2023). Strengthened biosecurity measures across these southern coastal regions are critical to ensuring early detection of suspected or confirmed avian influenza cases in both wild and domestic avian and mammalian populations. Of particular concern is the significant surge of HPAI H7 avian influenza outbreaks in Victoria between 2024 and 2025, including seven HPAI H7N3 outbreaks near Meridith and five near Lethbridge, one HPAI H7N9 outbreak near Terang, and three HPAI H7N8 outbreaks near Euroa (Kumar et al., 2024; World Organization for Animal Health, 2025). The emergence of these HPAI subtypes (H7N3, H7N8, and H7N9) highlights increased environmental and virological interaction at the poultry-wild bird interface. A critical next step is to implement coordinated surveillance and response strategies across Sub-Antarctic and Southern Australian regions to mitigate the risk of viral introduction and spread via Southern Ocean Flyway **(Figure 1)**.

Figure 1: Distributions of HPAI H5N1 detections across the Southern Ocean Region (World Organization for Animal Health, 2025). The green boundary denotes the Southern Ocean Flyway (Morten et al., 2025), manually drawn by the author.



Sources: Vantor, Airbus DS, USGS, NGA, NASA, CGIAR, GEBCO, N Robinson, NCEAS, NLS, OS, NMA, Geodatastyrelsen and the GIS User Community, Sources: Esri, USGS, Sources: Esri, TomTom, Garmin, FAO, NOAA, USGS, © OpenStreetMap contributors, and the GIS User Community, Esri, USGS

Ethics and Consent

This rapid report used open-source data and did not involve human participants or animal research; therefore, ethics approval was not required.

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