

Letter to the Editor: Australia's first detection of HPAI H5N1 in a wild bird: a regional sentinel for Indonesia's One Health preparedness

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To the Editor,

On 20 June 2026, Australia notified the World Organization for Animal Health of its first confirmed detection of highly pathogenic avian influenza (HPAI) H5N1 in a wild bird: a migratory brown skua (*Stercorarius antarcticus*) found near Cape Le Grand National Park, Western Australia. The virus was identified as H5N1 clade 2.3.4.4b, and its genomic sequence is available in the Global Initiative on Sharing All Influenza Data (GISAID) database (<https://gisaid.org>) under isolate ID EPI_ISL_20479340 (A/Brown Skua/Western Australia/AS-26-1348-1/2026). By 13 July 2026, Australian authorities had reported 13 H5 detections in individual wild seabirds: seven in Western Australia, five in South Australia, and one in New South Wales. All but one involved migratory seabirds; a greater crested tern detected near Robe, South Australia, represented the first confirmed H5 detection in a non-migratory Australian seabird. No mass mortality events, poultry infections, or broader agricultural involvement had been reported, and the public health risk remained low¹⁻³. Given the regional significance of HPAI H5N1 and Indonesia's proximity to Australia, these developments also warrant consideration in the context of Indonesia's One Health preparedness.

These findings should not be interpreted as evidence of a direct Australia-to-Indonesia transmission pathway.

Rather, they provide a regional sentinel signal that HPAI H5N1 clade 2.3.4.4b has reached wildlife in a

subregion that had previously remained free of this subtype. Notably, targeted surveillance conducted before the first mainland detection found no HPAI H5N1 in 924 avian samples or 38 Australian sea lions, highlighting both the value and the limitations of active surveillance for detecting sporadic incursions into wildlife populations⁴. Earlier assessments also identified important knowledge gaps regarding long-distance seabird movements, potential Southern Ocean introduction pathways, and surveillance of remote wildlife populations⁵.

Globally, HPAI H5N1 clade 2.3.4.4b has fundamentally altered the epidemiology of avian influenza. Unlike earlier poultry-associated H5N1 outbreaks, the current panzootic is characterized by an expanded host range, with repeated detections in wild birds, poultry, marine mammals, and terrestrial mammals. The latest joint FAO–WHO–WOAH assessment continues to classify the risk to the general population as low while emphasizing an elevated risk for occupationally and frequently exposed individuals⁶. Accordingly, Indonesia's response should be proportionate and evidence-based – not through alarm or unsupported trade restrictions, but by strengthening surveillance at the wildlife–poultry–human interface.

Indonesia possesses important foundations for H5N1 preparedness; however, several vulnerabilities remain. Human health authorities already conduct influenza-like illness (ILI) and severe acute respiratory infection (SARI) surveillance that incorporates information on exposure to sick or suddenly dead poultry



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and contaminated environments⁷. A district-level multisectoral One Health joint risk assessment has also been implemented in Bogor⁸. Accordingly, the priority should be to expand geographic coverage, standardize wildlife and live bird market surveillance, accelerate genomic sequencing turnaround, and improve interoperability across human, animal, and environmental surveillance systems, rather than establish entirely new preparedness structures. A recent Indonesian review⁹ similarly identified inconsistent biosecurity practices in live bird markets, limited routine genomic surveillance of poultry and wild birds, gaps in laboratory access and capacity, and fragmented intersectoral data sharing as persistent priorities for improvement.

Distinguishing endemic circulation from new viral introductions is essential for accurate epidemiological interpretation. Indonesia has experienced long-standing circulation of HPAI H5N1 in poultry, and clade 2.3.4.4b is not merely a hypothetical future introduction. Viruses belonging to this clade were isolated from domestic ducks during outbreaks in South Kalimantan in April

2022 and July 2023 and were genetically most closely related to viruses detected in East Asia. However, the exact route of introduction could not be determined¹⁰. Consequently, future H5 detections in Indonesia may reflect continued circulation of established viruses, additional introductions of genetically distinct clade 2.3.4.4b viruses, or reassortant viruses arising during co-circulation. Genomic characterization is essential to distinguish among these epidemiological scenarios.

Rather than designating entire provinces as uniformly high risk, Indonesia should prioritize surveillance according to documented epidemiological pathways. Selected pathway-specific settings and their supporting evidence are summarized in Table 1. The geographical labels correspond to the specific sites, sampled markets, outbreak settings, or administrative areas described in the cited sources and should not be interpreted as representing uniform risk across the surrounding provinces. Figure 1 complements this evidence-based framework by integrating the Australian HPAI H5N1 detection as a regional

Table 1. Selected pathway-specific settings to strengthen H5N1 surveillance in Indonesia.

Priority setting	Pathway and supporting evidence	Surveillance focus
Kupang Bay, East Nusa Tenggara	Ecological sentinel: an internationally important wetland supporting 2,000-5,500 shorebirds and a unique assemblage of Asian, Australian, and cosmopolitan waterbirds. This ecological connectivity does not demonstrate directional H5N1 transmission from Australia to Indonesia ^{11,12} .	Migratory waterbirds, unusual bird mortality, wetland environments, and nearby poultry populations.
Domestic duck outbreak settings in South Kalimantan	Confirmed HPAI H5N1 clade 2.3.4.4b infections in domestic ducks during 2022-2023, with affected farms associated with nearby marsh environments ¹⁰ .	Domestic ducks, farm-to-market poultry movements, marsh interfaces, and whole-genome sequencing.
Selected live bird markets in Banten, Jakarta, West Java, Central Java, and East Java	Market-associated maintenance and amplification: H5N1 was detected in poultry and environmental samples collected from selected live bird markets in Banten, Jakarta, West Java, Central Java, and East Java during 2014-2019, including viruses belonging to clades 2.1.3 and 2.3.2 and several reassortant lineages. More recent surveillance in selected markets in Surabaya, Sidoarjo, Pasuruan, and Malang also identified H5-positive poultry samples, including an H5N1 clade 2.3.2.1c virus isolated from an apparently healthy chicken ¹³⁻¹⁵ .	Repeated poultry and environmental sampling, source tracing, genomic sequencing, surveillance of apparently healthy birds, sanitation, and market biosecurity.
Bogor, West Java	District-level One Health joint risk assessment setting: influenza A virus was detected in two environmental samples, but no H5 subtype was identified. The likelihood of at least one locally acquired human infection was assessed as low, with moderate uncertainty ⁸ .	Joint risk assessment, integrated waste management, poultry-movement monitoring, occupational health surveillance, and multisectoral information sharing.
Duck-farming systems in Sidenreng Rappang Regency, South Sulawesi	HPAI H5N1 clade 2.3.2.1c was identified in clinically affected ducks during an outbreak in Sidenreng Rappang Regency, South Sulawesi in 2018 ¹⁶ .	Investigation of neurological signs and sudden duck mortality, with farm and environmental water sampling, poultry movement tracing, and genomic characterization.

As illustrated in Figure 1, the Australian HPAI H5N1 detection should be interpreted as a regional sentinel signal rather than evidence of a source-specific threat to Indonesia. The selected Indonesian settings represent distinct but complementary surveillance pathways, including ecological surveillance in Kupang Bay, East Nusa Tenggara, documented domestic duck outbreaks involving different H5N1 clades in South Kalimantan and South Sulawesi, multisite live bird market surveillance in selected parts of Java, and district-level One Health joint risk assessment in West Java.

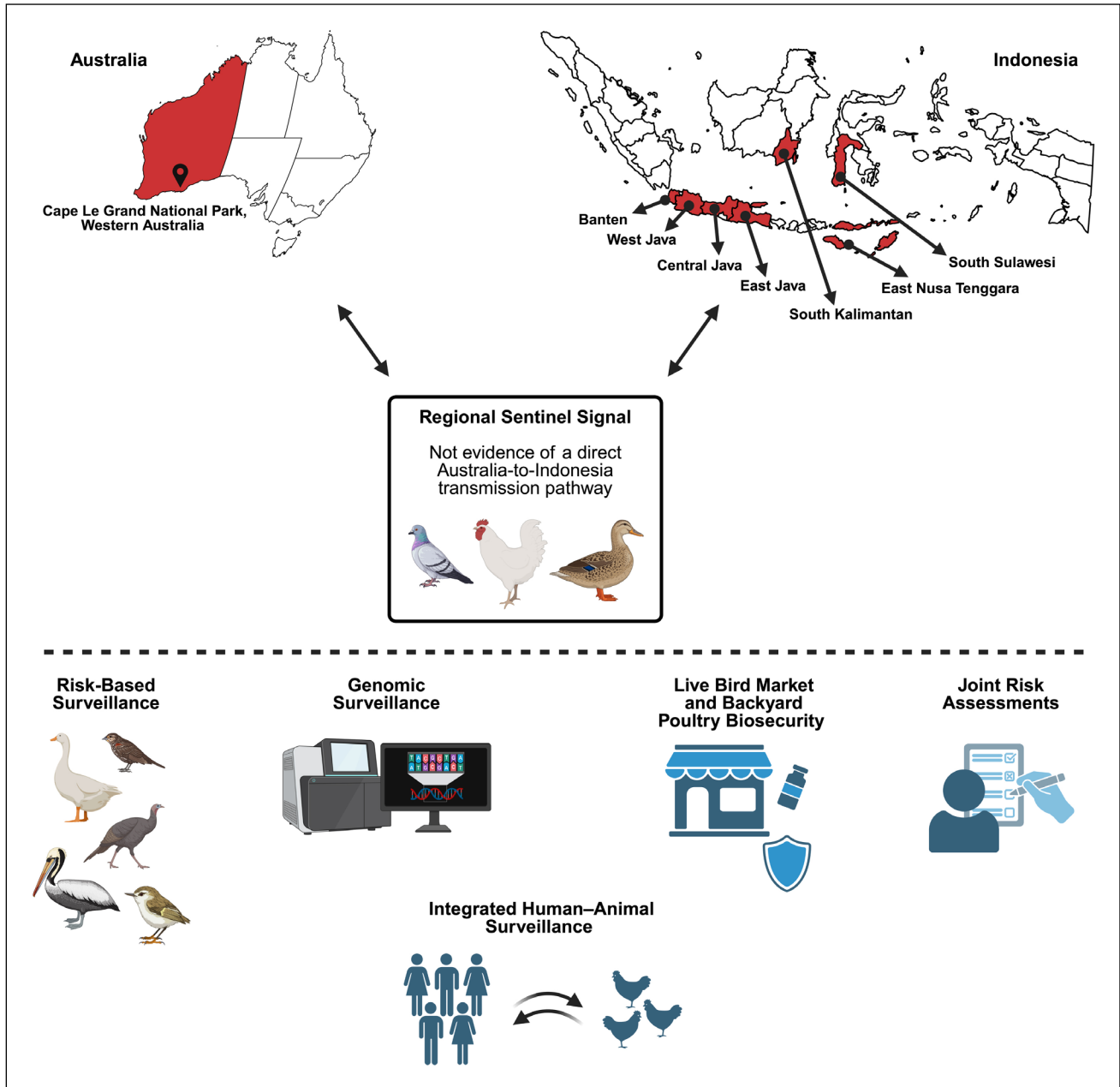


Figure 1. Schematic conceptual framework presenting Australia's HPAI H5N1 wild-bird detection as a regional sentinel signal, selected pathway-specific surveillance settings in Indonesia, and five complementary priorities for strengthening Indonesia's One Health preparedness. Geographical labels in the figure are presented schematically; the precise evidence-based setting names and geographical scopes are provided in Table 1. The figure does not depict a demonstrated direction of H5N1 transmission from Australia to Indonesia and does not represent a formal ranking or systematic prioritization of provincial H5N1 risk. Created with [BioRender.com](https://www.biorender.com) under a valid publication license.

sentinel signal with selected pathway-specific surveillance settings in Indonesia and five complementary priorities for strengthening One Health preparedness.

Together, Table 1 and Figure 1 illustrate that surveillance and preparedness strategies should be tailored to the underlying epidemiological pathways rather than applied uniformly across provinces. The recent H5N1 detection in Australia therefore provides an opportunity for Indonesia to shift from reactive outbreak response to proactive risk management by strengthening the five complementary domains outlined in Figure 1. First, risk-based surveillance should

be expanded using transparent prioritization criteria, including documented wild bird connectivity, previous H5 detections, poultry density and movement, live bird market activity, existing surveillance gaps, and laboratory diagnostic capacity.

Passive reporting of unusual wild bird mortality should be integrated with targeted surveillance of seabirds, shorebirds, domestic ducks, backyard chickens, and shared environments. Second, existing genomic surveillance systems should be standardized and strengthened to ensure that H5-positive samples are rapidly sequenced, compared with Indonesian and

regional reference genomes, and shared through appropriate data-sharing platforms. Cross-border genomic surveillance and data exchange with Australia, Timor-Leste, Papua New Guinea, and regional surveillance networks should be enhanced while avoiding any implication that a particular country is the source of a potential H5N1 introduction.

Third, live bird markets and backyard poultry systems should be prioritized for practical and enforceable interventions. This priority is consistent with broader evidence that migratory waterfowl, backyard and commercial poultry, live bird markets, and abattoirs represent multiple epidemiological interfaces requiring coordinated surveillance and strengthened biosecurity measures¹⁷. Recommended interventions include routine cleaning and disinfection, separation of ducks and chickens, avoidance of mixed-species cages, safe management of slaughter waste, exclusion of visibly sick birds from sale, regular disinfection of transport cages and vehicles, and improved access to handwashing facilities and personal protective equipment^{13,14,17}. Reporting systems should seek to minimize economic disincentives without assuming that concealment of poultry mortality is universal. Fourth, human health surveillance should be closely integrated with signals from animal health surveillance. Influenza-like illness (ILI) and SARI surveillance systems should consistently document occupational and environmental exposures among poultry traders, slaughterhouse workers, cullers, veterinarians, wildlife responders, and household contacts of suspected or confirmed cases.

Fifth, Indonesia should institutionalize district-level One Health joint risk assessments by strengthening and expanding existing local initiatives rather than establishing new systems. The Bogor assessment illustrated how live bird markets can be evaluated as local human–animal–environment interfaces: two environmental samples tested positive for influenza A virus, no H5 subtype or locally acquired human case was detected, and the estimated likelihood of at least one human infection remained low, albeit with moderate uncertainty⁸. Its primary value lies in identifying potential local transmission pathways and informing feasible control measures, rather than demonstrating ongoing H5N1 circulation.

Australia's first detection of H5N1 in a wild bird does not indicate that Indonesia is facing an imminent human epidemic, nor does it establish a direct route of viral spread. Nevertheless, it reinforces the need to strengthen Indonesia's existing One Health framework while differentiating between endemic circulation, new viral introductions, and reassortment events. An appropriate response is to enhance integrated surveillance across wildlife, poultry, live bird markets, genomic monitoring, and occupationally exposed populations to reduce the probability and consequences of future spillover events. The epidemiological information presented in this Letter was reviewed and updated on 13 July 2026.

CONFLICT OF INTEREST:

The authors declare that they have no conflict of interest.

ETHICS APPROVAL:

Not applicable.

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Not applicable.

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Data sharing is not applicable to this article because no original datasets were generated or analyzed.

AUTHORS' CONTRIBUTIONS:

MRA and ANMA conceived the study, developed the conceptual framework, and contributed to the preparation of the manuscript. MRA drafted the original manuscript. ANMA critically reviewed and revised the manuscript for important intellectual content. Both authors read and approved the final version of the manuscript and agree to be accountable for all aspects of the work.

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AI DISCLOSURE:

Grammarly was used solely for English-language proofreading, grammar correction, and sentence-level refinement to improve the scientific writing style of the manuscript. ChatGPT (OpenAI) was used only as a brainstorming aid to discuss the conceptual organization of Figure 1. Figure 1 and all of its graphical elements were independently prepared and assembled by the authors using BioRender.com. All scientific statements, references, geographical labels, and graphical elements were independently checked, critically revised, and approved by the authors. The authors take full responsibility for the accuracy, originality, integrity, and final content of the manuscript and Figure 1.

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