The detection of avian influenza virus in human pathology laboratories in Australia, New Zealand, and South Pacific nations

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ustralia has been relatively free from highly pathogenic avian influenza A (HPAI) virus outbreaks. HPAI viruses are primarily transmitted by wild birds, but avian influenza viruses have recently entered mammalian hosts, including cats and dairy cattle. 1-3 Reports of avian H5N1 influenza virus infections in humans have also increased. For example, 70 cases of H5N1 clade 2.3.4.4b virus infection in humans were reported in the United States in recent years, ⁴ and at least 83 cases in Cambodia during 2003–2025, including eleven cases (clade 2.3.2.1e) during 2025,³ almost all cases following documented contact with infected animals or contaminated environments. Although most recent H5N1 infections in humans in the United States have been mild,⁵ severe disease has also been reported, including six deaths in Cambodia during 2025. Serosurvey findings suggest that avian influenza infections in humans are not infrequent; in Michigan and Colorado, eight of 115 dairy workers (7%) were seropositive for H5N1 influenza A virus. These reports indicate the risks of intra-human viral genome mutations conferring increased human-to-human transmissibility or increased pathogenicity and genome reassortment from co-infection with other circulating influenza A subtypes.

In Australia, the first case of an H5N1 avian influenza infection in a human was reported in May 2024, a returning traveller infected with an Indian origin clade 2.3.2.1a virus. Within weeks, an HPAI H7N3 virus was reported in a poultry farm in Meredith (Victoria) and an HPAI H7N8 virus in the Hawkesbury region (New South Wales). HPAI H7 influenza A viruses were subsequently reported in sixteen poultry farms in Victoria, New South Wales, and the Australian Capital Territory, but all were successfully eradicated by decontamination processes. The first HPAI H7N6 virus infections in New Zealand poultry farms were also reported in 2024, as were fifteen infections of humans in China with avian H9N2 virus and a triple reassortment H3N3 virus derived from H3N8, H10N3 and H9N2.

Monitoring of avian influenza A infections in animals in Australia is performed by state departments of agriculture and primary industries, but the capability of human pathology laboratories to detect animal influenza viruses is unknown. Most instructions-for-use documents provided by manufacturers for Therapeutic Goods Administration-approved human diagnostic tests for influenza do not contain information about the polymerase chain reaction (PCR) target sequences, and few indicate that they can detect a range of avian influenza viruses, particularly the sequence-divergent and strongly animal-restricted H7 and H9 influenza A viruses.

During 1–3 July 2024 we assessed the detection of the NSW H7N8 HPAI virus by twelve diagnostic assays used by NSW Health Pathology (NSWHP) laboratories. We subsequently also reviewed the 12–25 November 2024 data from the Royal College of Pathologists of Australasia Quality Assurance Programs (RCPAQAP) Emerging Biological Threats survey, assessing the detection of five other avian influenza viruses: H5N1, H7N3, H7N9, H9N2, and H10N7. These assessments were needed because knowledge of the ability to detect avian influenza virus on human diagnostic platforms is critical for minimising public anxiety in the event of human infections, and facilitates public health response planning.

The New South Wales H7N8 avian influenza virus was diluted in viral transport medium (Tréidlia Biovet) and distributed at 4°C for blind testing in NSWHP laboratories. The H5N1, H7N3, H7N9, H9N2 and H10N7 viruses were de-identified and distributed through the RCPAQAP external quality assessment programs (EQAP) as diluted RNA from cultured virus. The diagnostic tests used were standard commercial molecular test kits for human respiratory viruses and a specialised influenza hemagglutinin (H)-subtyping test (Box). Human research ethics approval was not sought for this study, as human samples were not used.

The NSW avian influenza H7N8 virus was detected as influenza A virus by all twelve assessed diagnostic assays used by NSWHP laboratories. The H5N1, H7N3, H7N9, H9N2, and H10N7 viruses were each detected as influenza A viruses by all RCPAQAP EQAP 2024 survey test results. The RCPAQAP EQAP survey reports for Molecular Respiratory Pathogens and Molecular Rapid Diagnostics indicated that the diagnostic tests we assessed were representative of tests routinely used for the molecular detection of influenza A in Australia, New Zealand, and South Pacific nations, corresponding to 392 of 425 results submitted (Box).

We found that the probability of avian influenza virus being detected by human diagnostic testing platforms used in Australia and the region is extremely high. The 100% detection rate for all six avian influenza A viruses assessed alleviates concerns arising from the unstated information about PCR target sequences in commercial diagnostic test instructions-for-use documents. Our findings indicate that current human pathology respiratory virus diagnostic tests can reliably detect the H5, H7, H9, and H10 avian influenza virus strains as influenza A virus, including the HPAI strains involved in the 2024 Australian outbreaks and avian influenza A viruses detected during 2010–2022 (Box, footnotes).

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Detection of avian influenza A viruses and tests used in human pathology laboratories in Australia, New Zealand, and South Pacific nations*

Diagnostic test name	Detection of avian H7N8 influenza A virus (number of laboratories): NSW Health Pathology laboratories [†]	Detection of five avian influenza A viruses (number of laboratories): RCPAQAP 2024 Emerging Biological Threats Survey [‡]	Number of results for testing of influenza A virus in RCPAQAP 202 EQAP surveys [§]
2024 EQAP survey test results (all)	_	_	425
2024 EQAP test results excluded	_	_	33 [¶]
Total number of tests assessed	12	13	392
AusDiagnostics			
Respiratory pathogens (12-well)	NT	NT	2
Respiratory pathogens (24-well)	Detected (one)	All five detected (one)	4
Respiratory pathogens B (16-well)	Detected (one)	All five detected (one)	6
Respiratory pathogens C (16-well)	NT	NT	3
Upper respiratory pathogens (16-well)	Detected (one)	NT	6
SARS-CoV-2/Influenza/RSV (8-well)	Detected (one)	NT	1
bioMérieux			
BioFire respiratory RP2.1 panel	NT	NT	2
BioFire respiratory RP2.1 plus panel	Detected (one)	NT	11
Cepheid			
Xpert Xpress Flu/RSV (or XC)	NT	NT	29
Xpert Xpress SARS-CoV-2/Flu/RSV	NT	NT	54
Xpert Xpress CoV-2/Flu/RSV Plus	Detected (one)	NT	178
CerTest			
VIASURE SARS-CoV-2/Flu/RSV RT-PCR	Detected (one)	NT	5
Genetic Signatures			
EasyScreen Respiratory	NT	All five detected (one)	6
Hologic			
Panther Fusion SARS-CoV-2/Flu A/B/RSV	NT	All five detected (one)	17
In-house tests			
Real-time respiratory virus RT-PCR	Detected (one)	NT	0
Influenza A H-subtype multiplex RT-PCR	Detected (one)	All five detected (one)	0
Respiratory RT-PCR	NT	All five detected (four)	2
Roche			
Cobas Liat Flu/RSV	NT	NT	7
Cobas Liat SARS-CoV-2/FluA/B	Detected (one)	NT	37
Cobas SARS-CoV-2/Influenza A/B	NT	All five detected (one)	0
Seegene			
Allplex RV Essential assay	NT	All five detected (one)	7
Allplex RV Master assay	NT	All five detected (one)	11
Allplex Respiratory panel 1	NT	All five detected (one)	0
Allplex Respiratory panel 1A	Detected (one)	NT	2
Allplex SARS-CoV-2/FluA/FluB/RSV	Detected (one)	NT	2

EQAP = external quality assessment programs; NT = not tested; RT-PCR = reverse transcription polymerase chain reaction; RCPAQAP = Royal College of Pathologists of Australasia Quality Assurance Programs; RSV = respiratory syncytial virus; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2. * Qualitative results reported (not PCR cycle threshold data) because differences in nucleic acid extraction input/output volumes and testing volumes preclude direct comparisons. † Tests assessed for the detection in NSW Health Pathology laboratories of avian influenza virus, H7N8: A/chicken/NSW/Sydney/S119/2024 provided by the NSW Department of Primary Industries, Menangle. The examined tests are routinely used by NSW Health Pathology for influenza A virus testing. ‡ Tests assessed in the 2024 RCPAPQAP Emerging Biological Threats EQAP for the detection of five avian influenza A viruses — H5N1: A/Black faced spoonbill/HongKong /AFCD-HKU-22-21944-01009/2022; H7N3: A/chicken/Vic/24-01759-3/2024 (Meredith); H7N9: A/chicken/Vic/18/2024; H9N2: A/chicken/SouthEastA/2019; H10/N7: A/Ch/NSW/Aust/CV10-1004-12/2010. § Number of survey test results submitted in the RCPAQAP 2024 Molecular Respiratory Pathogen Survey 3 and the 2024 Molecular Rapid Diagnostics Influenza/RSV/SARS-CoV-2 Survey 3. ¶ Results were excluded because they were not examined in our study for the detection of avian influenza A virus. ◆

Research letter

Our findings raise some topics for consideration. First, assessing the ability to detect new avian influenza A viruses depends critically on access to outbreak virus and well defined, prearranged agreements between jurisdictions to share virus. Access to virus from early in an outbreak is highly important because, although synthetic nucleic acid-positive control reagents are helpful, it is prudent to test the detection of new virus strains on human diagnostic platforms, especially viruses that have evolved in non-human animal hosts (eg, the H5, H7, and H9 viruses). Second, identifying avian viruses as influenza A viruses is required before subtyping is undertaken, if required; for example, for people exposed to avian viruses, including those in the households of HPAI-exposed workers, or during periods of suspected human-to-human transmission. Molecular confirmation as influenza A virus also permits forwarding samples for sequencing, and data sharing ensures the ongoing suitability of assays and mapping of viral evolution. Third, accurate detection in Australia and the region of infrequent avian influenza infection in humans increases community confidence in public health responses and informs decisions about workforce management and the strategic use of test supplies. In our study, the levels of avian influenza in human respiratory samples was not assessed, but viral loads in people with symptomatic infections are generally sufficient for detection by PCR testing.³

Our findings support public confidence that respiratory virus PCR tests can detect avian influenza in humans, in Australia,

New Zealand, and South Pacific nations and highlight the benefits of collaboration between human and animal health authorities for detecting animal viruses that are rarely targets in human pathology testing.

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Data sharing: Detailed results, including Royal College of Pathologists of Australasia Quality Assurance Programs external quality assessment survey program reports, are available from the corresponding author on request.

Author contributions: Peter Kirkland supplied the H7N8 virus stock. Lisa Sedger, Vishal Ahuja, and Catherine Pitman prepared diluted samples and distributed H7N8 avian influenza for testing in NSW Health Pathology laboratories and analysed NSW Health Pathology data. Katherine Lau, Deane Byers, and Torsten Theis prepared Royal College of Pathologists of Australasia Quality Assurance Programs external quality assessment program survey samples, led survey programs, and analysed survey data. Lisa Sedger and Vishal Ahuja co-wrote the manuscript. Il authors have read and agreed with the final version of the manuscript.

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