Risk assessment of high pathogenicity avian influenza to Australian dairy cattle: final report

Robyn N Hall, Peter White, Duncan Worsfold, Nina Matsumoto, Ofir Schlosberg, Isabel MacPhillamy, Alison Hillman, Skye Badger, Emma Zalcman, Brendan C Cowled, Jaimie Hunnam

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Department of Agriculture, Fisheries and Forestry
GPO Box 858 Canberra ACT 2601
Telephone 1800 900 090
Web agriculture.gov.au

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Acknowledgement of Country

We acknowledge the continuous connection of First Nations Traditional Owners and Custodians to the lands, seas and waters of Australia. We recognise their care for and cultivation of Country. We pay respect to Elders past and present, and recognise their knowledge and contribution to the productivity, innovation and sustainability of Australia's agriculture, fisheries and forestry industries.

Summary

This summary provides a high-level overview of the final project report prepared for the Department of Agriculture, Fisheries and Forestry (the department) and Dairy Australia, assessing the risk of clade 2.3.4.4b high pathogenicity avian influenza (HPAI) to the Australian dairy industry. The report offers preliminary recommendations for national contingency and response planning, which may serve as a basis for further consultation with jurisdictional animal health authorities, the Australian dairy industry and other key stakeholders. This analysis is based on information available up to 23 May 2025, acknowledging the rapidly evolving nature of this area.

Background

Avian influenza, caused by infection with influenza A viruses (IAVs), is a globally significant disease with considerable implications for animal, ecological and public health, as well as potential food security and safety, socio-economic and cultural impacts. IAVs are notable given their wide host range, rapid mutation rate and potential for zoonotic transmission (MacLachlan et al. 2017). Of particular concern is the H5 HPAI lineage 2.3.4.4b (alternatively called clade 2.3.4.4b, Appendix A). This lineage first emerged in around 2016 and has now been detected in over 550 avian species and 87 mammalian species (Xie et al. 2023; Lee et al. 2017; Caliendo et al. 2022; Youk et al. 2023; Lee et al. 2016; FAO 2025). A novel clade 2.3.4.4b HPAI reassortant of the H5N1 subtype emerged in 2020, demonstrating unprecedented host adaptability and geographic spread and leading to a dramatic change in disease ecology. This reassortant has disseminated widely and is now found in all regions except Oceania (Wille et al. 2024). The clade 2.3.4.4b HPAI is different to the H7 HPAI viruses that have caused recent outbreaks in Australian poultry (e.g. 2020, 2024, 2025) (Queensland Department of Primary Industries 2025), having demonstrated sustained mammal-to-mammal transmission in several settings, including European fur farms, marine mammal populations and dairy cattle in the United States (US) (Peacock et al. 2024).

In 2023, a Wildlife Health Australia risk assessment estimated the likelihood of clade 2.3.4.4b HPAI incursion into Australia via wild birds as moderate, with moderate uncertainty (WHA 2023). A key consideration is that the assessment was conducted prior to the incursion of clade 2.3.4.4b HPAI into Antarctica (Banyard et al. 2024). There is now increased concern around HPAI entering southern Australia (where commercial poultry operations are concentrated) via subantarctic islands, as well as via northern Australia (Stock 14 August 2024).

In early 2024, clade 2.3.4.4b HPAI (H5N1 subtype, genotype B3.13) was identified as the cause of a novel syndrome in lactating dairy cattle in the US, characterised by a severe drop in milk production, abnormal thickened milk (described as ‘colostrum-like’) and accompanying non-specific systemic illness. Phylogenetic and epidemiological analyses initially indicated a single spillover event into cattle, most likely between September or October 2023 and January 2024 (Nguyen et al. 2025; Worobey et al. 2024), followed by sustained cow-to-cow transmission, although the spillover pathway was not definitively determined (Caserta et al. 2024). Subsequently, 2 more spillovers into dairy cattle (genotype D1.1) were detected in January and February 2025, identified through bulk milk testing from processing plant silos. Again, the spillover host(s) and pathway(s) were not determined; the D1.1 genotype was the dominant genotype in the North American flyways in

autumn 2024 and has been identified in wild birds, domestic poultry and mammals (APHIS 2025). As of 22 May 2025, at least 1,070 dairy herds across 17 US states have been impacted (APHIS 2024i). Although clade 2.3.4.4b HPAI is widespread globally, the infection of dairy cattle with this clade has only been reported from the US to date.

The bovine udder is the primary site of virus replication in lactating dairy cattle, leading to very high viral titres in milk of affected animals, up to 100 million infectious units per mL of milk in some cases (Caserta et al. 2024; Peña-Mosca et al. 2025; Halwe et al. 2024). Correspondingly, current evidence indicates that transmission is through exposure to raw milk (from both clinical and subclinical cows). This could be through contact with contaminated fomites (e.g. milking equipment, teat cup liners, gloves, intramammary treatments) or through splashing and/or aerosolisation of milk with subsequent ingestion, inhalation, mucous membrane contact, or intramammary inoculation (Nguyen et al. 2024; Ríos Carrasco et al. 2024; APHIS 2024g; Baker et al. 2024; Webby and Uyeki 2024; Halwe et al. 2024; Rodriguez et al. 2024; Campbell et al. 2025). The spread of clade 2.3.4.4b HPAI between states is linked to cattle movements (including subclinical animals) and animal movement is a known and recognised risk for disease transmission (APHIS 2024g). The movement of people (visitors or workers), shared vehicles and/or equipment contaminated with raw milk are also reported to be risk factors for disease spread (APHIS 2024g, 2024k; Caserta et al. 2024; CEZD 2024b; Molteni 20 December 2024). For example – at least half of new herd infections in the US reportedly did not involve movement of live cows (Payne and CDQAP 2024), and in those cases, spread was presumably through contaminated equipment such as trailers or potentially visitors. Current genomic and epidemiological evidence do not support that wild or peri-domestic birds are spreading HPAI between dairy herds (APHIS 2024g). However, based on experience with HPAI in poultry (Aha 2023c), it is assumed that birds and other animals (including domestic pets, other livestock and peri-domestic wildlife or feral animals) may act as fomites in transferring virus between cows either within a herd or between premises.

While typically a self-limiting infection that resolves in 1–3 weeks, a large proportion of lactating cows in an affected herd (3–20%) can become sick, leading to significant drops in milk yield (20–100%) in individual animals and resulting in considerable impact on overall herd health and productivity. Additionally, serological investigations on 1 US dairy farm indicated a large proportion (83.7%) of subclinical infections, which may complicate detection and disease control (Peña-Mosca et al. 2025). Mortality is generally low (less than 2%), although the case fatality rate may approach 7% among clinically affected lactating animals. Many additional animals may be prematurely removed from the herd for economic reasons, as milk production may be reduced for more than 2 months post-infection (Peña-Mosca et al. 2025). Substantial economic impacts have been experienced by US dairy producers due to decreased milk production, mortality and premature culling of affected animals. For example - the average cost per affected cow on 1 affected US farm was calculated to be USD$932 (Peña-Mosca et al. 2025). Another estimate from the American Association of Bovine Practitioners was USD$100 to $200 per infected cow (Larkin 2024). A report from a Michigan producer stated a total loss for a 500-head dairy herd of between USD$30,000 and $40,000 during the first 15 days of infection, due to lost milk production and treatment (Durst 2024). There has been no significant disruption or barriers to US dairy trade and exports according to the International Dairy Foods Association, although it is unclear whether this refers to exports of dairy products or also of live dairy cattle (International Dairy Foods Association 2024). Food standard pasteurisation is effective at inactivating clade 2.3.4.4b HPAI in milk and other dairy products (Suarez et al. 2025;

Caceres et al. 2024; Nooruzzaman et al. 2024; Kwon, Gebhardt, et al. 2024; Spackman et al. 2024; Alkie et al. 2025; Cui et al. 2024; Schafers et al. 2025). Enhanced controls for importation of live cattle were applied in some countries and some impacts on beef and other cattle products were experienced, although these were temporary (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). These restrictions had little appreciable effect on overall US beef/veal or live cattle trade volumes; indeed, US beef exports in 2024 were projected to decline due to factors preceding HPAI but ended up stronger than expected (Petry 12 March 2025).

In the US, clade 2.3.4.4b HPAI has transmitted from dairy cattle to other species, including domestic cats, wild birds, peri-domestic wildlife, poultry and humans (Peacock et al. 2024). Of the 70 confirmed human H5 cases in the US since 25 February 2025, 41 have been linked to exposure to affected dairy herds (CDC 2025a). Most human cases in the US have been mild, with conjunctivitis and/or upper respiratory symptoms, although 1 severe case resulting in death (not associated with dairy cattle exposure) was reported in Louisiana (CDC 2024b, 2024a).

Internationally, human infections with clade 2.3.4.4b HPAI have been reported from China, Chile, Ecuador, Spain, the United Kingdom and Canada (FAO et al. 2024a, 2024b, 2024c). Severe cases (n = 5) were documented in China, Chile, Ecuador and Canada, with one death in China (FAO et al. 2024a, 2024b, 2024c). All other severe cases recovered following hospitalisation.

The US response to HPAI in dairy cattle aims for containment and elimination, primarily through the National Milk Testing Strategy (NMTS), mandatory pre-interstate movement testing of lactating dairy cows, enhanced surveillance and federal support for producers, including enhanced biosecurity planning and implementation (APHIS 2024j). The NMTS involves testing of bulk tank milk samples to identify states with active clade 2.3.4.4b HPAI circulation (APHIS 2025c, 2025e, 2025h). This program led to the detection of the 2 genotype D1.1 spillovers in early 2025 (APHIS 2025a, 2025b), suggesting that this strategy is beneficial for early detection. However, not all states are enrolled in this program and it is also unclear how targeted this surveillance is; that is, how many individual farms are being captured. Since April 2024, pre-movement testing of lactating dairy cattle has been mandatory prior to interstate movement. Non-lactating cattle are exempt, although testing via nasal swabs is strongly encouraged. Intrastate cattle movement is governed by state-specific guidance (where available). Despite this mandated pre-movement testing, HPAI has continued to spread through the US dairy herd since April 2024. There is limited surveillance in other livestock species in the US, although the United States Department of Agriculture recommends testing other domestic animals showing illness on HPAI-affected farms and will conduct this testing at no cost to the producer (APHIS 2024). Some states may also conduct risk-based surveillance of livestock on HPAI-affected poultry or dairy premises during their epidemiological investigations. For example – this led to the detection of clade 2.3.4.4b HPAI infection in goat kids in Minnesota in March 2024, in alpacas in Idaho in May 2024 and in swine in Oregon in October 2024 (APHIS 2024a, 2024h). Unlike poultry, depopulation (culling) is not being recommended for dairy herds due to the self-limiting nature of the infection in most cattle (APHIS 2024), meaning that most cattle will recover.

It is unclear why clade 2.3.4.4b HPAI spillovers into dairy cattle have been restricted to the US (at least so-far). North American migratory bird flyways extend across Canada and indeed, the first clade 2.3.4.4b HPAI detections in North America were in Canada in December 2021 (Caliendo et al. 2022). Clade 2.3.4.4b HPAI has continued to spill over into domestic poultry in Canada since 16 December

2021, with active control measures in place in the poultry industry, such as movement controls and depopulation (CFIA 2024). Canada's national dairy herd is considerably smaller than the US industry. Average herd sizes in Canada are also much smaller than in the US (~100 milking cows), although housing systems are similar with most premises using tie stall or free stall housing (CFIA 2021). Relatively few operations in Canada use robotic milking systems (~14% of farms surveyed) (CFIA 2021). It is illegal to feed any form of poultry manure (including poultry litter) to livestock in Canada. Canada has tested over 1,200 samples of pasteurised retail milk and almost 3,500 raw (unpasteurised) milk samples collected at processing plants since mid-2024, with no positive detections (CFIA 2024; Wallace et al. 2025). Monthly testing of raw milk collected from processing plants is ongoing in Canada. In Europe, clade 2.3.4.4b HPAI viruses have been circulating at relatively high prevalence since around 2016 with no detections in cattle (FLI 2024). The European Union (EU) is the world's largest milk producer, with Germany accounting for more than 21% of the milk produced in the EU (Vinci 2024). Farming systems vary widely, from free-range farming in alpine areas (approximately 10% of EU milk production) to large-scale specialised farms and cooperatives (Vinci 2024). The feeding of poultry litter (and other processed animal proteins) to ruminants was banned in 2001 as part of the response to bovine spongiform encephalopathy (Regulation (EC) No 999/2001). Germany tested approximately 1,400 bovine (not stated whether beef or dairy) serum samples for antibodies to IAV, collected from regions severely affected by avian HPAI outbreaks, with no positive detections (Friedrich-Loeffler-Institut 2024). Additionally, around 350 bulk milk tank samples from Germany were tested for viral RNA and again, all were negative. As the spillover host(s) and pathway(s) into US dairy cattle has not been determined, the risk factors for spillover remain speculative and uncertain.

The dairy industries in Australia and the US differ with regards to scale, geographic distribution, production systems and market orientation. The US dairy industry operates on a significantly larger scale than the Australian industry. Recent reports indicate that the total national US herd was approximately 9.4 million milk cows (USDA 2024b), while the number of farms was reported to be about 23,153 (USDA 2024a). In contrast, the Australian dairy industry comprised a national herd of 1.33 million cows in milk across 3,889 dairy farms in 2024 (Dairy Australia 2024a). The average herd size across the entire US is comparable to Australia (337 in 2022), although this varies considerably by state; 22% of US states have an average herd size of greater than1000 head (Progressive Dairy 2023). While most dairy operations in the US are family-owned, many belong to national producer-owned cooperatives (USDA 2025), with reportedly frequent movement of animals and resources (equipment, vehicles and personnel) between premises (Rawson et al. 2025). However, data on dairy cattle movements, both in Australia and in the US, are not readily available, preventing detailed comparison. In terms of production systems, Australia primarily employs pasture-based dairying, frequently supplemented with grain concentrates, forages and by-products (Dairy Australia 2023). The number of farms feeding partial mixed rations (in addition to grazing) is growing (Dairy Australia, pers. comm., 6 June 2025). In contrast, the US relies heavily on intensive contained housing systems with cattle fed controlled diets (i.e. total mixed ration; TMR) (USDA 2011). In Australia, it is very rare for dairy cows to be housed and fed a TMR. Market orientation is another key distinction between the Australian and US dairy industry. Australia's industry is export-driven, with 32% of its milk production destined for global markets, particularly to Asia (Dairy Australia 2024a). The US allocates a larger proportion of production to the domestic market, with only 18% exported in 2022 (International Dairy Foods Association 2023; USDA 2011). From a public health perspective, the sale

of raw milk is legal in many US states, although federal law prohibits the sale of unpasteurised milk across state lines (CDC 2024a). The sale of raw cow's milk for human consumption is illegal in Australia.

Project objectives and scope

Australia remains free of clade 2.3.4.4b HPAI as of May 2025. However, the 2023 Wildlife Health Australia risk assessment considered there to be a moderate likelihood of incursion via wild birds (WHA 2023). The emergence of clade 2.3.4.4b HPAI in dairy cattle in the US, and the sporadic spillovers observed in other livestock species, has heightened concerns about potential risks to Australian livestock industries if clade 2.3.4.4b HPAI was to enter Australia via wild birds. Therefore, Ausvet Pty Ltd were engaged by to conduct a qualitative risk assessment evaluating the likelihood and consequences of clade 2.3.4.4b HPAI entering and spreading within and between Australian dairy herds in the 3 years following incursion of the virus into Australia via wild birds. The project encompassed several distinct components:

- A comprehensive literature review outlining the current state of knowledge around HPAI in dairy cattle (Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review)
- An assessment of the molecular epidemiology of the outbreak in dairy cattle and the risk of reassortment with IAVs currently in Australia in the event of an incursion (Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review)
- A formal qualitative risk assessment on the risk of entry and spread of clade 2.3.4.4b HPAI in the Australian dairy industry, including a report detailing practical recommendations to minimise the risk of HPAI to Australian dairy cattle and producers achievable within the unique setting of the Australian dairy industry (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). This was supported by:
    - on-farm biosecurity assessments on 25 representative Australian dairy farms.
    - the development of a stochastic, agent-based simulation model for within-farm spread of clade 2.3.4.4b HPAI in a 'typical' Australian dairy farm.
- Rapid risk appraisals for the risk of clade 2.3.4.4b HPAI entry and transmission in Australian beef (Risk of high pathogenicity avian influenza to Australian beef cattle: Rapid risk assessment), pig (Risk of high pathogenicity avian influenza to the Australian pig industry: Rapid risk assessment) and small ruminant (Risk of high pathogenicity avian influenza to Australian small ruminant industries: Rapid risk assessment) industries.
- A final project report detailing recommendations to inform national preparedness and response planning.

The project scope was limited to clade 2.3.4.4b HPAI.

Key assumptions and uncertainty

The risk assessments were conducted under a hypothetical scenario where clade 2.3.4.4b HPAI was present in the wild bird population and the incidence of infection in wild birds was moderate to high and geographically homogeneous across Australia. For our rapid risk appraisals, we assumed that infection was only present in wild birds, while for the comprehensive dairy cattle qualitative risk

assessment we assessed additional pathways including potential spillovers from wild birds into either domestic poultry or mammals. We assumed that the biology (including pathogenesis, virulence and transmissibility) of any virus entering Australia would not differ substantially to previously evaluated clade 2.3.4.4b HPAI viruses. We assumed that no specific control measures were in place to mitigate spread between premises at the time of an incursion. Additional assumptions specific to each assessment are detailed in the respective methodologies (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment, Risk of high pathogenicity avian influenza to Australian beef cattle: Rapid risk assessment, Risk of high pathogenicity avian influenza to the Australian pig industry: Rapid risk assessment, Risk of high pathogenicity avian influenza to Australian small ruminant industries: Rapid risk assessment). We did not assess the risk of clade 2.3.4.4b incursion into Australia; introduction via wild birds has already been comprehensively assessed by Wildlife Health Australia (WHA 2023).

Our assessments were based on data available at the time of the project. The global understanding of clade 2.3.4.4b HPAI disease ecology is evolving rapidly, and our findings should be interpreted considering new data as it becomes available. The assessments represent our situational understanding at a point in time and are specific to the scenarios assessed.

Our assessments were limited by high uncertainty around many aspects of clade 2.3.4.4b HPAI biology in livestock species. In particular, there is high uncertainty around the minimum infectious doses for different species, the amount of virus shed in excretions and secretions, and virus persistence in various substrates under Australian conditions. This assessment was necessarily constrained by the currently available dataset, which is limited to the US and may therefore have limited direct applicability to the distinct industry conditions in Australia. The on-farm biosecurity assessments underpinning many of the aspects of the risk assessment for dairy cattle involved a relatively small sample size (25 farms), which may have resulted in a level of bias. The disease spread simulation model is limited by a lack of quantitative data for many parameters (particularly the role of non-milk-associated transmission e.g. respiratory and fomite spread) and necessary simplifications given the limited time available for modelling (CDC 2025). These are described in detail in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Simulation modelling of within-herd transmission'. Our choice of risk assessment framework may influence the risk estimate, for example, by using a different number of likelihood and consequence categories or by defining categories differently. Our definitions may differ from those used by other organisations for specific purposes, such as the World Trade Organization.

Risk assessment findings for the Australian dairy industry

A qualitative risk assessment expresses outputs categorically (like low, medium, high). The qualitative approach is a reasoned and logical discussion of a given hazard and is suitable for most risk analyses, aligning with international guidelines for animal health risk assessment from the World Organisation for Animal Health (WOAH) (WOAH 2010). A key aspect is that the risk estimate must be considered along with the degree of uncertainty in the assessment. The risk estimate provides the most probable risk based on the assumptions and findings of the assessment. However, this must be interpreted in the context of our level of understanding or completeness of knowledge about a hazard (e.g. uncertainty around the minimum infectious dose for dairy cattle) and the natural

heterogeneity that exists within biological systems (e.g. different animals will vary in their inherent resistance to infection) (WOAH 2010). A more detailed introduction to risk analysis is provided in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

We assessed the following entry, within-farm and between-farm spread pathways for clade 2.3.4.4b HPAI in the Australian dairy industry:

- Entry of clade 2.3.4.4b HPAI
    - Spillover from wild birds (either exposure to faeces/environmental contamination, direct contact, or inadvertent consumption of a carcass)
    - Spillover from wild birds to poultry and then into dairy cows (either direct contact, exposure to faeces/environmental contamination, or inadvertent consumption of a carcass)
    - Spillover from wild birds to mammals and then into dairy cows (either direct contact with a non-human mammal, direct contact with a person contaminated or infected by poultry, or inadvertent consumption of an infected carcass or faeces)
- Within-farm spread of clade 2.3.4.4b HPAI
    - Contamination during milking (either raw milk contaminating milking equipment or splashing and aerosolisation of milk)
    - Contact with an infected dairy cow (non-milk associated transmission)
    - Contaminated floors or bedding
    - Feeding of raw milk
    - Exposure to milk for disposal or effluent containing raw milk
    - Spread facilitated by non-cattle hosts (with 6 sub-pathways depending on the host exposure pathway and host-cattle contact type)
- Between-farm spread of clade 2.3.4.4b HPAI
    - Movement of infected cattle
    - Movement of contaminated vehicles (excluding milk tankers) and equipment
    - Movement of milk tankers
    - Movement of raw milk
    - Spread to adjacent premises (either direct contact with adjacent stock or exposure to effluent containing raw milk)
    - Spread facilitated by non-cattle hosts, excluding people (with 4 sub-pathways depending on the host exposure pathway and host-cattle contact type)
    - Spread facilitated by people

The overall unrestricted risk (i.e. the level of risk that would be present if there were no risk mitigation measures in place) that clade 2.3.4.4b HPAI poses to the Australian dairy industry was assessed as low, with high uncertainty. A key outcome was that additional research is required to reduce the uncertainty in the assessment, particularly around the minimum infectious dose and infection pathways (e.g. role of respiratory transmission) in both lactating and non-lactating cattle.

Following aggregation of the different entry pathways, the likelihood of clade 2.3.4.4b HPAI entering the Australian dairy herd was assessed as low (i.e. unlikely to occur), with high uncertainty. Spillover from wild birds into poultry and then into dairy cows was assessed as more likely than spillover directly from wild birds into dairy cows. While direct contact rates between poultry and dairy cows was assessed as low, indirect exposure rates to poultry faeces was assessed as moderate (e.g. via poultry litter used as fertiliser). Based on current available evidence, poultry shed high concentrations of HPAI virus in faeces, while the concentration of clade 2.3.4.4b HPAI virus in wild bird faeces varies considerably by species (as does faecal volume, thus total amount of virus). Little is known about clade 2.3.4.4b HPAI dynamics in species relevant to the Australian dairy industry. The full rationale for these assessments is outlined in Tables 5 and 6 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'. Spillover from wild birds into mammals and then into dairy cattle was deemed less likely, due to lower contact rates and viral shedding. For full details of the assessment see Table 7 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

If the virus were to enter an Australian dairy herd, the likelihood of within-farm spread was assessed as high (i.e. very likely to occur) based on aggregation of the different within-farm spread pathways, with low uncertainty. The highest likelihood pathways were assessed as contamination during milking (splashing/aerosolisation of raw milk) and feeding raw milk to calves.

The likelihood of between-farm spread was assessed as very low (i.e. very unlikely to occur) based on aggregation of the different between-farm spread pathways, with very high uncertainty. The highest likelihood pathways in the Australian context were assessed as movement of infected cattle, direct contact with adjacent premises, and spread facilitated by non-cattle hosts. Other pathways, such as contaminated vehicles, milk tankers, and movement of raw milk, were assessed as extremely low likelihood. This finding differs considerably from the US experience, where between-farm spread has been substantial. Due to the distinct operational practices and structures of the Australian and US dairy industries, the probability of disease transmission via certain pathways may vary between the 2 countries. For example – anecdotally there is considerably greater movement of live animals, vehicles, equipment and people between dairy premises in the US industry. In contrast, available evidence suggested that the movement of lactating cattle in Australia was uncommon (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). It was beyond the scope of this project to conduct a detailed risk assessment for the US industry to explore these differences further. A comparative analysis of the structure and dynamics of the Australian versus US dairy cattle industries may provide further insights. Alternatively, this estimation of risk may be limited by the very high uncertainty in the assessment, particularly around the role of non-cattle hosts, including people, in spreading infection.

The consequences of a clade 2.3.4.4b HPAI outbreak in the Australian dairy industry were assessed as high (i.e. likely to be significant at the national level and highly significant within affected zones, of national concern), primarily driven by potential socio-economic impacts, with moderate uncertainty. Other consequences included animal health and welfare, human health, environmental and trade impacts, and food security and safety.

Key considerations for national contingency planning for the Australian dairy industry

Proactive consideration of disease mitigation measures is crucial, focusing on ensuring early detection and rapid response and enhancing on-farm and between-farm biosecurity. The results suggest that trying to control infection once present in a dairy herd is likely to be challenging. We therefore discuss several preliminary considerations around national contingency planning for clade 2.3.4.4b HPAI in the Australian dairy industry, noting that further consultation must be undertaken with jurisdictional governments, Australian dairy industry stakeholders, relevant non-government agencies and public health authorities. These considerations include:

- Epidemiological assessment: A clinical case definition and a surveillance definition should be established now. Following an incursion, it will be critical to identify the spatial distribution of infected populations, determine the source and incidence of infection, and understand pathways of spread in the context of the Australian dairy industry. Genomic sequencing will be beneficial for understanding spillover pathways and spread, and mechanisms for rapid sequence sharing must be established. An early understanding of the extent of spread will allow an optimal response to be implemented.
- Quarantine and biosecurity: Depending on the objective of an Australian response, quarantine of infected premises and the establishment of declared areas could aid in mitigating spread via lactating dairy cattle and raw milk. There is still a lack of empirical evidence on the role of vehicles, equipment and people in transferring infection between farms. Whilst research from the US experience will assist decision making, these may not be directly applicable to the Australian dairy industry.
- Movement controls and testing: Processes for the safe movement of live animals should be considered in the event of an outbreak in dairy cattle. This may involve pre-movement testing of specified populations, for example – either high-risk (lactating cows), all dairy cattle or all livestock co-mingling with dairy cattle. Alternatively, herd status and eligibility for movement may be more efficiently demonstrated through bulk milk testing, as for the US Dairy Herd Status Program (APHIS 2025). Clinically affected lactating cows should not be moved. Enhanced biosecurity protocols for vehicles, equipment and people moving from affected premises are crucial, although the significance of these transmission pathways is still unclear. Restrictions on dairy cattle shows and other events where dairy cattle congregate (e.g. saleyards) may be beneficial in the event of an outbreak.
- Tracing and surveillance: Passive surveillance is an essential component for early detection, aided by clear reporting mechanisms and enhanced producer awareness. Routine bulk milk sampling has proven effective for early detection in the US and could be adopted in Australia. The effectiveness of the NMTS in the US for detecting new spillover events into dairy cattle indicates that surveillance for early detection may be useful following incursion in wild birds and prior to an outbreak in dairy cattle. Risk-based surveillance could be undertaken if infection in wild birds (or other species) is restricted to a specific geographic area, or if regions of high incidence in wild birds (or other species) are identified. Several countries have reported conducting various forms of early detection surveillance activities for clade 2.3.4.4b HPAI in dairy cattle; these are discussed further in Section 2.2.4. Genomic sequencing is likely to be

helpful in understanding complex transmission chains between dairy herds and cross-species transmission in the event of a spillover into dairy cattle.

Tracing should prioritise movements of lactating dairy cattle and of raw milk (except raw milk contained in milk tankers) initially, as the highest virus concentrations are found in milk. Based on 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment', the likelihood of milk tankers spreading the virus between farms was assessed as extremely low, since cattle are extremely unlikely to have contact with milk from a milk tanker due to milk processor quality assurance requirements. Rapid antigen tests could have a valuable role in supporting point-of-care farm-level management decisions.

- Treatment of infected animals: In the US, treatment has focussed on supportive care (e.g. oral fluid therapy with or without anti-inflammatories). Depopulation is not recommended in the US due to the self-limiting nature of the infection in dairy cattle. Infection was also widespread (3 states) at the time of detection and no significant market access restrictions were imposed.
- Treatment and disposal of milk and other animal products: Contaminated raw milk must not be used for human consumption or fed to other animals and must be appropriately disposed of. Both vat/batch pasteurisation (63°C for 30 minutes) and high-temperature short-time (HTST) pasteurisation (72°C for 15 seconds) are effective at inactivating HPAI in milk. Food Standards Australia New Zealand require that 'milk for human consumption is only sourced from animals that do not show any evidence of infectious diseases transferrable to humans through milk, are in a good general state of health and are clearly identifiable through stock identification procedures' (FSANZ 2016). Thus, milk from clinically affected cows cannot enter the food chain. WOAH specifies that only milk produced by non-infected cows and that has been pasteurised (or otherwise inactivated) should be commercialised (WOAH 2024). However, milk from subclinical or preclinical cows may inadvertently enter bulk tank milk, as evidenced by detection of viral RNA in pasteurised retail milk in the US (Spackman et al. 2024; Suarez et al. 2025). The US Food and Drug Administration is confident that pasteurised retail dairy products are safe for human consumption, even when viral RNA (which is not infectious) is present (US FDA 2025). Decision-makers must decide whether bulk tank milk (potentially contaminated due to subclinical or pre-clinical cows) from affected premises can still be pasteurised and used for human consumption, or whether this must be disposed of in addition to milk from clinically affected animals. Based on the US experience, milk from infected animals is likely to make it into the retail food chain to some extent. On-farm treatment or disposal of large volumes of milk will be challenging, given the limited on-farm pasteurisation capacity in Australia and lack of data on effectiveness of other milk treatment methods. Considerations are discussed in the AUSVETPLAN operational manual for disposal (Aha 2021b). Transport to approved processing sites for pasteurisation and disposal could be considered, with appropriate enhanced biosecurity.
- Decontamination: The focus of decontamination efforts should be on areas and fomites (e.g. footwear, clothing, milking equipment) that may be contaminated with raw milk, although the significance of fomites in transmission is still unclear. Currently, there is insufficient evidence to understand how much of a transmission risk oronasal and other secretions from infected animals pose.
- Wild animal management: Destruction of wild birds is not supported as there is no genomic and epidemiological evidence that wild or peri-domestic birds are spreading HPAI between cattle

herds in the US. It would be prudent to limit access of wild birds and peri-domestic wildlife to dairy cattle feed, water and facilities, where practicable. Proactive monitoring for unexpected mortality events in wild birds or animals should be encouraged.

- Vaccination: No HPAI vaccines are currently available for dairy cattle in the US, although field trials to evaluate safety of at least 7 H5N1 vaccine candidates in dairy cows have been approved.

Rapid risk appraisals for other Australian livestock industries

Natural infection with clade 2.3.4.4b HPAI has been confirmed in various livestock species in addition to dairy cattle, including pigs, alpacas, goats and sheep, although sustained transmission within these species has not yet been documented. The susceptibility of dairy cattle to infection suggests that clade 2.3.4.4b HPAI may also pose a risk to beef cattle. Therefore, there is a need to also consider the risk of HPAI to other Australian livestock industries. The beef cattle, pig and small ruminant industries are signatories to the Emergency Animal Disease (EAD) Response Agreement (EADRA) and are integrated into Australia's EAD preparedness activities. Therefore, we conducted rapid risk appraisals on the risk of clade 2.3.4.4b HPAI entry and spread within these industries in Australia. Together with the formal dairy qualitative risk assessment, these provide coverage of the HPAI risk to Australia's major non-equine livestock industries.

Rapid risk appraisals are conducted over a limited time frame and result in a qualitative assessment of the risk of an event (FAO 2021). They are less comprehensive than a formal risk assessment. Therefore, we did not specifically evaluate individual entry and exposure pathways.

Beef cattle

The overall risk to the commercial beef cattle industry was assessed as negligible, with high uncertainty. Spillover likelihood was assessed as low and establishment and spread was assessed as negligible, as mammary glands are the main site of replication in dairy cattle and adult beef cattle have limited exposure to milk. There are no data to suggest that adult Australian beef cattle are routinely fed unpasteurised milk, whey or other dairy products or by-products. Clade 2.3.4.4b HPAI has never been detected in non-dairy cattle to date, although we are not aware of any routine surveillance in beef cattle in any country. In the United Kingdom (UK), surveillance of other mammalian species present on HPAI-affected poultry premises has been in place since 2024 (HAIRS 2025). Some US states may also conduct risk-based surveillance of livestock on HPAI-affected poultry or dairy premises during their epidemiological investigations. For example – this led to the detection of clade 2.3.4.4b HPAI infection in goat kids in Minnesota in March 2024, in alpacas in Idaho in May 2024 and in swine in Oregon in October 2024 (APHIS 2024a, 2024h). Consequences were assessed as minor, given current evidence indicates that clinical disease is mild in non-lactating cattle and milk is not a commodity for the beef industry.

Pigs

The overall risk to the Australian pig industry (excluding public health consequences) was assessed as low, with moderate uncertainty. Both the likelihood of spillover and of establishment and spread were assessed as low, as current evidence indicates that avian-adapted viruses require further adaptation for efficient respiratory transmission in pigs. Consequences were assessed as minor, with

both experimentally- and naturally-infected pigs either remaining healthy or showing a short duration of lethargy and fever. Public health considerations are discussed in the Consequence Assessment and full report 'Risk of high pathogenicity avian influenza to the Australian pig industry: Rapid risk assessment', however an evaluation of potential public health consequences was out of scope. A public health risk assessment is recommended to explore the risk to human health if clade 2.3.4.4b HPAI was to enter and spread within the Australian pig industry.

Small ruminants (sheep and goats)

The overall risk to Australian small ruminant industries was assessed as negligible, with very high uncertainty. Spillover likelihood was assessed as low and establishment and spread was assessed as negligible. Consequences were assessed as minor, as current evidence indicates that most infections are subclinical (based on serology studies). As discussed for beef cattle, based on WOAH principles trade restrictions are not recommended.

Conclusion

The overall risk of clade 2.3.4.4b HPAI to the Australian dairy industry was assessed as low, but with high uncertainty due to current knowledge gaps (detailed in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'). The high likelihood of within-farm spread, and high potential consequences, necessitate robust preparedness and response strategies. Early detection, enhanced biosecurity and clear communication with industry stakeholders are essential to minimise the impacts of a potential outbreak. Continuous review of the risk assessment and further research to address uncertainties are critical for maintaining the resilience of Australia's livestock industries against this evolving threat. Much of this research is currently underway in the US (US DHHS 2024), and once published, this risk assessment could be updated to include these new findings (i.e. in 6–12 months).

Recommendations for clade 2.3.4.4b HPAI preparedness and response in the Australian dairy industry

Based on the project's findings, Ausvet recommends several actions for clade 2.3.4.4b HPAI preparedness and response in the Australian dairy industry. We note that Ausvet does not have a comprehensive picture of current activities across all sectors—these are gaps identified during our assessment based on publicly available information. These recommendations should be discussed collaboratively with relevant stakeholders to ensure preparedness efforts are coordinated and prioritised appropriately.

Policy, legislation and regulatory aspects

1) Industry, state and federal government and other relevant stakeholders should develop and agree on the scope of preparedness and response activities now.

2) Emergency response plans, policies and governance structures for clade 2.3.4.4b HPAI should be developed, or updated to include dairy cattle. Specifically:

a) Clinical case and surveillance definitions should be developed that are applicable to the Australian context.

b) The objectives of an Australian response should be agreed upon.

c) AUSVETPLAN response strategies and the EADRA should be reviewed and updated to consider dairy cattle (and other livestock).

d) A strategy for multisectoral collaboration and coordination in the context of clade 2.3.4.4b HPAI in the dairy industry should be developed.

e) Mechanisms to support producers in the event of an outbreak should be agreed upon.

f) Guidance on diagnostic testing should be developed, including for point-of-care testing of raw milk.

g) Should a suitable vaccine be developed for cattle (domestically or internationally) and found suitable for use in Australia, processes must be established for rapid liaison with the Australian Pesticides and Veterinary Medicines Authority regarding emergency use permits. Additionally, vaccination guidelines for veterinarians and producers should be in place, and supply chain and logistical considerations understood. Therefore, a working group should be established with industry to begin to develop a vaccine strategy for dairy cattle. The costs and benefits of developing on-shore manufacturing capacity could also be considered.

h) Ensure that disinfectants effective against clade 2.3.4.4b HPAI and suitable for use in a dairy setting are approved with the Australian Pesticides and Veterinary Medicines Authority.

Organisational development, implementation and sectoral integration

3) The on-farm assessments revealed considerable confusion and uncertainty among Australian dairy producers concerning HPAI in dairy cattle. This indicates a clear need to enhance producer awareness and education. A communication and education plan targeted to producers should be developed. This should include early and clear communication of jurisdictional response plans (once developed) to improve farmer compliance and support of any future response.

4) Results of the risk assessment indicate that enhanced on-farm biosecurity should focus on mitigating the risk of spillover and the risk of between-herd spread. Guidelines should be developed particularly around mitigating risks associated with the movement of lactating animals. Farm-level recommendations are detailed in Section 1.3.4.

5) On-farm pasteurisation capacity should be increased on Australian dairy farms to manage contaminated milk from clinical cows. Producers should be encouraged to routinely treat milk prior to calf feeding in the event of a clade 2.3.4.4b HPAI incursion into Australia.

6) Best-practice treatment guidelines for affected cattle that facilitate rapid return to production should be developed following consultation with US dairy veterinarians and producers.

7) Training and multi-sectoral preparedness and response exercises specific to clade 2.3.4.4b HPAI in the dairy industry should be conducted with biosecurity response teams at the national and jurisdictional levels, and also within the Consultative Committee on Emergency Animal Diseases.

8) Industry liaisons should be connected within jurisdictional biosecurity preparedness and response teams now to provide input into response strategies.

9) Communications material and talking points for ministerial and public release should be prepared in advance of an outbreak.

10) Relevant supply chains should be reviewed. These could include for laboratory testing reagents and consumables, commercial electrolyte solutions and other treatments for affected cattle, suitable disinfectants for decontamination, personal protective equipment for dairy workers (and response teams), and chemicals appropriate for treatment of contaminated milk if such treatment is determined to be effective and practical.

11) Genomic sequencing should be utilised to generate data to understand spillover, between-farm transmission pathways and zoonotic risk in the event of incursion. This requires data sharing frameworks and systems to be established in advance across jurisdictions and across sectors (e.g. with public health agencies). It is important to ensure that sufficient genomic sequencing and data sharing capability (and laboratory diagnostic capability) are available in the event of an incursion.

Data, evidence and knowledge

12) Key research gaps (provided in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle') should be addressed to reduce uncertainty in the assessment. Research on many of these gaps may already be occurring in the US and other countries. There is a need to engage internationally to understand what research is happening overseas and ensure coordination of international research efforts.

13) The assessment revealed a lack of detailed, current information regarding the structure and movement dynamics of the dairy industries in both Australia and the US. Movement networks within the dairy industry are a critical control point for managing between-farm spread of disease. This analysis should be undertaken as a priority. A state-based analysis of the US industry may help to explain why some states (e.g. California) were impacted more severely than others.

14) A surveillance plan should be developed for early detection of clade 2.3.4.4b HPAI in the Australian dairy herd. The effectiveness of the NMTS in the US suggests that surveillance for early detection could be initiated following incursion in wild birds to detect new spillover events into dairy cattle. Other surveillance components should be agreed upon by an expert working group comprising jurisdictional and federal governments, industry and other relevant stakeholders.

15) Alternative approaches to early detection of infection should be investigated further. These could include coordinated research into point-of-care test development and validation in the Australian context and understanding the role of rumination collars and other 'wearable devices' for early detection.

16) Research and development into large-volume milk treatment options suitable for use in the Australian context is required. The effectiveness of (and barriers to) alternative milk treatment options, such as acidification, should also be explored.

17) Consideration should be given as to whether local vaccine development is warranted, given this is already occurring in the US.
18) Consider conducting an updated incursion risk assessment for clade 2.3.4.4b HPAI. The previous assessment was performed in July 2023 prior to arrival of the virus in Antarctica and sub-Antarctic islands. Non-wild bird sources may also be considered, for example – subclinically infected travellers.
19) Advanced modelling is required as further quantitative data become available from the US.
20) Detailed economic analyses are required to better understand the potential economic consequences of an outbreak in the Australian dairy industry. These analyses should consider seasonal, batch and year-round calving herds at different stages of lactation and should be based on current Australian milk prices.
21) A trade impact analysis would be useful given the uncertainty around trade and market access impacts.

Contents

Tables

Figures

Introduction

This is a rapidly evolving area and new information is being released regularly. This analysis was conducted based on information available up to 23 May 2025.

Background to the clade 2.3.4.4b HPAI outbreak in dairy cattle

In early 2024, a syndrome of non-specific systemic illness, milk abnormalities and an abrupt, severe drop in milk production was observed in lactating dairy cattle in Texas, New Mexico and Kansas in the United States (US) (Caserta et al. 2024; Oguzie et al. 2024). Clade 2.3.4.4b high pathogenicity avian influenza (HPAI) of the H5N1 subtype (Appendix A) was identified as the cause of the syndrome, specifically a single genotype, B3.13 (Oguzie et al. 2024). Phylogenetic and epidemiological analyses indicated a single spillover event into cattle at that time, with subsequent sustained cow-to-cow transmission, although the spillover host and transmission pathway into cattle are still not definitively known (Worobey et al. 2024; Caserta et al. 2024). Subsequently, 2 more spillovers into dairy cattle were detected in January and February 2025, respectively (APHIS 2025a, 2025i; CIDRAP 2025; APHIS 2025b; AZDA 2025). Genotype D1.1 was identified in both of those later events; however, virus sequences from each event are genetically distinct, indicating 2 separate spillovers (APHIS 2025b). The D1.1 spillover events were both detected through testing of milk from processing plant silos. Three of 11 silo samples collected in Nevada tested positive and trace-back revealed that 2 herds were infected with this D1.1 genotype (APHIS 2025i). The Arizona D1.1 spillover was attributed to a single dairy (AZDA 2025).

The first spillover of clade 2.3.4.4b HPAI genotype B3.13 into dairy cattle led to sustained transmission within and between dairy herds in the US, leading to a large-scale epidemic. It is not clear whether genotype D1.1 is continuing to spread through dairy herds as genotype is not being publicly reported at the herd level (APHIS 2024i). As of 22 May 2025, clade 2.3.4.4b HPAI has impacted at least 1,070 dairy herds across 17 states (APHIS 2024i). While IAV infections of cattle have been recognised since 1949, including as a cause of sporadic milk drop in dairy cows, sustained cow-to-cow transmission was not knowingly observed prior to the current clade 2.3.4.4b HPAI outbreak in US dairy cattle (Saito 1951; Gunning and Pritchard 1997; Gunning et al. 1999; Sreenivasan et al. 2019).

The bovine udder is the main site of virus replication in lactating dairy cattle, resulting in necrosis and destruction of milk-secreting epithelial cells, likely leading to the systemic clinical signs seen in lactating animals (Caserta et al. 2024; Peña-Mosca et al. 2025). Clinically affected animals show a drastic drop in milk yield (20–100% of baseline production), abnormal thickened milk (described as ‘colostrum-like’), a severe decline in rumen motility, markedly reduced feed and water intake, severe dehydration, lethargy and fever (sometimes exceeding 40.5°C) (APHIS 2024g; Baker et al. 2024; Caserta et al. 2024; Oguzie et al. 2024; Burrough et al. 2024; Rodriguez et al. 2024; El Masry et al. 2024; Halwe et al. 2024). While clinical disease is typically self-limiting and resolves in 1 to 3 weeks in most cases, the potential for a large proportion of lactating cows to become sick (generally 3–20%) indicates considerable impact on overall herd health and productivity (Caserta et al. 2024; Baker et al. 2024; Peña-Mosca et al. 2025). Mortality (the percentage of the herd that die or are euthanised) is

typically low (less than2%) (Caserta et al. 2024). However, the proportion of clinically affected animals that die (i.e. the case fatality rate) has been estimated at 6.8% in one study and many additional animals may be prematurely removed from the herd for economic reasons, as milk production may be reduced for more than 2 months post-infection (Peña-Mosca et al. 2025). Clinical disease is primarily restricted to lactating dairy cows, although non-lactating cattle may be subclinically infected (Peña-Mosca et al. 2025).

Significant economic impacts have been experienced by US dairy producers at the farm level due to decreased milk production, mortality and early herd removal (Peña-Mosca et al. 2025). Accounting for the expected milk loss and replacement costs across all animals that died, were prematurely removed from the herd, or were temporarily affected, the average cost per affected cow on an affected Ohio farm was calculated to be USD$932 (Peña-Mosca et al. 2025). Another estimate from the American Association of Bovine Practitioners was USD$100 to $200 per infected cow (Larkin 2024). A report from a Michigan producer stated a total loss for a 500-head dairy herd of between USD$30,000 and $40,000 during the first 15 days of infection, due to lost milk production and treatment (Durst 2024). The International Dairy Foods Association reported that there have been no known disruptions or barriers to US dairy trade and exports, despite the widespread outbreak in US dairy cattle (International Dairy Foods Association 2024). Enhanced controls for importation of live cattle from the US were applied by some countries. For example – Canada and Mexico implemented enhanced controls for importation of lactating dairy cattle from the US, including enhanced certification prior to export and pre-movement testing (Hunter 29 October 2024). Non-lactating cattle, including beef cattle, were not subject to these enhanced controls. In contrast, Israel requires pre-export testing for all cattle types (Hunter 29 October 2024). Turkey prohibited importation of all live cattle from the US (Hunter 29 October 2024). Some impacts on beef meat and cattle products were experienced, although these were temporary. For example – Colombia closed markets (valued at USD$40 million) for live US cattle, beef meat/meat products and cattle germplasm in April 2024 (Huffstutter and Polansek 26 April 2024). While most restrictions were lifted in September 2024, restrictions on live cattle originating from HPAI-affected states remain. The Dominican Republic market for US beef and live cattle was closed from May to June 2024 but restrictions have since been removed (Hunter 29 October 2024). These restrictions had little appreciable effect on overall US beef/veal or live cattle trade volumes; indeed, US beef exports in 2024 were projected to decline due to factors preceding HPAI but ended up stronger than expected (Petry 12 March 2025).

Dairy cattle have transmitted infection onward to several other species, including domestic cats, wild birds that congregate in barns (such as grackles, rock pigeons and blackbirds), wild terrestrial mammals (i.e. peri-domestic wildlife, such as foxes, raccoons and mice), poultry and humans (Peacock et al. 2024; Nguyen et al. 2024; Worobey et al. 2024; Burrough et al. 2024; Caserta et al. 2024). Of the 70 confirmed human cases in the US since February 2025, 41 had exposure to affected dairy herds, with the bulk of the remainder (24 cases) being exposed to poultry farms and culling operations (CDC 2025a). Current evidence suggests that infected dairy workers acquired infection through exposure to raw milk or through close contact with secretions from clinically affected animals (Morse et al. 2024). Food standard milk pasteurisation is effective at inactivating HPAI in milk and other dairy products (Suarez et al. 2025; Caceres et al. 2024; Nooruzzaman et al. 2024; Kwon, Gebhardt, et al. 2024; Spackman et al. 2024; Alkie et al. 2025; Cui et al. 2024; Schafers et al. 2025). Most human cases of clade 2.3.4.4b HPAI infection have been mild, with conjunctivitis and/or upper respiratory symptoms reported most commonly (CDC 2025b; Morse et al. 2024; Mellis et al. 2024).

However, there have also been 6 severe cases of clade 2.3.4.4b HPAI in humans since the emergence of this virus lineage, although to date no human deaths were associated with exposure to infected cattle (FAO et al. 2024a, 2024b, 2024c; CDC 2025a).

US response to the clade 2.3.4.4b HPAI outbreak in dairy cattle

The aim of the US HPAI response in dairy cattle is containment and elimination of HPAI from the national dairy herd (APHIS 2024k). Previously, elimination was considered feasible because transmission appeared to occur primarily through contact with milk from infected animals rather than via respiratory droplets or aerosols, which are more difficult to control (Peacock et al. 2024). With evidence now for 3 spillover events into dairy cows, some experts now question whether elimination is truly viable given the risk of repeated introduction (Schreiber 23 February 2025). Critically, if the spillover pathway into dairy cows was understood, targeted mitigation measures may be able to reduce the likelihood of future introductions.

The US response strategy centres on the National Milk Testing Strategy (NMTS), along with mandatory testing of lactating dairy cows prior to interstate movement, enhanced surveillance and financial support for producers, including for implementation of enhanced biosecurity measures (APHIS 2024j). Other mandated control measures vary between states.

Unlike in domestic poultry, where the primary control and elimination strategy for HPAI has been depopulation or 'stamping-out', there is no recommendation to depopulate dairy herds since 'in most cattle, this appears to be a self-limiting disease' (USDA 2017; APHIS 2024a). The US response strategy is discussed further in the introduction of this report.

Risks in livestock industries

The potential future introduction of clade 2.3.4.4b HPAI virus into Australian livestock presents a spectrum of risks to Australian livestock industries. At highest risk are the poultry industries and wild bird populations. Wild birds (classically waterfowl) are reservoir hosts for clade 2.3.4.4b HPAI and poultry are highly susceptible to the avian-adapted strains circulating in wild bird populations. Poultry HPAI outbreaks are thought to be principally initiated via exposure to wild bird faeces (Aha 2023c). Once a poultry flock is infected, HPAI spreads rapidly due to the close contact between birds in commercial poultry operations and the high level of virus replication in poultry species. HPAI strains, including clade 2.3.4.4b HPAI, produce severe systemic disease in gallinaceous poultry, while clinical disease and mortality is variable in other poultry species (e.g. ducks, ratites) (Swayne et al. 2020). HPAI in gallinaceous poultry is an acute fulminant disease leading to death within 3 to 5 days in most infected birds (Swayne et al. 2020). Mortality can reach 100% in some flocks. The presence of HPAI may restrict international trade in live birds and poultry meat, which can impact national economies (WOAH n.d.).

Wild birds are likewise susceptible to severe disease caused by clade 2.3.4.4b HPAI (WHA 2024; Wille and Barr 2024). Waterfowl, shorebirds, seabirds and predatory or scavenging birds have been infected most commonly (WHA 2024; Wille and Barr 2022). Population monitoring data indicate significant population declines in some wild bird species (Pearce-Higgins et al. 2023; Wille and Barr 2022). Ecological behaviours which increase exposure to the virus include residing in water,

predating or scavenging other birds, and congregating in large colonies (Pearce-Higgins et al. 2023). If clade 2.3.4.4b HPAI were to arrive in Australia, there is potential for widespread, long-term population loss or local extinction of wild bird species (WHA 2023).

IAVs have long been recognised as a cause of disease, classically respiratory disease, in a wide range of non-avian species, including humans, horses, pigs and dogs (Swayne et al. 2020). Sporadic infections have been recorded in various mammal species, including cattle, sheep, goats, camelids, marine mammals and various predatory and scavenging species (e.g. cats, foxes, mink). Further details are discussed in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review'. The clinical presentation in species of the order Carnivora is generally severe. Cats, foxes, mink and other predatory species frequently present with severe encephalitis and death, due to neurological invasion of the virus (Butt et al. 2024; Plaza et al. 2024). Similar neurological signs have been reported in H5N1-infected marine mammals (also order Carnivora) (Banyard et al. 2024; Uhart et al. 2024; Leguia et al. 2023). This presentation is not specific to clade 2.3.4.4b HPAI viruses and has been recognised in big cats (e.g. tigers) fed contaminated chicken carcasses since 2005 (Thanawongnuwech et al. 2005). In vivo studies show that HPAI neurovirulence is determined in part by the route and dose of inoculation, as well as virus strain and infected animal species (Bauer et al. 2023).

Like non-lactating cattle, other artiodactyls, such as pigs, goats and alpacas, reportedly show minimal clinical disease with H5N1 infection (Kwon, Trujillo, et al. 2024; Plaza et al. 2024; APHIS 2024f). However, these are typically individual case reports with small sample sizes, so generalisations should be made cautiously.

The emergence of sustained mammalian transmission in dairy cattle marks an unprecedented shift in HPAI epidemiology. The cells of the bovine udder express α-2,3-linked sialic acids that avian-adapted IAVs can bind to without having to evolve specific mammalian genetic adaptations (Peacock et al. 2024; Good et al. 2024; Kristensen et al. 2024). Because of this, IAV infection in dairy cattle is mostly localised to the mammary tissue, which during lactation contains abundant target cells that support viral replication, leading to shedding of virus in extremely high concentrations in milk (e.g. up to 109 50% tissue culture infectious doses (TCID50), a measure of the amount of virus, per ml) (Mitchell et al. 1954, 1953; Halwe et al. 2024; Caserta et al. 2024). Hence, exposure of susceptible individuals to raw milk or colostrum (either through direct contact with infected cows or via exposure to contaminated fomites) is currently thought to be the primary pathway for transmission between cows (Halwe et al. 2024; Zhou et al. 2024).

Studies on sialic acid distribution in other livestock species are limited. One recent study examined the expression pattern of different sialic acids in mammary gland tissue of various livestock species (Nelli et al. 2025). It is worth noting that this study assessed sialic distribution via histochemistry, not direct virus binding and replication. Both α-2,3- and α-2,6-linked sialic acids were identified in mammary epithelium of ruminants (cattle, sheep, goats) and non-ruminants (alpaca, pig), suggesting that both mammalian-adapted and avian-adapted IAVs have the potential to bind to mammary tissue of a wide range of livestock species. This was supported by the recent detection of a lactating ewe in the UK testing positive for clade 2.3.4.4b HPAI and showing clinical signs of mastitis (HAIRS 2025).

While these findings may suggest a similar pathogenesis of clade 2.3.4.4b HPAI infection in lactating livestock beyond just dairy cattle, there are considerable evidence gaps that limit our ability to assess

risk in other species with any certainty (HAIRS 2025). For example – the routes of infection (e.g. intramammary, oral, respiratory) and infectious dose across different mammalian species are not known. How host factors may limit susceptibility to infection are not known. Whether co-infections with other pathogens or differences in management systems influence susceptibility to clade 2.3.4.4b HPAI infection are not known. The duration of infection, clinical disease and virus shedding are not known, as well as which secretions and/or excretions may be infectious. The spectrum of clinical disease in different livestock species is not known, nor are any long-term effects on infection on relevant production parameters, such as fertility, weight gain and wool production. However, the currently available evidence indicates that gallinaceous poultry and some wild bird populations are at highest risk from clade 2.3.4.4b HPAI (i.e. likelihood of infection and consequences of infection), followed by populations of lactating mammals where sustained transmission occurs, particularly those with closely networked populations (e.g. dairy animals), predator and scavenger species, due to the severe neurological disease that often results, and animal populations where mammalian-adapted IAVs circulate enzootically, due to the risk of the emergence of novel reassortants with pandemic potential. While other non-lactating livestock may be infected with clade 2.3.4.4b HPAI, the consequences of infection in terms of clinical disease and production impacts and the likelihood of sustained mammal-to-mammal transmission would currently appear to be limited, noting the high uncertainty and need for further research. With the continued evolution of clade 2.3.4.4b viruses and the emergence of novel genotypes, the biological properties (such as pathogenesis, virulence and transmissibility) of these viruses may change over time, which may change the results of this risk assessment.

This general introduction provides an overarching framework for the more detailed, industry-specific risk assessments that follow in Sections 1 and 3.

Australian dairy industry

The Australian dairy industry represents the third largest rural industry in the nation (following the red meat and wheat sectors) and contributed approximately AUD$6.2 billion in farmgate value during the 2023–24 financial year (Dairy Australia 2024a). In 2024, the industry comprised 3,889 dairy farms with a national herd of 1.33 million cows in milk and an average herd size of 385 cows per farm (Dairy Australia 2024a). There is an emerging trend of large farm operations milking more than 700 cows. The industry produced 8.4 billion litres of milk over the 2023–24 season, with about 32% of production exported to Greater China, Japan, Singapore, Indonesia and Malaysia (Dairy Australia 2024a). This makes the Australian dairy industry a major dairy exporter. The total value of Australia's dairy exports in 2023–24 was AUD$3.6 billion (Dairy Australia 2024a).

Australian dairy operations are predominantly pasture-based and are located across temperate and some subtropical regions, with most milk production occurring in south-eastern regions given the favourable climate and natural resources for dairying (Dairy Australia 2024a; AHA 2022). The distribution of dairy farms varies significantly across states, with Victoria being the largest contributor to milk production (Dairy Australia 2024a). In 2023–24, Victoria accounted for 63.2% of the national milk output, supported by 2,552 farms, which represented 65.6% of all Australian dairy farms (Dairy Australia 2024a). Production volume is generally seasonal, reflecting pasture quality, with peaks in October and lower production over the cooler winter months (AHA 2022).

Milking typically occurs twice daily, although milking once-a-day, 3 times daily or 3 times every 2 days is done on some farms (AHA 2022). For milking, cows are collected from a paddock and walked to the milking shed, where they are held in close confinement in concrete yards while awaiting milking. After milking they either walk back to a paddock or are held together in a loafing area or feed pad.

Australian dairy farms can be broadly classified according to operating structure, although these structures are not necessarily mutually exclusive (e.g. family farms may be within a corporate structure) (AHA 2022). Operating structure can influence biosecurity risk; for example – businesses that involve a structure with multiple farms are more likely to share resources, such as machinery and farm personnel, particularly on larger corporate farms and equity partnerships (AHA 2022). The movement of animals between premises is also more likely within larger corporatised systems, although empirical data demonstrating this are lacking. These types of movements may become more common as Australia's dairy industry continues to become more horizontally integrated. Since animal movements are a key determinant of disease spread, an updated review of the structure and dynamics of the Australian dairy cattle industry would be of benefit. This should include an understanding of between-'milking herd' movements in multi-herd businesses.

Dairy cattle are likely to move between farms in the 'dry period', in regions with mostly split or seasonal calving (AHA 2022). The choice of calving system can be driven by climatic variables affecting pasture quality, by market factors and by disease patterns.

Comparison with the US dairy industry

The dairy industries in Australia and the US differ with regards to scale, geographic distribution, production systems and market orientation. The US dairy industry operates on a significantly larger scale than the Australian industry. Recent reports indicate that the total national US herd was approximately 9.4 million milk cows (USDA 2024b), while the number of farms was reported to be about 23,153 (USDA 2024a). In the US, 5 milk-producing states—California, Wisconsin, Idaho, Texas and New York—collectively account for more than 50% of the nation's annual milk supply (USDA 2025). The average herd size across the entire US is comparable to Australia (337 in 2022), although this varies considerably by state; 22% of US states have an average herd size of greater than 1,000 head (Progressive Dairy 2023). In 2023, US milk production was 98.4 billion litres. While most dairy operations in the US are family-owned, many belong to national producer-owned cooperatives (USDA 2025), with reportedly frequent movement of animals and resources (equipment, vehicles and personnel) between premises (Rawson et al. 2025). Some of these cooperatives have high vertical integration, operating their own processing and manufacturing plants.

In terms of production systems, Australia primarily employs pasture-based dairying, where cows graze on open pasture (Dairy Australia 2023). This system is cost-efficient but highly dependent on favourable seasonal conditions and rainfall, supplemented with irrigation and supplemental feeding in drier regions. In contrast, the US relies heavily on intensive contained housing systems with cattle fed controlled diets (i.e. TMR) (USDA 2011). In 2013, less than 8% of dairy operations were primarily pasture-based (USDA 2022). Approximately 40% of dairy operations primarily used freestalls (with or without access to an open/dry lot), 39% used tie stalls or stanchions, and 14% used various other housing types (USDA 2022).

Market orientation is another key distinction between the Australian and US dairy industry. Australia's industry is export-driven, with 32% of its milk production destined for global markets, particularly to Asia (Dairy Australia 2024a). The US allocates a larger proportion of production to the domestic market, with only 18% exported in 2022 (International Dairy Foods Association 2023; USDA 2011). From a public health perspective, the sale of raw milk is legal in many US states, although federal law prohibits the sale of unpasteurised milk across state lines (CDC 2024a). The sale of raw cow's milk for human consumption is illegal in Australia.

While a recent study of biosecurity practices among Australian dairy farmers was done in 2019 (Aleri and Laurence 2020), no such comprehensive review of biosecurity practices on US dairy farms is available, with the most recent relevant study dating to 2000 (Wells 2000). There is a need to better understand on-farm biosecurity practices in the US to be able to make robust comparisons with the Australian industry.

Additional background information on the Australian and US dairy industries is provided in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review'.

Risk assessments for clade 2.3.4.4b HPAI in dairy cattle

Globally, we identified 8 risk assessments on HPAI in dairy cattle. Additionally, several risk assessments have been conducted by various countries and organisations assessing the public health risks associated with clade 2.3.4.4b HPAI. Since this review focuses on HPAI in dairy cattle, we do not discuss the risk assessments for public health further. Regarding risk assessments specific to cattle:

- Belgian authorities conducted a risk assessment for entry of clade 2.3.4.4b HPAI into cattle and goat populations in April 2024 (RAG-V-EZ 2024). The likelihood of exposure of cattle and goats was assessed as very low to low. In the Belgian epidemiological context, the main source of infection was assessed as direct or indirect contact with infected birds (wild birds and poultry). Wild mammals were also considered a potential source of exposure. The authors recommended active surveillance of cattle and goat populations in Belgium to monitor for sub-clinical infection.
- In July 2024 a rapid risk assessment for clade 2.3.4.4b HPAI was conducted for Germany (FLI 2024). This assessment encompassed domestic poultry, wild birds and cattle. For cattle, the risk of genotype B3.13 entering German cattle herds, including dairy farms, was assessed as very low. The most likely routes of introduction of genotype B3.13 were trade in live cattle and contaminated raw milk products, although neither raw milk nor live cattle are imported into Germany from the US. The risk of infection of German cattle with other H5 HPAI viruses was estimated to be very low. This was based on historical circulation of H5 HPAI viruses in many countries for several decades without spillover into cattle or other bovids.
- In August 2024 Canadian government experts conducted a rapid qualitative risk assessment on the risk to Canadian dairy cattle from the US genotype B3.13 outbreak (CEZD 2024b). They concluded that the risk of at least 1 dairy cattle herd in Canada being infected with genotype B3.13 over the next 6 months (to 31 October 2024) was: 1) very high via dairy cattle imported from the US, with moderate to high uncertainty; 2) very low to low via migratory wild birds, with moderate uncertainty; and 3) low via the movement of cattle transport trucks from the US, with

high uncertainty. Strengthened import conditions around testing and health certification of lactating dairy cattle entering Canada from the US were thought to mitigate most of the risk. However, residual risk remained, for example – if cattle were tested early in the incubation period before infection becomes detectable, or if cattle were infected after samples were collected. Additionally, some categories of animals were exempt from testing, such as Canadian cattle returning to Canada. There was residual risk around non-lactating dairy cattle movements, although the authors noted that significant information gaps remain. For example – there is uncertainty around the ability of non-lactating cattle to shed an infectious dose of virus and the epidemiological importance of non-milk-associated transmission routes between cattle.

- In November 2024 Canada updated their public health rapid risk assessment for clade 2.3.4.4.b HPAI, which stated that the likelihood of a random individual animal being infected during the following 3 months was very low for livestock, with moderate uncertainty (Public Health Agency of Canada 2024). They concluded that, while the virus may enter Canadian cattle herds within this timeframe, it would likely take longer to spread significantly.
- A qualitative risk assessment for HPAI in mammals in Belgium was published in November 2024 (Van Leeuw et al. 2024). The likelihood of cattle infection in Belgium was assessed as high, while the clinical consequences were assessed as minor to medium, resulting in an overall risk of low to moderate, with high uncertainty. This was based on several factors. Cattle were considered to have very high susceptibility to HPAI. Contact with wild birds was assessed as moderate, while the likelihood of ingestion of raw infected product was assessed as very low (this was limited to poultry meat and did not consider raw milk). For the consequences, clinical signs were assessed as ‘mild’ to ‘major but without death’.
- In February 2025 an assessment of the risk of introduction and spread of HPAI in cows in Bulgaria was published (Goujgoulova and Koev 2025). The likelihood of HPAI affecting Bulgarian dairy herds was assessed as low to medium, due to a high concentration of dairy herds in geographic areas where HPAI outbreaks occurred in wild and domestic birds in 2024. The risk was thought to increase during the autumn period due to the increased migration of wild birds.
- In March 2025 the UK Health Security Agency released a risk assessment for influenza of avian origin in all lactating livestock (including dairy cattle) (HAIRS 2025). Notably, this was primarily focused on the risk of human exposure. While not explicitly assessing the risk of likelihood of entry and exposure of lactating livestock, they considered that there was satisfactory evidence to demonstrate that there were routes of introduction of clade 2.3.4.4b HPAI into livestock in the UK and that the disease was not endemic in animals within the UK.
- In April 2025 a Danish team developed a quantitative model to estimate the spillover rate of clade 2.3.4.4b HPAI from wild birds to cattle (both dairy and beef) (Chang et al. 2025). Overall, they assessed the risk to cattle as low, with highest risk between December and March, driven by seasonal migration of wild birds. The highest risk geographical areas were located along the Danish coastline and near the German border. The estimated number of spillover events in 2024 was 1.96 (95% confidence interval (CI) 0.48–4.98). The authors concluded that the risk of further transmission within Danish cattle could be influenced by factors such as livestock density, movement patterns and farm management practices, including biosecurity standards.

Of relevance to the Australian context, an incursion risk assessment for clade 2.3.4.4b HPAI via wild birds was completed by Wildlife Health Australia in July 2023 (WHA 2023). This is discussed further in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review'. Briefly, at the time of the assessment the risk of clade 2.3.4.4b HPAI entry and establishment in Australia via wild birds was assessed as high, with moderate uncertainty. Entry and establishment within wild mammals was assessed as low risk, with high uncertainty. The risk to livestock was not assessed, since this was prior to the US HPAI detections in dairy cattle.

Response guidance for Australia

In Australia, emergency animal disease (EAD) responses are guided by the Australian Veterinary Emergency Plan (AUSVETPLAN). AUSVETPLAN consists of a series of manuals that describe the nationally agreed approach for responding to EAD incidents of national significance. These manuals include disease-specific response strategies and response policy briefs, operational manuals, enterprise manuals, management manuals, and guidance and resource documents. The aim is to develop accurate but concise references that are relevant and useful to jurisdictions and industries, facilitating a rapid response. As they are developed prior to an outbreak their key role is to provide an immediate starting point for drafting EAD response plans early in an outbreak when little is known. The manuals are managed by Animal Health Australia and are developed in consultation with Australian national and jurisdictional governments, the relevant livestock industries, non-government agencies and public health authorities, where relevant. The relevant AUSVETPLAN disease-specific manuals for IAVs include:

- the response strategy for avian influenza in poultry, cage (aviary) or zoo birds
- the response policy brief for IAVs in swine (covering swine-origin, human-origin and avian-origin IAVs)
- potentially the response strategy for equine influenza (though this classically refers to the equine-adapted H3N8 subtype and the historical H7N7 subtype).

There is currently no nationally agreed-upon disease-specific response strategy that covers clade 2.3.4.4b HPAI in dairy cattle (or other non-avian hosts beyond IAVs in pigs generally). Additional relevant AUSVETPLAN documents for a potential clade 2.3.4.4b HPAI incursion into Australian dairy cattle include the enterprise manual for the dairy cattle industry, the various operational manuals, and guidance documents such as those on movement controls and tracing and surveillance.

AUSVETPLANs are relatively high-level documents, which are complemented by more detailed nationally agreed standard operating procedures (NASOPs) developed by jurisdictions that outline how to undertake specific actions during an EAD response (Aha 2023a). Other relevant response guidance may include jurisdictional or industry policies, jurisdictional-level standard operating procedures and work instructions. Responses are also governed by Commonwealth and jurisdictional legislation and legal agreements, including the Emergency Animal Disease Response Agreement (EADRA).

The EADRA is a contractual arrangement between the Australian and jurisdictional governments and signatory livestock industries that outlines the roles and responsibilities of industries and governments to reduce the risk of EAD incursion, as well as the approach to contributing to a response, including cost-sharing (Aha 2023b). Current signatory industries are:

- Poultry (Australian Chicken Meat Federation Limited, Australian Duck Meat Association Inc, Australian Eggs Limited)
- Dairy (Australian Dairy Farmers Limited)
- Beef cattle (Cattle Australia Limited, Australian Lot Feeders' Association Inc)
- Pigs (Australian Pork Limited)
- Sheep and small ruminants (Sheep Producers Australia Limited, WoolProducers Australia Limited, Goat Industry Council of Australia)
- Horses (Racing Australia Limited, Harness Racing Australia Incorporated, Australian Horse Industry Council, Equestrian Australia Limited).

EADs are categorised according to the impact they may have on livestock production, human health and the environment—the category determines how costs are shared between affected industries and governments. In return, industry representatives are involved with maintaining a surveillance and response capacity and in assisting with response strategies, including development and review of the AUSVETPLAN manuals. Avian influenza in poultry (HPAI subtypes H5 and H7) is a category 2 disease, while IAV of swine and equine influenza are category four diseases (Table 1).

Table 1 Categorisation of emergency animal diseases

Category	Definition
1	Serious effects on human health and/or the environment (depletion of native fauna); may only have minimal direct consequences to the livestock industries.
2	Potential to cause major national socio-economic consequences through very serious international trade losses, national market disruptions and very severe production losses; OR significant public health and/or environmental consequences.
3	Generally moderate national socioeconomic consequences through international trade losses, market disruptions involving 2 or more states and severe production losses, but potential to be significant, with minimal or no effect on human health or the environment.
4	Mainly production loss diseases.

Source: Aha 2023a

AUSVETPLAN manuals are drafted and maintained by industry–government expert writing or working groups with technical expertise in the subject matter (Aha 2023a). Drafted manuals are reviewed by the AUSVETPLAN Technical Review Group, approved by the Industry Forum and endorsed by the Animal Health Committee, which includes the chief veterinary officers of the Commonwealth and jurisdictions, along with representatives from the Australian Centre for Disease Preparedness, the Department of Agriculture, Fisheries and Forestry (the department) and various observers. Once support is demonstrated from all relevant government and industry signatories to the EADRA, the manuals are authorised by the National Biosecurity Committee under the Intergovernmental Agreement on Biosecurity. The six phases in the development and approvals process for AUSVETPLAN manuals are identification, prioritisation, drafting, consultation, approval/endorsement and publication. More detail on each of these steps can be found in the AUSVETPLAN Overview document (Aha 2023a).

Project objectives

Australia remains free of clade 2.3.4.4b HPAI as of October 2025. However, the recent outbreak in dairy cows in the US has heightened concerns about the potential risk to the Australian dairy industry following a potential clade 2.3.4.4b HPAI incursion. In 2023, a Wildlife Health Australia risk assessment estimated the likelihood of clade 2.3.4.4b HPAI incursion via wild birds to moderate, with moderate uncertainty (WHA 2023). A key consideration is that the assessment was conducted prior to the incursion of clade 2.3.4.4b HPAI into Antarctica (Banyard et al. 2024). There is now increased concern around HPAI entering southern Australia (where commercial poultry and dairy cattle operations are concentrated) via subantarctic islands, as well as via northern Australia (Stock 14 August 2024).

To address this heightened concern, Ausvet were contracted by the department and Dairy Australia (DA) to evaluate the risk of entry and between- and within-farm transmission of HPAI in the Australian dairy industry. The hazard of interest was initially identified as H5N1 HPAI in dairy cattle. This was refined over the course of the project, in consultation with the department and DA, to be clade 2.3.4.4b HPAI in dairy cattle.

Mammals appear to be unusually susceptible to clade 2.3.4.4b HPAI (Peacock et al. 2024), although the reasons for this remain unclear. In theory, other H5 or H7 HPAI subtypes could perhaps also spillover into cattle. However, H7 viruses have never been detected in cattle and other H5 HPAI viruses have never been detected in Australia despite circulating in south-east Asia for many years (Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review). Thus, other non-clade 2.3.4.4b H5 and H7 HPAI viruses were not considered further, to focus project resources on the highest risk lineage.

The project encompassed several distinct components:

- A comprehensive literature review outlining the current state of knowledge around HPAI in dairy cattle (Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review)
- An assessment of the molecular epidemiology of the outbreak in dairy cattle and the risk of reassortment with IAVs currently in Australia in the event of an incursion (Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review)
- A formal qualitative risk assessment on the risk of entry and spread of clade 2.3.4.4b HPAI in the Australian dairy industry, including a report detailing practical recommendations to minimise the risk of HPAI to Australian dairy cattle and producers achievable within the unique setting of the Australian dairy industry (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). This was supported by:
    - On-farm biosecurity assessments on 25 representative Australian dairy farms
    - Development of a stochastic, agent-based simulation model for within-farm spread of clade 2.3.4.4b HPAI in a ‘typical’ Australian dairy farm
- Rapid risk appraisals for the risk of clade 2.3.4.4b HPAI entry and transmission in Australian beef (Risk of high pathogenicity avian influenza to Australian beef cattle: Rapid risk assessment), pig (Risk of high pathogenicity avian influenza to the Australian pig industry: Rapid risk assessment)

and small ruminant industries (Risk of high pathogenicity avian influenza to Australian small ruminant industries: Rapid risk assessment).

- A final project report detailing recommendations to inform national contingency and response planning.

1 Qualitative risk assessment: Clade 2.3.4.4b HPAI in the Australian dairy industry

This assessment was conducted based on information available up to 23 May 2025.

This is a summary of the comprehensive assessment provided in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'. Further details are provided in that document.

The recent emergence of clade 2.3.4.4b HPAI in dairy cattle in the US has raised concerns about the potential risk to the Australian dairy industry. In response, a qualitative risk assessment was conducted to evaluate the risk (i.e. likelihood and consequences) of clade 2.3.4.4b HPAI entering and spreading within and between Australian dairy herds. This assessment aims to provide an evidence-based understanding of the risk, inform preparedness activities, and recommend updates to on-farm biosecurity plans.

1.1 Risk questions

1) Assuming clade 2.3.4.4b entered Australia via wild birds, what is the risk (likelihood and consequences) of entry and within- and between-farm transmission of HPAI in the Australian dairy industry in the 3 years following incursion?

    a) Assuming clade 2.3.4.4b HPAI was introduced into Australia via wild birds, what is the likelihood of clade 2.3.4.4b HPAI infecting at least 1 Australian dairy cow in the 3 years following incursion?

    b) If at least 1 Australian dairy cow was infected with clade 2.3.4.4b HPAI, what is the likelihood of spread within the affected dairy farm?

    c) If at least 1 Australian dairy farm was infected with clade 2.3.4.4b HPAI, what is the likelihood that infection would spread to other Australian dairy farms?

    d) What are the consequences of clade 2.3.4.4b HPAI entering and spreading within the Australian dairy industry in the 3 years following incursion?

1.2 Methodology

The risk analysis followed a structured process aligned with WOAH guidelines, comprising hazard identification, risk assessment (entry, within- and between-farm establishment and spread and consequence assessments and risk estimation), risk management and risk communication (WOAH 2010). The final pathways selected for assessment were:

- Entry of clade 2.3.4.4b HPAI into a dairy farm via various pathways including:
    - Spillover from wild birds (either exposure to faeces, direct contact, or inadvertent consumption of a carcass)

  - Spillover from wild birds to poultry and then into dairy cows (either direct contact, exposure to faeces/environmental contamination, or inadvertent consumption of a carcass)
  - Spillover from wild birds to mammals and then into dairy cows (either direct contact with a non-human mammal, direct contact with a person contaminated or infected by poultry, or inadvertent consumption of an infected carcass or faeces)

- Within-farm spread of clade 2.3.4.4b HPAI via various pathways including:
  - Contamination during milking (either raw milk contaminating milking equipment or splashing and aerosolisation of milk)
  - Contact with an infected dairy cow (non-milk associated transmission)
  - Contaminated floors or bedding
  - Feeding of raw milk
  - Exposure to milk for disposal or effluent containing raw milk
  - Spread facilitated by non-cattle hosts (with 6 sub-pathways depending on the host exposure pathway and host-cattle contact type)
- Between-farm spread of clade 2.3.4.4b HPAI via various pathways including:
  - Movement of infected cattle
  - Movement of contaminated vehicles (excluding milk tankers) and equipment
  - Movement of milk tankers
  - Movement of raw milk
  - Spread to adjacent premises (either direct contact with adjacent stock or exposure to effluent containing raw milk)
  - Spread facilitated by non-cattle hosts, excluding people (with 4 sub-pathways depending on the host exposure pathway and host-cattle contact type)
  - Spread facilitated by people

For each pathway, scenario trees (i.e. risk pathway) outlined the individual steps or nodes necessary for the event to occur (see 'Qualitative risk assessment for clade 2.3.4.4b HPAI in the Australian dairy industry'). Data were gathered through the literature review, on-farm biosecurity assessments and within-spread simulation modelling to parameterise each node. Qualitative likelihood and consequence categories were combined to assess overall risk, and uncertainty was explicitly evaluated in the assessment (Table 2, Table 3, Table 4).

Table 2 Qualitative likelihood categories used in this assessment

Qualitative category	Definition
High	Event would be very likely to occur
Moderate	Event is equally likely to occur or not occur
Low	Event would be unlikely to occur
Very low	Event would be very unlikely to occur
Extremely low	Event would be extremely unlikely to occur
Negligible	Event would almost certainly not occur

Table 3 Qualitative consequence categories used in this assessment

Qualitative category	Definition
Extreme	Effect is likely to be highly significant at the national level. Implies that economic stability, societal values or social well-being would be seriously affected.
High	Effect is likely to be significant at the national level and highly significant within affected zones. Implies that the effect would be of national concern. However, serious effects on economic stability, societal values or social well-being would be limited to a given zone.
Moderate	Effect is likely to be recognised on a national level and significant within affected zones. The effect is likely to be highly significant to directly affected parties.
Low	Effect is likely to be recognised within affected zones and significant to directly affected parties. It is not likely that the effect will be recognised at the national level.
Very low	Effect is likely to be minor to directly affected parties. The effect is unlikely to be recognised at any other level.
Negligible	Effect is unlikely to be recognised at any level within Australia.

Table 4 Qualitative uncertainty categories used in this assessment

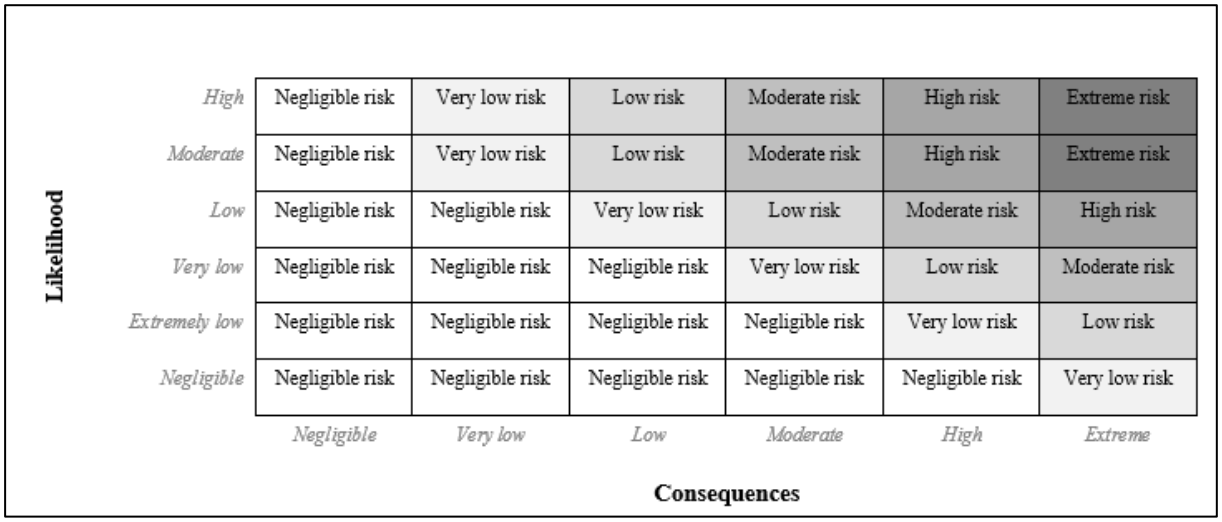
Qualitative category	Definition
Very low	Reliable data and information are available in sufficient quantity; results strongly anchored in empiric data or concrete information
Low	Reliable data and information available but may be limited in quantity, or be variable; results based on expert consensus
Moderate	Some gaps in availability or reliability of data and information, or conflicting data; results based on limited consensus
High	Limited data or reliable information available; results based on educated guess
Very high	Lack of data or reliable information; results based on crude speculation only

(FAO et al. 2020)

Figure 1 Matrix for iteratively combining likelihoods

Likelihood $n+1$ \ Conditional likelihood to n	*Negligible*	*Extremely low*	*Very low*	*Low*	*Moderate*	*High*
High	Negligible	Extremely low	Very low	Low	Moderate	High
Moderate	Negligible	Extremely low	Very low	Low	Low	Moderate
Low	Negligible	Extremely low	Very low	Very low	Low	Low
Very low	Negligible	Extremely low	Extremely low	Very low	Very low	Very low
Extremely low	Negligible	Negligible	Extremely low	Extremely low	Extremely low	Extremely low
Negligible	Negligible	Negligible	Negligible	Negligible	Negligible	Negligible

Figure 2 Risk estimation matrix



1.2.1 Assumptions

The risk assessment was made with the following assumptions:

- That clade 2.3.4.4b HPAI is present in wild birds across Australia. This is a hypothetical assumption for the purpose of this assessment. As of October 2025, Australia remains free of clade 2.3.4.4b HPAI.
- That the biology (including virulence and transmissibility) of any virus entering Australia is not substantially different to the genotype B3.13 clade 2.3.4.4b HPAI virus in dairy cattle in the US. Similarly, that the pathogenesis of infection in Australian dairy cattle is comparable to that observed in US dairy cattle. This is because data on which to assess the risk are primarily limited to genotype B3.13. Differences in husbandry practices, host genetics or potentially environmental factors may alter the epidemiology of clade 2.3.4.4b HPAI in Australia.
- That no specific control measures are in place to mitigate spread of clade 2.3.4.4b HPAI between dairy premises at the time of an incursion (i.e. animal, people, vehicle and equipment movements continue as normal).

1.3 Key findings

1.3.1 On-farm biosecurity assessments

A summary of key findings from the on-farm biosecurity assessments is provided here. Further detailed information is provided in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

The average milking herd size of farms visited was 415 cows (range 200 to 1,000). Non-lactating dairy cattle present on dairy farms included dry cows (median 100, interquartile range (IQR) 25 to 209), heifers (median 136, IQR 55 to 400), bulls/steers (median 7, IQR 4 to 25) and calves (median 102, IQR 70 to 280). Twenty-one out of 25 dairy farms visited had at least 1 neighbouring property with dairy cattle.

Forty percent of producers inspected all stock, including dry cows and heifers, daily for illness. For the other farms, lactating cows were generally inspected daily, while dry stock were inspected

regularly, but not necessarily daily. When detected, sick stock were reported to management on most farms and usually this occurred within 1–2 days. Producers reportedly had good relationships with their veterinarians and veterinary advice was sought in relation to unusual illness or death in the majority of cases.

On 44% of premises, mastitic cows were always milked separately from the main herd. This indicates that on many dairies, mastitic animals are not always milked separately. One producer mentioned that sick animals tended to naturally come in last. Producers noted that infrastructure challenges made management of a separate sick herd difficult. Two farms reported that milking equipment was washed and sanitised after sick cows. When handling sick cattle, 38% of farms reported that staff always followed appropriate biosecurity practices.

On 36% of farms staff always wore site-specific clothing when handling cattle. A higher proportion (64%) always used boots and an apron or wet weather gear when milking. Seventy-two percent of farms reported that staff always wore gloves during milking and when handling milk and colostrum (e.g. for calf feeding). Twenty percent said that staff always washed their hands with detergent before and after milking. One producer noted that staff used gloves instead of practising handwashing. Staff on most of the Australian dairy farms visited (64%) never wore eye protection during milking or when handling milk. Of the farms that sometimes did, 56% very rarely cleaned or disinfected their eye protection and 44% never did. Staff on most farms (83%) never used respiratory protection during milking or when handling milk. Of the farms that sometimes did, 50% very rarely replaced or disinfected their respiratory protection.

Teats were rarely disinfected prior to milking, although 1 producer reported using teat disinfectant wipes and 1 producer reported that chlorine dioxide foam was applied to every teat. Most farms (60%) always used a teat disinfectant after milking, typically iodine-based. Both automated sprayers and manual spray systems were used.

On 66% of dairies visited, hosing down of the milking shed commenced while cows were still present. Producers noted that it was not practical to wait, given the time required for milking (e.g. milking takes 8 hours). Producers often noted that they were cautious to avoid washing down near cows.

Eighty four percent of Australian dairy farms visited regularly fed calves raw waste milk and 79% of farms regularly fed calves raw vat milk. One farm reported pasteurising waste milk prior to calf feeding due to the risk of Mycoplasma, although this was done rarely. Another farm reported occasionally pasteurising vat milk prior to feeding. No producers mentioned any other form of milk treatment prior to calf feeding (e.g. acidification). Four farms regularly used milk replacer for calf feeding, although most producers noted this was too expensive to be practical on a routine basis. Only 1 out of 25 farms ever brought raw milk onto the property from other premises and this was done very rarely.

Unpasteurised milk was frequently consumed by either owners, staff, family and/or visitors on 68% of farms interviewed, while 12% of farms reported that people never consumed raw milk. On 88% of farms, staff with flu-like symptoms sometimes worked with or handled cattle. Three producers noted that staff were often casual (i.e. no sick leave) and needed the income. Labour shortages were also highlighted.

Milk was occasionally disposed of on-farm when not able to be collected (e.g. vat breakdown, refrigeration issues, power outage). Twenty producers stated that, when required, milk was disposed of into effluent ponds. Three producers mentioned they were able to spray milk for disposal onto paddocks if required. Milk was not treated prior to disposal (e.g. heat-treated or acidified). 100% of farms spread effluent across grazing areas as fertiliser, although 20% only did so occasionally (e.g. a couple of times a year).

Not unexpectedly, wild birds were observed frequently on dairy farms. Waterfowl, corvids, psittacines (e.g. cockatoos, corellas) and small passerines (e.g. perching birds like swallows, sparrows, starlings, mynas) were commonly encountered in large numbers. Other groups, including pigeons, doves, raptors, gulls and terns, were less commonly reported. Seven farms reported seeing more than 1,000 waterfowl per week on at least one area of the property. The most common areas where birds congregated were reported to be irrigated pastures, pastures where cattle graze, ponds (including effluent ponds) and cattle watering points. Stock feed was regularly accessible to wild birds on 72% of premises. Corvids and small passerines were the most common bird group reported around feed troughs and/or feed pads and within the dairy shed. One farm highlighted swallows as an issue for faecal contamination of feed. One farm noted large numbers of ducks were often observed around the feed pad. Ibis, cockatoos, corellas, swallows and sparrows were noted by at least one producer to be present around feed/silage storage. One farm noted issues with ibis contaminating troughs. Two producers reported major issues with ibis fouling the dairy (including defecating on milking cups and in feed troughs in the dairy shed). One producer reported a previous experience where a dead bird was present in a paddock during hay making. The paddock was slashed and hay was spread onto a neighbouring paddock, resulting in a mass mortality event in dairy cattle. During our assessments we observed a wild bird carcass in 1 paddock.

The feed infrastructure used for lactating cattle varied widely by farm. Infrastructure included feed pads, troughs, pellet feeders, hay rings/feeders or feeding hay and/or silage directly from the ground. One farm reported using a TMR mixer. The frequency with which feed infrastructure was cleaned varied widely between farms. Two farms stated daily cleaning, 2 said weekly, 1 said monthly, 4 said once or twice a year and 1 said not cleaned. Two producers stated that cleaning was on an as-needs basis. Regarding cow housing, 2 producers had free stall barns for cows and 3 had shade sheds or other paddock shelters. One additional farm had an open-sided shed that covered the feed pad.

Cow bedding was used regularly on 26% of dairies visited. Bedding material was mostly stored in open sheds and was regularly accessible to wildlife (including vermin), domestic animals and wild birds on 83% of dairies. Bedding materials included sand, straw and wood chips. Where bedding was used, 2 producers spread used bedding directly onto paddocks. One recycled used bedding directly into the emergency calving area. Many other producers composted used bedding.

Of the 25 dairy farms visited during our on-farm assessments, 1 property also raised broiler chickens commercially and 12 out of 25 kept pet poultry. Two premises had neighbouring properties that raised chickens commercially, while 12 out of 25 premises had neighbours with pet poultry. Thirteen farms reported having staff members who owned poultry. None reported employing staff who also worked at poultry farms. Most producers (56.2%) reported that poultry (pet or commercial) never accessed land grazed on by dairy cattle, 93.8% reported that poultry never accessed cattle watering points, and 87.5% reported that poultry never accessed feed troughs/pads. Two out of 25 farms

stated that poultry litter was regularly used as fertiliser on the property. Two producers mentioned that while they themselves don't use poultry litter, it is used commonly in the dairy industry as fertiliser. Despite two farms reporting the use of poultry litter as fertiliser, 100% of producers stated that their cattle never had any exposure to eggs, poultry carcasses, feather meal or poultry litter. One farm reported that poultry regularly had access to raw milk and another mentioned that chickens may be able to access spilt calf milk.

Thirteen out of 25 premises kept beef cattle, as well as dairy cattle. Three properties kept pigs, 9 properties kept sheep, 8 properties kept horses, 1 property kept goats, and 1 property kept camels. Most properties kept domestic pets (cats and dogs), with only 1 out of 25 not having either a cat or a dog on site. Feral cats were also frequently reported around dairy premises. Dogs and cats had free access to dairy cattle or the milking or calf sheds on 30% and 27% of the farms visited, respectively. Off-property cats (e.g. feral, stray, from neighbouring properties) had access to dairy cattle or the dairy environment on 79% of premises, suggesting that contact with healthy cats is common. On 54% of farms, dogs, cats and/or other livestock had regular access to raw milk.

Seventy-nine percent of farms stated that wildlife had regular contact with dairy cattle, either directly or via a shared environment. Reported wildlife species included foxes, deer, kangaroos, wallabies, bandicoots, rabbits/hares, possums, quolls, echidnas and, in Tasmania, Tasmanian devils. No producers interviewed reported issues with feral pigs. Fifty-eight percent of premises applied a continuous rodent control program in the dairy shed, suggesting that exposure to rodents would be unlikely on these premises. However, 8% of farms did not have a rodent control program. Stock feed was regularly accessible to wildlife (including vermin), domestic animals and/or wild birds on 72% of premises. In particular, hay was usually accessible, while grain and/or other concentrates was stored in silos on at least 13 farms. Cattle carcasses were able to be accessed by livestock, feral animals and/or wildlife at least occasionally on most farms.

One out of 25 farms interviewed had purchased lactating dairy cattle during 2024, suggesting that the purchase of lactating animals is relatively uncommon. Three farms had purchased non-lactating cattle during 2024. Forty-six percent of producers reported sending cattle off-property for agistment or contract rearing; these were typically calves and/or heifers. However, 1 farm reported agisting 300 cows during 2024. Three out of 25 dairies reported sometimes milking cows from other farms. Eighty-seven percent of producers reportedly never sold cattle, apart from cull animals. All producers reported that they only ever transported clinically healthy cattle. Only 1 producer reported that they exhibited dairy cattle at shows, and only very rarely. Noting that producers rarely purchased lactating cattle at our farm visits, greater than75% reported that if milking cows were purchased, they were never grazed separately or milked separately from the main herd. Twenty-one percent of producers reported that they always quarantine new arrivals for at least 21 days.

Twenty-five percent of premises visited regularly used farm vehicles across multiple dairy premises. This included across multiple land parcels within the same business or when visiting other premises. Two producers said that farm vehicles and equipment were regularly lent to or used on other properties. No property routinely cleaned and disinfected vehicle tyres when entering and leaving the property. Only 21% of respondents said that they would regularly clean and disinfect equipment/vehicles before and after use if they lent them out. On most premises cattle did not regularly have contact with vehicles.

Seven out of 25 of the farms interviewed reported that staff from other dairies visited occasionally. One property had a family member working at another dairy. Two farms reported that at least 1 staff member worked across multiple dairies. Visitors were always aware of farm biosecurity requirements and movements were always controlled around the site on 44% of premises interviewed. However, no farms always kept a dedicated up-to-date visitor log. Site-specific clothing was not generally provided to visitors (84% of farms responded that it never was), although many premises (52%) said that visitors regularly provided their own clean protective clothing (e.g. gumboots and overalls). Visitors' boots were not routinely cleaned before entering areas where cattle or milk were present on 92% of premises. On 75% of premises interviewed visitors did not always wash their hands or wear gloves when handling cattle. Eighty-eight percent of respondents stated that visitors did not always clean their boots and/or equipment when leaving the premises.

These on-farm visits provided an up-to-date understanding of current biosecurity practices in the Australian dairy industry relevant to clade 2.3.4.4b HPAI. This information, along with evidence from the peer-reviewed and grey literature, informed the qualitative likelihood category assignments to each node within each transmission pathway evaluated in the risk assessment.

1.3.2 Qualitative risk assessment

Following aggregation of the different pathways, the likelihood of clade 2.3.4.4b HPAI entry into the Australian dairy herd was assessed as low, with high uncertainty.

Details on the individual pathways are provided in Section 1.2.

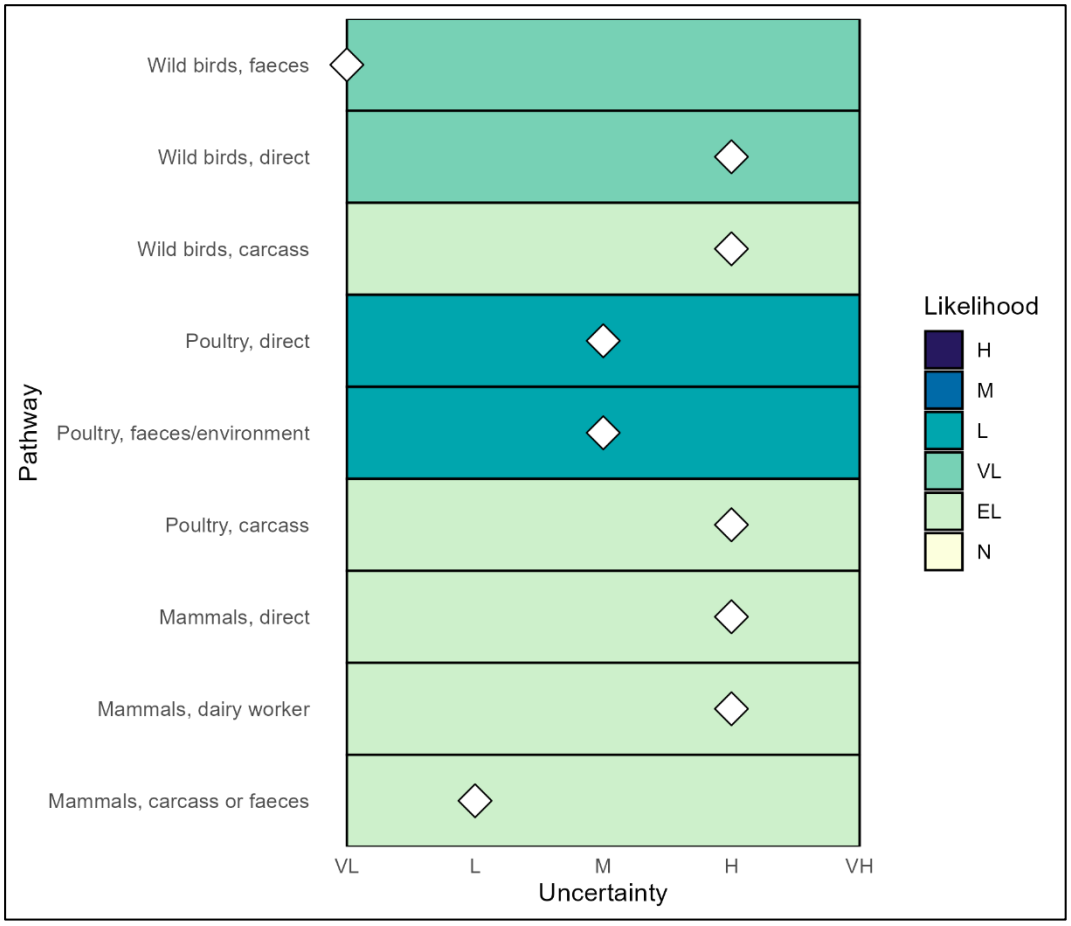
Spillover from wild birds to poultry and then into dairy cows was considered more likely than spillover directly from wild birds into dairy cows, due to the higher virus concentrations and shedding volumes associated with an outbreak in poultry compared to carriage in wild birds (Figure 3). Our assessment considered not only direct and indirect contact rates with dairy cattle, but also other steps in the spillover pathway, such as whether an exposure is likely to contain sufficient virus levels to initiate an infection in a dairy cow. For the complete rationale, please see Section 2.1 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

Spillover from wild birds into mammals and then into dairy cows was considered less likely due to lower contact rates with dairy cattle and lower viral shedding. We assessed evidence around the likelihood of respiratory transmission from infected mammals, transmission from a person infected or contaminated following contact with affected poultry, or inadvertent consumption of a carcass or faeces of an infected mammal. For the complete rationale, see Section 2.1.3 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

There is significant uncertainty around many factors in this assessment. Of particular note are uncertainties around the minimum infectious dose of clade 2.3.4.4b HPAI in cattle, the role of non-milk associated transmission routes, and the long-term impacts of an outbreak. Detailed discussion of uncertainty for each pathway is provided in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'. Key research gaps identified during the assessment are detailed in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'.

Risk assessments for other countries have assessed the likelihood of clade 2.3.4.4b HPAI entry into cattle as very low to high, based on their specific epidemiological circumstances (see introduction).

Figure 3 Likelihood assessments for entry of clade 2.3.4.4b HPAI into dairy cattle



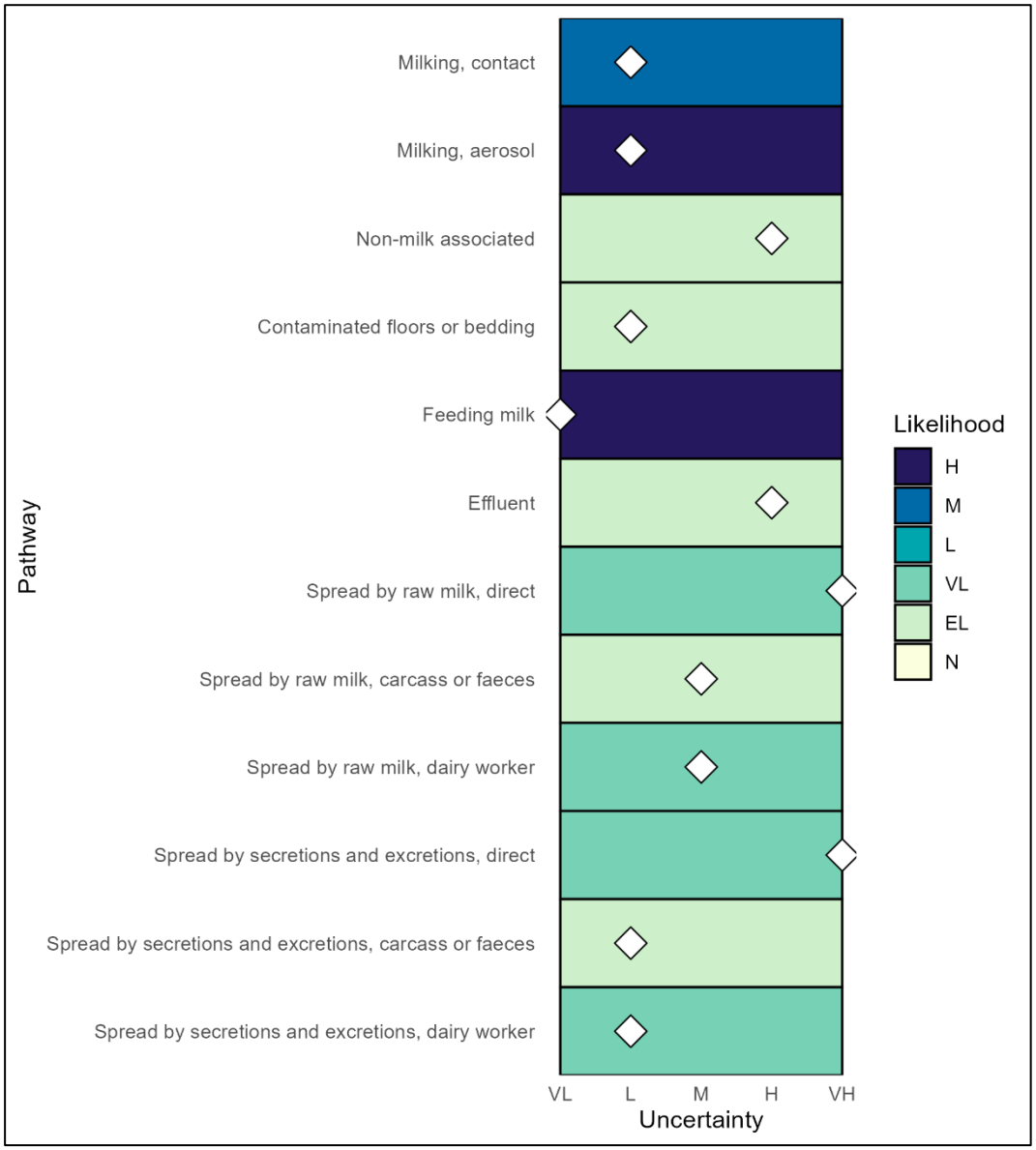
The likelihood for each entry pathway (y-axis) is indicated by the box fill colour. Uncertainty is shown on the x-axis and represented by a white diamond for each pathway. Abbreviations: VH very high, H high, M moderate, L low, VL very low, EL extremely low, N negligible.

If clade 2.3.4.4b HPAI entered a dairy herd, the likelihood of within-farm spread was assessed as high based on aggregation of the different within-farm spread pathways, with low uncertainty.

The highest assessed likelihood pathways were contamination during milking through splashing or aerosolisation of raw milk and feeding of raw milk to calves (Figure 4).

Other pathways, such as contact with infected cows (non-milk associated), contaminated floors or bedding, and spread in effluent, were assessed as having lower likelihood.

Figure 4 Likelihood assessments for within-farm spread of clade 2.3.4.4b HPAI



The likelihood for each within-farm establishment and spread pathway (y-axis) is indicated by the box fill colour. Uncertainty is shown on the x-axis and represented by a white diamond for each pathway. Abbreviations: VH very high, H high, M moderate, L low, VL very low, EL extremely low, N negligible.

The likelihood of between-farm spread was assessed as very low based on aggregation of the different between-farm spread pathways, with very high uncertainty.

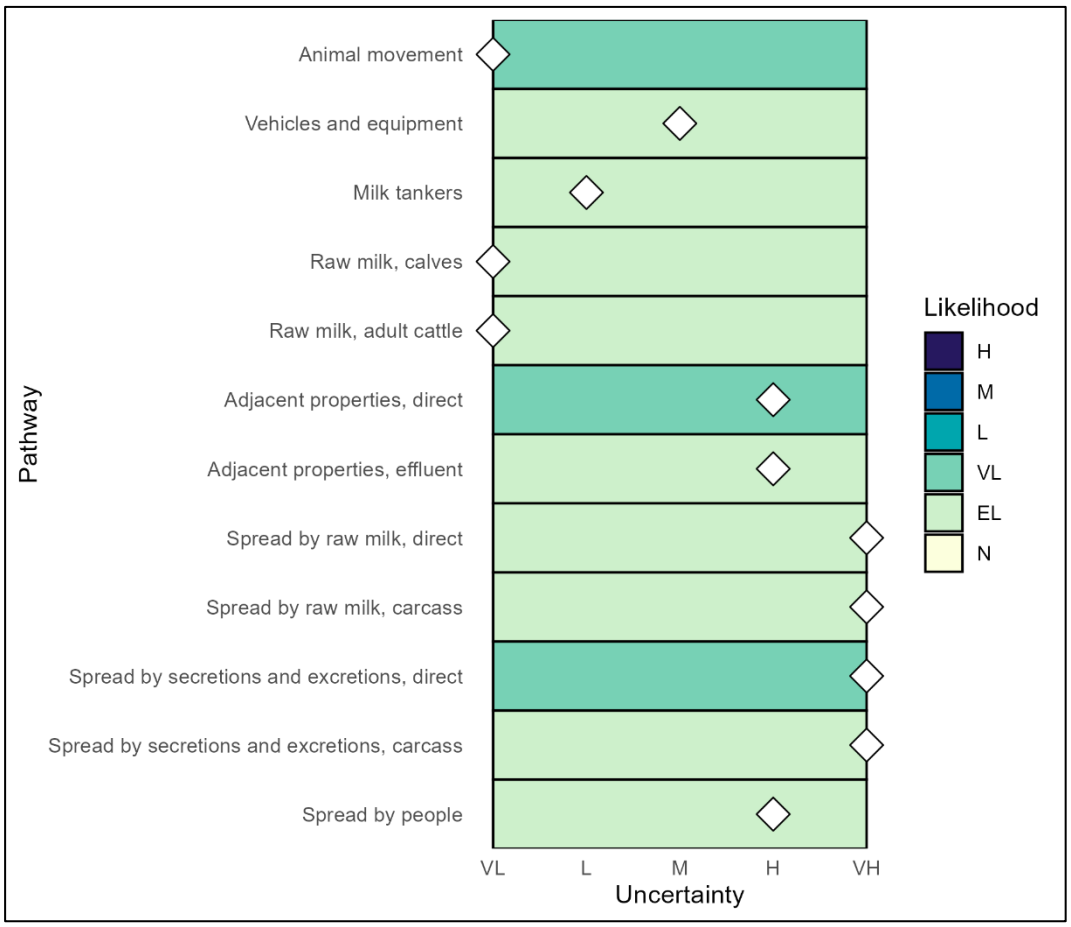
The highest assessed likelihood pathways were movement of infected cattle, spread to adjacent premises via direct contact, and spread facilitated by non-cattle hosts (e.g. on contaminated animals) (Figure 5).

Other pathways, such as movement of contaminated vehicles and equipment, spread via milk tankers, and other movements of raw milk, were assessed as having extremely low likelihood. The evidence used to inform these likelihood ratings is detailed in Section 2.3 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'.

This finding differs considerably from the US experience, where between-farm spread has been substantial. Differences between the Australian and US dairy industries could lead to pathways having different likelihoods in the 2 regions. For example – anecdotally there is considerably greater movement of lactating cows, vehicles, equipment and people between dairy premises in the US industry. In contrast, the evidence indicated that between-farm movements of lactating dairy cows were uncommon in Australia and dairy cows were rarely exposed to vehicles or equipment from other farms (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). It was beyond the scope of this project to conduct the same detailed risk assessment for the US industry to explore these differences further, which would require extensive consultation with US industry representatives.

While the on-farm assessments indicated that movement of lactating cattle in Australia was uncommon, these results were based on responses from 25 dairy farms. Our analysis revealed a lack of detailed, current information regarding the structure and movement dynamics within the Australian dairy industry. Movement networks are a critical control point for managing between-farm spread of disease. Additionally, with the continued corporatisation of the dairy industry, analyses need to distinguish between within-business movements in multi-herd operations and between-business movements. An updated movement analysis should be undertaken as a priority.

Figure 5 Likelihood assessments for between-farm spread of clade 2.3.4.4b HPAI



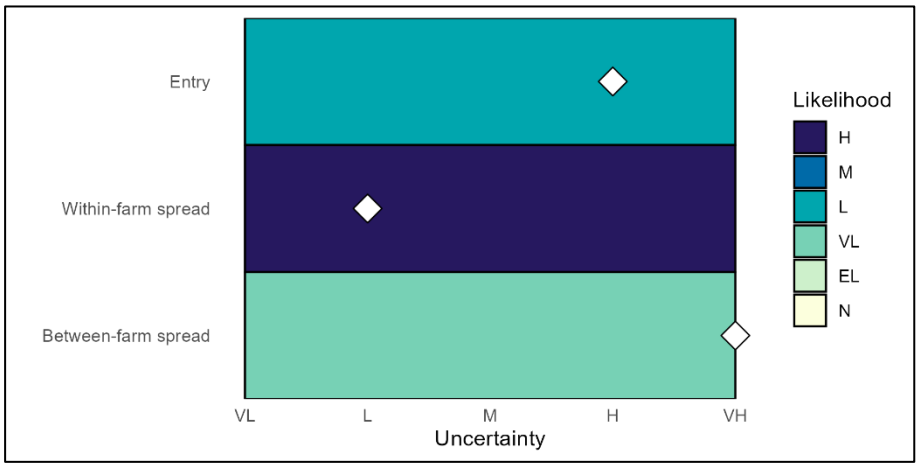
The likelihood for each between-farm establishment and spread pathway (y-axis) is indicated by the box fill colour. Uncertainty is shown on the x-axis and represented by a white diamond for each pathway. Abbreviations: VH very high, H high, M moderate, L low, VL very low, EL extremely low, N negligible.

The consequences of a clade 2.3.4.4b HPAI outbreak in the dairy industry were assessed as high, driven by the magnitude of socio-economic impacts experienced by producers in the US, with moderate uncertainty.

That is, effects of an outbreak are likely to be of national concern and highly significant within affected zones. However, this depends on the size and scale of an outbreak and associated response measures. Other consequences considered included animal health and welfare, human health, environmental and trade impacts, and food security and safety.

The overall risk of clade 2.3.4.4b HPAI to the Australian dairy industry was assessed as low. This was based on an entry assessment of low likelihood, a within-farm spread assessment of high likelihood, and a between-farm spread assessment of very low likelihood, together with a high consequence assessment (Figure 6). However, the overall uncertainty in the risk assessment was high.

Figure 6 Likelihood assessments for entry, within-farm and between-farm spread of clade 2.3.4.4b HPAI in Australian dairy herds



The likelihood for each assessment (y-axis) is indicated by the box fill colour. Uncertainty is shown on the x-axis and represented by a white diamond for each pathway. Abbreviations: VH very high, H high, M moderate, L low, VL very low, EL extremely low, N negligible.

1.3.3 Limitations

A comprehensive discussion of the risk assessment findings is provided in '[Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment]'. However, we note here several key limitations:

- There is significant uncertainty around many factors in this assessment. Of particular note are uncertainties around the minimum infectious dose of clade 2.3.4.4b HPAI in cattle, the role of non-milk associated transmission routes, and the long-term impacts of an outbreak. Additional research gaps are detailed in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'.
- Data on clade 2.3.4.4b HPAI biology, pathogenesis and transmissibility in dairy cattle in a field context were based on the US experience, where the industry is heavily reliant on contained housing and dairy herd sizes can be extremely large. These data may not be relevant to the Australian industry with smaller herd sizes and predominantly pasture-based grazing system.
- The on-farm biosecurity assessments involved a relatively small sample size (25 farms). The geographic distribution of the selected farms approximated the distribution of dairy farms by

state. Farms within each state/district were convenience sampled based on their willingness to participate, which may have resulted in a level of selection bias.

- There are considerable assumptions and limitations associated with the simulation modelling relating to transmission pathways and production systems that are described in detail in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Simulation modelling of within-herd transmission'.
- The potential for the emergence of new HPAI virus genotypes with altered virulence or transmissibility remains an ongoing source of uncertainty.

1.3.4 Farm-level recommendations for Australian dairy producers

1) Prevent entry (spillover) into dairy cattle:
    a) Implement measures to prevent direct and indirect contact between dairy cattle and poultry, including avoiding the use of poultry litter as fertiliser.
    b) Monitor wild bird populations for signs of HPAI (such as sudden death) and implement enhanced biosecurity measures on dairy farms if infection is detected locally.
    c) Where possible, minimise access of wild birds, poultry and other animals to dairy cattle feed and water sources. Opportunities for both faecal contamination of dairy cattle feed and inadvertent contamination with carcasses should be minimised.
    d) Update biosecurity plans.
    e) Be alert and report illness promptly.
2) Reduce within-farm spread:
    a) Controlling an outbreak on an affected premises once the virus has entered is likely to be challenging.
    b) Implement strict hygiene practices during milking, including regular cleaning and disinfection of equipment.
    c) Do not feed milk from mastitic cows to calves.
    d) Consider treating milk before feeding it to calves, such as through pasteurisation or potentially acidification. While calves are not thought to be epidemiologically relevant in disease spread, current recommendations from the US are not to feed calves raw milk from exposed cattle. The aim should be to limit the number of infections in any mammalian species to reduce opportunity for mammalian adaptation.
    e) Implement early detection and isolation of clinically affected animals.
3) Reduce between-farm spread:
    a) Minimise animal movements, especially of lactating cows, and implement pre-movement testing (if available) and strict quarantine for at least 14 days.
        - Implement strict biosecurity protocols for people, vehicles and equipment moving between farms. There is currently insufficient evidence to implicate specific pathways. This limits our ability to provide advice on targeted and effective biosecurity that is practically implementable on farm. Research gaps are detailed further in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'.

b) Avoid moving raw milk between farms.

4) Reduce the impacts:

a) Prepare for the treatment of sick animals, including having equipment and supplies (e.g. electrolytes) on hand for oral rehydration therapy (see Section 2.2.5).

b) To mitigate public health risks, consider the use of personal protective equipment (such as gloves, apron, respiratory protection and eye protection) in certain circumstances (e.g. during milking or when in close contact with secretions from sick animals, like during drenching/stomach tubing).

c) Don't consume raw milk or other raw dairy products.

d) If an inexpensive, accurate pen-side test to diagnose clade 2.3.4.4b HPAI in the milking herd was readily available, a farm-specific surveillance plan could be developed (e.g. systematic testing of vat milk) for early detection to facilitate rapid treatment and management of an infected herd and hopefully faster recovery.

1.3.5 Recommendations for national contingency and response planning

1) The on-farm assessments revealed considerable confusion and uncertainty among Australian dairy producers concerning HPAI in dairy cattle. This indicates a clear need to enhance producer awareness and education. This could be achieved through: HPAI-specific training for industry, a simulation exercise(s) around clade 2.3.4.4b HPAI targeted to producers and/or the development of clear guidelines for enhancing on-farm biosecurity in the context of clade 2.3.4.4b HPAI. A communication and education plan targeted to producers should be developed.

2) The consequences of a positive test result need to be clearly communicated by policy and decision-makers. Empowerment of farmers and producer cooperation is critical to optimising both active and passive surveillance systems (i.e. for rapid investigation and reporting of outbreaks) (Gates et al. 2021). Various factors influence the willingness of producers to report suspect emergency animal diseases, including (1) uncertainty around the clinical signs and situations that warrant reporting, (2) fear over the social and economic consequences from both positive and false positive reports, (3) negative beliefs regarding the efficacy and outcomes of response measures, (4) mistrust and dissatisfaction with animal health authorities, (5) absence of sufficiently attractive financial and non-financial incentives for submitting reports, and (6) poor awareness of the procedures involved with the submission, processing, and response to reports (Gates et al. 2021). These factors need to be proactively addressed by government and industry.

3) Similarly, response strategies in dairy cattle should be considered now (i.e. before an outbreak) and clearly communicated so that industry can better understand the likely impacts of potential control measures. Ongoing consultation with a wide range of industry stakeholders during the development of response plans will be crucial to ensure their practicality and acceptance.

4) Further guidance for policy makers around national-level contingency planning will be explored further in the final project report.

5) Key research gaps must be addressed to reduce uncertainty in the assessment. Research gaps identified through the assessment are provided in 'Research gaps identified for clade 2.3.4.4b

HPAI in dairy cattle'. Research on many of these gaps may already be occurring in the US and other countries. There is a need to engage internationally to understand what research is happening overseas and ensure coordination of international research efforts.

6) In particular, the assessment revealed a lack of detailed, current information regarding the structure and movement dynamics of the dairy industries in both Australia and the US. Movement networks within the dairy industry are a critical control point for managing between-farm spread of disease. In particular, a better understanding is required of between-'milking herd' movements in multi-herd businesses. This analysis should be undertaken as a priority. A state-based analysis of the US industry may help to explain why some states (e.g. California) were impacted so much more severely than others.

7) Best-practice treatment guidelines for affected cattle that facilitate rapid return to production should be developed following consultation with US dairy veterinarians and producers. These should be tailored for mild, moderate and severe clinical cases. Training should be provided to producers where required, for example – in the delivery of large volumes of oral fluids.

8) Alternative approaches to early detection of infection should be investigated further. These could include coordinated research into point-of-care test development and validation in the Australian context and understanding the role of rumination collars and other 'wearable devices' for early detection.

9) Research and development into large-volume milk treatment and disposal options suitable for use in the Australian context is required. The impact of milk disposal needs to be better quantified and understood. While on-farm pasteurisation is ideal, this is not widely available on Australian dairy farms and is currently restricted to small volumes. Options for larger volume on-farm pasteurisation capacity (or local/regional capacity) should be investigated. The effectiveness of (and barriers to) alternative milk treatment options, such as acidification, should also be explored.

10) Advanced modelling is required as further quantitative data become available from the US.

11) Detailed economic analyses are required to better understand the potential economic consequences of an outbreak in the Australian dairy industry. These analyses should consider seasonal, batch and year-round calving herds at different stages of lactation and should be based on current Australian milk prices.

1.4 Conclusion

The findings of the qualitative risk assessment have several important implications for the Australian dairy industry. While the overall risk was assessed as low, the high likelihood of within-farm spread of clade 2.3.4.4b HPAI and the potential for significant consequences necessitate proactive consideration of disease mitigation measures. Efforts should focus initially on enhancing farm biosecurity to prevent spillover of clade 2.3.4.4b HPAI. If it does become established in Australian dairy cattle, enhancing between-herd biosecurity will be critical to mitigating the consequences of an outbreak. Further research to address the many identified uncertainties, and continuous review of the risk assessment in light of new information, is recommended.

2 Response guidance for clade 2.3.4.4b HPAI in dairy cattle

2.1 Response measures used in the United States

As discussed in the Introduction, the US response to clade 2.3.4.4b HPAI in dairy cattle has centred on the NMTS, mandatory testing of lactating dairy cows prior to interstate movement, enhanced surveillance, and financial support for producers, including enhanced biosecurity planning and implementation.

2.1.1 National Milk Testing Strategy

The US Department of Agriculture (USDA), in collaboration with state veterinary officials, established the NMTS in December 2024 to monitor the presence and spread of clade 2.3.4.4b HPAI in dairy herds nationwide. Bulk tank milk samples are collected and tested by reverse transcription quantitative polymerase chain reaction (RT-qPCR) to identify states with active clade 2.3.4.4b HPAI circulation (APHIS 2025c, 2025e, 2025h). Sampling is coordinated at the state level; states may sample individual farm bulk tanks, tankers or at processing silos (see Section 2.2.4). Any positive detections trigger additional epidemiological investigations at the state level, including trace-back of all farms contributing to the milk sample. Once identified, infected herds are subject to enhanced biosecurity, movement controls, contact tracing and enhanced surveillance until infection is resolved. Ongoing testing using representative serial sampling and a phased approach for sampling frequency supports demonstration of freedom in unaffected and previously affected states.

As of 16 May 2025, 45 states were enrolled in the NMTS. This program led to the detection of the 2 genotype D1.1 spillovers in early 2025 (APHIS 2025a, 2025b), suggesting that this strategy is beneficial for early detection. However, limited participation will reduce the coverage, representativeness and therefore sensitivity of this surveillance approach. It is also unclear how granular this surveillance is; that is, how many individual farms are being captured.

2.1.2 Mandatory testing of lactating dairy cows prior to interstate movement

In April 2024, to control the interstate spread of clade 2.3.4.4b HPAI in the dairy industry, a federal order was issued that mandated pre-movement testing for lactating dairy cattle in the US. All interstate movements must be accompanied by a Certificate of Veterinary Inspection. The requirement specifically applies to lactating cows, as they are considered the primary infection source through virus shedding in milk (APHIS 2024b). Non-lactating cattle (heifers, dry cows, and bull calves) are exempt from mandatory testing, although testing via nasal swabs is strongly encouraged**.** Lactating dairy cattle must receive a negative IAV RT-qPCR test from an approved National Animal Health Laboratory Network (NAHLN) laboratory within the 7 days prior to interstate movement**.** Milk samples are collected from individual cows, with each quarter sampled. Lactating cattle from infected herds are restricted from interstate movement for 30 days following the most recent positive sample from the herd and positive herds are subject to an epidemiological investigation,

including movement tracing. Intrastate cattle movement is governed by state-specific guidance (where available).

2.1.3 Enhanced surveillance

To encourage widespread testing and alleviate the financial burden on producers, the USDA is fully funding HPAI testing at NAHLN laboratories (APHIS 2024m). This applies to testing of:

- suspect cattle
- any cattle that have been exposed to or epidemiologically linked to suspect or confirmed HPAI cases
- cattle from producers concerned their cattle may have HPAI
- sick or dead domestic animals near affected dairy premises
- wildlife
- monitoring of healthy cattle via the Dairy Herd Status Program.

The voluntary Dairy Herd Status Program allows dairy producers to monitor their herd HPAI status via weekly bulk milk sample testing at an NAHLN laboratory (APHIS 2025d). Weekly samples must represent all animals in the milking strings, but do not need to include samples from animals not contributing to the vat milk. Field data show that bulk tank milk testing for clade 2.3.4.4b HPAI is very sensitive, and positive results occur in bulk tank/vat milk before widespread clinical illness in the herd (APHIS 2025d). Therefore, testing milk from sick or newly freshened cows (i.e. those that have recently calved and are in the early stages of lactation) does not significantly increase the sensitivity of this surveillance. Like for the NMTS, any positive detections trigger a state-level epidemiological investigation and movement restrictions. As of 23 May 2025, 100 herds across 18 states have enrolled in the program, representing 0.4% of the approximately 23,153 dairy farms in the US (USDA 2024). The barriers to enrolment have not been reported.

Some states have additionally implemented their own voluntary herd-level monitoring programs. For example – California provides producers with options to conduct regular surveillance through sampling of bulk milk, individual cow milk or nasal swabs from non-lactating cattle (California Department of Food and Agriculture 2024a). Sampling protocols are detailed further in Section 2.2.4.

Laboratories and state veterinarians must report positive IAV nucleic acid detections or serology results in livestock to the USDA in compliance with Federal Orders.

2.1.4 Support for producers

Recognising that biosecurity is the most effective way to prevent and control the spread of clade 2.3.4.4b HPAI in the US dairy industry, the USDA offers education for producers as well as several programs and resources to support enhanced on-farm biosecurity measures and surveillance (APHIS 2025f).

All dairy producers are eligible for:

- up to USD$1,500 for biosecurity planning and implementation, plus USD$100 for an in-line milk sampler

- up to $100 per premises per month to offset shipping costs for laboratory testing.

Affected dairy producers are eligible for:

- up to USD$10,000 per premises to offset veterinary costs associated with HPAI treatment
- up to USD$2,000 per month for provision of personal protective equipment (PPE) or uniform laundering (subject to participation in a US Centers for Disease Control and Prevention epidemiological study)
- up to USD$8,000 per premises to offset heat treatment for milk disposal
- compensation for milk losses via the Emergency Assistance for Livestock Program. Producers receive payments at 90% of lost production per cow for 28 days (Farm Service Agency 2024).

Unaffected producers are eligible for:

- up to USD$2,000 to offset veterinary costs associated with sample collection.

The Farm Service Agency is also providing direct and guaranteed loans to assist with implementation of various biosecurity measures, including physical infrastructure, purchase of disinfectant and PPE, costs associated with cleaning and disinfecting livestock transportation.

2.2 Australian control and elimination policy recommendations

Following on from 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review' and 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment', here we discuss various considerations for national contingency planning in the event of an incursion into dairy cattle in Australia. This broadly follows the format used in the AUSVETPLAN disease-specific response strategies under 'Control and eradication policy'. A central finding was that there was high uncertainty around the findings from the qualitative risk assessment due to a lack of information around the epidemiology of infection in dairy cattle, such as the minimum infectious dose, relevant transmission pathways between cattle, and role of non-lactating cattle in disease spread. Further research is required to address these key information gaps. The recommendations outlined here should continue to be reviewed as new data become available. These are preliminary recommendations based on the scientific evidence gathered throughout this project and may not fully consider the broader economic, political, social, legal and regulatory context of EAD responses in Australia. Further consultation should be undertaken with jurisdictional governments, Australian dairy industry stakeholders, relevant non-government agencies and public health authorities.

2.2.1 Epidemiological assessment

This section broadly follows the guidance provided in the AUSVETPLAN manuals for avian influenza in poultry and for foot-and-mouth disease (FMD), with modifications relevant to clade 2.3.4.4b HPAI and the Australian dairy industry.

Epidemiological investigation or assessment draws on multiple sources of information to build understanding of the disease and how it is behaving in an outbreak. This helps inform response decision making.

To facilitate epidemiological assessment, a case definition appropriate for the local context must be agreed upon. The AUSVETPLAN disease-response manual for avian influenza in poultry defines avian influenza as laboratory-confirmed infection with avian influenza virus in a susceptible animal with or without clinical signs. Positive serology in the absence of other clinical, epidemiological or laboratory evidence supporting infection does not constitute a case. In the US, the USDA has adopted the following case definitions for clade 2.3.4.4b HPAI in non-avian species:

1) Suspect case
    a) Illness compatible with clade 2.3.4.4b HPAI infection, or
    b) Detection of IAV antigen in milk using an approved commercially available influenza A antigen test kit, or
    c) Detection of IAV RNA by RT-qPCR at a private laboratory where the host species virus lineage has been ruled out (e.g. swine lineage H1/H3, equine/canine H3).
2) Presumptive positive case
    a) Detection of IAV RNA by RT-qPCR at an approved laboratory where the host species virus lineage has been ruled out, with or without the presence of compatible illness.
3) Confirmed positive case
    a) Identification of clade 2.3.4.4b HPAI at the national reference laboratory by molecular assay OR genome sequencing.
        i) An animal may be excluded as a confirmed case after review of all available case information if an alternative diagnosis can fully explain the illness or detection or if test result(s) are poorly or not repeatable and resampling is either not possible or testing from resampling is negative.

In Australia, the key objectives for an epidemiological assessment will be to identify:

- the spatial distribution of infected and free animal populations (dairy cattle, poultry, wild birds, potentially other peri-domestic mammals)
- the source of infection
- the prevalence of infection and the likely size of the outbreak
- pathways of spread and their risk profiles, including potential mechanical vectors involved (as well as potential biological vectors)
- risk factors for the presence of infection and susceptibility to disease (including weather and wild bird populations).

Epidemiological assessment and tracing and surveillance activities (Section 2.2.4) in an EAD response are interrelated activities. Early findings from tracing and surveillance will be inputs into the initial epidemiological assessment (e.g. considering the temporal and spatial distribution of infection). The outcomes of the initial epidemiological assessment will then guide decisions on subsequent tracing and surveillance priorities. The outcomes of the epidemiological assessment will be used initially to determine the feasibility of elimination versus long-term control, and then to guide the selection of other appropriate response measures (including the application of movement controls).

Ongoing epidemiological assessment is important for any EAD response to aid evaluation of the continued effectiveness and value of response measures, and assessment of the progress of the disease response. Ongoing epidemiological assessment will consider the outcomes of tracing and surveillance activities and will contribute evidence to support any later claims of disease freedom.

If infection is detected, genomic sequencing of positive cases will provide a more detailed epidemiological understanding of spillover pathways into dairy cattle and the temporal and spatial spread of infection between herds, as conclusively demonstrated in Australia during the COVID-19 pandemic (Hall et al. 2023; Lane et al. 2021). It may also provide useful information to support ongoing epidemiological assessment. Furthermore, it will be critical information for public health agencies to monitor for sequence changes at biologically relevant sites that may indicate mammalian adaptation or antiviral resistance (CDC 2024). For genomic sequencing to be of most use, it must be comprehensive, rapid, and utilise a shared nomenclature that can adapt to ongoing emergence of new strains/variants (such as Genoflu in the US). Data sharing mechanisms must also be developed and agreed to by all jurisdictions in advance of an outbreak. Specific guidance for strategies for genomic surveillance of IAVs is provided by the European Union Reference Laboratory.

2.2.2 Quarantine and biosecurity

In the US, the approach to managing infected dairy premises is governed by the individual state. For this assessment, we relied on publicly accessible information to understand US response strategies. While some states, like Texas and Arizona, do not appear to mandate quarantine for infected dairy premises, other states, such as California, Idaho, Wisconsin and New York state, do.

California places all dairies that test positive for clade 2.3.4.4b HPAI under quarantine and enforces enhanced biosecurity measures on affected premises (California Department of Food and Agriculture 2025, 2024b). Premises are released from quarantine following 3 negative tests on creamery samples (presumably vat milk) collected at least 7 days apart, starting from 60 days post-diagnosis and after resolution of clinical signs. During quarantine, affected dairies in California must:

- Activate an Enhanced Biosecurity Plan with initial verification audit. This includes:
    - posting signage at the farm entry point and at every human entry point into and out of the milking shed
    - installing footbaths at all human entry and exit points at the milking shed, near cattle feed storage areas, to feeding areas, corrals and cattle pathways or alleyways
    - implementing hand washing or sanitisation before and after contact with cattle, milk or related equipment; or the use of disposable gloves when handling milk or cattle
    - disinfecting vehicle tyres, including milk trucks, feed delivery trucks, shared premises mixing trucks or push-up tractors, cattle transport trucks, calf haulers, deadstock haulers, manure haulers, or other visitors (e.g. nutritionists, veterinarians, hoof trimmers).
- Provide biosecurity training to employees.

- Isolate cows showing clinical signs in a hospital pen. All hospital milk must be heat-treated, diverted from the human food supply and disposed of in accordance with regulatory requirements.
- Conduct vat and hospital milk sampling as directed.
- Hold cattle on the premises except under the following conditions:
    - Non-clinical dry cull cattle and mature dairy bulls can move directly to a slaughter plant establishment.
    - Calves less than 7 days old may move directly to a specified calf ranch that has adopted enhanced biosecurity practices. The interior and exterior of the calf trailer must be decontaminated at various stages.
    - Bull calves may be sold to bull calf buyers or dealers.
    - Special cases may be moved under approved movement permits.
    - Any cattle moved off the premises must be under daily active observational surveillance for 30 days.
    - Maintain records of all movements on and off the premises for the duration of quarantine.
- Feed calves only pasteurised colostrum and milk, or colostrum/milk replacer.

Idaho's quarantine requirements are less detailed. Infected cattle must be isolated from the rest of the herd on the premises. Lactating cows may continue to produce milk, although milk from sick cows must be diverted from the human food supply and destroyed. A testing and surveillance strategy will be developed with Department of Agriculture staff to monitor the herd. It is not clear whether any quarantine requirements are placed on non-lactating dairy cattle.

Wisconsin provides the following guidance for affected producers, although no cases in dairy cattle have been detected there as of 23 May 2025. Affected properties will be subject to an epidemiological investigation and enhanced biosecurity measures, although specific details are not stated. Following the epidemiological investigation, movement of non-lactating animals may be allowed under permit. Lactating cull cows must be dried off and then moved directly to slaughter. Movement of bulk milk intended for pasteurisation will not be restricted. Raw milk and waste milk cannot be moved off site without a permit. Premises will be released from quarantine based on serial negative results from bulk milk testing, anticipated to be within 60 to 90 days of detection in most cases.

New York state, like Wisconsin, is a major dairy producing state but is currently free of clade 2.3.4.4b HPAI in dairy cattle. If a case is detected, cattle movements off the premises will be prohibited during quarantine, with the exception of approved necessary animal movements. Following an epidemiological investigation, movements of non-lactating cattle may be considered following a risk assessment and implementation of enhanced biosecurity measures. No animals from the affected premises will be allowed to enter livestock markets or other areas where animals congregate. Premises can continue to ship milk intended for pasteurisation. Premises will be released from quarantine at least 2 weeks after clinical signs have resolved, following 2 consecutive negative weekly bulk milk tests and 1 negative hospital and fresh pen test. Farms (dairy and poultry) within 3 km of an affected dairy will be in the 'infected zone' and will be tested weekly for the duration of

quarantine. Farms within 10 km of an affected dairy will be in the 'surveillance zone' and should implement enhanced biosecurity practices.

In the context of an Australian response, legally declared areas and premises classifications used in EAD responses are detailed in the AUSVETPLAN guidance document on declared areas and allocation of premises classifications in an emergency animal disease response. The implementation of quarantine and mandatory biosecurity measures in the event of a clade 2.3.4.4b HPAI in Australian dairy cattle will be underpinned by these classifications.

If the aim of an Australian response to an outbreak is eradication, it would be prudent to quarantine affected premises and high-risk premises, as for avian influenza in poultry. Given the potential for spread to adjacent properties and local movement of contaminated (or infected) non-cattle hosts (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment), it would also be justified to declare areas around affected premises, within which movement controls, enhanced surveillance and related measures were implemented. These areas should include poultry operations given the high risk (i.e. severe consequences) of an outbreak in poultry. Likewise, it would be justified to include dairy premises around infected poultry enterprises in any outbreak surveillance plan. Given the potential for clade 2.3.4.4b HPAI to infect a wide range of mammalian species, including various livestock, a decision needs to be made as to which premises are considered 'at-risk'. Many US states do not report defining declared areas around affected dairies. However, as discussed previously in this report, New York state will declare a 3 km 'infected zone' and a 10 km 'surveillance zone' around affected dairies, although no dairy cattle cases have been detected there to date.

Based on current evidence, it is clear that lactating dairy cattle, including both clinical and subclinical/preclinical animals, and raw milk are major sources of infectious virus. Therefore, quarantine must focus on mitigating spread from these sources. The epidemiological importance of non-lactating cattle on affected premises, and of contaminated vehicles, non-cattle hosts (including people), and equipment in transferring infection, is less clear. Conservatively, until more information becomes available quarantine and enhanced biosecurity should also address these sources. This is discussed further under Section 2.2.3.

The findings of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Simulation modelling of within-herd transmission' suggest that isolation of affected animals for 14 days following arrival will abrogate the risk of outbreaks. Modelling results suggest that isolation of pre-clinical animals (e.g. through rumination monitoring) could reduce the impacts of an outbreak to some extent. Isolation may also reduce the amount of virus entering the dairy environment, thereby reducing the likelihood of an exposure being infectious, and may reduce the severity of clinical disease if transmission occurs, although both the minimum infectious dose for cattle and how infectious dose relates to disease severity remain unknown; these are both identified as research gaps in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'. Isolation will also facilitate surveillance and management of contaminated milk. For example – California requires quarantined commercial dairy premises to isolate cows with clinical signs and requires activation of an enhanced biosecurity plan.

People managing sick animals should protect themselves from potential droplet and/or aerosol exposure. The US Centers for Disease Control and Prevention outline a series of engineering controls,

administrative controls and PPE recommendations for workers in high exposure settings (e.g. contact with confirmed infected animals or products) and medium exposure settings (e.g. contact with animals when there are confirmed infections in the region) (CDC 2025a, 2025b, 2025c). Recommended engineering controls include proper ventilation and automated milking systems to reduce contact with lactating animals (CDC 2025a). Recommended administrative controls include monitoring and testing of animals and workers, training of workers around infection control, and implementing work practices that reduce the duration, frequency or intensity of exposure (CDC 2025b). Recommended PPE for high exposure settings include respiratory and eye protection, fluid-resistant outer wear (e.g. coveralls), disposable gloves, a head cover and dedicated footwear. For medium exposure settings, respiratory and eye protection and disposable gloves are recommended. We note that, while recommended to protect against infection, based on our on-farm visits this level of PPE is not likely to be considered practical by industry in the Australian context, particularly during summer. Support may be required to ensure availability and access to PPE in the event of an extensive outbreak, particularly if concurrent outbreaks are being experienced in the poultry industry.

Similarly, enhanced hygiene at milking, while unlikely to completely eliminate within-farm spread based on 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment' and 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Simulation modelling of within-herd transmission', may reduce the exposure rate and dose (for both other cattle and for farm staff). Teat disinfection post-milking reduces the potential for spread of many contagious pathogens. However, its effectiveness specifically against clade 2.3.4.4b HPAI in dairy cattle has not been studied, given the route of entry into lactating cattle is still unknown (e.g. infection may require inoculation of the virus directly into the teat canal or may be respiratory/oral with subsequent dissemination to the mammary gland) (Lombard et al. 2025).

Raw milk or colostrum should not be fed to calves (or other animals, such as domestic cats) on quarantined premises. Given the high proportion of subclinical animals in an affected herd (Peña-Mosca et al. 2025), even the vat milk on an affected farm is likely to contain infectious virus. Alternatives could include heat-treated or appropriately acidified milk/colostrum or milk replacer. Raw milk should not be consumed by people.

Biosecurity controls to prevent contact between dairy cattle and other animals (wild and domestic) should be implemented, where practicable, to mitigate the risk of non-cattle hosts moving virus off-farm, either mechanically or biologically (i.e. being infected). For example – domestic cats that consume raw milk on affected dairy farms are at a high risk of infection (Burrough et al. 2024). Transmission has also been detected from dairy cattle to several other peri-domestic species, including wild birds that congregate in barns, wildlife mammals (e.g. foxes, mice) and poultry (Peacock et al. 2024; Nguyen et al. 2024; Worobey et al. 2024; Caserta et al. 2024).

Enhanced biosecurity should be encouraged on all premises with susceptible animals within declared areas. Biosecurity measures should be targeted to relevant transmission pathways, if known. For example – measures may differ if spillover into cattle was determined to be via affected poultry instead of via wild birds. Access to dairy cattle feed by wild birds, poultry and other mammals should be strictly prevented, to avoid both faecal contamination and accidental contamination of feed with carcasses.

A testing and surveillance strategy should be developed based on the epidemiological characteristics of the outbreak. Release from quarantine should be based on molecular testing at an approved laboratory, once diagnostic test characteristics are determined for the Australian context (e.g. diagnostic sensitivity/specificity in milk matrices). There are no reports of persistent infection or of a carrier state following infection; indeed, there is no robust evidence for a true carrier state for IAVs in any species (MacLachlan et al. 2017). Bulk milk testing is likely to be more efficient and cost-effective than testing of individual animals. Further research is needed to understand whether testing should also be applied to non-lactating cattle. While this is not being done in the US, neither has control been effectively achieved.

Critically, molecular tests such as RT-qPCR (that detect viral RNA) may remain positive once an animal/herd is no longer infectious. For example – viral RNA was consistently detected in milk samples from infected cows for up to 31 days post infection (CEZD 2024a), while infectious virus was detected in pooled milk for up to 12 days following infection (Baker et al. 2024). Unfortunately, inexpensive and high-throughput testing methods that detect infectious virus are not available. If a herd continues to test positive by RT-qPCR over an extended period, special consideration may need to be given as to whether the herd is truly still infectious.

2.2.3 Movement controls and testing

As a general principle, the aim of movement controls is to reduce the spread of infection between premises by preventing the movement of infected animals, infected animal products and infected vectors (where relevant for the disease), and by allowing or permitting movements that pose minimal risk. The stringency of movement controls will depend on the aim of the response (e.g. mitigation versus elimination) and the characteristics of an outbreak. We discuss various options that will need to be decided through the standard AUSVETPLAN drafting process through negotiation between industry and government. General guidance is provided in the AUSVETPLAN guidance document on movement controls.

Movement of infected lactating cattle (including subclinical/preclinical animals) into naïve herds was quickly identified as the primary transmission pathway for between-farm spread of clade 2.3.4.4b HPAI in the US (APHIS 2024l; Caserta et al. 2024; Nguyen et al. 2025; Peña-Mosca et al. 2025). In response, a federal order was issued in April 2024 that mandated testing of healthy lactating dairy cattle prior to interstate movement. Clinically affected dairy cows are prohibited from moving interstate or to slaughter (APHIS 2024a). For healthy cows, milk samples/udder secretions must test negative for IAV by RT-qPCR at an approved laboratory within the 7 days prior to movement (APHIS 2024m). For large groups of animals (greater than or equal to 30), at least 30 must be tested from each lot; for smaller groups, all animals must be tested (APHIS 2024a). The specific details of this calculation (e.g. design prevalence, test characteristics) are not given. All 4 quarters must be sampled from each animal, as there have been reports of only a single quarter testing positive (APHIS 2024m).

Non-lactating cattle, including heifers, dry cows and bull calves, are not subject to this mandatory federal movement testing because current evidence suggests that raw milk is the primary source of infectious virus in dairy cattle. However, given the high uncertainty around the epidemiological role of non-lactating cattle in HPAI transmission, residual risk may remain around their movements (CEZD 2024b). Depending on risk appetite, movement controls and testing could also be applied to non-lactating cattle. For example – in the context of imports, Israel requires pre-export testing for all US

cattle and Turkey has prohibited importation of all live cattle from the US (Hunter 29 October 2024). Arizona requires all mobs of non-lactating dairy cattle being imported into a licenced dairy premises to test negative for IAV on nasal swab samples. Animals imported direct to slaughter or to a terminal feedlot are exempt from testing. Critically, diagnostic sensitivity and specificity have not been determined for samples from non-lactating cattle and diagnostic testing may not be reliable in this group, although the USDA continues to recommend voluntary pre-movement testing of non-lactating cattle and provides this at no cost to producers (APHIS 2024a).

Intrastate cattle movements and testing are under the authority of the relevant state Department of Agriculture; thus, intrastate movement controls vary by jurisdiction. In California, no movement controls are in place for non-infected premises, although bulk milk surveillance is recommended prior to sale of lactating dairy cattle or cows due to calve within a month. Bulk milk testing provides surveillance at the herd level. Affected premises are subject to movement controls for some, but not all, groups of cattle. For example – the following movements may continue through quarantine:

- Dry cull cows (greater than or equal to 10 days dry) or mature dairy bulls (no clinical signs) moving directly to slaughter
- Calves less than 7 days old moving to a quarantined calf ranch
- Bull calves being sold to a bull calf buyer or dealer.

Additionally, the following movements may be allowed under special permit, with enhanced biosecurity requirements and other conditions:

- Dairy cows currently lactating or due to calve within a month moving between affected premises or direct to slaughter for welfare reasons
- Dry cull cows moving to a quarantined saleyard or cattle broker for slaughter only sale
- Mature dairy bulls moving between affected premises or to a quarantined saleyard or cattle broker for slaughter only sale
- Feeder cattle 3 to 14 months moving to any saleyard or direct to feedlot where they will not comingle with dairy replacements
- Weaned but unbred dairy heifers moving to a quarantined heifer ranch.

Since January 2025, a statewide ban on the exhibition of some dairy cattle (lactating or recently dried off adult cows, heifers and springers) at fairs and shows has been implemented in California. Dairy bulls, feeder calves and steers can continue to be exhibited. Other states continue to exhibit dairy cattle, either requiring a negative RT-qPCR for IAV within the 7 days prior to intrastate movement (e.g. Texas, Wisconsin, Iowa) or with no additional requirements (e.g. New Mexico).

Arizona has ordered that all imported dairy cattle must be quarantined from the main herd for at least 21 days, with dedicated personnel and equipment for the quarantine herd.

Movement controls on vehicles and equipment appear to be limited to enhanced biosecurity for vehicles moving cattle from affected dairies. For example – California requires that cattle haulers must avoid poultry premises, cannot mix exposed and non-infected cattle in a single load, and must be cleaned and disinfected following transport. Detailed cleaning and disinfection protocols must be

followed for calf trailers. The affected dairy must be the last stop of the day for any vehicles (e.g. milk tankers, cattle/calf haulers, feed delivery trucks).

In the Australian context, various movement controls could be adopted depending on the objective of a response. These could be applied at various control levels (e.g. affected dairies only; all affected and high-risk premises; all dairy premises within a declared area). The following measures could be considered, subject to risk assessments and characteristics of the outbreak:

- Restrictions on live animal movements from affected and/or high-risk premises or areas.
    - Prohibit movement of only animals showing clinical signs consistent with clade 2.3.4.4b HPAI, or
    - Prohibit movement of only lactating dairy cattle and those due to calve within a month, or
    - With or without enhanced measures for movement of non-lactating cattle (e.g. quarantine at destination)
    - Prohibit movement of all dairy cattle, or
    - Prohibit movement of all livestock that co-mingle with dairy cattle.
    - Any animal movement controls enacted must make allowance for animal movements for welfare purposes, for example – in the event of acute injury.
    - Exemptions could be made for movements directly to slaughter or movements that are made within a declared area (i.e. not out of the declared area) or between separate properties within the same business (e.g. properties used for heifer agistment).
    - Risk-based permitting processes for exemptions must be developed to allow the ongoing operations of a dairy.
- Mandatory pre-movement testing (not restricted to declared areas or premises)
    - For all dairy cattle or only lactating dairy cattle and those due to calve within a month.
    - Exemptions could be made for movements directly to slaughter.
    - The timeframe must be defined (e.g. 7 days before a movement, or shorter, depending on realistic laboratory turnaround times).
    - The test type and sampling protocol (e.g. all 4 udder quarters) should also be stipulated.
    - Sample size for mobs should be calculated based on sound epidemiological principles.
    - Some residual risk may remain if an animal is at a very early stage of infection at the time of testing or becomes infected after sampling, leading to false negative results (CEZD 2024b).
    - If mandatory testing is not enforced, voluntary testing should be accessible for producers and supported by government.
- Enhanced biosecurity for vehicles, equipment, people and animal products moving from affected or high-risk premises

  - For all vehicles or specific vehicle classes.
  - Enhanced cleaning and disinfection protocols (exterior only versus both interior and exterior).
  - Mandatory visitor/vehicle logs.
  - Dedicated vehicle routes onto affected premises.
  - IPs should be the last premises visited for the day.
  - Milk and carcasses are discussed separately under Section 2.2.7. Briefly, current evidence indicates that raw milk, other raw dairy products and carcasses may be safely moved from affected dairies directly to approved processing sites for pasteurisation with appropriate biosecurity; however, other off-site movements should be prohibited.

- Other considerations
  - Restrictions on dairy cattle shows, exhibits, sales/saleyards and other events, either for all classes of dairy cattle or only lactating cattle or those near calving.
    - Complete ban
    - Enhanced testing
    - Stricter conditions on arrival (e.g. isolation, decontamination protocols)
  - Restrictions on other congregations of dairy cattle (e.g. at saleyards or other locations where commingling of animals from different origins occurs).
  - Mandatory on-farm quarantine protocols for animals moving between dairy premises or from animal congregation points.
  - Manure: There is currently no evidence that either viral RNA or infectious virus are present in manure from infected cattle. However, studies to date are limited.
  - Effluent: 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment' assessed the likelihood of between-farm spread via effluent as extremely low, with high uncertainty.
  - People: 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment' assessed the likelihood of between-farm spread via people acting as mechanical or biological vectors as extremely low, with high uncertainty. This was based on the findings from on-farm visits that people moving directly between dairy premises and having contact with animals generally had good biosecurity awareness and would regularly provide their own clean protective clothing and boots (e.g. 'come clean go clean') (see Table 20 of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'). However, the USDA still considers this an important risk factor for disease spread (APHIS 2024j). Our on-farm assessments highlighted potential areas for strengthening visitor biosecurity and personal decontamination protocols on some Australian dairy farms. Stand-down periods (or other risk reduction methods like showering between premises) could be considered for people moving between dairy premises or from poultry to dairy premises.
  - Crops, grains, hay, silage and mixed feeds: The persistence of infectious clade 2.3.4.4b HPAI virus on feedstuffs relevant to the Australian dairy industry has

not been determined. It is assumed that cattle can be infected via the oral route, given that calves can be infected by consuming raw milk from infected cows (Davila et al. 2025). However, the minimum infectious dose via the oral route is not known. Until the persistence of infectious virus on relevant feedstuffs is known, movement of any feedstuffs from affected or high-risk premises should be limited, particularly any that may have been exposed to raw milk, poultry litter or effluent.

Based on the findings of our qualitative risk assessment (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment), movements of lactating dairy cattle between premises are relatively uncommon in Australia, suggesting that the impact of live animal movement restrictions (of lactating cows) on industry may be minimal, although enhanced vehicle biosecurity would be laborious to implement. This should be further verified with industry stakeholders, noting that our sample of 25 surveyed dairy farms is not large enough to estimate movements with confidence. Understanding barriers to the implementation of movement controls will be essential to maximise industry cooperation. While movement controls should prioritise lactating dairy cattle and raw milk, the epidemiological role of non-lactating cattle and milk-contaminated fomites in an outbreak is still unclear. Risk-based movement controls and/or testing protocols for other lactating and/or non-lactating livestock species from affected dairies could also be considered.

Prioritisation of movement controls should be based on the best available scientific evidence regarding transmission pathways and risk factors for clade 2.3.4.4b HPAI in dairy cattle. Rapid risk assessments should be conducted regularly to review the highest-risk animal movements and implement controls accordingly. Movement controls should be proportionate to the risks posed by different animal categories, movement types and area classifications, minimising disruption to the industry. Controls should be flexible and adaptable as an outbreak evolves and as new information becomes available. Like the US, individual jurisdictions may apply specific import requirements for receiving dairy cattle during a response. Clear communication of movement control measures and enforcement are crucial for achieving compliance and industry buy-in.

2.2.4 Tracing and surveillance

A detailed guide to developing a surveillance strategy for influenza A(H5N1) in cattle has been written by the Food and Agriculture Organization of the United Nations (FAO) (El Masry et al. 2024) and is discussed further in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review'. Guidance on tracing and surveillance for EAD responses in the Australian context can be found in the AUSVETPLAN tracing and surveillance guidance document. It is beyond the scope of this report to design a comprehensive surveillance plan for clade 2.3.4.4b HPAI. We discuss general considerations that could guide a future surveillance plan, based on the US experience.

Following an incursion into Australia in wild birds (no disease detected in cattle)

A key surveillance objective should be early detection of spillover events from birds to non-avian species, including cattle (El Masry et al. 2024). Therefore, surveillance for infection in wild birds and poultry populations is critical. Passive surveillance in dairy cattle plays a key role in early detection of clade 2.3.4.4b HPAI spillover in Australia, given the pronounced clinical appearance in affected herds and intensive nature of production (twice daily milking allowing close observation of cattle). This

could be aided by listing it as a notifiable disease and having clear reporting mechanisms (El Masry et al. 2024). In the US, while reporting of suspicion of disease in cattle is not mandatory, the April 2024 federal order introduced mandatory reporting of laboratory detections of IAV in livestock (nucleic acid and serology). Clear communication to producers is essential so that they understand how they can access testing, when testing can be requested (e.g. what clinical signs are eligible) and what costs may be incurred (e.g. laboratory costs, costs of sample collection, shipping costs).

The sensitivity of passive surveillance is enhanced by increasing producer awareness, directed at clinical disease recognition and the importance of notification and investigation of clinical cases (Sergeant et al. 2022). During our on-farm assessments, a notable degree of confusion was observed among producers concerning HPAI in dairy cattle. This primarily manifested as a misunderstanding of the epidemiological differences between the H7 outbreaks in Australian poultry and the H5 outbreaks in US dairy cattle. Furthermore, producers frequently expressed the belief that HPAI was already established within Australia, indicative of a need for clearer communication regarding the different HPAI subtypes. This confusion may affect the sensitivity and specificity of passive surveillance.

Various factors influence the willingness of farmers to report suspect EADs (Gates et al. 2021), including:

- uncertainty around the clinical signs and situations that warrant reporting
- fear over the social and economic consequences from both positive and false positive reports
- negative beliefs regarding the efficacy and outcomes of response measures
- mistrust and dissatisfaction with animal health authorities
- absence of sufficiently attractive financial and non-financial incentives for submitting reports
- poor awareness of the procedures involved with the submission, processing, and response to reports.

Response strategies in the event of an outbreak in Australia need to be developed now (i.e. before an outbreak) and clearly communicated with industry, to gain producer cooperation and encourage early reporting of suspect cases. There is also a need to develop messaging around what support and compensation (e.g. under EADRA versus national disaster relief) would be provided in the event of an outbreak. Again, this was raised by producers during our on-farm assessments.

A key limitation of the US clade 2.3.4.4b HPAI surveillance strategy is the lack of sequencing of poultry outbreaks. Such sequencing could have greatly aided our understanding of spillover pathways into dairy cattle, leading to targeted disease control measures to reduce the likelihood of entry (spillover) into dairy cattle populations. While it is not feasible to sequence every wild bird infection, if sequencing results had been available for each US poultry outbreak, spillover from poultry could have rapidly been ruled out (or in). That is not intended to make a target of the poultry industry, but rather to understand where to prioritise disease prevention and control efforts. For example – if poultry are a significant source of infection, biosecurity protocols around poultry-to-dairy farm movements could be relatively easily enhanced, as compared to trying to reduce contact between dairy cattle and wild birds. Along with representative sequencing of poultry in the event of an Australian outbreak, increased wild bird surveillance should also be considered, perhaps targeted

to dairying regions (and regions with high poultry farm densities). An expanded surveillance program, representative in terms of time, species, geography and disease severity, would aid our ability to assess spillover risks to mammalian species and monitor for the emergence of novel genotypes that may arise through reassortment with local LPAI lineages. Specific guidance for strategies for genomic surveillance of IAVs (in poultry, wild birds and mammals) is provided by the European Union Reference Laboratory. Genomic sequencing is also discussed in Section 2.2.1. Sequencing can be very cost-effective when samples are multiplexed and high-throughput methodologies are applied (e.g. amplicon sequencing).

Early detection of clade 2.3.4.4b HPAI in dairy cattle could be supported through routine bulk milk sampling, herd surveillance programs, risk-based surveillance or enhanced passive surveillance. Several countries have reported conducting various forms of early detection surveillance activities. For example:

- Canada has tested over 1,200 samples of pasteurised retail milk and almost 3,500 raw (unpasteurised) milk samples collected at processing plants since mid-2024, with no positive detections (CFIA 2024; Wallace et al. 2025). Monthly testing of raw milk collected from processing plants is ongoing in Canada.
- Risk-based HPAI surveillance in livestock on HPAI-affected poultry premises has been in place in the UK since 2024 (HAIRS 2025). This led to the detection of clade 2.3.4.4b HPAI infection in a ewe with mastitis in early 2025. Additionally, a cross-sectional survey was carried out in the UK from May to June 2024 that tested 508 bulk milk samples from 455 dairy farms distributed across England, Scotland and Wales by RT-qPCR (Animal and Plant Health Agency 2024). All milk samples tested negative.
- In June 2024, approximately 1,400 bovine serum samples (not stated whether beef or dairy) collected from regions in Germany severely affected by avian HPAI outbreaks were tested for antibodies to IAV, with no positive detections (Friedrich-Loeffler-Institut 2024). Additionally, around 350 bulk milk tank samples from Germany were tested for viral RNA and again, all were negative.

The cost-effectiveness of such early detection programs has not been assessed.

Routine bulk milk sampling at processing plants

Bulk milk testing has proven to be an effective and efficient surveillance method for early detection of clade 2.3.4.4b HPAI in US dairy populations. This is highlighted by the detection of the 2 genotype D1.1 spillovers in Nevada and in Arizona in early 2025 (APHIS 2025a, 2025b). Three of 11 silo samples collected in Nevada tested positive and trace-back revealed that 2 herds were infected (APHIS 2025i). The Arizona event was attributed to a single dairy (AZDA 2025). The effect of dilution at the vat, tanker and silo level on test performance is not known; that is, how many infected animals must contribute to the pooled sample to still be detected as positive. However, the Nevada D1.1 detections in processing silo samples suggests a high sensitivity for pooled testing. False negative results may also occur if sick animals are not contributing to vat milk (e.g. due to cessation of milk production or isolation from the milking herd).

The US NMTS relies on testing (RT-qPCR) of raw milk samples collected from dairy processing plant silos holding milk intended for pasteurisation (APHIS 2025e). Sampling is implemented at the state

level, depending on state resources and industry workflows (APHIS 2025c). For example – New York state collects monthly samples from every processing plant silo containing grade 'A' milk (i.e. fluid grade milk suitable for beverage consumption) intended for pasteurisation, which would provide a census of all dairy farms producing pasteurised milk. Wisconsin is also conducting comprehensive sampling monthly, although farms are tested individually through samples submitted to milk quality laboratories as part of normal dairy quality control procedures. Colorado initially tested bulk milk samples weekly, when the state-level incidence of HPAI in dairy herds was high, but from February 2025 has reduced sampling to every second week. Bulk milk samples are collected from all licenced dairy cow farms by certified sample collectors, but it is not specified if the samples are collected on-farm, at processing facilities or elsewhere. Raw milk permit holders are not included in the NMTS, as their milk is not intended for pasteurisation. Some states, such as New York state, additionally require mandatory monthly testing of milk from these permit holders.

Canada's milk testing strategy, like that of New York state, relies on sampling of raw milk at dairy processing plants. Monthly samples are collected that provide surveillance coverage of approximately 1,500 of the 9,256 dairy farms in Canada across all provinces. While not specific to clade 2.3.4.4b HPAI, New Zealand's Mycoplasma bovis national milk surveillance strategy requires tanker operators to submit samples from all commercial dairy farms at the point of collection. Non-commercial dairies must submit their own samples. Tanker operators already send milk samples to a milk quality laboratory for routine testing, and it is those samples that are additionally tested for M bovis monthly (pers. comm., A. Burroughs, OSPRI, 14/05/2025). This provides comprehensive coverage of New Zealand's dairy herds. In New Zealand, this is streamlined because a single central laboratory is responsible for all milk testing. Australia has previously used a national bulk milk testing strategy for the eradication of enzootic bovine leukosis from the national dairy herd, funded and coordinated by Dairy Australia (Kirkland and Rodwell 2005).

In the Australian context, milk samples could be collected from individual farm vats, tankers, or processing facility silos. As part of routine milk quality testing, samples are already taken automatically during pumping, when milk is being collected on-farm (AHA 2022). Dip samples are generally no longer taken. According to the AUSVETPLAN dairy cattle enterprise manual, samples are couriered to an independent laboratory for testing. Additionally, pooled samples from tankers are collected at processing factories (AHA 2022). Producers may also send individual cow milk samples to a herd test centre for testing (AHA 2022). RT-qPCR testing for clade 2.3.4.4b HPAI could be added on to any of these existing samples. Producers, industry and testing laboratories must be consulted to understand which sampling methodology would result in minimal disruption to operations. Australia's existing milk traceability framework will enable trace-back of any positive tanker or processing silo samples.

The testing frequency should take into account the acute nature of clade 2.3.4.4b HPAI infection in dairy cattle. Ideally, comprehensive coverage of all dairy farms would be achieved. Risk-based surveillance targeting farms with a higher risk profile for clade 2.3.4.4b HPAI could also be considered, if farm risk profiles are known. If a census approach is not used, sample size calculations should be based on sound epidemiological principles.

Risk-based surveillance

Some US states have implemented risk-based surveillance approaches to clade 2.3.4.4b HPAI in dairy cattle. For example – Iowa has implemented mandatory sampling of dairy herds within 20 kilometres of an infected poultry premises since June 2024.

The USDA suggests that animals introduced into the herd within 6 months of lactation should be sampled upon freshening (i.e. calving and commencing a lactation cycle) (APHIS 2024b).

Pre-movement testing may also be considered a form of risk-based surveillance (see Section 2.2.3).

Enhanced passive surveillance

A cornerstone of Canada's national African swine fever surveillance program is enhanced passive surveillance through rule-out testing on samples that meet certain clinical criteria. For clade 2.3.4.4b HPAI in Australia, clinical mastitis cases submitted to government laboratories could perhaps undergo exclusion testing for IAVs. Alternatively, individual cow milk samples submitted to a herd test centre (i.e. routine quality control sample) could be tested (AHA 2022). The relevant legal and regulatory frameworks around additional testing of samples without explicit producer consent would need to be considered.

Response to an outbreak in dairy cattle

If infection with IAV has been confirmed in Australian dairy cattle, surveillance objectives may include early detection of new cases, characterisation of circulating viruses (e.g. measure level of disease or monitor for biologically relevant viral mutations), or demonstration of freedom from infection in certain herds, regions or sectors to support zoning and/or compartmentalisation (El Masry et al. 2024).

In the event of an outbreak in Australia, tracing all cattle movements involving the affected dairy should be undertaken as a matter of priority. Trace-back and trace-forward of cattle movements is essential to identify the source of infection and for early detection of other infected herds. Given the acute nature of clade 2.3.4.4b HPAI infection and relatively short incubation period of 12 to 21 days at the herd level (FAO 2024; Payne and CDQAP 2024), trace-back may be restricted to a limited time period (e.g. 1–2 months). Adjacent properties should also be investigated, and all lactating cattle should be tested (most practically through testing of vat and waste milk samples). Tracing should focus initially on lactating dairy cattle, raw milk, and vehicles, equipment or people potentially contaminated with raw milk.

Assuming depopulation is not used, herds on affected dairies should undergo health monitoring and surveillance. The owner or manager should report regularly to animal health authorities describing clinical signs, morbidity, mortality and production effects in the herd. Release from quarantine should be based on resolution of clinical signs as well as molecular testing at an approved laboratory, as discussed in Section 2.2.2. Bulk milk testing (e.g. RT-qPCR) is likely to be more efficient and cost-effective than testing of individual animals. Further research is needed to understand whether testing should also be applied to non-lactating cattle.

Genomic sequencing is advised for at least 1 positive sample from each outbreak (Monne 2021). Phylogenetic and phylodynamic analyses of dairy cattle sequences in the context of other clade 2.3.4.4b HPAI sequences from wild birds, poultry and other species can provide evidence on likely

reservoirs/sources of infection, spillover pathways and transmission pathways between herds. Sequences should be interrogated for any potentially biologically relevant mutations that may indicate mammalian adaptation or resistance to antivirals. Dairy cattle sequences should be compared to any sequences from human infections to increase our understanding of cattle-to-human transmission pathways and risk. Genomic sequencing will also facilitate enhanced contact tracing.

Within a declared area, surveillance may include:

- identification and mapping of all at-risk premises, with each producer advised to immediately report clinical signs consistent with clade 2.3.4.4b HPAI to animal health authorities.
- mandatory monitoring may be requested (e.g. regular health monitoring).
- regular sampling may be conducted (e.g. vat milk from affected dairies).
- any mortalities in wild birds or other domestic species (e.g. cats on dairy farms) or peri-domestic wildlife should be investigated.
- active surveillance may be initiated in declared areas, such as sampling local wetlands and/or wild birds, testing at-risk species (e.g. cats, sheep, pigs).

In the outside area, disease awareness should be raised amongst dairy producers, animal health and service providers and members of the public, with clear avenues for immediate reporting of suspect cases. Based on the US response, an appropriately designed national milk testing strategy is likely to be very effective in detecting new cases, delineating areas where infection is present versus absent, and identifying herds requiring more detailed epidemiological assessment (Section 2.2.1). Considerations for developing a milk testing strategy have already been discussed. Herd-level surveillance programs could also be considered.

Herd surveillance programs

Various voluntary herd surveillance programs have been offered in the US. California offers both bulk tank (vat) and individual cow milk surveillance protocols for lactating cows, and nasal swab sampling for non-lactating cattle, at the individual herd level to help producers verify their herd status (California Department of Food and Agriculture 2024a). The program is state-funded; that is, testing is free to producers. Vat sampling is the preferred protocol.

For vat sampling at the herd level, the sample needs to be representative of all cattle in a lactating herd in a 24-hour period. A minimum of 7 ml of milk is collected from the bulk tank/vat and a second sample is collected from the sick/hospital pen. The hospital pen sample can be individual cow samples from all functional quarters of up to 30 head of sick cattle or a single bulk milk sample representative of the hospital pen. Sampling is conducted once per week for 3 weeks and then fortnightly for healthy strings. The hospital sample is collected monthly.

Individual cow milk sampling uses the following protocol. Sample size depends on the milking herd size; for milking herds with less than 33 head all cows are sampled, for milking herds with less than or equal to 1000 head 33 animals are sampled, for milking herds with greater than 1000 head 34 animals are sampled. Cows with clinical signs consistent with HPAI are prioritised for sampling, followed by cows in a hospital pen, cows with health alerts through activity monitors, cows 30 to 150

days in milk, and then other cohorts. A minimum of 7 ml of milk from all functional quarters is collected into a single collection tube. Samples are collected weekly for 3 weeks and then fortnightly.

Nasal swab sampling of non-lactating cattle is offered to aid producers in assessing the risk of movement of non-lactating dairy cattle. Sample size is as described in the previous paragraph for individual cow milk sampling. Both nostrils of each animal are sampled using a sterile sab. The swab is eluted in suitable viral transport media and then removed and safely disposed of. Sampling is on an 'as needed' basis.

The USDA offers an alternative bulk milk sampling program for producers to monitor individual herds without requiring testing of individual animals (APHIS 2025d). Bulk milk samples are collected on-farm weekly for IAV testing using sampling kits and shipping labels provided by USDA at no cost to the producer. Provided all samples are negative, no additional pre-movement testing is required for animals in the herd.

Such herd-level surveillance programs could similarly be implemented in the Australian context.

Rapid antigen tests (RATs) (also referred to as lateral flow assays) could hold considerable potential as a point-of-care, preliminary screening tool for Australian dairy producers in specific contexts. This is because of the extremely high virus (and therefore antigen) levels in the milk of infected animals, making detection relatively straightforward compared to many other pathogens and sample matrices. The use of RATs on milk from infected cows has been successfully demonstrated experimentally (Halwe et al. 2024). Commercial human IAV RATs have been shown to detect both genotype B3.13 and D1.1 (although that study used spiked human nasal swab samples) (Bassit et al. 2025). Further validation would be required before RATs could be recommended as a field test, but these tests may offer an inexpensive, rapid indicator of infection, empowering farmers and veterinarians to make informed decisions regarding milk segregation, disposal protocols and targeted RT-qPCR testing, thereby enhancing on-farm biosecurity. For example – RATs could be used when moving cattle (either when leaving the origin premises or on arrival), if mandatory RT-qPCR testing is not required. Testing could be performed on the day of movement, reducing the residual risk associated with animals becoming infected after sampling. RATs could be used to determine when a mob can be released from on-farm quarantine following movement (note that this does not refer to quarantined premises, where more stringent testing will likely be required). They could also be used to test milk prior to calf feeding (particularly mastitic milk). There are many considerations around the use of point-of-care testing; for example – once rapid antigen tests became widely available during the COVID-19 pandemic, underreporting of test results quickly led to high uncertainty around true case numbers. A framework for point-of-care testing in the context of clade 2.3.4.4b HPAI in the Australian dairy industry should be developed, considering also data collection mechanisms. The consequences of a positive test result must also be clearly communicated to producers. However, there is the potential for RATs to be a valuable farm-level risk mitigation tool for clade 2.3.4.4b HPAI in the dairy industry.

The use of precision wearable technologies may also aid early diagnosis of clade 2.3.4.4b HPAI infection in dairy cattle. The adoption of wearable technologies, such as collar-based monitoring systems and intraruminal automated sensor devices, is accelerating in both the US and Australian dairy industries (Dairy Australia, pers. comm., 6 June 2025). Such technologies have previously been evaluated for disease detection purposes in dairy cattle (Rodriguez et al. 2023; Adams et al. 2013). In

the context of clade 2.3.4.4b HPAI in dairy cows, one case study looked at rumination times measured by the AfiCollar® monitoring system and found that rumination time started to decrease around 5 to 7 days prior to clinical diagnosis (Peña-Mosca et al. 2025). Another case study looked at health-related fever alerts from smaXtec intraruminal boluses and found that observation of clinical signs was delayed by at least one week relative to fever alerts (Rodriguez et al. 2025). The authors concluded that early detection via such automated sensor devices may allow for timely intervention that could minimise production losses and improve herd health management during an outbreak. Further studies (both field and modelling studies) are needed to better understand how to most effectively use rumination collars and other 'wearable devices' for early detection of clade 2.3.4.4b HPAI. Guidance will need to be developed on how to interpret data from wearable devices in the context of early disease detection, how to investigate initial alerts, and how to manage animals until confirmatory testing results are received.

Proof of freedom

If the aim of a response to clade 2.3.4.4b HPAI in Australian dairy cattle is eradication, surveillance will be required to demonstrate population freedom and enable any remaining movement controls to be lifted. Proof of freedom will also be required to regain access to international markets, if these are affected.

The US approach to demonstrating freedom from clade 2.3.4.4b HPAI in dairy cattle is through the NMTS. After all states have demonstrated absence/elimination through 4 rounds of negative plant silo testing, 3 months of targeted risk-based sampling will be conducted to support national freedom (APHIS 2025e). A similar approach could be applied in Australia.

2.2.5 Treatment of infected animals

Treatment of clade 2.3.4.4b HPAI in dairy cattle in the US has focused on supportive care. Treatment is aimed at correcting dehydration and re-establishing rumination as quickly as possible (Payne and CDQAP 2024). The mainstay of treatment is large volume oral fluid therapy (~20 litres of electrolytes given 1–2 times per day). Restoring hydration and rumination quickly minimises secondary pneumonia, abortions, mortalities and culls (Payne and CDQAP 2024).

During the peak of an outbreak producers may be providing oral fluid therapy for up to 40% of the herd daily for a week or more (Payne and CDQAP 2024). US dairy farmers experienced supply chain challenges concerning commercial drench carts. Shortages may also be experienced for commercial electrolyte preparations. Stomach tubing infected cattle is a known human health risk and PPE should be worn during procedures where there will be direct contact with oral secretions (Morse et al. 2024). High demand for PPE may lead to supply chain issues.

Anti-inflammatories (i.e. non-steroidal anti-inflammatory drugs) may be administered but should be used cautiously in dehydrated animals. Probiotics and injectable B vitamins have been used in some cases, although data on effectiveness in reducing mortality or returning to production are not yet available. Intravenous fluids have been used in rare cases but are generally expensive and impractical (Payne and CDQAP 2024). Any secondary bacterial infections, such as bacterial pneumonia, should be treated appropriately (Payne and CDQAP 2024). There are no specific antivirals licenced for use in cattle (although antivirals are available for human infections). Residue concerns, cost and

development of resistance impacting human treatment options will likely preclude their use in veterinary species.

California requires that clinically affected cows are isolated immediately to a hospital pen. While the findings of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment' suggest that this is unlikely to stop within-farm spread, isolation of sick animals will reduce the level of exposure of other cattle to potentially infectious secretions/excretions (including raw milk). This may reduce the likelihood of an exposure being infectious and may reduce the severity of clinical disease if transmission occurs, although both the minimum infectious dose for cattle and how infectious dose relates to disease severity remain unknown; these are both identified as research gaps in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'.

There is little benefit in drying off affected cows. Early drying off takes about 2 weeks and can create a number of health and welfare issues for cows (AHA 2022). Since the infectious period for clade 2.3.4.4b HPAI in dairy cows is thought to be 1–2 weeks (Halwe et al. 2024; Baker et al. 2024; Caserta et al. 2024), drying off affected cows may not offer additional benefits in controlling disease spread. Sick animals should be separated from the unaffected herd by moving them to a dedicated hospital or sick pen that, if possible, should not share confined air space, fence lines, feeding or watering space with other animals (APHIS 2024). The milk should be treated and disposed of appropriately (see Section 2.2.7) and all equipment should be thoroughly decontaminated after use with sick animals with a disinfectant effective against clade 2.3.4.4b HPAI (APHIS 2024c). It is important that suitable disinfectants are approved for use with the Australian Pesticides and Veterinary Medicines Authority. Milk production will already be substantially reduced in many affected animals and frequently remains at sub-optimal levels for several months post-infection (Caserta et al. 2024; Rodriguez et al. 2025; Peña-Mosca et al. 2025). Many affected cows (e.g. 31.6% in 1 case study) will be prematurely removed from the herd due to ongoing production impacts (Peña-Mosca et al. 2025).

2.2.6 Stamping out

Australia's general policy for control of an EAD (where technically feasible and approved by the National Management Group) is stamping out (Aha 2021a). Stamping out is primarily used for diseases that cause significant morbidity or mortality, result in production losses, pose a threat to international trade or are a public health risk (Aha 2021a). The department has stated that in the event of an incursion in dairy cattle in Australia, depopulation is unlikely to be the mainstay of a response (pers. comm., DAFF, 8/9/2025).

2.2.7 Treatment of milk and other animal products

The primary product of concern in dairy cattle is raw milk, as the main site of viral replication is in the bovine udder. Very high levels of infectious virus are present in milk from affected animals, up to 109 TCID50 per mL (Halwe et al. 2024).

Milk poses a risk to other dairy cattle, mammal and bird species and humans via ingestion or via contact with mucous membranes. For example – in 1 human case, conjunctivitis developed following milk splashing into the eye (Morse et al. 2024). Unpasteurised milk from infected cows must not be used for human consumption (or fed to other animals) (FSANZ 2016). The sale of raw cow's milk for human consumption is illegal in Australia; however, there may be variability in compliance to this regulation. Raw milk and raw milk products may be sold as cosmetics (e.g. 'bath milk', soaps),

although these must be treated, packaged, labelled and presented in a manner that deters human consumption, such as the addition of a bittering agent. While no human infections have been linked to raw milk cosmetic products to date, potential exposure pathways exist through inhalation, accidental ingestion, or contact with mucous membranes. Raw milk cheese also presents a potential food safety risk. Infectious virus was found to be stable in raw milk cheese and was detected for at least 60 days of aging in commercial raw milk cheeses inadvertently prepared with contaminated raw milk (Nooruzzaman et al. 2025). Raw milk cheese (either imported or locally produced) is permitted to be sold in Australia under certain conditions; however, very low volumes are sold and consumed. Other exposure pathways to raw milk may include via aerosolisation of milk (e.g. during the milking process) or through raw milk contaminating fomites.

In the US, heat-treatment is the only currently approved method for inactivating clade 2.3.4.4b HPAI in raw milk. Both vat/batch pasteurisation (63°C for 30 minutes) and high-temperature short-time (HTST) pasteurisation (72°C for 15 seconds) are effective at inactivating HPAI in in raw milk and other dairy products, including retail cheese, butter and ice cream (Suarez et al. 2025; Caceres et al. 2024; Nooruzzaman et al. 2024; Kwon, Gebhardt, et al. 2024; Spackman et al. 2024; Alkie et al. 2025; Cui et al. 2024; Schafers et al. 2025). Food standard milk pasteurisation in Australia is heating to a temperature of no less than 72°C and retaining at such temperature for no less than 15 seconds, or heat treatment of an equivalent or greater lethal effect (e.g. 63°C for 30 minutes) (FSANZ 2016).

Acidification may have potential for inactivating clade 2.3.4.4b HPAI in milk, although this is not currently an approved treatment method in the US (see Section 2.2.7).

No special processing is required for meat or meat products produced from affected cattle. Clade 2.3.4.4b HPAI is only rarely detected in muscle tissue. All evidence to date indicates that the virus is inactivated with thorough cooking. The USDA has conducted 3 safety studies around clade 2.3.4.4b HPAI in beef and concluded that the meat supply is safe (APHIS 2025g). Testing of cull dairy cows detected clade 2.3.4.4b HPAI nucleic acid (not infectious virus) in 1 of 333 diaphragm muscle samples (APHIS 2025g). Muscle tissues from the same animal corresponding to common retail cuts of meat in that animal were negative. No evidence of clade 2.3.4.4b HPAI was detected in samples of retail ground beef in the US (APHIS 2025g). The Government of Canada has stated that HPAI is not a food safety concern when safe food handling, preparation and good hand hygiene are practiced.

2.2.8 Disposal of animal products (milk and carcasses)

In the US, the federal Grade 'A' Pasteurized Milk Ordinance states that milk from sick cows must be collected separately and not allowed to enter the supply chain. California requires that milk from clinically affected cows is diverted from the human food supply and is disposed of in accordance with regulatory requirements. Vat milk from non-clinical cattle can continue to be moved to milk handlers using appropriate biosecurity practices. The USDA is encouraging affected producers to establish on-farm systems to heat-treat milk for disposal (or prior to calf feeding) by providing financial support of up to USD$8,000 per affected premises (APHIS 2025f). Current US guidance recommends heat-treatment or pasteurisation of milk followed by dumping in effluent ponds or application of waste solids (APHIS 2024b). On-farm pasteurisation units are reportedly very rare in Australia and are only capable of treating small volumes (AHA 2022).

Food Standards Australia New Zealand require that '"milk for human consumption is only sourced from animals that do not show any evidence of infectious diseases transferrable to humans through milk, are in a good general state of health and are clearly identifiable through stock identification procedures' (FSANZ 2016). Thus, milk from clinically affected cows cannot enter the food chain. However, milk from subclinical or preclinical cows may inadvertently enter bulk tank milk, as evidenced by detection of viral RNA in pasteurised retail milk in the US (Spackman et al. 2024; Suarez et al. 2025). WOAH specifies that only milk produced by non-infected cows and that has been pasteurised (or otherwise inactivated) should be commercialised (WOAH 2024). The US Food and Drug Administration is confident that pasteurised retail dairy products are safe for human consumption, even when viral RNA (which is not infectious) is present (US FDA 2025). Australian decision-makers must decide whether bulk tank milk (potentially contaminated due to subclinical or pre-clinical cows) from affected premises could continue to be safely transported for pasteurisation, given the findings of 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment', and used for human consumption. This approach is being taken by some US states (e.g. New York state, Wisconsin, California). While movement of raw milk and dairy products from an infected premises is not permitted under Australia's FMD response guidance, FMD virus is also excreted in high concentrations in the faeces of infected animals, unlike HPAI virus in dairy cattle; manure may arguably be more likely to contaminate milk tankers and other fomites. Biosecurity measures that could be adopted to allow approved milk processing plants to receive milk from a declared area are discussed in the AUSVETPLAN enterprise manual for the dairy cattle industry.

Disposal of milk during EAD responses is covered in Section 5 of the AUSVETPLAN disposal manual. In general, following treatment to inactivate the infectious agent, milk could be incinerated, sprayed on pasture, fed to animals, or processed to remove a high proportion of the water content and then incinerated or buried (Aha 2021b). Milk must be disposed of in accordance with environmental guidelines, which may vary by jurisdiction. Given the large volumes of milk involved, treatment and disposal on-farm in the event of a clade 2.3.4.4b HPAI outbreak will be challenging. Consideration should be given as to whether waste milk from affected premises could be safely transported to approved disposal sites (i.e. specified processing facilities) for pasteurisation and disposal (if these were available and if large volumes of waste milk were accumulating).

If milk must be disposed of on-site in the absence of heat treatment options, acidification to inactivate clade 2.3.4.4b HPAI may also be considered. This is not currently an approved treatment method in the US. A recent pilot study demonstrated that treatment with citric acid to a pH between 4.1 and 4.2 for 6 hours, but not pH 4.4, inactivated clade 2.3.4.4b HPAI genotype B3.13 in milk (Crossley et al. 2025). This is more stringent than for FMD (pH less than 5 for at least 1 hour) (AHA 2022). The practicalities of on-farm acidification must also be considered. For example – a herd of 720 milkers with 5% of cows affected, each producing 5 to 10 litres of milk per day (assuming a 60–85% drop in production), would generate 180 to 360 litres of milk per day to be treated. To achieve a pH of ~4.1, thiswould require 0.8–1.6 kg of citric acid per day. If the decision was made to disinfect vat milk (15,000 litres) as well, that would require ~65 kg of citric acid each day. The acidified milk would then need to be disposed of, which would require dilution, generating a larger volume again. Treated milk could potentially be disposed of off-site if an appropriate disposal site is available (such as landfill, composting or a central effluent wastewater disposal site) (Aha 2021b). Milk must be disposed of in accordance with environmental guidelines, which may vary by jurisdiction. Access to the required amounts of citric acid, disposal of acidified milk and workplace health and safety issues

for dairy farm staff may limit the utility of this approach. Critically, further research is required to understand whether acidification and other chemical treatments of milk are practical in a field setting.

Chemicals such as formalin should not be used to treat milk because this would create a hazardous substance (Aha 2021b).

While the herd-level mortality rate in dairy cows infected with clade 2.3.4.4b HPAI is typically low (Less than 2%), anecdotally, mortality up to 20% in some Californian dairy herds has been reported in the news media, noting that this has not been confirmed by official sources (Douglas 18 October 2024; Rust 4 October 2024). It is important to acknowledge that this is all-cause mortality on affected farms (i.e. mortality due to not only HPAI but also other causes, such as other disease or environmental conditions); other factors, such as extreme heat stress, may also have contributed to these high mortality rates (Douglas 18 October 2024; Rust 4 October 2024). This emphasises that in an outbreak, even without depopulation, carcass management needs to be considered. Infectious virus has been recovered from mammary gland tissue of infected cattle on day 24 post-infection in 1 study (Baker et al. 2024) and on days 9 and 13 in a second study (Halwe et al. 2024). Viral RNA is only occasionally found in muscle tissue and infectious virus has not been recovered (see Section 2.2.8). Low levels of viral RNA and antigen were detected in the lung, supramammary lymph nodes, spleen, heart, colon and liver of affected cows in 1 study (Caserta et al. 2024). Together, these findings suggest that most of a carcass (apart from the udder) is not likely to be highly infectious.

In California, carcasses from affected dairy farms are disposed of using standard methods at the discretion of the quarantined premises (on-site or off-site). In Australia, routine on-site disposal methods recommended by Dairy Australia, such as on-farm composting or appropriate burial, would likely be appropriate provided that carcasses are dealt with immediately and are not accessible to other cattle or wildlife. Carcasses must be disposed of in accordance with environmental guidelines, which may vary by jurisdiction. Current evidence suggests that off-site disposal may be safely achieved with the implementation of specific movement controls and enhanced biosecurity measures such as vehicle decontamination (see Section 2.2.3).

2.2.9 Depopulation

Stamping out by humane depopulation (culling of animals) is an epidemiological strategy for disease control and eradication in animal populations in certain contexts (Geering et al. 1999; Thrusfield 2008). Because of the self-limiting nature of infection in dairy cattle, depopulation is not being recommended in the US (USDA 2017; APHIS 2024a). Furthermore, by the time clade 2.3.4.4b HPAI was identified in the US dairy cattle population it was widespread across at least 3 states and there were no significant trade or market access restrictions arising from infection (Nguyen et al. 2024; International Dairy Foods Association 2024). The US represents one specific incursion scenario and response policy decision. Targeted depopulation as a response measure in Australia in the event of an HPAI incursion could be considered, alongside other response measures, depending on the outbreak context. In the author's opinion, policy deliberations on the implementation of targeted depopulation measures should consider whether:

- the outbreak is associated with a mammalian-adapted strain that poses a high risk of zoonotic transmission, or an avian-adapted strain with low public health risk

- the outbreak is limited in size and swift elimination might quickly restore export markets
- there are indications that significant pressure may be exerted by trading partners
- depopulation would facilitate eradication in a shorter time frame and for a lower overall cost (Geering et al. 1999)
- affected premises can be appropriately quarantined (e.g. stringent movement controls) and affected animals treated until the herd recovers
- significant trade or market access restrictions may be imposed following an outbreak
- infection is widespread at the time of detection
- there is a high frequency of spillover from a reservoir population that cannot be controlled
- an effective vaccine is available (Geering et al. 1999).

Social, economic and other factors need to be carefully evaluated before selecting depopulation as part of a disease control strategy (Geering et al. 1999). The transparent, early and clear communication of jurisdictional response plans in the event of a HPAI incursion in dairy cattle is critical for farmer compliance and support of the response.

2.2.10 Decontamination

Decontamination entails cleaning and disinfection of the infected site to remove all infective material. The AUSVETPLAN operational manual for decontamination provides guidance on the most appropriate means and methods of decontamination.

Raw milk from infected cows contains very high levels of infectious virus, up to 109 50% TCID50 per mL (Halwe et al. 2024). Experimental studies suggest that viral shedding in milk is of relatively short duration, around 1–2 weeks, peaking early in infection, around days 2–3 (Caserta et al. 2024; Halwe et al. 2024; Baker et al. 2024). Low levels of infectious virus (101 to 103 TCID50 per mL) have been recovered from nasal swabs of non-lactating cattle for up to 7 days following experimental intranasal infection (Halwe et al. 2024; Kalthoff et al. 2008). Viral RNA has been detected in other samples at low levels, such as urine, ocular swabs, whole blood and serum, although infectious virus has not been recovered and results vary between studies (Caserta et al. 2024; Halwe et al. 2024; Baker et al. 2024; Facciuolo et al. 2025; Davila et al. 2025). Further studies are required to investigate the infectivity of these sample types. Rectal swabs and faeces have been consistently negative when tested. Together, these findings suggest that decontamination should focus on areas/fomites (e.g. footwear, clothing, equipment) that may be contaminated with raw milk (and potentially oro-nasal secretions). People that may have been exposed to raw milk from infected cows should undergo personal decontamination procedures.

Genotype B3.13 clade 2.3.4.4b HPAI can remain infectious on stainless steel and rubber for at least 1 hour (CEZD 2024b; Le Sage et al. 2024). The authors estimated that milk deposited on milking equipment could remain infectious for over 3 hours. Environmental persistence depends on various factors, including temperature and humidity. At 4°C and 80% relative humidity, the half-life of genotype B3.13 was 1.4 days on polypropylene and 1.2 days on stainless steel (Kaiser et al. 2025). Half-lives were lower at 22°C and 65% relative humidity—2.5 hours on polypropylene and 3.3 hours on stainless steel. In raw milk, the half-life of genotype B3.13 was found to be 2.1 days at 4°C and 0.74 days at 22°C (Kaiser et al. 2024). Given that approximately 69 days is required for a 10 log10

reduction in virus titre at 4°C (24 days at 22°C), raw milk with a sufficiently high initial virus titre may remain infectious in a refrigerator for weeks (Kaiser et al. 2024).

IAVs are susceptible to a wide range of disinfectants including iodine, hydrogen peroxide and other agents, although contact time is important for disinfectant effectiveness (The Center for Food Security & Public Health 2024; EPA 2025). An extensive list of disinfectants approved for use against HPAI on dairy premises is provided by the California Department of Food and Agriculture. This list includes hydrogen peroxide, peracetic acid, sodium hypochlorite (i.e. bleach), and iodine. It is important that suitable disinfectants are approved for use with the Australian Pesticides and Veterinary Medicines Authority. Organic material must be removed by dry or wet cleaning before disinfectants will work properly (Aha 2023c). As for avian influenza in poultry, detergent, steam, alkalis and phenolic compounds can be used to remove organic material prior to the application of disinfectants (Aha 2023c). The high protein content of milk may stabilise the virus, making it more resistant in milk compared to other matrices (Kaiser et al. 2025). Other decontamination methods, such as ultrafiltration and ultraviolet irradiation, may have applications in some dairy byproduct and whey processing situations (Martin et al. 2024), but have not yet been widely studied.

Decontamination should include standard rodent control measures to minimise mechanical spread of the virus to nearby premises.

California requires that affected dairies implement disinfectant footbaths, hand washing or sanitisation, and disinfection of vehicle tyres while in quarantine (see Section 2.2.2). General guidance for decontamination of vehicles in the context of the Australian dairy industry is provided in Appendix 6 of the AUSVETPLAN enterprise manual for dairy cattle. Critically, while the movement of vehicles or equipment contaminated with raw milk are reported to be risk factors for disease spread in the US (APHIS 2024g, 2024j; Caserta et al. 2024; CEZD 2024b; Molteni 20 December 2024), this transmission pathway was assessed as extremely low likelihood (with moderate uncertainty) in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment' when considered in the context of the Australian dairy industry. Decontamination has environmental and workplace health and safety implications and may not be cost-effective if performed inappropriately or not relevant to the infectious agent of interest. It may also compromise stakeholder compliance around other, more critical, disease control measures (e.g. the 'hygiene theatre' experienced during the COVID-19 pandemic). More research is required to determine whether infectious virus can be recovered from vehicles and equipment on affected dairy premises and under what circumstances, so that targeted, cost-effective decontamination guidance can be developed. Decontamination recommendations for clade 2.3.4.4b HPAI in the dairy industry are likely to look very different to those for diseases such as HPAI in poultry or FMD, where depopulation of infected premises is applied.

2.2.11 Wild animal management

General guidance on the management of wild and/or feral animals in an EAD response is provided in the AUSVETPLAN wild animal response strategy operational manual.

The role of wild birds and peri-domestic wildlife in facilitating spread of clade 2.3.4.4b HPAI between dairy premises is highly uncertain, but was assessed as very low to extremely low in 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment'. Note that this

relates to spread from an affected dairy premises, not initial spillover risk. Current genomic and epidemiological evidence do not support that wild or peri-domestic birds are spreading HPAI between cattle herds in the US (APHIS 2024g), although mechanical vectoring cannot be ruled out. Rather, all evidence suggests that there were 3 independent spillover events into US dairy cattle, followed by sustained cow-to-cow transmission within the industry. Notably, transmission has been detected from dairy cattle to several other species, including domestic cats, wild birds that congregate in barns (such as grackles, rock pigeons and blackbirds), terrestrial mammals (such as foxes, raccoons and mice) and poultry (Peacock et al. 2024; Nguyen et al. 2024; Worobey et al. 2024; Burrough et al. 2024; Caserta et al. 2024).

Scientifically, destruction of wild waterfowl (or other wild birds) is not supported, either during an outbreak or preventatively (Aha 2023c). Experts do not recommend the lethal removal of wild birds to prevent the spread of HPAI, particularly in dairy cattle where the US outbreak has been driven by cow-to-cow spread. Because of the high number and constant movement of wild birds, the use of lethal control methods is neither practical nor environmentally sound.

Standard rodent control measures should be continued during an outbreak to minimise mechanical spread of the virus to nearby premises.

It is prudent to minimise access of wild birds and peri-domestic wildlife to dairy cattle feed, feed storage, water sources, bedding materials and facilities, where possible. Arguably, the most practical control measure to mitigate the likelihood of spillover is to detect infection in local wildlife populations early and instigate temporary intensive biosecurity measures if virus is present in local populations. Therefore, proactively monitor for and report any unexpected mortality or behaviours in wild birds (or wild animals).

Any dead or dying wild birds or other wildlife around affected premises should be tested for clade 2.3.4.4b HPAI (APHIS 2024m). Recommended samples for birds are oropharyngeal and cloacal swabs and for mammals include brain tissue or oral, nasal or rectal swabs. The US does not recommend euthanising apparently healthy wildlife solely for sampling (APHIS 2024m).

2.2.12 Vaccination

No HPAI vaccines are currently available for use in dairy cattle in the US, although field trials to evaluate safety of at least 7 H5N1 vaccine candidates in dairy cows have been approved. Further details on vaccine types and preliminary results are not yet publicly available. These observational field studies are restricted to nonviable, non-replicating vaccines (such as inactivated virus, recombinant protein subunit or mRNA vaccines) and do not involve deliberate virus challenge. Studies utilising live vaccines or interventional studies involving virus challenge (i.e. controlled trials) continue to require laboratory containment.

Safe and effective vaccines can increase resistance to infection, protect against clinical disease and production losses, reduce or prevent viral shedding, thereby reducing transmission and environmental contamination (Swayne et al. 2023, 2014). Ideal IAV vaccines for dairy cattle should:

1) Be safe
2) Be protective against high environmental exposure

3) Prevent virus replication and shedding (i.e. induce sterilising immunity)
4) Provide protection with a minimum number of doses (ideally single-dose protection)
5) Have a long duration of immunity
6) Be easy to administer
7) Be inexpensive
8) Be broadly usable in multiple species
9) Enable differentiation of infected and vaccinated animals (DIVA)
10) Have minimal or no withholding periods (residues) for dairy (and meat) products.

These criteria are not trivial to achieve. In poultry, when using high potency vaccines with sufficient antigenic match to the field viruses, resistance to infection can be increased such that a 3 to 4 log10 increase in virus exposure is required to produce infection (Swayne et al. 2014). However, birds can still be infected following high-dose exposure. Given the extremely high virus levels present in the milk of clade 2.3.4.4b HPAI-affected dairy cows, they are likely to regularly be exposed to high virus levels. How this impacts HPAI vaccine effectiveness is yet to be determined.

Sterilising immunity is difficult to achieve in practice. Non-sterilising vaccines may still protect against clinical disease and production losses but may accelerate the rate of pathogen evolution and select for higher levels of intrinsic virulence, leading to more severe disease in unvaccinated individuals (and species) (Gandon et al. 2001; Aha 2023c). For a pathogen like HPAI, with potential for zoonotic transmission, this needs to be carefully considered. Vaccines that protect against clinical disease but not viral shedding can promote silent spread of infection, masking virus circulation and jeopardising early detection surveillance systems (Aha 2023c; Swayne et al. 2023).

HPAI vaccines for poultry, particularly less expensive inactivated whole virus vaccines, typically require a prime-boost strategy with a minimum of 2 (sometimes 3) doses, with additional boosters at 6 to 12 month intervals (Swayne et al. 2014). This may not be practical or cost-effective in longer-lived species such as dairy cattle. A cost-benefit analysis would be required to determine how the cost of vaccination (and the associated operational costs) over the animal's productive life span compare with the loss of production due to HPAI infection. Additionally, because of the high mutation rate of IAVs (i.e. antigenic drift), vaccines must be regularly updated to ensure they are antigenically matched to circulating field strains, like seasonal influenza vaccines in people (Swayne et al. 2014). This may increase the cost of HPAI vaccines relative to other viral vaccines.

Given that clinical disease is primarily limited to lactating cattle, maternal antibody interference is not likely to be an issue as vaccination will be limited to older animals and not calves (Windeyer and Gamsjäger 2019).

A barrier to implementing vaccination for HPAI is the potential trade implications. The WOAH Terrestrial Animal Health Code allows use of vaccination (of poultry) under specific conditions and without negatively impacting HPAI-free status if appropriate surveillance is conducted (Swayne et al. 2023). Zoning and compartmentalisation can be used to facilitate safe trade (Swayne et al. 2023). It is technically feasible with some vaccine types (e.g. mRNA vaccines, recombinant protein subunit vaccines, virally-vectored vaccines) to implement a DIVA surveillance strategy. This will need to be

considered following demonstration of safety and effectiveness. Some considerations from the poultry perspective are given in Suarez et al. (2012).

The most appropriate vaccine strategy (e.g. barrier, blanket, ring, targeted vaccination) would depend on the specific vaccine characteristics, including cost and vaccination availability. General guidance is provided in the WOAH Terrestrial Animal Health Code Chapter 4.18 (WOAH 2022). If the Australian Government were to implement a policy allowing for the vaccination of dairy cattle against HPAI in Australia, the decisions around use of a vaccine (if/when available) will be under the control of the chief veterinary officer for each jurisdiction.

2.3 Recommendations for clade 2.3.4.4b HPAI preparedness and response in the Australian dairy industry

Based on the project's findings, Ausvet recommends several actions for clade 2.3.4.4b HPAI preparedness and response in the Australian dairy industry. We note that Ausvet does not have a comprehensive picture of current activities across all sectors—these are gaps identified during our assessment based on publicly available information. These recommendations should be discussed collaboratively with relevant stakeholders to ensure coordinated efforts and to prioritise activities.

Policy, legislation and regulatory aspects

1) Industry, state and federal government and other relevant stakeholders should develop and agree on the scope of preparedness and response activities now.
2) Emergency response plans, policies and governance structures for clade 2.3.4.4b HPAI must be developed, or updated to include dairy cattle, as a matter of priority. Specifically:
    a) Clinical case and surveillance definitions must be developed that are applicable to the Australian context.
    b) The objectives of an Australian response should be agreed upon.
    c) AUSVETPLAN response strategies and the EADRA should be reviewed and updated to consider dairy cattle (and other livestock).
    d) A strategy for multisectoral collaboration and coordination in the context of clade 2.3.4.4b HPAI in the dairy industry should be developed.
    e) Mechanisms to support producers in the event of an outbreak should be agreed upon.
    f) Guidance on diagnostic testing should be developed, including which animals are eligible for testing, appropriate sample types and collection methods, considerations around specimen transport, validated test protocols, the consequences for producers/industry of positive (or indeterminate) results, and how testing will be funded.
    g) Guidelines around point-of-care testing for clade 2.3.4.4b HPAI in raw milk should be developed, including data collection mechanisms for testing results.
    h) Should a suitable vaccine be developed (domestically or internationally) and found suitable for use in Australia, processes must be established for rapid liaison with the Australian Pesticides and Veterinary Medicines Authority regarding emergency use permits.

Additionally, vaccination guidelines for veterinarians and producers should be in place, and supply chain and logistical considerations understood. Therefore, a working group should be established with industry to begin to develop a vaccine strategy for dairy cattle. The costs and benefits of developing on-shore manufacturing capacity should be considered.

i) Ensure that disinfectants effective against clade 2.3.4.4b HPAI and suitable for use in a dairy setting are approved with the Australian Pesticides and Veterinary Medicines Authority.

3) To understand movement patterns relevant to the spread of clade 2.3.4.4b HPAI, the National Livestock Identification Scheme should be updated to distinguish between beef and dairy cattle movements, identify whether cows being moved are lactating or dry, and provide the production or operation system (e.g. corporate) for origin and destination premises.

Organisational development, implementation and sectoral integration

4) The on-farm assessments revealed considerable confusion and uncertainty among Australian dairy producers concerning HPAI in dairy cattle. This indicates a clear need to enhance producer awareness and education. This could be achieved through: HPAI-specific training for industry,simulation exercises around clade 2.3.4.4b HPAI targeted to producers and/or the development of clear guidelines for enhancing on-farm biosecurity in the context of clade 2.3.4.4b HPAI.

5) Results of the risk assessment indicate that enhanced on-farm biosecurity should focus on mitigating the risk of spillover and the risk of between-herd spread. Guidelines should be developed particularly around mitigating risks associated with the movement of lactating animals. Farm-level recommendations are detailed in Section 1.3.4.

6) On-farm pasteurisation capacity should be increased on Australian dairy farms to manage contaminated milk from clinical cows. Producers should be encouraged to routinely treat milk prior to calf feeding in the event of a clade 2.3.4.4b HPAI incursion into Australia.

7) A communication and education plan targeted to producers should be developed. This should include early and clear communication of jurisdictional response plans (once developed) to improve farmer compliance and support of any future response.

8) Best-practice treatment guidelines for affected cattle that facilitate rapid return to production should be developed following consultation with US dairy veterinarians and producers. These should be tailored for mild, moderate and severe clinical cases. Training should be provided to producers where required, for example - in the delivery of large volumes of oral fluids.

9) Training and multi-sectoral preparedness and response exercises specific to clade 2.3.4.4b HPAI in the dairy industry should be conducted with biosecurity response teams at the national and jurisdictional levels, and also within the Consultative Committee on Emergency Animal Diseases.

10) Industry liaisons should be connected within jurisdictional biosecurity preparedness and response teams now to provide input into response strategies. For example – industry can assist with:

a) Developing processes for the safe transport of vat milk (i.e. milk collected from non-clinical cows) from affected premises to pasteurisation or treatment facilities. This would avoid having to treat and dispose of large volumes of milk on-farm.

b) Developing plans for use/disposal of treated contaminated milk.

c) Developing practical and effective quarantine requirements for affected premises and high-risk premises.

d) Developing practical and effective movement controls in the event of an outbreak. This should include both lactating and non-lactating cattle, as well as protocols for dairy shows and exhibits.

11) Communications material and talking points for ministerial and public release should be prepared in advance of an outbreak.

12) Relevant supply chains should be reviewed. These could include for laboratory testing reagents and consumables, commercial electrolyte solutions and other treatments for affected cattle, suitable disinfectants for decontamination, personal protective equipment for dairy workers (and response teams), and chemicals appropriate for treatment of contaminated milk if such treatment is determined to be effective and practical.

13) Genomic sequencing should be utilised to generate data to understand spillover, between-farm transmission pathways and zoonotic risk in the event of incursion. This requires data sharing frameworks and systems to be established in advance across jurisdictions and across sectors (e.g. with public health agencies). While some capacity for genomic sequencing exists within Australia, data sharing is still limited, which restricts the inferences that can be drawn from genomic data. It is important to ensure that sufficient genomic sequencing and data sharing capability (and laboratory diagnostic capability) are available in the event of an incursion.

Data, evidence and knowledge

14) Key research gaps must be addressed to reduce uncertainty in the assessment. Research gaps identified through the assessment are provided in 'Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle'. Research on many of these gaps may already be occurring in the US and other countries. There is a need to engage internationally to understand what research is happening overseas and ensure coordination of international research efforts.

15) The assessment revealed a lack of detailed, current information regarding the structure and movement dynamics of the dairy industries in both Australia and the US. Movement networks within the dairy industry are a critical control point for managing between-farm spread of disease. In particular, a better understanding is required of between-'milking herd' movement in multi-herd businesses. This analysis should be undertaken as a priority. A state-based analysis of the US industry may help to explain why some states (e.g. California) were impacted so much more severely than others.

16) A surveillance plan should be developed for early detection of clade 2.3.4.4b HPAI in the Australian dairy herd. Consider the following components:

a) The effectiveness of the NMTS in the US suggests that surveillance for early detection should be initiated following incursion in wild birds to detect new spillover events into dairy cattle and delineate infected areas.

b) A framework for bulk milk surveillance should be developed now, leveraging existing bulk milk surveillance activities where possible. Guidance should be developed around where bulk milk samples are collected, where they are sent for testing, what testing is performed, how testing is funded, and processes in the event of a positive result. The bulk milk testing framework for enzootic bovine leukosis developed by Dairy Australia may be a useful reference.

c) Alternatively, retail milk sampling could be conducted, as is done in Canada. Trace-back would presumably be more complex than for bulk milk tank surveillance.

d) Exclusion testing for HPAI on mastitis case submissions could be conducted by laboratories if the regulatory framework allows (i.e. testing without specific submitter request).

e) Testing of suspect cases in dairy cattle should be encouraged to increase the sensitivity of passive surveillance.

f) Testing of any mortality events in wild birds and/or peri-domestic mammals (especially predatory or scavenging species) around dairy farms should be strongly encouraged. Guidance should be provided for dairy producers to enact stringent biosecurity measures, at least temporarily, if infection is detected in the vicinity.

    i) Testing prior to movement of cattle, especially lactating cows, should be strongly supported, particularly in declared areas. Communications material on HPAI testing targeted to producers should be developed.

17) Alternative approaches to early detection of infection should be investigated further. These could include coordinated research into point-of-care test development and validation in the Australian context and understanding the role of rumination collars and other 'wearable devices' for early detection. Guidance will need to be developed, for example – around interpretation of data from wearable devices, next steps in investigation, how to manage animals until confirmatory testing results are received.

18) Research and development into large-volume milk treatment and disposal options suitable for use in the Australian context is required. The impact of milk disposal needs to be better quantified and understood. While on-farm pasteurisation is ideal, this is not widely available on Australian dairy farms and is currently restricted to small volumes. Options for larger volume on-farm pasteurisation capacity (or local/regional capacity) should be investigated. The effectiveness of (and barriers to) alternative milk treatment options, such as acidification, should also be explored. Training in the appropriate use of on-farm pasteurisation units should be provided.

19) Consideration should be given as to whether local vaccine development is warranted, given this is already occurring in the US.

20) Consider conducting an updated incursion risk assessment for clade 2.3.4.4b HPAI. The previous assessment was performed in July 2023 prior to arrival of the virus in Antarctica and sub-Antarctic islands. Non-wild bird sources may also be considered, for example – subclinically infected travellers, imported bovine reproductive materials.

21) Advanced modelling is required as further quantitative data become available from the US.

22) Detailed economic analyses are required to better understand the potential economic consequences of an outbreak in the Australian dairy industry. These analyses should consider

seasonal, batch and year-round calving herds at different stages of lactation and should be based on current Australian milk prices.

23) A trade impact analysis would be useful given the very high uncertainty around trade and market access impacts.

3 Rapid risk appraisals: Clade 2.3.4.4b HPAI in Australian livestock industries

3.1 Beef cattle

This assessment was conducted based on information available up to 6 March 2025.

This is a summary of the comprehensive assessment provided in 'Risk of high pathogenicity avian influenza to Australian beef cattle: Rapid risk assessment'. Further details are provided in that document.

Here, we synthesise the latest scientific evidence on HPAI in cattle to inform an evidence-based rapid risk appraisal for the Australian beef cattle industries.

3.1.1 Risk questions

1) Assuming clade 2.3.4.4b HPAI was present in Australia, what is the risk (likelihood and consequences) to the Australian commercial beef cattle industry?
    a) Entry assessment: Assuming clade 2.3.4.4b HPAI was present in Australia, what is the likelihood of clade 2.3.4.4b HPAI spilling over into at least 1 commercial beef animal in Australia in the year following incursion?
    b) Establishment and spread assessment: If clade 2.3.4.4b HPAI were to infect 1 or more commercial beef animals in Australia, what is the likelihood of spread within and between commercial beef production premises in the year following incursion?
    c) Consequence assessment: What are the consequences of clade 2.3.4.4b HPAI infection in the Australian beef cattle industry?

3.1.2 Overall assessment

Overall, assuming clade 2.3.4.4b HPAI was present in Australia, the risk to commercial beef cattle industry was assessed as negligible, with high uncertainty.

Key findings supporting this assessment include:

Entry assessment

The likelihood of clade 2.3.4.4b HPAI spilling over into at least 1 commercial beef animal in Australia was assessed as low, with low to moderate uncertainty.

Despite high levels of HPAI circulation in wild bird and poultry populations globally, spillovers of IAVs into cattle remain rare, even in environments with high cattle exposure (e.g. agricultural operations with significant bird presence). Current evidence points to 3 spillovers of clade 2.3.4.4b HPAI into dairy cattle, which have so far been restricted to the US (Nguyen et al. 2024).

Spillovers of clade 2.3.4.4b HPAI have not been detected in dairy cattle populations outside the US where active surveillance is being conducted. For example – Canada, Germany, Pakistan and the UK have conducted targeted surveillance for HPAI in dairy cattle with no positive detections (CFIA 2024; Wallace et al. 2025; Ahmed et al. 2024; Friedrich-Loeffler-Institut 2024; Animal and Plant Health Agency 2024).

There have been no reports of clade 2.3.4.4b HPAI infections in US beef cattle despite the widespread outbreak in dairy cattle, although active surveillance is not being conducted.

Establishment and spread assessment

The likelihood of clade 2.3.4.4b HPAI establishing and spreading within and between commercial beef production premises was assessed as negligible, with low uncertainty.

Sporadic IAV infections (with various HxNx subtypes and genotypes) have been recognised in cattle for decades, without documented mammal-to-mammal transmission (Sreenivasan et al. 2019; Mostafa et al. 2024).

There are several barriers that avian-adapted IAVs must overcome to transmit efficiently amongst mammalian hosts (Long et al. 2019). Generally, multiple infection events in a new host species are required for mammalian-adaptive genetic mutations to emerge and establish (become fixed) in a virus population (Arruda et al. 2024). Dairy cattle are an exception because 'avian-type' receptors (α-2,3-linked sialic acids) are abundantly expressed in the mammary gland (Peacock et al. 2024; Good et al. 2024). Therefore, minimal adaptation is required for avian-adapted viruses to spread between lactating dairy cows.

The mammary gland is the main site of virus replication in dairy cattle (Mitchell et al. 1953; Caserta et al. 2024; Halwe et al. 2024; Ríos Carrasco et al. 2024). While non-lactating cattle can be infected with clade 2.3.4.4b HPAI, the level of virus in non-lactating cattle is much lower than in lactating dairy cows (Halwe et al. 2024).

Within-farm and between-farm transmission of IAVs in US dairy cattle is thought to be primarily through exposure to unpasteurised (raw) milk (i.e. direct contact with either clinically infected or subclinical animals or contact with milk during milking or via contaminated fomites) (APHIS 2024g). Adult beef cattle generally have limited exposure to milk from other animals.

Non-milk-related transmission routes appear to be of little epidemiological relevance in cattle (but cannot be definitively ruled out). For example – no onward transmission was observed in experimental infections of non-lactating cattle with clade 2.3.4.4b viruses (Halwe et al. 2024).

Consequence assessment

The consequences of clade 2.3.4.4b infection in the Australian beef cattle industry were assessed as minor, with high uncertainty.

Experimental infection studies have demonstrated that clinical disease following clade 2.3.4.4b infection in non-lactating cattle is mild and short-lived (at least with those genotypes investigated) (Halwe et al. 2024; Kalthoff et al. 2008; Davila et al. 2025; Peña-Mosca et al. 2025). Morbidity in infected dairy herds is generally between 3 and 20% (primarily restricted to lactating cows) (Caserta et al. 2024; Oguzie et al. 2024; Burrough et al. 2024), although anecdotal reports from California

suggest that up to 50–60% of some milking herds can be clinically affected (Douglas 18 October 2024; Rust 4 October 2024).

Impacts on beef cattle production at an industry level are anticipated to be minor, since mortality in dairy cattle (at least with genotype B3.13) has been low on average (less than 2%) (Caserta et al. 2024). Anecdotally, herd-level mortality rates of up to 20% in some Californian dairy herds have been reported in the news media (Douglas 18 October 2024; Rust 4 October 2024), but this has not been confirmed by official sources. These mortality rates were also reported during extreme heat waves.

Significant economic impacts to the dairy industry are due to decreased milk production, mortality and early herd removal (Peña-Mosca et al. 2025). These impacts are primarily related to clinically affected lactating cows. Milk is not a commodity for the beef cattle industry.

The impacts of HPAI infection on long-term liveweight gain, fertility and other metrics relevant to beef cattle production have not been investigated.

Public health consequences are negligible, since humans are unlikely to be exposed to milk from beef cattle. Current evidence suggests that infected dairy workers acquired infection through exposure to raw milk or through close contact with secretions from clinically affected animals (CDC 2025b; Morse et al. 2024).

The potential trade impacts of clade 2.3.4.4b HPAI infection in the Australian beef industry are difficult to predict, adding considerable uncertainty to the assessment. It is possible that trading partners may impose restrictions or additional testing requirements if clade 2.3.4.4b HPAI was detected in Australian beef cattle. Australia relies heavily on access to premium export markets. Based on what has been observed for US dairy cattle, trade impacts are more likely to affect live cattle movements than animal products (Hunter 29 October 2024).

Some impacts on beef meat and cattle products were experienced following the incursion of clade 2.3.4.4b HPAI into dairy cows in the US, although many of these impacts were temporary. Colombia closed markets (valued at USD$40 million) for live US cattle, beef meat/meat products and cattle germplasm in April 2024 (Huffstutter and Polansek, 2024). While most restrictions were lifted in September 2024, restrictions on live cattle originating from HPAI-affected states remain. The Dominican Republic market for US beef and live cattle was closed from May to June 2024, although restrictions have since been removed (Hunter 29 October 2024). Turkey prohibited importation of all live cattle from the US (Hunter 29 October 2024). Israel now requires pre-export testing for all cattle types from the US (Hunter 29 October 2024). These restrictions had little appreciable effect on overall US beef/veal or live cattle trade volumes (Risk of high pathogenicity avian influenza to Australian dairy cattle: Qualitative risk assessment). Indeed, US beef exports in 2024 were projected to decline due to factors preceding HPAI, but ended up stronger than expected (Petry, 2025).

Response measures may also result in significant industry disruption and socio-economic impacts, if implemented. An agreed response policy to be followed in the event of an outbreak in beef cattle in Australia has not yet been developed. This adds further uncertainty to the assessment.

With the continued evolution of clade 2.3.4.4b viruses and the emergence of novel genotypes, the biological properties (such as pathogenesis, virulence and transmissibility) of these viruses may change over time, which may change the results of this risk assessment.

3.2 Pigs

This assessment was conducted based on information available up to 6 March 2025.

This is a summary of the comprehensive assessment provided in 'Risk of high pathogenicity avian influenza to the Australian pig industry: Rapid risk assessment'. Further details are provided in that document.

In October 2024, clade 2.3.4.4b HPAI was detected in 2 non-commercial pigs in the US (APHIS 2024n). The pigs were sampled as part of the response to an HPAI outbreak in poultry (specifically, chickens and ducks) on the same farm. Three other pigs on the premises tested negative (APHIS 2024e). The source of the infection was determined to be co-mingling of the pigs with infected poultry and sharing of water sources, housing and equipment (APHIS 2024e). Although the pigs remained heathy, they were humanely killed as part of the investigation. The genotype detected in these pigs, D1.2, is not the same as the genotypes currently impacting dairy cattle in the US (i.e. genotypes B3.13 and D1.1). Here, we synthesise the latest scientific evidence on HPAI in pigs to inform an evidence-based rapid risk appraisal for the Australian pig industry.

To note that an evaluation of the public health consequences was out of scope for this assessment, however some public health considerations are discussed in the report.

3.2.1 Risk questions

1) Assuming clade 2.3.4.4b HPAI was present in Australia, what is the risk (likelihood and consequences) of HPAI to the Australian pig industry?
    a) Entry assessment: Assuming clade 2.3.4.4b HPAI was present in Australia, what is the likelihood of clade 2.3.4.4b HPAI spilling over into at least one commercial pig in Australia in the year following incursion?
    b) Establishment and spread assessment: If clade 2.3.4.4b HPAI were to infect one or more commercial pigs in Australia, what is the likelihood of spread within and between commercial piggeries in the year following incursion?
    c) Consequence assessment: What are the consequences of clade 2.3.4.4b HPAI infection in the Australian pig industry (excluding public health consequences)?

3.2.2 Overall assessment

Overall, assuming clade 2.3.4.4b HPAI was present in Australia, the risk to the Australian pig industry was assessed as low, with moderate uncertainty.

Key findings supporting this assessment include:

Entry assessment

The likelihood of clade 2.3.4.4b HPAI spilling over into at least one commercial pig in Australia was assessed as low, with low to moderate uncertainty.

Spillovers of novel IAV genotypes into pigs appear to be rare, despite high levels of circulation of HPAI in global wild bird and poultry populations in recent years.

Two natural infections with clade 2.3.4.4b (genotype D1.2) HPAI have been detected in pigs (APHIS 2024n). These were non-commercial animals that shared an environment with an infected poultry flock. Three other pigs on the premises were exposed but did not become infected.

Seroconversion to clade 2.3.4.4b HPAI (indicating past exposure to the virus) was detected in pigs on several occasions between 2016 and 2021 (Hervé et al. 2021; Schülein et al. 2021; Rosone et al. 2023). These detections were made in pigs co-housed with infected poultry (1 farm in Italy and 1 in France) and in 3 wild boar from southern Germany. Specifically, exposure to H5N1 and H5N8 subtypes of clade 2.3.4.4b HPAI were detected. However, infectious virus was not recovered in these investigations.

To date, no further reports of clade 2.3.4.4b HPAI infections have been reported in pigs in the US or elsewhere despite widespread disease and infection reported in wild birds, dairy cattle and poultry. However, active surveillance in pigs appears to be limited to research studies and case reports.

Establishment and spread assessment

The likelihood of clade 2.3.4.4b HPAI establishing and spreading within and between piggeries in Australia was assessed as low, with moderate uncertainty.

There are several barriers that avian-adapted IAVs must overcome to transmit efficiently amongst mammalian hosts (Long et al. 2019). Generally, multiple infection events in a new host species are required for mammalian-adaptive genetic mutations to emerge and establish in a virus population (Arruda et al. 2024). Dairy cattle are an exception because 'avian-type' receptors (α-2,3-linked sialic acids) are abundantly expressed in the mammary gland (Peacock et al. 2024; Good et al. 2024). Therefore, minimal adaptation is required for avian-adapted viruses to spread between lactating dairy cows. In contrast, other mammalian species, including pigs, require further adaptations to transmit effectively.

Experimentally, only clade 2.3.4.4b viruses isolated from mammals have been able to transmit between pigs (i.e. not viruses sampled directly from birds) (Arruda et al. 2024; Kwon et al. 2025; Graaf et al. 2023). Therefore, spillover from peri-domestic wildlife (e.g. rats, cats, foxes) may be of more concern than spillover from wild birds. As an example, this may occur if pigs scavenge infected carcasses.

Consequence assessment

The consequences of clade 2.3.4.4b HPAI infection in the Australian pig industry were assessed as minor, with moderate uncertainty.

Experimental infection studies suggest that clinical disease following clade 2.3.4.4b infection in pigs is inapparent or mild and short-lived (at least with those genotypes investigated) (Arruda et al. 2024; Kwon et al. 2025; Graaf et al. 2023). However, the spillover risk could be underestimated because infections may go unrecognised, particularly as no active surveillance is occurring beyond research studies and risk-based surveillance on affected poultry premises in some countries (Hervé et al. 2021; Schülein et al. 2021; Rosone et al. 2023; HAIRS 2025; APHIS 2024). For endemic swine IAVs, virus shedding typically ceases by 7–10 days post infection (WOAH 2023). There is no robust evidence for a true carrier state for IAVs in any species (MacLachlan et al. 2017).

The impacts of clade 2.3.4.4b HPAI infection on important production metrics for the pig industry, particularly on reproduction, have not been investigated. Swine-adapted IAVs may cause reproductive problems in sows, depending on the stage of gestation at infection (Gumbert et al. 2020; Madec et al. 1989; Grøntvedt et al. 2011; Kwit et al. 2015).

Pigs raise additional concerns around their potential role as 'mixing vessels' for the emergence of novel IAVs (Public Health Agency of Canada 2024). For example – the 2009 pandemic H1N1 virus was a reassortant of avian-, human- and classical swine-origin IAV lineages (Smith et al. 2009). An evaluation of the public health consequences was out of scope for this rapid risk appraisal. A detailed public health risk assessment is warranted to further explore the risk to human health if clade 2.3.4.4b HPAI was to enter and spread within the Australian pig industry.

With the continued evolution of clade 2.3.4.4b viruses and the emergence of novel genotypes, the biological properties (such as pathogenesis, virulence and transmissibility) of these viruses may change over time, which may change the results of this risk assessment.

3.3 Small ruminants (sheep and goats)

This assessment was conducted based on information available up to 7 May 2025.

This is a summary of the comprehensive assessment provided in 'Risk of high pathogenicity avian influenza to Australian small ruminant industries: Rapid risk assessment'. Further details are provided in that document.

The ongoing HPAI outbreak in dairy cattle has now affected at least 1,048 dairy farms across 17 states (APHIS 2024i). Small ruminant infections have also been reported. For example – in March 2024, clade 2.3.4.4b HPAI genotype B3.6 was detected in neonatal goat kids on a farm following an outbreak in backyard poultry (APHIS 2024f). Adult goats on the same premises tested negative. Chickens and ducks on the premises were found to be infected with the same genotype as the kids and shared the same pasture and water source. Then in March 2025, a lactating ewe tested positive for clade 2.3.4.4b HPAI in the UK on a premises experiencing an outbreak in captive birds (DEFRA and APHA 2025; Schnirring 2025; HAIRS 2025). Detections of clade 2.3.4.4b HPAI in the US have also been confirmed in other livestock, including in pigs (genotype D1.2) and alpacas (genotype B3.13) (APHIS 2024f, 2024h, 2024n), highlighting the potential for infection in species beyond dairy cattle. Here, we synthesise the latest scientific evidence on HPAI in dairy cattle to inform an evidence-based rapid risk appraisal for the Australian small ruminant industries.

3.3.1 Risk questions

1) Assuming clade 2.3.4.4b HPAI was present in Australia, what is the risk (likelihood and consequences) to Australian small ruminant industries?
    a) Entry assessment: Assuming clade 2.3.4.4b HPAI was present in Australia, what is the likelihood of clade 2.3.4.4b HPAI spilling over into at least 1 small ruminant in Australia in the year following incursion?
    b) Establishment and spread assessment: If clade 2.3.4.4b HPAI were to infect 1 or more small ruminants in Australia, what is the likelihood of spread within and between small ruminant production premises in the year following incursion?

c) Consequence assessment: What are the consequences of clade 2.3.4.4b HPAI infection in Australian small ruminants?

3.3.2 Overall assessment

Overall, assuming clade 2.3.4.4b HPAI was present in Australia, the risk to Australian small ruminant industries was assessed as negligible, with very high uncertainty.

Key findings supporting this assessment include:

Entry assessment

The likelihood of clade 2.3.4.4b HPAI spilling over into at least 1 small ruminant in Australia was assessed as low, with moderate uncertainty.

Despite high levels of HPAI circulation in wild bird and poultry populations globally, spillovers into small ruminants are detected rarely. One infection has been reported from a sheep in the UK (HAIRS 2025) and 5 infections were reported in newborn goat kids in the US (APHIS 2024f).

These spillover events were associated with infected backyard poultry flocks, with contaminated environment and water sources implicated as the potential sources of infection (AVMA 2024; APHIS 2024f; DEFRA and APHA 2025). Other factors likely contributed to the severe clinical presentations in the newborn goats, as 5 others also died on the premises but tested negative for HPAI. This could suggest that host compromise or poor husbandry may have weakened immunity, increasing susceptibility to infection.

It is worth noting that limited surveillance is being done for HPAI infection in small ruminants. Therefore, infection rates may be underestimated. Active surveillance is limited to risk-based surveillance on affected poultry premises in some countries (HAIRS 2025; APHIS 2024i). The sensitivity of passive surveillance is likely to be limited; for example – in the UK mastitis in sheep is only rarely reported to or diagnosed by the Animal and Plant Health Agency, although it is consistently the primary cause in sheep of premature culling, loss of udder function, and reduction in milk yield (HAIRS 2025). One serological study conducted in Pakistan in 2023 found that 23.9% of goat and 31.0% of sheep samples were positive for antibodies against clade 2.3.4.4b HPAI, indicating prior exposure (Wong et al. 2024). If accurate, this suggests that most infections in small ruminants are subclinical, as no history of clinical disease was reported in that study.

Establishment and spread assessment

The likelihood of clade 2.3.4.4b HPAI establishing and spreading within and between small ruminant production premises was assessed as negligible, with high uncertainty.

No other adult sheep on the property were infected following the detection in the UK (HAIRS 2025). The lambs of the infected ewe tested negative for viral RNA, although 1 lamb returned a weakly positive serological reaction on an unaccredited test, indicating either exposure to the virus or a false positive result. No adult goats on the infected property in the US tested positive.

Of the various samples collected, including nasal swabs, only the milk of the infected ewe tested positive (at relatively high cycle threshold values) and infectious virus was not recovered, noting that sampling only occurred late in infection (HAIRS 2025). Virus levels in the samples collected from the goat kids were not reported.

In dairy cattle, exposure to milk from infected cows is thought to be the primary mode of transmission. This is because 'avian-type' receptors (α-2,3-linked sialic acids) are abundantly expressed in the bovine mammary gland (Peacock et al. 2024; Good et al. 2024). Therefore, minimal adaptation is required for avian-origin viruses to infect the bovine udder, and virus can replicate to very high levels, facilitating spread in milk. Although studies are limited, preliminary investigations indicate that mammary tissues from small ruminants also express these 'avian-type' receptors (Nelli et al. 2025). If virus biology is similar to dairy cattle, most animals will not be exposed to milk from other small ruminants. However, animals within the sheep and goat dairy sectors would therefore likely be at a higher risk of exposure.

Although limited data are available, Australian sheep and goat dairy industries appear to have limited connectedness. That is, animals (especially lactating ewes/does), vehicles and equipment are not frequently moved between premises (Zalcman and Cowled 2017).

Critically, no experimental infection studies with clade 2.3.4.4b HPAI have been conducted in small ruminants. Therefore, the dynamics of virus shedding in small ruminants, over time and in different tissues, secretions and excretions, are not known. Routes of infection in sheep (e.g. respiratory, ingestion, intramammary) are not known. This adds significant uncertainty to our assessment.

To transmit efficiently amongst mammalian hosts via non-milk associated routes, avian-adapted influenza A viruses must overcome several barriers (Long et al. 2019). Generally, multiple infection events in a new host species are required for mammalian-adaptive genetic mutations to emerge and establish in a virus population (Arruda et al. 2024). So far, sustained mammal-to-mammal transmission has only been documented in limited cases: fur farms in Europe, in wild marine mammals in South America, and in dairy cows in the US (Peacock et al. 2024).

Consequence assessment

The consequences of clade 2.3.4.4b infection in Australian small ruminants were assessed as minor, with very high uncertainty.

Animal health and welfare impacts in small ruminants are not known. The single infection in a sheep was associated with localised mastitis, but no other clinical signs (e.g. no respiratory signs) (HAIRS 2025). The infections in goat kids were associated with neurological signs; however, a clear link to HPAI was not established, as 5 others also died on the premises but tested negative (APHIS 2024f).

The Australian sheep and goat dairy industries are relatively small (AHA 2022). The economic impact of mastitis in Australian small ruminant dairy industries has not been examined. The severity of mastitis caused by clade 2.3.4.4b HPAI in small ruminants, and how this compares with the clinical disease in cattle, is based on a single infection in a non-commercial lactating ewe.

Impacts on meat and fibre production are anticipated to be minor, based on limited mortality in other artiodactyl species (e.g. non-lactating cattle, pigs, alpacas). This is speculative and thus highly uncertain. Critically, the impacts of HPAI infection on liveweight gain, reproduction, wool quality and other metrics relevant to small ruminant meat and fibre production have not been investigated.

The potential for trade impacts of clade 2.3.4.4b HPAI infection in Australian small ruminants are difficult to ascertain, adding uncertainty to the assessment. To our knowledge, there have been no reported impacts on sheep or goat trade following the UK and US isolated detections. However,

those detections were in non-commercial animals and export of live animals for slaughter and fattening has been banned in the UK since 2024. No studies have investigated the presence of clade 2.3.4.4b HPAI RNA or infectious virus in meat or meat products from small ruminants.

Response measures may result in significant industry disruption and socio-economic impacts, if implemented. An agreed response policy to be followed in the event of an outbreak in small ruminants in Australia has not yet been developed. This adds further uncertainty to the assessment.

Public health consequences are negligible, since humans are unlikely to be exposed to raw milk from small ruminants in most circumstances. Current evidence suggests that infected dairy workers acquired infection through exposure to raw milk or through close contact with secretions from clinically affected animals (CDC 2025b; Morse et al. 2024). Certain activities (e.g. stomach tubing sick animals) may increase the risk of zoonotic transmission.

With the continued evolution of clade 2.3.4.4b viruses and the emergence of novel genotypes, the biological properties (such as pathogenesis, virulence and transmissibility) of these viruses may change over time, which may change the results of this risk assessment.

3.4 Recommendations for the Australian beef cattle, pig and small ruminant industries

1) To reduce the likelihood of entry (spillover) into Australian livestock populations:
    a) Where possible, limit direct contact with wild birds, poultry and peri-domestic wildlife (e.g. rats, foxes, feral cats).
    b) Where possible, prevent or limit access of wild birds, poultry and peri-domestic wildlife to livestock feed, feed storage, water sources, bedding material, facilities and equipment.
    c) Avoid feeding unpasteurised (raw) milk and colostrum, poultry carcasses and poultry by-products (e.g. poultry litter, offal) to pigs (and other animals).
    d) Avoid access to poultry by-products (e.g. poultry litter or manure used as fertiliser).
    e) Avoid co-mingling livestock and poultry and limit contact with potentially contaminated environments.
    f) Avoid sharing (unclean) equipment or vehicles with poultry (and dairy) farms.
2) To reduce the likelihood of transmission between premises:
    a) Minimise unnecessary animal movements and keep detailed movement records.
    b) Maintain good farm biosecurity (e.g. pro-actively manage movement of people, equipment and vehicles).
    c) Enhance passive surveillance (e.g. monitor for sick livestock, wild birds or wildlife and report; consider HPAI as a differential diagnosis for unexplained illness).
    d) Jurisdictions and the Commonwealth should establish testing protocols for HPAI in non-avian species to facilitate testing of suspect cases.
    e) Surveillance of enzootic IAVs in Australian pig populations may better inform the likelihood of IAV reassortment in swine, which could lead to sustained pig-to-pig transmission.

f) Consideration should be given as to whether an evidence-based active surveillance strategy is required, following detection of a clade 2.3.4.4b HPAI spillover event. This would need to be assessed within the specific context of an incursion. The US is not currently conducting active surveillance in beef cattle, pigs or small ruminants (APHIS 2024d). In the UK, risk-based surveillance is being conducted in mammalian species co-mingling with poultry on HPAI-affected poultry premises (HAIRS 2025).

3) To reduce impacts:

a) Response strategies in non-avian species should be considered now (i.e. before an outbreak) and clearly communicated so that industries can better understand the likely impacts of potential control measures.

b) Consider the use of personal protective equipment (PPE) (e.g. gloves, apron, respiratory protection and eye protection) in certain circumstances (such as managing sick animals) to reduce the risk of human infection.

c) Do not consume raw milk, colostrum or raw milk products from small ruminants.

Appendix A: Influenza virus nomenclature

There are 4 types (genera) of influenza viruses: A, B, C and D (MacLachlan et al. 2017):

1) IAVs infect birds and some mammals, as well as causing seasonal flu in humans.
2) Influenza B viruses also cause seasonal flu in humans and can infect certain mammal species, but not birds.
3) Influenza C viruses infect humans and pigs.
4) Influenza D viruses infect pigs and cattle.

Within the IAVs, viruses are frequently grouped by either 1) their pathogenicity in domestic poultry (i.e. HPAI and LPAI), or 2) based on the key surface proteins of the virus, haemagglutinin (H) and neuraminidase (N). There are currently 18 recognised H types and 9 recognised N types (Sreenivasan et al. 2019). While all H subtypes can exist as LPAI viruses, only H5 and H7 can become HPAI viruses (MacLachlan et al. 2017).

Within a given IAV subtype (e.g. H5), there can be many different lineages or clades (e.g. clade 2)—that is, not all H5s are the same. Over time, as these lineages continue to transmit and evolve, these clade names can be made more specific (e.g. clade 2.3.4.4b). Importantly, these lineage or clade names only refer to the H genetic segment. Because influenza viruses are segmented viruses, as well as mixing the H and N genetic segments they can also mix the other 6 segments. This mixing in IAVs is referred to as reassortment and 'mixed' viruses are referred to as reassortants.

An IAV *genotype* refers to the full gene constellation of all 8 genetic segments. That is, clade 2.3.4.4b represents many different gene constellations, all with the same clade 2.3.4.4b H segment. While many biological properties of IAVs depend primarily on the H gene segment (e.g. receptor binding, antibody and vaccine evasion), biological properties can also vary between genotypes due to variation in the other genetic segments.

For further detail on IAV nomenclature and evolutionary history, see 'Risk of high pathogenicity avian influenza to Australian dairy cattle: Literature review'.

Appendix B: Research gaps identified for clade 2.3.4.4b HPAI in dairy cattle

- How does clade 2.3.4.4b HPAI enter the cattle host?
    - Is virus infectious via the oral route, respiratory route, contact with conjunctival membranes, direct intramammary inoculation?
    - What is the minimum infectious dose and probability of infection via each route of entry?
    - Does disease severity vary depending on route of entry and/or infectious dose?
- Under Australian conditions, what are the relevant transmission pathways between lactating cows?
    - How much raw milk are cows exposed to at milking via the different entry routes in Australian dairies (e.g. intramammary vs aerosol vs oral)?
    - What are the sources of intramammary exposure (e.g. milking cups/liners, gloves/hands of dairy workers, intramammary treatments) in Australian dairies? What proportion of farms automatically flush clusters and liners between cows?
    - Is infectious virus present in aerosols in Australian milking sheds? This may indicate whether hosing down is a transmission risk. How do virus concentrations in milking shed air change over the course of a milking session?
    - How frequently are Australian dairy cattle exposed to milk from mastitic animals? For example – how often are mastitic animals separated from the main herd? How often are they milked last? What enhanced hygiene is used following milking of mastitic animals? The on-farm assessments in the current project were conducted at a higher level and did not interrogate this level of detail.
    - What is the incidence of milk leakage in Australian dairy herds?
    - What other secretions/excretions contain infectious virus apart from milk? For example – respiratory aerosols vs droplets, oronasal secretions, urine, blood. What are the peak virus concentrations in relevant secretions/excretions? How do virus levels change over time? Is shedding continuous or intermittent? How do shedding dynamics change in subclinical vs clinically infected cows?
    - How long does infectious clade 2.3.4.4b HPAI persist in the Australian environment on relevant matrices? Or more specifically, what is the rate of loss of infectivity in different sample types on different matrices under different environmental conditions (e.g. temperature, humidity, UV exposure)? For example – on pasture, in the dairy shed, on concrete, on typical bedding materials, on feed pads, in water troughs, on hay, in concentrates.
    - What range of virus concentrations could be expected in effluent during an HPAI outbreak? How long does infectious clade 2.3.4.4b HPAI persist in effluent under typical Australian conditions? What is the frequency of contact with effluent and duration of exposure on Australian dairy farms? This could be via direct contact

with effluent ponds or run-off or after spraying on pasture if infectivity is shown to persist.
  - How frequently are lactating cows moved between premises? What are the movement patterns/networks for lactating dairy cows between Australian dairy farms? It is unclear whether beef and dairy movements, and movements of lactating versus non-lactating cattle, can be easily distinguished in NLIS data; if not, this needs to be addressed in the system.
  - How frequently is raw milk/whey fed to adult dairy cattle?
  - How frequently is raw milk moved between Australian dairy premises?

- What risk do non-lactating cattle and calves pose to milking cows?
  - We know these groups can be infected, but how can we minimise infection rates in these groups?
  - How frequently are calves fed milk from mastitic cows in the Australian context? What are the barriers to treating milk (e.g. pasteurisation, acidification) prior to calf feeding in the Australian context?
  - How are dry cows exposed, given the main transmission route between lactating dairy cows is thought to be via intra-mammary inoculation at milking?
  - Once infected, what are the infection dynamics of clade 2.3.4.4b HPAI in these groups? What secretions and excretions are infectious? What are the peak virus concentrations in relevant secretions and excretions? How do virus levels change over time? Is shedding continuous or intermittent? What is the duration of viral shedding? Can they develop clinical disease? What are the risk factors for developing clinical disease?
  - If non-lactating cattle and calves are shown to be a transmission risk, what are the movement patterns and networks between Australian dairy farms?

- What risk do wild birds pose to Australian dairy cattle?
  - What are the infection dynamics of clade 2.3.4.4b HPAI in wild birds relevant to the Australian context? These may include Australian waterfowl, ibis, corvids, psittacines (e.g. cockatoos, corellas, galahs), small passerines (e.g. swallows, sparrows, starlings, mynas, pigeons, doves), raptors, gulls and terns. What are the peak virus concentrations in faeces versus oropharyngeal samples? How do virus levels change over time? Is shedding continuous or intermittent? How long are different species infectious for? How do shedding dynamics change in subclinical versus clinically infected birds? What are the risk factors for clinical versus subclinical infection?
  - How long does infectious clade 2.3.4.4b HPAI in wild bird faeces persist in the Australian environment in different matrices?
  - Regarding mechanical carriage by wild birds (e.g. following potential exposure to raw milk), how long does infectious clade 2.3.4.4b HPAI persist on feathers?
  - How frequent is direct contact between cattle and wild birds in the Australian context? How frequently would Australian dairy cattle consume a wild bird

carcass? How frequently would wild birds be exposed to raw milk? These questions were explored in the on-farm assessments, but results were limited to the 25 visited premises.

- What risk do domestic poultry pose to Australian dairy cattle?
  - Can we rule out domestic poultry as a spillover pathway in the US? Sequences or samples from US poultry outbreaks between September 2023 and January 2024 could be requested from US authorities and phylodynamic analysis may be able to rule out domestic poultry as the spillover host.
  - How frequently are cattle exposed to domestic poultry in the Australian context? This includes direct contact with poultry and indirect contact, such as via people, equipment or vehicles contaminated with poultry faeces or dander or exposure to poultry litter. Do contact rates vary by poultry species? For example – ducks may be subclinically infected and therefore shed virus for longer periods. These questions were explored in the on-farm assessments but results were limited to the 25 visited premises.
  - Do plumes from infected poultry houses contain sufficient infectious virus to infect dairy cattle? Over what distance?
- What risk do non-human mammals pose to Australian dairy cattle?
  - Can infected mammals transmit infection onwards (i.e. are they biological vectors or only mechanical vectors)? Relevant species in the Australian context include cats, rodents, peri-domestic wildlife (e.g. foxes, deer, kangaroos, wallabies, bandicoots, rabbits/hares, possums, quolls, echidnas, Tasmanian devils).
  - What are the infection dynamics of clade 2.3.4.4b HPAI in mammals relevant to the Australian context? What secretions and excretions contain infectious virus (particularly faeces)? What are the peak virus concentrations in relevant secretions and excretions? How do virus levels change over time? Is shedding continuous or intermittent? How long are mammals infectious for? How do shedding dynamics change in subclinical versus clinically infected mammals? What are the risk factors for clinical versus subclinical infection?
  - How frequently are Australian dairy cattle exposed to the relevant species (or secretions and excretions)? What is the duration of exposure? How frequently would Australian dairy cattle consume a mammal carcass? The on-farm assessments in the current project were conducted at a higher level and did not interrogate this level of detail.
  - How long does infectious clade 2.3.4.4b HPAI persist on fur/skin?
  - Regarding mechanical transmission, how frequently would different mammal species be exposed to infectious secretions andexcretions from cattle (e.g. raw milk)?
- What risk do people pose to Australian dairy cattle?

  - Can infected people transmit infection onwards (i.e. are they biological vectors or only mechanical vectors)?
  - What are the shedding dynamics of clade 2.3.4.4b HPAI in infected people? What secretions and excretions contain infectious virus? What are the peak virus concentrations? How do virus levels change over time? How long are people infectious for? How do shedding dynamics change in subclinical versus clinically infected people? For example – would it be transmission be reduced by limiting people with flu-like symptoms from working with cattle?
  - How long does infectious clade 2.3.4.4b HPAI from cattle secretions/excretions persist on skin, clothing, footwear, hair?
  - How frequently do high-risk people (e.g. those that have had contact with infectious cattle secretions and excretions) move between dairy farms without changing clothing and/or showering? What are the movement patterns/networks for people between Australian dairy farms?

- What risk do vehicles and fomites pose to Australian dairy cattle?

  - How frequently are milk tankers, other vehicles and different categories of farm equipment contaminated with raw milk (or other infectious cattle secretions and excretions)?
  - How long does clade 2.3.4.4b HPAI from cattle secretions/excretions persist on relevant fomites?
  - How frequently are high-risk vehicles or fomites (i.e. those that may have had contact with infectious cattle secretions/excretions) moved between Australian dairy farms? How frequently and through which pathways are cattle exposed to high-risk vehicles or fomites? For example – crossing tracks that vehicles have driven on vs being drenched with the same equipment. The on-farm assessments in the current project were conducted at a higher level and did not interrogate this level of detail.
  - How frequently is there spillage of milk from milk tankers in the Australian context?

- How can we minimise the impacts of clade 2.3.4.4b HPAI infection in Australian dairy cattle?

  - What host factors influence resistance to infection in the Australian context? For example – can we boost innate immunity to increase resistance to either infection?
  - What factors influence disease severity (and duration) in lactating dairy cattle in the Australian context? For example – virus dose, route of infection, host genetics, physiological characteristics, environmental factors (e.g. concurrent heat stress), co-infections with endemic pathogens.
  - What are the long-term impacts of clade 2.3.4.4b HPAI infection in dairy cattle? What are the impacts on future milk production? Are long-term impacts observed if cattle are infected in the dry period? Are there impacts on fertility? Does infection increase susceptibility to endemic pathogens?

- What are the optimal isolation and treatment protocols for clinically affected animals in the Australian context to minimise production losses?
- What are the optimal methods for early detection of clade 2.3.4.4 HPAI in Australian dairy cattle? For example – physiological monitors such as boluses or rumination collars, point-of-care testing and on-farm surveillance.
- What are appropriate disinfection and decontamination protocols for different matrices in the Australian context? For example – which approved disinfectants effective against clade 2.3.4.4b HPAI? Can milk for disposal be effectively inactivated on-farm (e.g. acidification)?
- Is consumption of raw milk and raw milk cheeses a transmission risk to humans?
- While clade 2.3.4.4b HPAI vaccines are being evaluated for dairy cows in the US, do these vaccines protect Australian dairy cattle from either infection or clinical disease?

Glossary

Term	Definition
AUSVETPLAN	Australian Veterinary Emergency Plan
DA	Dairy Australia
DIVA	differentiation of infected and vaccinated animals
EAD	emergency animal disease
EADRA	Emergency Animal Disease Response Agreement
EU	European Union
FAO	Food and Agriculture Organization of the United Nations
FMD	foot-and-mouth disease
HA/H	haemagglutinin, an IAV gene and protein
HPAI	high pathogenicity avian influenza
HTST	high-temperature short-time
IAV	influenza A virus
LPAI	low pathogenicity avian influenza
NA/N	neuraminidase, an IAV gene and protein
NAHLN	National Animal Health Laboratory Network
NASOP	nationally agreed standard operating procedures
NMTS	national milk testing strategy
PPE	personal protective equipment
RAT	rapid antigen test
RT-qPCR	reverse transcription quantitative polymerase chain reaction
$TCID_{50}$	50% tissue culture infectious dose
TMR	total mixed ration
USDA	US Department of Agriculture
WOAH	World Organisation for Animal Health

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