Surveillance for farm-to-farm wind dispersion during outbreaks of highly pathogenic avian influenza in southeastern Australia: from integrated research to decision-making

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Summary

Although spatio-temporal clustering of outbreaks of highly pathogenic avian influenza has been consistently observed, there is little agreement as to the exact transmission mechanism. This in turn creates challenges in developing and implementing efficient surveillance. Building on advances in atmospheric dispersion modelling, a structured, modular approach ("SPREAD-HPAI") was developed which should enable veterinary authorities to define the epidemiological and atmospheric conditions under which farm-to-farm wind dispersion (FFWD) occurs. However, a challenge is the lack of fundamental research on which to base model parameters, and to overcome this we present a framework which serves to both identify research priorities and to assemble the interdisciplinary team needed to resolve the uncertainties.

Introduction

Outbreaks of highly pathogenic avian influenza (HPAI) in Australian commercial poultry have a unique virology, all being caused by distinct lineages of H7 strains [2]. These strains have been shown to circulate in the low pathogenic form in wild ducks in Australia with sporadic spillovers to commercial poultry [3]. Previously these spillovers were sporadic and confined to only one or two infected premises (IPs). However, in recent years these outbreaks have increased in frequency and seriousness, particularly with respect to farm-to-farm spread within defined spatio-temporal clusters.

The exact pathway of transmission of the HPAI viruses between farms is uncertain, as the secondarily infected premises (IPs) have generally had in place high standards of biosecurity. There is evidence, albeit somewhat anecdotal, from field investigations of outbreaks in Europe and North America of the role of windborne fine dust aerosols as a transmission pathway [4]. However, confirming farm-to-farm wind dispersion (FFWD) has proved challenging using conventional field sampling [5]which indicates the need for novel approaches. Herein we describe the development of a holistic approach which combines field epidemiology, laboratory investigative experiments and integrated epidemiological-environmental modelling with the goal of arriving at outbreak surveillance system to inform farms at risk of aerosol transmission and to inform infected premise (IP) management to minimise risk of onward transmission.

Methods

The development of a FFWD surveillance system for HPAI outbreaks is an evolving series of projects which has as its origin the investigation of an outbreak of HPAI H7N7 in southern Victoria in July/August 2020. This outbreak involved 3 IPs, with the virus being detected in IP2 and IP3 within three weeks of that in the index IP. All three IPs had a high standard of biosecurity and whilst the pathway of infection of IP3 is uncertain, integrated environmental and epidemiological modelling provided evidence that a plausible pathway of infection of IP2 was FFWD, with the latter conclusion supported by a network analysis of full viral genomes collected during the outbreak [1].

Further outbreaks of HPAI occurred in both Victoria and New South Wales in 2024, during which there was a general consensus between both the industry and veterinary authorities that FFWD might have been responsible for transmission to some of the secondary IPs. This led the industry, via its research funding body, Australian Eggs, to request an investigation into aerosol spread during destruction and disposal on HPAI-infected farms in an outbreak response. Industry is now funding integrated studies to quantify the emission of fine dust aerosols from sheds at end-of-production (field study) and the viability of HPAI virus in shed litter substrates under different environmental conditions (laboratory study) to improve understanding of factors that prolong virus viability within layer sheds.

The findings of these studies will subsequently be integrated in the epidemiological-environmental modelling framework *SPREAD-HPAI* to investigate the epidemiological and atmospheric conditions which favour farm-to-

farm wind dispersion (FFWD).

Results

At the outset of the investigation of the farm-to-farm transmission of H7N7 HPAI in Victoria in 2020 outbreak, a literature review revealed that there was little consensus amongst virologists on whether aerosol transmission of avian influenza virus might occur over inter-farm distances of 1-10 km. Nevertheless, there was a broad agreement in the aerobiological community that a suitable approach for investigating windborne dispersion of pathogens was to define three sequential stages, *viz*. “emission”, “transport” and “deposition” [6]. This approach was built into an integrated field and genomic epidemiology system to investigate farm-to-farm transmission of foot-and-mouth disease virus (FMDV), which we had formalised into a software application *SPREAD* (System for Preparedness and Response to Emergency Animal Disease) [7]. *SPREAD-FMD* provided an exemplar to develop *SPREAD-HPAI*. Given the urgency to resolve the role of FFWD in the transmission of HPAI during outbreaks in Australia, initial investigations with *SPREAD-HPAI* involved a global sensitivity analysis to guide research priorities, which identified the potential impact of culling operations on the production of fine dust (Figure 1a).

Now, our studies are underway, with field sampling that has quantified the production of fine dust (PM10 and PM2.5) during routine culling of layer hens and litter disposal at the end of production (Figure 2), activities which approximate the impact of depopulation, disposal and decontamination during the management of a HPAI outbreak. The associated laboratory study is studying the impact of environmental conditions - principally temperature and humidity - on the viability of avian influenza viruses on litter substrates.

Discussion

During the past 50 years, considerable progress has been made in developing efficient surveillance systems for production animal diseases [8]. However, there remain disease scenarios which continue to be problematic. Most obvious is where there is the lack of a sensitive diagnostic test for diseases with long incubation periods, but a second challenging problem arises where the transmission pathway is variable and/or uncertain. With regards to the specific example of HPAI this uncertainty is well illustrated from a recent investigation of H5N1 2.3.4.4b outbreaks during 2022-23 in British Columbia, wherein integrated field and viral genomic epidemiological investigations were not able to assign the transmission pathway for the majority of the 127 infected commercial premises [9]. Rather, for 82 of the IPs, the pathway was assigned to be “local spread” which was defined as occurring if a secondary IP was genetically and spatially connected but no epidemiological links were identified. The exact transmission pathway for local spread could not be further defined, and although windborne spread was listed as one of these mechanisms, this was not specifically assessed due to limitations in available weather data and microclimates in the Fraser Valley, the principal affected site.

In the case of the relatively small H7N7 HPAI cluster in 2020, initial investigation encountered the same problem of not having weather data at a high spatio-temporal resolution, but this was resolved by engaging with climatologists and pollutant dispersion modellers. Combining weather data with a high-resolution atmospheric dispersion model, enabled hourly simulations at a very high spatial resolution. The results from this dispersion modelling were instructive showing that potential transmission of virus by FFWD might occur for only one or two hours in a day. By contrast, investigation limited to averaged daily wind directions - as has been used by comparable investigations [10]- would have incorrectly concluded that FFWD was unlikely.

Having demonstrated that FFWD was plausible, the next step was to determine if it was the probable pathway. Undertaking a sensitivity analysis of the SPREAD-HPAI output demonstrated the overriding importance of the concentration of contaminated dust into downwind farms. This requires that we develop a model for fine dust emission from poultry sheds which also accounts for the viability of the virus on the surfaces from which the fine dust is produced. We are now achieving this by the combined expertise of a team of domain specialists, *viz*. aerobiologists familiar with dust sampling and virologists experienced with the culture of avian influenza viruses, along with experts in poultry health, epidemiology and biosecurity who have strong industry linkages.

At this stage (April 2026), the field and laboratory work is still too preliminary to make definitive conclusions. However, what is recognised by both the industry and the funding bodies is the benefit of using a modelling framework to define the most important research gap and to specifically assemble interdisciplinary teams of domain specialists who can apply their knowledge and expertise to enable field and laboratory studies. This experience suggests that this might be a useful and generalisable approach for complex surveillance and disease control problems (Figure 1b).

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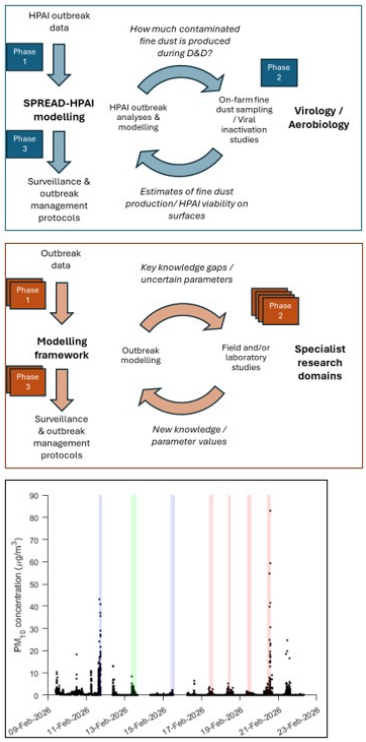


Figure 1a. Schematic of the research path for developing an integrated research framework and enhanced surveillance for managing farm-to-farm wind dispersion of contaminated dust aerosols in commercial layer flocks. Figure 1b. Generalised framework for developing an integrated research surveillance system. This generalised framework may go through a number of iterations which, with increasing knowledge, can lead to a "virtuous cycle". Figure 2. Field sampling of fine dust (PM10) from a commercial layer shed during routine end-of-lay depopulation and decontamination. Blue are cull periods, green is dry cleaning and red is manure removal.

Keywords: Farm-to-farm windborne dispersion, Highly pathogenic avian influenza, Integrated surveillance system.

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