Modeling long-distance airborne transmission of highly pathogenic avian influenza carried by dust particles

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Abstract

Highly pathogenic avian influenza (HPAI) is continuously causing significant economic losses with massive depopulations. Airborne transmission of HPAI was suspected, as initial bird mortalities were reported near air inlets of poultry houses. In addition, infected farms were distant, indicating that the viruses carried by dust particles might help the viruses travel for long distances in the environment. The objective of this study focused on simulating the airborne transmission of HPAI by using computational modeling to assess the risk of airborne and deposited avian influenza (AI) carried by poultry-litter dust particles. The Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) modeling was used in this study. Data from 168 infected cases in the mid-western area of U.S. were obtained from the Animal and Plant Health Inspection Service (APHIS) and Watt Poultry. The concentration simulation modeling was performed to estimate the airborne and deposited AI concentration carried by PM2.5 dust particles. Results showed that concentrations of airborne AI, deposited AI, and combined AI transmitted to other farms in a day were lower than the minimal infective dose for poultry. In most of the scenarios, the predicted probability of infection showed that Iowa-infected farms and turkey poultry houses had the highest infection probability. The findings may provide an understanding of the risk of airborne HPAI virus carried by dust particles and suggest the factors that influence long-distance airborne transmission.

Keywords: Airborne transmission, dust particles, highly pathogenic avian influenza, HYSPLIT modeling, poultry

Introduction

The U.S. poultry industry is among the world's largest poultry producers. It includes meat products from turkeys and broilers, and eggs from laying hens. The combined values of these products exceeded 35 billion U.S. dollars in 2020 (USDA-NASS, 2020). Poultry products are affordable and important sources of daily protein. In addition, about 18% of U.S. poultry products are exported annually, and the industry provides over 1 million jobs for national populations. However, this important industry is extremely vulnerable to infectious diseases caused by pathogenic microorganisms such as highly pathogenic avian influenza (HPAI). The HPAI virus is one of the biggest challenges facing the poultry industry. In 2015, an outbreak of HPAI in the Mid-Western U.S. resulted in a significant loss of over 50 million birds and 3.3 billion U.S. dollars (Torremorell et al., 2016). This showed the vulnerability of the U.S. poultry industry to viral infectious diseases such as HPAI.

Avian influenza (AI) or bird flu refers to the infectious disease caused by the infection of type A avian influenza. These viruses are found in wild aquatic birds all over the world and can infect domestic poultry as well as other bird and mammal species. Although avian influenza A viruses can infect wild aquatic birds' intestines and respiratory tracts, other species, such as wild ducks, may not become ill. Avian influenza A viruses, on the other hand, are highly infectious among commercial poultry, and some of these viruses can sicken and even kill certain domesticated bird species such as chickens, domestic ducks, and turkeys. As of November 2022, approximately 50 million birds including 265 commercial flocks and 358 backyard flocks have been affected by the 2022 AI outbreak (USDA-APHIS, 2022a). AI type A viruses can be found in infected

birds' saliva, nasal secretions, and feces. Transmission of the pathogen to naive (susceptible) birds can result from direct contact between birds or by indirect contact with virus-contaminated fomites (Swayne and Suarez, 2000).

In the poultry house, the major components of the air include gases, odors, and numerous pathogens carried by dust particles or droplet nuclei such as AI viruses. AI viruses are first secreted via birds' nasal secretions, feces, and saliva. The bird secretions can either be dried and suspended in the air for a long period of time or deposit on the poultry litter surface. The deposited secretions which carry AI are then mixed with poultry litter particles and re-aerosolized into the air by dust bathing behavior of birds. Both droplet nuclei and dust particles that carry AI may then be distributed into the poultry house environment and transmitted from barn to barn via ventilation system and transport of air.

At susceptible farms, the AI can be sucked in through the ventilation system and be distributed inside the farms. The airborne HPAI viruses are then deposited onto the surface of poultry litter on which they can survive up to 5 days at 24° C (Kurmi et al., 2013). In previous studies, authors have reported that most airborne AI viruses are found in dust particles as small as 1 μ m – 5 μ m in size (Bertran et al., 2017; Zhou et al., 2016) at 0.5 m away from poultry housing. It is important to note the fine dust particles (or dust particles with diameters that are generally 2.5 μ m and smaller) can travel hundreds of miles. With the long dispersion range, the AI viruses carried by fine dust particles can be a possible transmission pathway of HPAI.

To determine the possibility of long-distance airborne transmission of HPAI carried by poultry dust particles, this study aims at simulating the airborne transmission of HPAI by using the Hybrid Single-Particle Lagrangian Integrated Trajectory model (HYSPLIT) to assess the risk of airborne and deposited AI carried by poultry litter dust particles. Compared to other models such as Computational fluid dynamics (CFD) which is also able to simulate the flow of the air, the advantage of HYSPLIT is to integrate the meteorological data into the model which improves the accuracy of the simulation.

Materials and methods

Infected farm data

Data from 168 infected cases in the U.S. were obtained from the Animal and Plant Health Inspection Service (APHIS) and Watt Poultry (WattPoultry.com). Each confirmed case datum included physical address, county and state, infection confirmation date, and the number of birds infected. In this study, 168 infected commercial poultry cases (72% of the national total of commercial farm infections) in the Mid-Western U.S. were focused on, and data from the period of February 08th, 2022 to May 22nd, 2022, were included in the model. The dispersion simulation modeling was performed to examine if the confirmed cases in the Mid-West received air from other farms before being infected and estimate the concentration of airborne AI received. The reason for selecting data from the commercial farms and excluding data from backyard farms in the Mid-Western area was that although the number of backyard flocks infected was higher than commercial flocks, the number of infected birds per backyard flock was significantly lower than the number of birds infected per commercial farm (USDA-APHIS, 2022a).

HYSPLIT model

The HYSPLIT model (Hybrid Single-Particle Lagrangian Integrated Trajectory model, National Oceanic and Atmospheric Administration, Washington, D.C., U.S) is a computer model used to compute air parcel trajectories, which determines how far and in which direction a parcel of air, and hence air contaminants, will move. HYSPLIT may also estimate air pollutant dispersion, chemical transformation, and deposition. In the study, the HYSPLIT model was used to simulate the air movement of $PM_{2.5}$ which carries AI to examine if the $PM_{2.5}$ particles travel passing through other farms before the farms became infected. The modeling also

computed the concentration of airborne and deposited AI carried by PM_{2.5} dust particles (or fine dust particles) in the farms. The AI survival time of 24 h at 28 °C and period of 21 days prior to the infection confirmation dates (Zhao et al., 2019) were applied in the modeling. Three different periods, namely 8 a.m., 4 p.m., and 12 a.m. were calculated separately to reduce the temporal wind speed and direction varied effects. Airborne and deposited AI were examined at the height of 6 m above ground level (m agl), considering the typical height of the poultry houses. The height of typical air inlets which is 1.5 m was applied in the model.

The concentration of airborne AI carried by $PM_{2.5}$ was assessed by using both default and ceiling input data in the HYSPLIT model. The AI concentration has been reported to be detected predominantly from fine dust particles (Zhou et al., 2016), and with the long range of transmission, the $PM_{2.5}$ size can be a big concern for public health. The default input data are collected from scientific references, and the ceiling data are hypothetical data that are designed to simulate the worst scenarios where the virus survive longer and travel for a longer distance. The required parameters were provided in Table 1.

Parameter	Unit	Value
Total run time per cycle	h	24
Trajectory modeling direction	-	Forward
Top of the model	m	1,500
Incubation period	day	7 (USDA-APHIS, 2022b)
Virus emission duration	h	24
Height of concern	m	o-6 (airborne) & o (deposit)
		1 (laying hen) (Cambra-López et al., 2010; Li et al.,
$PM_{2.5}$ emission rate	mg/bird/d	2011; Shepherd et al., 2015)
		38 (turkey) (Cambra-López et al., 2010; Li et al., 2011; Shepherd et al., 2015)
PM density	g/cm³	1.5 (Rosenthal et al., 2007)
PM deposition velocity	m/s	0.001 (PM _{2.5}) (Lin et al., 1994)
Half-life	day	1.0/1.5 (default/ceiling) (Shaman and Kohn, 2009)
Percentage of manure in dust	%	5 (laying hen) (Cambra-López et al., 2010; Zhao et al., 2014) 40 (turkey) (Cambra-López et al., 2010; Zhao et al., 2014)
Viral shedding rate	Log EID ₅₀ /[g feces]	4/5 (default/ceiling) (Forrest et al., 2010)
Viral survival reduction	%	60 (after 24 h) (Kurmi et al., 2013)

Table 1: Input parameters used for concentration modeling in the HYSPLIT model.

Model processing

Forward concentration modeling was used to assess the possibility of infections from infected poultry farms to other farms. Data from168 infected farms from March 05th, 2022 to May 25th, 2022, in the Mid-Western area were utilized in the study. First, the AI data collected daily from APHIS and Watt Poultry websites were imported into HYSPLIT. The AI data were divided into four categories including default PM_{2.5}, ceiling PM_{2.5}, deposit default PM_{2.5}, and deposit ceiling PM_{2.5}. Default PM_{2.5} and ceiling PM_{2.5} stands for the airborne AI

concentration carried by PM_{2.5} with the default scenario and worst scenario, respectively. Deposit default PM_{2.5} and deposit ceiling PM_{2.5} are the AI concentration carried by PM_{2.5}, after being aerosolized, being deposited on the surface of poultry facilities with the default scenario and worst scenario respectively. Meteorological data was downloaded from the National Oceanic and Atmospheric Administration (NOAA, Washington, D.C., U.S.) website for each day. To reduce the variability of wind direction as well as meteorological data, the model is run every 8-hr interval which results in three trajectories covering the air arrival time at 8 a.m., 4 p.m., and 12 a.m. local standard time (LST). After processing the data, airborne AI concentration data collected from the model were then exported as kmz files which were then loaded in Google Earth Pro (Google LLC, Mountain View, CA, U.S.). With concentration data corresponding to the 4 scenarios and types of poultry farms would be reported. The modeled concentrations of AI were then compared to the minimal infective doses of airborne AI viruses and deposited AI viruses calculated based on formula (1) (2) and were utilized to assess the possibility of infection for each case.

Minimal infective doses for airborne transmission

Minimal infective dose for airborne transmission (MIDa) is the quantity of airborne AI (measured in EID_{50} m⁻³) that is necessary to cause infection in a healthy bird. The MIDa were calculated based on the general minimal infective dose (MIDt). MIDt were 10³ 50% egg infective dose (EID₅₀) for turkeys (Spackman et al., 2016) and 10^{3.5} EID₅₀ for laying hens (DeJesus et al., 2016). The same MIDa was used for laying hens, broilers, breeders, and pullets. The MIDa values were calculated by the following formula (1):

$$MIDa = MIDt \times \frac{1}{v \times r \times 24}$$
(4)

where MIDt is the general infective dose, EID_{50} ; v is the tidal volume of the bird, m³; r is respiratory rate, time h⁻¹; and MIDa is the Minimal infective dose for airborne transmission, EID_{50} m⁻³ for a day (24 hr).

Minimal infective dose for deposited (MIDd) AI is the quantity of deposited AI (measured in EID_{50} m⁻²) that is necessary to cause infection in a healthy bird. The same MIDd was used for laying hens, broilers, breeders, and pullets. The MIDd values were calculated by the following formula (2):

$$MIDd = MIDt \times \frac{1}{s}$$
(2)

where MIDt is the general infective dose, EID_{50} ; s is the area that a bird needs in the house, which are 0.11 m² per bird (or stocking density of 9 birds per m²) for laying hen (Krause and Schrader, 2019) and 0.3525 m² per bird (or stocking density of about 3 birds per m²) for turkey (Bartz et al., 2020), m² bird⁻¹; and MIDd is the Minimal infective dose for deposited AI viruses, EID_{50} m⁻² for a day.

Infection probability

The probability of farm infection (formula 4) is determined by the probability of individual-bird infection (formula 3) at a given dosage (d) and flock size (nf). We assumed that 95% of birds might get infected at the (d) dosage, θ was 0.00069 for turkeys and 0.00022 for laying hens (Zhao et al., 2019).

$$Pi = 1 - (1 - 9)^d$$
(3)

$$Ph = 1 - (1 - Pi)^{nf}$$
 (4)

where P_i is probability of individually bird infection, %; θ is probability of one ID₅₀ infect to bird, %; d is dosage of viruses exposed to a bird, EID₅₀ bird⁻¹ day⁻¹; P_h is is probability of farm infection, %; nf is size of flock, bird.

Results and discussion

Minimal infective doses

The infective dosage, lung capacity, breathing rate, and exposure duration were all used to compute the MIDa and MIDd. Lung capacity and respiratory rate in turkeys are 7.7×10^{-5} m³ and 2.4×10^{3} times h⁻¹, respectively, and 1.4×10^{5} m³ and 1.6×10^{3} times h⁻¹ in laying hens. Over a day of exposure, the resulting MIDa values were 210 EID₅₀ m⁻³ for turkeys and 5,880 EID₅₀ m⁻³ for laying hens. MIDd values were 2,837 EID₅₀ m⁻² for turkeys and 28,460 EID₅₀ m⁻² for laying hen.



(c)

(d)

Figure 1: Concentrations of airborne and deposit highly pathogenic avian influenza (HPAI) viruses at the recipient farms. The concentration of avian influenza (AI) viruses is reported according to two categories, scenario (worst or default) and transmission state (deposited or airborne). Concentration of (a) deposited AI viruses in worst scenario, 50% egg infective dose (EID50) m-2; (b) airborne AI viruses in worst scenario, EID50 m-3; (c) deposited AI viruses in default scenario, EID50 m-2; and (d) airborne AI viruses in default scenario, EID50 m-3. The blue solid line stands for the minimal infective dose of airborne AI (MIDa) values of turkey, the red dashed line stands for the MIDa values of laying hen, the red solid line stands for the MIDd values of turkey, and the green dashed line stands for the MIDd values of laying hen.

Viral concentrations in different types of poultry houses

The viral concentrations of AI in different types of poultry houses are reported in Figure 1. The figure shows the viral concentrations carried by $PM_{2.5}$ dust particles in 5 different types of poultry houses with 4 different

scenarios including deposit ceiling, ceiling, deposit default, and default. Results show that in all categories, the viral concentrations were lower than MIDa and MIDd lines. This implies that under all scenarios, these commercial farms are likely not to have received viral loads above their MIDa and MIDd. This suggests that there is little risk of sludge development under normal conditions.

The resulting hypothetical virus carried by PM_{2.5} concentrations generated by the HYSPLIT model was relatively low in all types of poultry farms. The concentration of airborne and deposited AI in these poultry farms are insignificant compared to their MIDa and MIDd values. It indicates that most recipient farms that get airborne AI from previous infected farms do not get enough viral dose to cause the AI infection. Compared to previous studies (Zhao et al., 2019), the authors also noted that the AI concentrations received by poultry farms from infected farms were relatively much lower than the MIDa and MIDd thresholds. When traveling through the air for a long distance, the AI virus can be greatly affected by outdoor conditions. This causes them to be inactivated extremely quickly. A previous study (Shahid et al., 2009) reported that the AI virus could live for more than 100 days at 4°C but was inactivated after 24 hours at 28°C and 30 minutes at 56°C. The outbreak of AI in 2022 happened in late spring and early summer when the temperature is typically above 25°C which can be a possible explanation for the short survival of the AI virus.

Infection probability

The farm infection probabilities of poultry farms that have received AI viruses from different locations in the Mid-Western area have been reported based on two categories, scenarios (default or ceiling) and transmission states (airborne or deposited). First, in the default scenario, deposited AI data show three remarkable results that Iowa, Nebraska, and South Dakota farms have 14.8%, 11.3%, and 7.5% chance of being infected by AI viruses from the previously infected farm from the Mid-Western area. Minnesota, Missouri, Oklahoma, and Kansas farms have unremarkable percentages with the highest infection probability of 1.7% of having the chance to be infected from the Mid-Western area. Airborne AI data in the default scenario show low infection probability that Iowa farms, South Dakota farms, Missouri farms, and North Dakota farms have 2.1%, 1.2%, 1.2%, and 0.6% chance to be infected. Kansas, Minnesota, Nebraska, and Wisconsin have lower than 0.5% of chance that can be infected by AI. The results of ceiling scenarios of airborne and deposited AI data show significantly high infection probabilities with the highest probability of 79.0% in South Dakota. However, the chance of the ceiling scenario happening is relatively low compared to the default scenario. The remarkable infection probabilities of deposited AI viruses imply that in the ceiling scenario, susceptible farms in South Dakota can be infected by AI viruses from previously infected farms with a probability up to approximately 79.0%.

Conclusions

This paper simulated the airborne transmission of HPAI by using HYSPLIT modeling to assess the risk of airborne and deposited AI carried by poultry-litter dust particles. Although the majority of poultry farms receive a relative viral load well below the MIDa and MIDd thresholds, the highest infection probabilities of airborne AI viruses in the ceiling scenario imply that susceptible farms in the surrounding Mid-Western area may have received airborne AI viruses from previously infected farms with the probability up to approximately 79.0% in South Dakota. In the default scenario, Iowa has the highest infection probability of 14.8%. However, the chance of the ceiling scenario happening is low compared to the default scenario. These findings provide insight into the possible role of the airtransmission of AI viruses between infected barns or facilities and the recipient farms.

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