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as a recognition for participating and presenting at the

International Conference on Environmental Research and Technology (ICERT) 2008

held on the

28 – 30th May 2008

at

Parkroyal Hotel, Penang, Malaysia

Organized by

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Proceedings International Conference on Environmental Research and Technology (ICERT' 08)

Environmental Technology for a Greener Tomorrow

28 - 30 May 2008
Parkroyal Penang,
MALAYSIA

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UNIVERSITI SAINS MALAYSIA

Editors:
Teng Thoon Tow
Fera Fizani Ahmad Fizri
Norli Ismail
Fazilah Arifin

ISBN 978-983-3986-29-3

ICERT 08

Proceedings of the International Conference on Environmental Research and Technology 2008
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Organised by:

School of Industrial Technology
Universiti Sains Malaysia
Penang, Malaysia

Distributed & Published by:

School of Industrial Technology
Universiti Sains Malaysia
11800 Minden
Penang, Malaysia
Tel: 04-6532119
Fax: 04-6573678
Email: icert@usm.my

Malaysian National Library Cataloguing-in-Publication Data

International Conference on Environmental Research and Technology (1st: 2008: Penang)
ICERT 2008: Proceedings of the International Conference,
Parkroyal Hotel,
28th-30th May, 2008 / Editor Teng Tjoon Tow ... [et al.]

ISBN 978-983-3986-29-3

1. Environmental management and policy
2. Environmental education
3. Environmental engineering
4. Environmental technology & process
5. Ecology & biodiversity
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MODELING OF EPIDEMIC TRANSMISSION OF AVIAN FLU

Tertia Delia Nova, Herman Mawengkang
Fakulty of Animal Husbandry, Andalas University

Abstract

Bird flu, or sometimes called avian flu, is an epidemic caused by H5N1 virus that primarily affects birds such as chickens, wild water birds, etc. These infuenza viruses occur naturally among birds. The transmission mode of avian flu can occur due to the spread from one farm to another farm of chickens or birds. This paper addresses a transmission model of avian flu taking into account the factors that affect the epidemic transmission such as source of infection, social and natural factors and various control measures.

1. Introduction

Bird flu also known as avian influenza is an infection caused by a virus known as orthomyxoviridae in virus classification . Influenza virus has only one species in it, which is called influenza A virus. These influenza viruses occur naturally among birds. Wild birds worldwide carry these viruses in their intestine but usually do not get sick from them. However, avian influenza is very contagious among birds and can make some domesticated birds including chickens, ducks and turkeys very sick and kill them [15,19,24,34]. Infected birds shed influenza viruses from their saliva, nasal secretions, etc. Susceptible birds become infected when they come in contact with the contaminated surfaces. Domesticated birds may become infected with avian influenza viruses through direct contact with infected waterfowl or other infected poultry [19,23,29] or through contact with surfaces (such as dirt or cages) or materials (such as water or food) that have been contaminated with the virus [1,12,30,35,37].

Infection with bird flu viruses in domestic poultry causes two main forms of disease that are distinguished by low and high extremes of virulence. The "low pathogenic" form may go undetected and usually causes only mild symptoms (such as ruffled feathers). However, the highly pathogenic form spreads more rapidly through flocks of poultry. This form may cause diseases that affect multiple internal organs and has a mortality rate that reaches 90–100% often within 48 hours [6].

Since 1997 when H5N1 spread from a bird to a human in Hong Kong, significant events have centered around this emerging international problem. These events include human deaths, culling infected birds, surveillance and control, emergency public health preparations, possible future pandemic, research, conferences and extensive news coverage. The avian (bird) influenza (flu) H5N1 infecting birds and a limited number of humans in some countries has again raised awareness about the link between the environment and human health. The avian (bird) flu viruses can be present in the intestinal tract of some wild birds. This evolutionary relationship usually does not cause a significant concern for the overall health of these wild bird populations. The concern heightened when domesticated

chickens, ducks and turkeys became ill and died with this contagious disease among birds. The destruction of domesticated birds used for human food has occurred in some countries to aid in preventing the spread of this disease. This has not been entirely successful. It is a challenge to cull 100% of the diseased domestic birds and implement quarantines in all necessary areas, especially if the disease is not immediately reported and infrastructure is not in place to deal with the problem and the extent of the problem is unknown.

Moreover, humans have died of this disease in numerous countries. Infected birds shed the virus particles in their fecal matter, saliva and nasal secretions. These virus particles contaminate the immediate environment and surfaces where other birds and humans can come into contact with the infectious virus particles. Especially humans working in poultry facilities on a daily basis or raising poultry in open environment conditions with humans in the same locations. Mortality is about 50% in humans. The spread of avian flu viruses [or mutated strain(s)] from human to human is a worldwide concern. If not controlled, the outcome could be one or more local outbreaks becoming a pandemic, with no vaccine available on a national and worldwide basis. The avian flu is an example of the complex relationships between viruses (requiring a host for replication) living organisms and contamination of our environment (our common biosphere) and the relationship between a pathogen and the one or more hosts it can infect. It is also an excellent example of the ability of infectious agents to spread throughout the environment or biosphere with the potential to mutate and become new strains. The recent events surrounding H5N1 also demonstrate the need for local, national and international surveillance, control procedures, vaccine development and testing, vaccine manufacturing facilities and distribution, anti-viral drugs, diagnostic methods for viruses and other infectious microorganisms, laboratory infrastructure, occupational and public health training, risk assessment and communication personal protection (e.g., hygiene, gloves, gowns, eye protection, respirators, high efficiency particulate air filtration, standard operating procedures, recognizing symptoms of illness, appropriate medical attention), biological research and international cooperation. These avian flu events also demonstrate that engineering infrastructure is required to properly disinfect animal wastes for disposal as well as the facilities the poultry is raised in.

The linkages between wild birds, their migration routes, domesticated poultry, the environment or our common biosphere and humans illustrates the need to research local, national and international pollution, especially with infectious microorganisms that are spread within and between species.

For more than two years, the virus has ravaged poultry and caused human illness and death in many Southeast Asian countries and China. Between April and June 2005, a large number of wild water birds at Qinghai Lake in western China perished after being infected by the virus. During, July–August 2005, outbreaks involving the virus were reported from Mongolia, Siberia and Kazakhstan. The virus reached Turkey, Croatia, Romania and Greece by October 2005. Ukraine reported outbreaks in November 2005. The virus was infecting chicken and humans in northern Iraq by January 2006. In early February 2006, Nigeria became the first African nation to report the bird flu virus, with an outbreak at a large commercial poultry farm. In February 2006, many European countries, Egypt and Iran found wild birds infected with H5N1 virus [9,11,12,18,21,31,33].

Avian influenza or bird flu can result in immediate and severe disaster, for example, the outbreak in USA [36] in 1983–1984 led to destruction of more than 17

million birds at a cost of nearly US $56 million [16]. Similar case again happened in Hong Kong in 1997–1998 [9,12,29,30,33]. Therefore rapid and effective measures must be taken to stop the spread of epidemics. The most effective measures to prevent the transmission of bird flu are rapid destruction of all infected or exposed birds, proper disposal of carcasses and excrement, the quarantining and rigorous disinfectioning of farms and timely use of vaccine [4,20,27,28,38]. The information relating to the spread of this epidemic in Canada may be obtained from the website [3].

In general, the influenza virus or flu virus can be classified into three categories: types A, B and C, which are distinguished by differences in two major internal proteins. Influenza virus type A is the most significant epidemiologically and the most interesting from an ecological and evolutionary stand point, because it is found in a wide variety of bird and mammal species [7,32] and can undergo major shifts in immunological properties. Type B is largely confined to humans and very little is known about type C. Type A virus is responsible for causing bird flu, which was first found in Italy in 1878. Type A virus is further divided into subtypes based on differences in membrane proteins HA and NA, which are the most important targets for the immune system. The notation HhNn is used to refer to the subtype comprising the hth discovered HA proteins and the nth discovered NA protein. The subtype H5N1 virus of type A virus is the main cause of the bird flu [9,12,18,25,33]. Subtype is further divided into strains; each genetically distinct virus isolated is usually considered to be a separate strain [8,26].

According to the research of World Health Organization (WHO), the transmission mode of bird flu can be divided
into following two types [16]:

- spread from one farm to another within a country and
- spread from country to country.

Generally, the virus resides in bird droppings, contaminated soil and airborne virus. Contaminated equipments, vehicles, food, cages and clothing like shoes can carry the viruses from farm to farm. Some evidence suggests that flies can also act as mechanical vectors [13]. Wet markets where live birds are sold under crowded and sometimes unsanitary conditions can be another source of spread. These constitute the main cause of the former transmission. Export and import of poultry products are the main cause of the latter transmission, since they can carry the viruses for long distances freely when artificial factors are prevented. Migratory birds can also be a cause of transmission between the countries [5,22]. Efforts have been made on the study of avian influenza and most of the recent papers focus on topics such as the route of transmission, physiological and biological properties, etc. The bird flu virus of low pathogenicity can mutate into highly pathogenic one after a short time; the virus is sensitive to temperature change (it was found that the virus survives for shorter time at a higher temperature). This kind of influenza is able to transmit to humans under some circumstances , however, no sufficient and clear evidences of human-to-human transmission have been found up to now [16].

Among these researches, an important approach to study bird flu is to establish a statistical transmission model, from which the general trends of epidemics can be predicted, and the effect of various control measures can be assessed [10].

In general, the outbreak of an infectious disease is dependent upon three necessary conditions as the source of an infection, the route of transmission and the herd susceptibility [16]. Other social and natural factors also play an important role in the transmission of infection, for example, the control measures and the change in

temperature. The source of infection that led to the outbreak is not clear. In some researcher's view migratory birds are thought to be carrying the virus [5,22]. So we consider in our problem the source of outbreaks of bird flu to be the transportation of infected poultry as globalization has turned the chicken into the world's number one migratory bird species. We have assumed that it is mainly the human activities of commerce and trade that this epidemic has spread. Also, we acquired some of the important information about bird flu such as, the virus H5N1 is sensitive to temperature changes, and the virus survives for shorter time at a high temperature. Also there are many effective control measures to block the virus transmission such as compulsory vaccination, culling of all infected or exposed birds [2].

2. Modeling bird flu

We know the major factors that play an important role in the transmission of bird flu are the way the infected poultry products are transported, air temperature, the control measures (for example, culling the poultry in the infected form, introducing compulsory vaccination to enhance the resistibility of poultry in the non-infected farms forbidding live birds being sold under crowded and unsanitary conditions, etc.), migratory birds and other infected transportation vehicles (which means the vehicles carry infected poultry or bird dropping or contaminated soil, etc.). Also there are some other factors not considered in our model, viz. bird flu transmitting to human beings, viruses of low pathogenicity mutating into high pathogenicity after some time, etc. since these elements will not contribute much to the usual transmission of bird flu [17].

How do these factors affect the transmission? The infected animals are the source of the infection, higher air temperature can drastically cut down the lifetime of the virus, and transportation of infected poultry is the route of transmission. Control measures such as active and effective actions play an important role in preventing and destroying the epidemics, which can effectively block the route of transmission of the infection, diminish the source of infection and promote the resistibility of susceptible poultry [16]. So we must take all the major factors into account in the formulation of our transmission model.

We define the following parameters:

$N(n)$ is the total number of regions of outbreak on the nth day.

$D(n)$ is the lifetime of the virus regarding the nth day since the beginning of the epidemic which implicitly corresponds to air temperature.

$I(n)$ is the resistibility of the poultry on the nth day since from the beginning of the epidemic many of the above control measures objectively promote the resistibility of poultry and even human beings.

$f(r)$ is the distribution of the probability that infected poultry products are transported a distance r.

The following are necessary assumptions for our model:

Let $P(n, r)$ represent the probability for a new outbreak to take place, then

$$P(n, r) \propto N(n),$$
$$P(n, r) \propto D(n),$$
$$P(n, r) \propto 1/I(n),$$
$$P(n, r) \propto f(r).$$

Considering the above assumptions, we obtain our proposed model for transmission of bird flu as under:

$$P(n,r) = f(r) \cdot R \cdot D(n) \cdot N(n) \cdot \frac{1}{I(n)} \quad (1)$$

where

$f(r) = r^{-(1+\beta)}$

β is taken close to 0.6 [17] and R is a reproduction number.

At every farm location, the (basic) reproduction number R can be calculated, which equals the expected number of secondary infections caused by one infected farm in the early stages of an epidemic. The good approximation of R is given by

$$R = 2\pi \int_0^\infty f(r) r dr$$

The integrand f(r) determines the contribution of farms at distance r to the reproduction number. If R <1, the pathogen is able to cause a major epidemic.

3. Methodology

In this section, we have discussed the methodology that we have used for simulation experiments. We first discuss, one by one the various parameters taken in our model. Also we explain, how we have computed these parameters and finally how we have given the methodology used to predict a new outbreak with the help of a flowchart suggested by Li et al. [16].

- In our model, we have used the random float number R which we have generated in our program by using random number generator. Why do we need R in our model? As we know the outbreak of bird flu is a probabilistic instance and not a deterministic one, even though $f(r)$, $D(n)$, $N(n)$ contribute much to $P(n, r)$, we cannot definitely assure that there will be a certain outbreak of bird flu in a region but can only say that there is enormous possibility or danger for an outbreak to take place. So an additional random parameter R is introduced to reflect the uncertainty.
- $D(n)$ denotes the lifetime of the virus of bird flu on the nth day. The H5N1 virus can survive at cool temperatures in contaminated manure for at least three months; in water, the virus can survive for up to 30 days at 0° C; about four days at 22° C; about 3 hours at 56° C and only 30 min at 60° C [16]. By means of fitting the above data by curve fitting method, we obtained an approximate formula as follows:

  $D(t) = e^{3.4-0.0915t^{1.1}}$ (2)

  where t represents the air temperature.

  Hence the temperature change may be taken as a linear approximation regarding the epidemic duration, that is,

  $t(n) = t_1 + t_2 n$ (3)

  in which t_1 and t_2 are two constants that can be determined by fitting the average temperature of the various countries through which the virus reached India. In this model $t_1 = 0.2$ and $t_2 = 2.2286$. So the relation between the lifetime of the virus and the epidemic duration shall be a compound form of (2) and (3) as

$$D(n) = e^{3.4-0.0915(0.2+2.2286n)^{1.1}} \quad (4)$$

- I (n) stands for the resistibility of poultry on the nth day. Obviously the resistibility will increase with the artificial interventions and the control measures. We assume the increase abides by law similar to Sigmoid function $1/(1 + e^{-x})$.
  Thus $I(n)$ assumes the following form:

$$I(n) = \frac{B}{1+(B-1)e^{-n/C}} \quad (5)$$

  Apparently, this is a modified sigmoid form. When $n = 0$, $I(0) = 1$, and when $n = \infty$, $I(n) = B$; which indicates the resistibility is impossible to approach a very big number [16].
- $f(r)$ is the distribution of the probability that infected poultry products are transported a distance r. The basic idea for taking the above mentioned form of $f(r)$ stems from Howlett [14]. Since the poultry products are also imported and exported very frequently, to various countries, we can assume its transport to be very similar to the human movement. So the probability that
  $f(r) = r^{-(1+\beta)}$
  infected poultry product is transported from the farm may assume a distance r, for r larger than 10 km with close to 0.6.
  This distribution behaves like a power law. This function decreases as r grows larger, meaning that transportation of poultry over a long distance is less common than short ones. However, it does not decrease as fast as other common probability distributions, which means that transportation over long distances are still common enough to have a significant effect. Poultry products make many short journeys, but the occasional long haul ensures that they disperse widely.
- A threshold value S is necessary which acts as a criterion: when $P(n, r)$ is greater than S there will be an outbreak; otherwise not. However, how to determine the possible number of outbreaks per day denoted by $K(n)$? Intuitively, $K(n)$ shall be in direct proportion to $N(n)$; however, since only the nearest several outbreaks have notable contribution to the probability of a new outbreak a number of distant outbreaks contribute little, so dependent relation of $K(n)$ upon $N(n)$ is of the form [16]

$$K(n) = A\,N(n)^b \quad (6)$$

  where $A \geq 1$ and $0 < b << 1$, that is, $K(n)$ increases slowly with the augment of $N(n)$.

We provide a short description of the algorithm. Suppose the epidemic has begun, we compute the number of actual outbreaks on the nth day. First we generate $K(n)$ according to (6). Then we calculate each $P(n, r)$ according to (1); when $P \geq S$, a new outbreak will take place, otherwise not. So, the total number of new outbreaks is always less than $K(n)$.

In our model, there are six parameters β, A, b, B, C and S which are all adjustable. So one may argue that too many adjustable parameters may not be an advantage for a "good" model. However, we must analyze independence of these parameters. Here S is not an independent parameter, rather dependent on $f(r)$, hence on β. Parameter A controls the initial possible number of outbreaks the epidemic may abort if A is too small and overflow if A is large. So there shall be a proper intermediate value for A. b denotes the general trend of the outbreaks, the total number of outbreaks will grow too rapidly to be practical if b is a big number and may be too flat if b is too small. B determines the

ultimate resistibility, which reflects the final degree of stringency of artificial interventions; the greater B is the more stringent the interventions are. As of C, it reflects the average degree of stringency throughout the epidemics; the smaller C is the more stringent the control measures are. In other words, B determines the final height of the curve $I(n)$ and C controls the shape or the process of $I(n)$.

Therefore each parameter has a definite meaning and a specific role and has little overlap regarding the role, so the model is reasonable.

4. Conclusions and discussion

Bird flu is a highly pathogenic epidemic that can result in serious disaster in many areas. Immediate and effective control measures are of great importance in preventing the transmission of avian influenza. So it is challenging to study it from various angles, and develop statistical–mathematical transmission models [16]. In this research, we put forward a statistical transmission model, which exhibits satisfactory results verified through simulations. These results may be used for the prediction of the future situation of the epidemics. Meanwhile (as many control measures have been taken into account in the formulation of the model) if the actual effect of these measures are assessed, then useful and effective control measures can be proposed for the prevention of the epidemic. Our ongoing investigations relate to the question of how to assess the actual control measures and assign the parameters in the model with proper numerical values.

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