

Global GIS model on Avian Influenza in Humans

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Avian Influenza is a virus among birds that poses a great threat to humans. Experts believe that when this virus becomes anthroponotic (human to human transmittable), it may infect 20-50% of the total human population and result in 2-50 million deaths. The goal of this project is to create a solid knowledge base and to facilitate the development of a collaborative real-time geospatial model to identify geographic areas that may be susceptible to future AI outbreaks. Human case study data will be analyzed using Geographic Information System (GIS) technology, a computer-based tool that is commonly used for mapping and interpreting data. Most of the documented human and animal case studies available in the public domain (online) have been collected. A preliminary model has been constructed using human and animal case study and data sheets such as: population density, poultry density, swine density, major wetlands, migratory routes of key reservoir species and geospatial data. The collaboration of various international agencies may be needed for a project of this magnitude. This is an ongoing project that will provide insight into the transitory mechanisms of this disease.

Introduction/Background

Avian Influenza (AI) is a virus that can infect all types of birds. This virus may cause severe respiratory disease, which often results in death, depending on the resistance of the species infected. Waterfowl, such as ducks, have a very high resistance to disease and are thus able to live normally when infected, displaying little or no symptoms. They are the natural reservoirs of the virus and are the common source of distribution. The transitory mechanisms of AI are not exactly known; however, it is suspected that direct contact, nasal and ocular discharges, and fecal matter, which may contaminate water sources or be caught in air blown soil particles, are responsible for the propagation of this virus.

Avian influenza, in its native form, should not be able to infect humans (because of the differences in influenza receptors between species), although there have been several instances that have proven otherwise. The first documented case of a direct transmission from poultry to humans was in Hong Kong, 1997, when 6 out of 18 people died from severe respiratory disease. There have been a dozen or so of these sporadic small-scale breakouts since 1997 that have mainly appeared in Southeast Asia, although human infections have also taken place in the Netherlands (H7N7, 2003), and Canada (H7N3, 2004).

Avian Influenza is divided into a number of subtypes classified by two surface proteins: hemagglutinin and neuraminidase. Currently, 15 hemagglutinin and 9 neuraminidase proteins have been identified and are the basis for the nomenclature, i.e. H7N1, H5N1, etc. Hemagglutinin functions as the attachment protein that allows the virus to bind to the host cell. Neuraminidase is the enzyme that releases the virus into the

cell in order for it to replicate and frees it from the cell after replication so that it can repeat the infection process.

The pathogenicity of an AI strain depends on the hemagglutinin present. Hemagglutinin is synthesized as a precursor and requires post-transcriptional modification by host proteases before it becomes functional. This cleavability allows the virus to produce infectious particles and thus determines the pathogenicity. This is the reason why only a few strains are highly pathogenic, most notably H5 and H7. High pathogenic AI causes a severe and highly contagious illness marked by mortality approaching 100%. In contrast, low pathogenic AI is widespread in wild birds and causes only a mild respiratory disease in domestic poultry.

The genome of the virus consists of eight segments of single-stranded reverse RNA. The segmented nature allows for reassortment of genes when a host is infected with two different influenza virus subtypes. Novel strains can be produced, which introduces serious implications for humans. For example, a person could be infected with AI and a human strain of influenza at the same time. Theoretically, an AI virus with a hemagglutinin (against which humans have little or no immunity) that reassorted with a human influenza virus (highly contagious) could result in a highly virulent and contagious strain of AI.

Outbreaks of highly pathogenic AI have had devastating impacts on the poultry industry as well as the general population. For example, an outbreak of HPAI in 1983–1984, confined mostly to Pennsylvania, resulted in the destruction of more than 17 million birds at a cost of over \$63 million in Federal funds and an additional \$350 million

in increased consumer costs. In 1918-1920, an estimate of 50 million people died from an outbreak (H1N1) dubbed the Spanish flu. The World Health Organization called it "the most deadly disease event in the history of humanity," killing more than even the Bubonic Plague of 1347-1351. Two other pandemics occurred in 1957 and 1968 that claimed more than 100,000 American lives.

In the past two years there have been 108 human infections in Southeast Asia, from which 54 people have died. Although the death toll has steadily decreased, there are a number of disturbing trends that are emerging. One such trend is the clustering of human infection, commonly within the same family. According to Professor Osterhaus, this could mean the virus is becoming more efficient at infecting humans. Another ominous trend is the drop in the death rate. This is an indication that the virus is mutating to become more "user friendly to the host". The rationale is that if the host dies, the virus also dies. To propagate, viruses often become less virulent as a tradeoff for more time to infect others. This was apparent in the Spanish Flu pandemic, a pandemic that had only a death rate of 2.5%, but catastrophic results nonetheless. Experts predict that the next AI pandemic could infect 20-50% of the world's total population and result in 2-50 million deaths, an estimate that is scientifically grounded.

Currently, there are several treatments for AI: Amantadine or Rimantadine for chemoprophylaxis (disease prevention) and use of Oseltamivir or Zanamivir for treatment. These drugs have been shown to be effective in the prevention and treatment of AI; however, there is no guarantee that these antiviral drugs will be effective against novel strains of hybrid influenza. This may be troublesome in an event of a pandemic, especially since it takes at least four months to produce a vaccine for a new subtype.

Perhaps one of the best ways to combat the spread of this disease is to take the necessary precautionary measures. This may include a plan to minimize the risk of transmission by vigilant surveillance, and to maximize containment efforts by the culling of chickens within the infected zone.

The goal of this project is to create a model that will determine the factors for the occurrence and the spread of Avian Influenza. Human and animal case study data will be analyzed using Geographic Information System (GIS) technology. GIS is a computer-based tool that is commonly used for mapping and analyzing data. It has been proven as an effective means in the control of diseases and minimization of economic loss by predicting outcomes and planning control strategies. GIS technology has many applications because it can accept a great number of parameters that can be identified, queried, and interpreted to visually represent a situation.

Most of the documented case studies available in the public domain have been collected. A preliminary model has been constructed using human and animal case study and data sheets such as: population density, poultry density, swine density, major wetlands, migratory routes of key reservoir species and geospatial data. The collaboration of various international agencies may be needed for a project of this magnitude. This is an ongoing project that will eventually lead to an interactive map that displays the occurrences of Avian Influenza along with all pertinent information and data in a way that elicits the underlying factors for the occurrence and spread of this disease. Buffer zones around an infected area can then be created along with a list of potential farms or cites that would need rapid surveillance testing and a possible quarantine.

