

Geospatial Overview of 2009-H1N1 Influenza A Pandemic

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Abstract

In 2009, the fatal outbreak of H1N1 influenza A became one of the most serious global concerns since mid-April. Within two months, the outbreak spectrum surged to pandemic. After one year, H1N1 caused at least 18,000 deaths in more than 200 countries worldwide. However, with timely collaborative responses among various organizations worldwide, the spread of the disease was finally brought back to normal. Swift action and cooperation through sharing relevant and comprehensive information played a crucial role for decision makers to issue pertinent measures and guidelines for preparedness and response. By deploying web-based technology and geographic information systems (GIS), these planning and intervention processes were achieved more economically and effectively.

1. Introduction

The world was still recovering from the scare of Avian Influenza (H5N1) and SARS. Suddenly, in March, 2009, the first case of swine-origin H1N1 influenza occurred in Mexico. According to the US Centers for Disease Control and Prevention (CDC, 2009), this novel influenza A (H1N1) was caused by a new influenza virus originating from swine. H1N1 was able to infect people and spread from human to human. It diffused throughout not only within the United States but also worldwide. During the first few months, confirmed infected cases and deaths from H1N1 rapidly increased daily, especially in the United States, Mexico and several European countries (Gallaher, 2009 and WHO, 2010a). Since it was a new hybrid strain of swine, avian and human viruses, most people did not have immunity to this virus (Gallaher, 2009). At the time it was first detected, there was no vaccine to protect against it. In the first week of June 2009, WHO declared the spread of the swine influenza was pandemic (WHO, 2010a). From the onset, scientists and public health officials collaborated to handle with this deadly disease. By August 2010, 11 months later, WHO announced the end of the pandemic (WHO, 2010a). Influenza pandemics are recurrent and much can be learned from the H1N1 recent pandemic. It is the responsibility of the global communities to learn from the success and continually improve research, technology, and intervention measures. This is to get ready for the next pandemic to come. In this article, nomenclature of influenza viruses and a brief history of influenza pandemics will be reviewed.

Then, clinical characteristics and treatment of the recent pandemic influenza will be analyzed. Finally, global spread, outbreak modeling approaches, and activities including intervention measures of related communities to support the outbreak monitoring processes and responses will be explored.

2. Nomenclature of Influenza Viruses

There are three major types of influenza virus that cause influenza: types A, B, and C. Type A viruses cause illness in humans and many animals include avian, swine, equine, and canine. It causes more severe illness compared to the other two types. Type B viruses only cause illness among humans but not other animals, while type C causes illness in both humans and pigs (Kanchanachitra et al., 2006 and Spickler, 2009). These viruses are further classified into strains. Most animals have their own particular strain of virus, which is usually named after them, such as "human influenza", "swine influenza" and "equine influenza." Likewise, avian influenza spreads easily among different bird species. Therefore, it is called "bird flu" (Kanchanachitra et al., 2006). Only influenza A viruses, including swine influenza, are divided into subtypes based on two proteins on their surface: the hemagglutinin (H) and the neuraminidase (N) (CDC, 2010a). The virus strains are categorized according to the structure of these proteins which differ from strain to strain. Numbers are assigned to H and N to specify the strains. According to Spickler (2009), there are 16 hemagglutinin antigens (H1 to H16) and nine

neuraminidase antigens (N1 to N9). Only H 1, 2 and 3, and N 1 and 2 are commonly found in humans (Lynch and Walsh, 2007, cited in Wikipedia, 2009). Specifically, H 1 and N 1 are assigned to the virus that causes swine flu (CDC, 2009).

3. History of Influenza Pandemics

According to the World Health Organization (2009c), influenza pandemics are unpredictable but recurring events that can have severe consequences on global communities. Influenza pandemics have been described at intervals ranging between 10 and 50 years with varying severity and impact. WHO classifies these recurring pandemics into three categories: Spanish Flu, Asian Flu and Hong Kong Flu. Brief details of each subtype are illustrated in Table 1. Later, in 1997, an avian influenza A virus of subtype H5N1 was first detected in humans after causing disease outbreaks in poultry in Hong Kong. Although never been ranked as a pandemic, an unusual high percentage of human infections and deaths compared to the 1918 pandemic were reported. There were over millions of poultry infections and more than four hundred human cases since its widespread reemergence in 2003-2004 (WHO, 2009c). It was found that, in rare occasions, H5N1 spreads from a person to another person - usually among family members. However, none of cases has resulted in sustained community-level outbreaks so far (WHO, 2009c). At the genetic level, pandemic influenza viruses may emerge in two manners: genetic mutation (genetic drift) and genetic reassortment (genetic shift). Genetic mutation happens during virus replication causing change of genes in an animal influenza virus. This allows virus to be able to infect humans and transmit among them (Spickler, 2009 and WHO, 2009c). Spickler (2009) added that genetic shift occurs when genes from animal and human influenza viruses assemble. This happens when two distinct viruses infect a cell at a time, causing an abrupt change and generating a human-animal

influenza reassortment. The hybrid virus may consist of some genes from one predecessor and some from the other. It is believed that both antigenic drift and antigenic shift bring about occurrence of new influenza viruses which are capable of causing epidemics and pandemics (Spickler, 2009). As an example, the recent pandemic H1N1 virus is a reassortment of avian, human, and swine influenza viruses. This particular combination of genes from American and Eurasian swine viruses had never been seen before in humans or animals. Genetic sequence of its gene revealed that the virus was a descendant of the 1918 pandemic strain. As well as persisting in pigs, the descendants virus have also circulated in humans through the 20th century (CDC, 2010e, Taubenberger and Morens, 2006). In those intervening 9 decades, it had evolved independently in swine and became different enough to now appear to humans as a novel strain which was very different from seasonal viruses (CDC, 2010e). Heinen (2002) claimed that the retention of influenza strains in pigs after these strains have disappeared from the human population might make pigs a reservoir where influenza viruses could persist, later emerging to reinfect humans once human immunity to these strains has diminished.

4. Transmission Characteristics of the H1N1 Pandemic Virus

In the past, swine-origin influenza has been reported only rare in humans. Generally, it affected young people and their household members with history of exposure to pigs (Wells et al., 1991). Some cases with no recent exposure to pigs have also been reported (Naffakh and van der Werf, 2009 and Galwankar and Clem, 2009). Despite scant reports, it is believed that human-to-human transmission is possible (Petrosillo et al., 2009). As for the recent swine influenza, CDC (2010a) reported that the causative virus is not considered zoonotic.

Table 1: Characteristics of the three pandemics of the 20th century

Pandemic	Area of emergence	Influenza A virus subtype	Estimated case fatality rate	Estimated Attributable Excess Mortality Worldwide	Age groups most affected
1918-1919 "Spanish Flu"	Unclear	H1N1	2-3%	20-50 million	Young adults
1957-1958 "Asian Flu"	Southern China	H2N2	<0.2%	1-4 million	Children
1968-1969 "Hong Kong Flu"	Southern China	H3N2	<0.2%	1-4 million	All age groups

This is because it only transmitted from person to person, not from pigs to humans. It is thought that novel influenza A (H1N1) influenza and regular seasonal influenza spread in the same manners; mainly through the coughs and sneezes of people who are sick with the virus (CDC, 2009, CDC, 2010d and Gallaher, 2009). The disease can be spread via droplets from a sick people to the others up to six feet away. Since the droplets do not remain for long, close contact between the source and recipient is required (Grayson et al., 2009). This makes the spread more conducive in populated places. Additionally, the disease can be transmitted if a person touches contaminated objects, then touches their own mouth or nose (CDC, 2009).

5. Clinical Signs, Symptoms and Treatment

According to the Centers for Disease Control and Prevention, the symptoms of the 2009 H1N1 influenza in human are similar to those of influenza and of influenza-like illness in general. These include fever, cough, sore throat, body aches, headaches, chills and fatigue. The 2009 outbreak has shown an increased percentage of patients reporting diarrhea and vomiting. Severe complications might be found in people with underlying medical condition such as diabetes, respiratory disease and obesity. Because these symptoms are not specific to swine flu, a differential diagnosis of probable swine flu requires not only symptoms but also a high likelihood of swine flu due to the person's recent history (CDC, 2009). As for pharmaceutical treatment, to date, four drugs have been developed to fight influenza infections; amantadine, rimantadine, oseltamivir (Tamiflu) and zanamivir (Relenza) (FAS, 2009). However, it was found that the pandemic H1N1 viruses were resistant to amantadine and rimantadine, but they were sensitive to oseltamivir and zanamivir (CDC,

2010g). Additionally, oseltamivir and amantadine have both been shown to be effective against hybrid viruses containing the parts of the 1918 flu and vaccines have also protected mice against viruses with some of the 1918 influenza components (FAS, 2009).

6. Pandemic Preparedness and Response

From the very beginning of the disease outbreak, WHO (2009c) recommended all countries to perform pandemic preparedness activities within the context of national and international priorities, competing activities, and limited resources. This was because uncertainties surrounding the timing of the next influenza pandemic. In order to ensure long-term sustainability of pandemic preparedness, integration of pandemic influenza preparedness into national emergency preparedness plans, framework, and activities should be done. Additionally, pandemic preparedness activities to strengthen basic and emergency health related capacities, and to actively build continuity plans specifically tailored to pandemic influenza should be performed. Finally, there should be periodic reassessment and updating of current plans based on new developments and information gained from exercises. In order to facilitate the world in pandemic preparedness and response planning, WHO (2009c) also provided guidance to a global framework. According to the guidance, the pandemic is divided into phases based on transmissibility of the disease (Figure 1). Phases 1 to 3 of the pandemic are related to preparedness. These include capacity development and response planning activities. Phases 4 to 6 clearly signal the need for response and alleviation efforts, while phases after the first pandemic wave are elaborated to facilitate post pandemic recovery activities (WHO, 2009c).

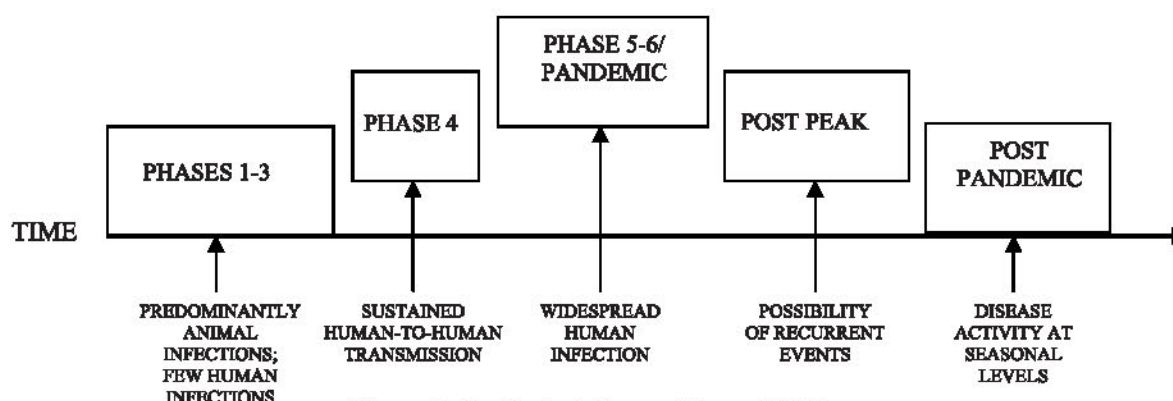


Figure 1: Pandemic Influenza Phases (2009)
Source: Adapted from World Health Organization (2009c)

These phases are intended to be used as a planning tool. It was not designed to predict what will happen during a pandemic and it will not always going to proceed in numerical order. In terms of global response, several local health authorities had enhanced their regular activities in many aspects to ensure the effectiveness of the response. For example, vaccination planning and implementation was developed; healthcare professionals were trained; and non-pharmaceutical communities were continuously guided. Furthermore, the information regarding the influenza was tracked and distributed among the global communities. These could be seen from many websites such as WHO (<http://www.who.int/csr/disease/swineflu/en/>), Flu.gov (<http://pandemicflu.gov/>), Pan American Health Organization (PAHO) (<http://ais.paho.org/flu/sm/en/atlas.html>), and mapcruzin.com (<http://www.mapcruzin.com>).

7. Global Outbreak

The H1N1 virus was first identified around mid April 2009 from two children in Southern California who suffered from mild respiratory illnesses. It was soon reported that cases of more severe respiratory disease which occurred in Mexico one month earlier were caused by the same virus (CDC, 2010b). On 24 April 2009, only two countries were affected. Within a very short period, the number of affected countries, confirmed cases and deaths rapidly increased. After detection of 20 confirmed cases on April 26, the United States declared a health emergency, and on the same day WHO declared a Public Health Emergency of International Concern. Only one day after that, WHO raised the influenza

pandemic alert from phase 3 to phase 4. Then, on April 29, the spectrum of outbreak was raised to phase 5. During the first month (24 April – 23 May 2009), number of daily confirmed cases and deaths drastically increased from 25 to 12,021 cases (Figure 2) and 86 deaths within 43 countries. According to the reports from affected countries, a younger age group has been affected than seen during seasonal epidemics of influenza. Though cases have been confirmed in all age groups, the youth or patients with severe or lethal infected cases were commonly found during early outbreak (WHO, 2009a). Therefore, on June 11, WHO eventually announced that the outbreak had reached the pandemic phase (WHO, 2009d). After that, the number of laboratory confirmed cases still kept on rising. The number of countries reporting cases of the disease increased to nearly double from mid-June 2009 to early July 2009 (CDC, 2010g). Fortunately, since the end of July, it was found that the overall situation was quite stable. As of 1 August 2010, more than 214 countries and overseas territories or communities worldwide have reported laboratory confirmed cases of pandemic influenza H1N1 2009, including over 18449 deaths (Figure 3). Most of the fatal cases were found in the United States, Mexico, Southern America, Europe, Asia and Australia respectively (WHO, 2009d, and WHO, 2010b). On 10 August 2010, after the overall situation remains largely unchanged, WHO announced that the H1N1 pandemic influenza had shifted into the post-pandemic phase (WHO, 2010a). Summarized timeline of the pandemic since the beginning of the outbreak is illustrated in Figure 4.

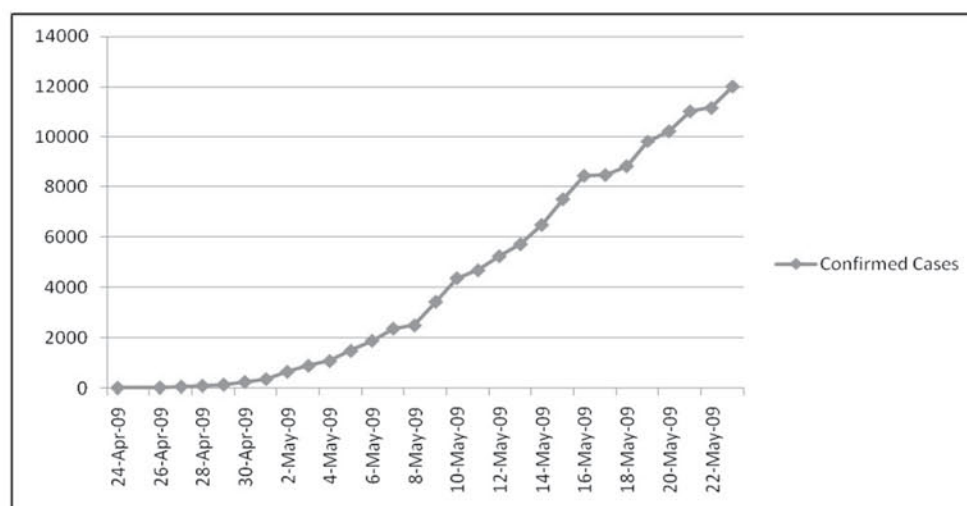


Figure 2: Numbers of confirmed cases and Deaths caused by Swine Flu from 24 April to 23 May 2009 Source: World Health Organization (WHO, 2009d)



Figure 3: Pandemic (H1N1) 2009 laboratory confirmed cases and cumulative number of deaths as reported to WHO as of 1 August 2009. Source: The World Health Organization (WHO, 2009d)

The 2009 H1N1 Pandemic Timeline

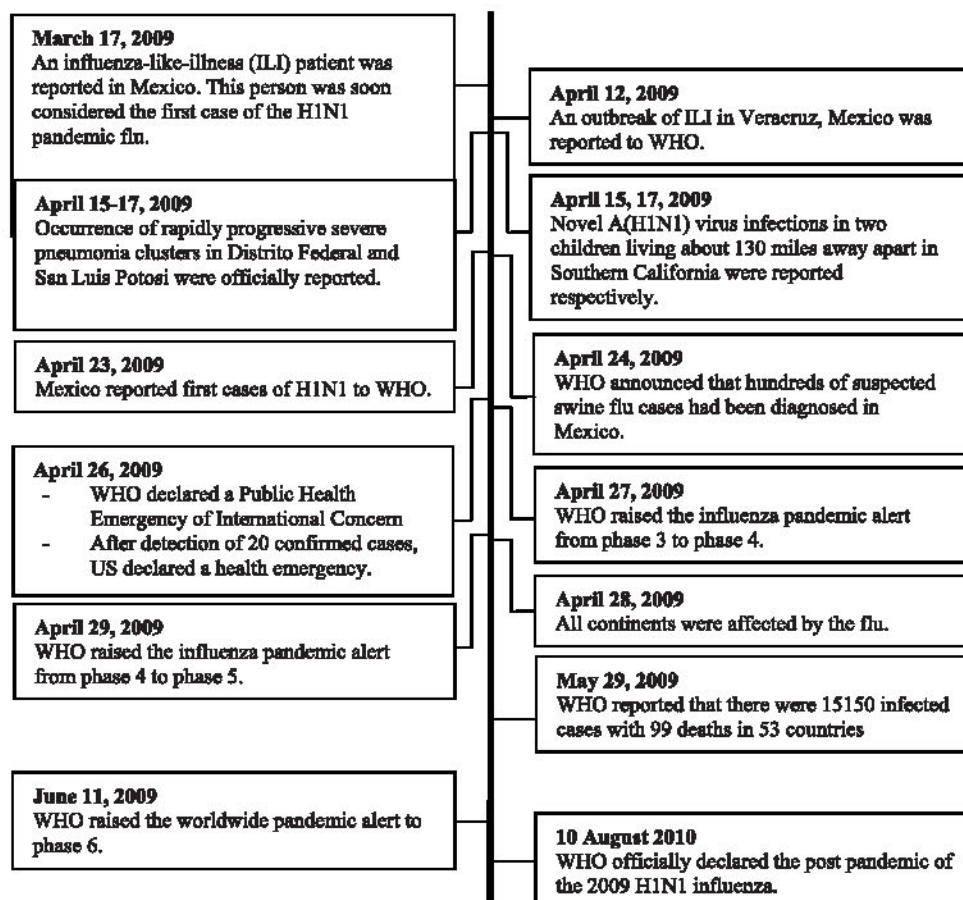


Figure 4: Timeline of the 2009 H1N1 pandemic flu

8. Spatial Path of the 2009-H1N1 Virus Spread

As seen in several international public health reports, it is clear that the 2009 pandemic H1N1 virus infection spreads easily across countries and continents. The emergence of the infection among humans is the greatest pandemic threat ever after the Hong Kong Flu in 1968 (Dawood et al., 2009). Various studies confirmed that globalized travel and trade networks played crucial roles in accelerating the spread of the recent pandemics (Khan et al., 2009, Lee and Wong, 2010, Wang et al., 2010, and Zhang et al., 2010). In the early epidemic phases, most of the cases were imported by air travelers from the previously affected countries, whereas the majority of cases afterwards were domestic (BEID, 2009, Lee and Wong, 2010, and Gutiérrez et al., 2009). It has been found that, after importation of

affected persons, the disease was then easily spread throughout the countries via close contact and crowding. Schools, private parties, and events involving crowds – such as rock festival are examples of possible scenes (Novel influenza A (H1N1) investigation team, 2009, Komiya et al., 2009, Gutiérrez et al., 2009). Being inspired by the phenomenon, Khan and colleagues (2009) then conduct an investigation based on an intensive database of global air traffic and passenger itineraries in March and April. In this case, the research team had to use 2008 flight information due to unavailability of the 2009 data, noting that air travel pattern during the period change little from year to year (Khan et al., 2009). An overview of the world airports and flight patterns are illustrated in Figure 5.



Figure 5: World airline routes, Source: Open Flight (2011)

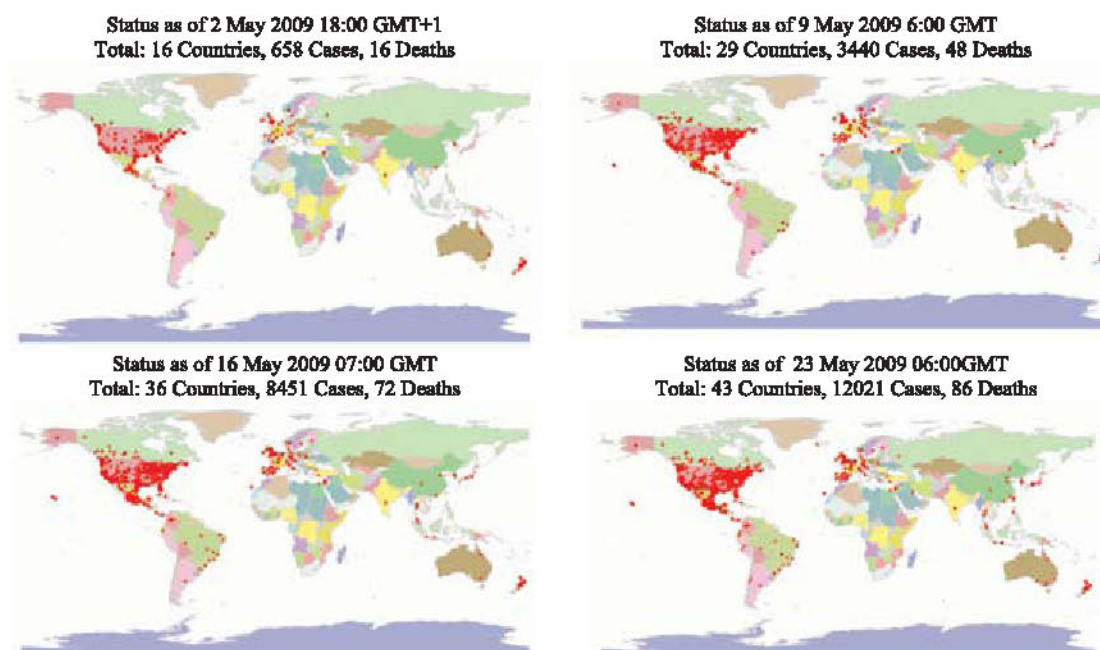


Figure 6: Weekly status of Swine Flu Global outbreak from 2 May to 23 May 2009
Source: The World Health Organization (WHO, 2009d) and Mapcruzin.com (2009)

From the study, Khan and coworkers found very strong correlation between the traffic and disease occurrences. Almost all the imported cases were found in the nations with high-traffic volumes of passengers from Mexico, while the countries that were not among the top-20 destinations of the flights from Mexico had few or no cases of travel-associated swine influenza (Khan et al., 2009). Distribution map of case notifications in May 2009 (Figure 6) is an evidence to support the findings. Similarly, models of human mobility in relation to disease outbreaks have been generated. For example, Balcan and colleagues developed a global structured 'metapopulation' model called Global Epidemic and Mobility (GLEaM) model based on Monte Carlo likelihood analysis. The model incorporated mobility and worldwide transportation data in order to simulate the worldwide spread of influenza A (H1N1), and to assess the effect on the whole world epidemic resulting from people's travel and seasonal transmission (Balcan et al., 2009). The result showed the potential for an early epidemic peak occurring in October/November in the Northern hemisphere, likely before large-scale vaccination campaigns could be carried out. The baseline results refer to a worst-case scenario in which additional alleviation policies are not applied. Zhang and coworkers believe that, although mathematic model can be used to calculate the number of cases, it is not an appropriate tool to visualize and analyze the complicated, spatial-temporal process of an epidemic. Conversely, Geographic Information System (GIS) provide powerful tools for spatial analysis and display. Therefore, they developed a spatially explicit epidemiological simulation system by integrating GIS and mathematic epidemic model to study the outbreak and transmission of influenza A (H1N1) in mainland China. In this model, the spread was processed at three scales: imported cases from abroad, cases flowing among provinces and the spread of influenza A (H1N1) in each province. It was found that the dynamics of all influenza cases from the simulation results were similar to reported statistics. Likewise, the distribution of infected provinces was reasonable (Zhang et al., 2010). Wang et al. (2010) also implemented a spatial explicit epidemiologic model of influenza for a better understanding of spatial diffusion of the disease through human network based on the assumption that propagation of influenza through a population is an inherent spatial-temporal process. The research group integrated GIS to an agent-based modeling (ABM) in order to simulate the spread of the H1N1 influenza in 2009 in an urban environment in Kunming, Yunnan province,

southwest of China. It was found that the GIS-agent based model can be easily customized to study the dynamicity of the H1N1 influenza by simply adjusting the disease parameters. Wang and team claimed that the model was applicable for any other influenza as well (Wang et al., 2010). Computer models have become important tools to study the transmission of influenza for both decision-makers and public. These models offer a global insight of an infectious disease outbreak by analyzing geographic and demographic features of the spread of the disease in a given population. Computer models have an advantage in representing and understanding the complex social structure and the heterogeneous patterns in the contact networks of real-world populations determining the transmission dynamics. By using this kind of simulations, comprehension of disease spread dynamic can be improved which, in turn, increase the effectiveness of prevention and control of an influenza outbreak (Wang et al., 2010).

9. Conclusion

Swine Flu is a global concern due to its rapid transmissions among swine and humans. Countries in every region of the world were affected and numbers of laboratory confirmed cases have increased hundreds folds within one month. Since the earliest days of the outbreak, main health organizations, including WHO and CDC, had been struggling to mitigate this severe situation but the outbreak increasingly expanded until it reached the pandemic period. However, with collaborative efforts from communities worldwide, the deadly phenomenon was brought to an end. It can be said that timely response, data sharing, and comprehensive and clear communications were the core components behind the achievement. Many scientists also played critical roles in investigations. Various mathematical and computerized models have been developed with spatial enabling capacity in order to obtain better understandings about spatial pattern of the disease transmission. Integration of information and communication approaches, especially web-based technologies and GIS, were extensively adopted in order to enhance the potential of the efforts. We were lucky that the recent pandemic emerged in the highly developed region of the world where sophisticated systems exist and information and resources were freely shared. Although there were several successes of the response to the pandemic, various disparities in many aspects including understanding, capacities, resources, and socioeconomic impact were experienced. Many challenges, especially information sharing and equitable access to

resources in rapidly changing and complex environment, are left to the world communities to develop effective strategic plans to cope with the other emerging pandemic to come.

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