Linda Young Landesman
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CASE STUDIES IN Public Health Preparedness
and Response to Disasters

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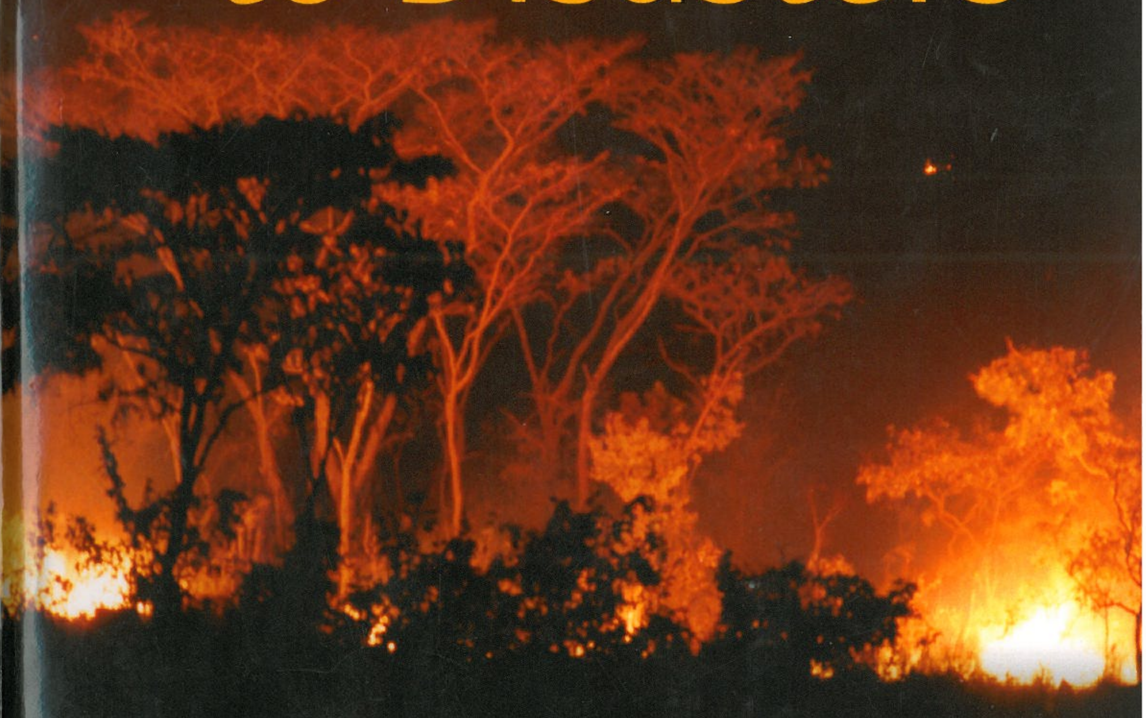

Linda Young Landesman

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Surveillance in Emergency Preparedness: The 2009 H1N1 Pandemic Response

Michael A. Jhung

INTRODUCTION

In 1997, the first human case of H5N1 avian influenza was identified in a 3-year-old boy in Hong Kong. Within a few months, several more cases of human infection with avian influenza A (H5N1) in Hong Kong were confirmed, and public health officials began a fervent investigation to determine whether these cases were the start of a global influenza pandemic. In due course, the investigation revealed that this influenza virus was not transmitted efficiently from person to person, and that most of these cases had exposure to a live poultry market, where they likely became infected. This, as it turned out, was not the start of a pandemic, but it did mark the beginning of a period of time that saw unprecedented funding, effort, and attention directed toward preparing for what many people thought would be the next global public health disaster.

By 2009, more than 400 cases of H5N1 infection had been reported, and the case fatality ratio exceeded 60%.[1,2] Most of these cases were in Asia (China, Indonesia, Thailand, and Vietnam, among other countries), but by 2005 to 2006, the virus had spread, and Africa, Europe and the Middle East had seen their first cases as well.[3] Public health officials around the world were keenly aware of the threat posed by avian influenza and were preparing for the worst. Their biggest fear was that we would see another pandemic like the 1918 disaster, which caused up to 100 million deaths worldwide.[4] Pandemic planning had become an important part of the influenza agenda—all signs were pointing to some form of avian flu as the likely cause, and the expectation was that it would start somewhere in Africa or Asia. The U.S. government developed a comprehensive national pandemic response plan that, although broad in scope, identified H5N1 avian influenza as the greatest pandemic threat.[5] As it turned out, the next pandemic would start in neither Africa nor Asia, and would come from a different animal as well.

A STEEP LEARNING CURVE INDEED

At the time of the Hong Kong outbreak of H5N1, I was busy applying to medical school 12 time zones away, and it took a while for news of these events to catch up with me—but when they did, I was riveted by accounts of how a team of epidemiologists from the Centers for Disease Control and Prevention (CDC) flew to Hong Kong from Atlanta to investigate the outbreak. I remember thinking at the time—this sounds like something I would really like to do! After medical school, I completed residency training in preventive medicine and public health and then joined CDC's Epidemic Intelligence Service (EIS) program in 2005[6] as an officer with a group responsible for hospital-acquired infections. In August 2009, I transitioned from the hospital infections group at the CDC to the Influenza Division. As we will soon see, this was about 4 months into the 2009 pandemic, right before the start of the second wave in the United States. So, after spending 4 years studying hospital infections (which, by the way, rarely include influenza), I had a lot of catching up to do and little time in which to do it.

Of course, I was not the only one at the CDC making changes, and the adjustments made in the very early phases of the pandemic were a little unexpected. As the nation's premier public health agency, it fell to the CDC to lead the scientific response to the first influenza pandemic in over 40 years. Throughout the rest of this case study, we will see what this entailed and discuss how the clinical, laboratory, and epidemiologic data the CDC collected were used to help guide the public health response. For now, it is interesting to note that much of the early effort in the response was spent revising our pandemic plans, which were based on the 1997 outbreak of avian influenza in Hong Kong, an outbreak that had much greater clinical severity than what the 2009 H1N1 pandemic ultimately showed. Toby Crafton, chief of staff during the 2009 H1N1 pandemic response at the CDC, puts it this way:

> We had to make huge modifications because the assumptions in our planning process were based around an H5N1 kind of response, and it starting somewhere else. Basically, what happened was it was not an H5N1, and it started here—actually in Mexico. But it came here real quick, and what we were expecting was it would start somewhere in Asia and we would have several weeks before it came to the United States, and that's not what happened at all. And of course most of our planning was around a real severe pandemic H5N1, where the mortality rate is up around 60% for that virus. This particular pandemic was not anywhere near that severe, so we need to do more planning around general scenarios and general principles as opposed to specific viruses, and a lot of our planning in the past was done around a specific virus.[7]

IT'S JUST A COLD, RIGHT?

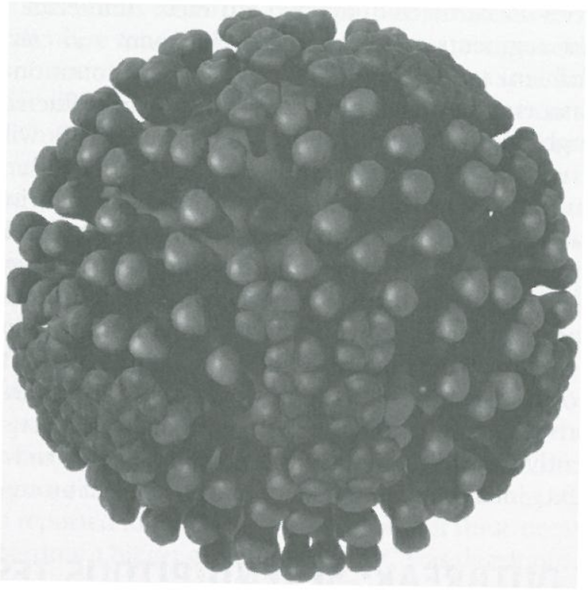
Most people know enough about influenza to realize that, for the most part, it causes relatively mild illness.[8] In fact, if you are one of the 15 to 60 million people who get the flu every year, you might be tempted to ask what the fuss is all about. First, although the majority of influenza cases are mild and self-limiting, complications can occur. The primary complication of influenza is pneumonia, and each year hundreds of thousands of people in the United States are hospitalized with,[9] and 3,000 to 49,000 people die from influenza.[10] Most of the really severe diseases occur in the elderly (people over 65 years of age), but children younger than 5 years of age, pregnant women, and people with underlying medical conditions are also at increased risk for hospitalization or death.[11] Along with this characteristic age distribution, seasonal influenza epidemics in the Northern Hemisphere also follow a predictable time course, with activity typically beginning in October, ending in May of the following year, and peaking sometime between February and March.

Most experts think that flu viruses are spread mainly by respiratory droplets made when people with the flu cough or sneeze. That means people with influenza can spread it to others up to about 6 feet away. These respiratory droplets can land in the mouths or noses of people who are nearby or possibly be inhaled into the lungs. Less often, a person might also get influenza by touching a surface or object that has virus on it and then touching his or her own mouth or nose. Most healthy adults may be able to infect others beginning 1 day before symptoms develop and up to 5–7 days after becoming sick. Children may pass the virus for longer than 7 days. Symptoms start 1–4 days after the virus enters the body. Some persons can be infected with the influenza virus but have no symptoms. During this time, those persons may still spread the virus to others.[8]

Vaccination is the best method for preventing influenza and its complications, but it must be given every year, and it works best when the vaccine strain matches the circulating virus (see **Figure 13-1**). Antiviral medications can also reduce serious morbidity and mortality related to influenza, but there is growing concern that circulating virus strains will become resistant to the few antiviral medicines that we currently have.

Figure 13-1

Artist's rendering of influenza A virus.



Source: Dan Higgins, CDC.

THE VIRUSES, THEY ARE A-CHANGING

This brings us to the second reason why you should care so much about influenza. Unlike many other organisms, the influenza virus is *always* changing, and changes in the virus, whether they are big or small, lead to the two things people worry about the most—resistance to antiviral medications and emergence of a novel influenza strain. Novel influenza strains are what cause pandemics. Small changes within the genetic material of influenza viruses occur frequently. This genetic drift does not lead to emergence of a new virus with pandemic potential, but can cause changes in virulence or transmissibility that can make influenza vaccines and antiviral medications less effective.

Without getting too bogged down with details, influenza viruses come in three flavors: types A, B, and C. Of the three, type A is the most alarming because it can infect both animals and humans, and thereby initiate a big change—an antigenic shift. An antigenic shift occurs when different influenza viruses exchange genetic material, resulting in major changes in viral surface proteins. When a single host cell is coinfected by two different influenza viruses, their genome segments can undergo reassortment and create an entirely new influenza virus. Pigs are thought to be a common mixing vessel for reassortment of avian, swine, and human influenza strains, and although relatively uncommon, human infections with reassortant swine viruses do occur.[12] These new viruses quickly die out, however, unless they retain the ability to replicate well in humans and are transmissible among humans. Prior to 2009, this had only happened three times in the last century, leading to influenza pandemics in 1918, 1957, and 1968. The worst of these pandemics (and some argue, the worst public health disaster of any kind) occurred in 1918, when up to 100 million people died from influenza.[4] By 2009, it had been over 40 years since the last pandemic, and there was growing concern that a new influenza virus might soon emerge and become efficiently transmitted among humans. This concern was justified, as the next global pandemic turned out to be right around the corner.

THE OUTBREAK: SERENDIPITOUS TESTING

On April 15, 2009, the first case of the 2009 pandemic was identified in a 10-year-old boy in Southern California; two days later, a second case of infection with the same pH1N1 virus was confirmed in a 9-year-old girl in an adjacent county in California.[13] The story of how these viruses were discovered is an interesting one and one of the first great successes of the pandemic response.

The diagnostic test used to identify influenza by most public health laboratories in the United States employs a molecular technique called reverse-transcription polymerase chain reaction (RT-PCR). Using RT-PCR, scientists can take a small amount of an unknown influenza virus and amplify its genetic material (in this case, RNA) until they have enough to "match" it against samples of virus whose identity they already know and have cataloged. In this way, they are able to describe influenza virus *type* (either A, B, or C) and *subtype*—a combination of letters and numbers that describes the composition of two important viral proteins (hemagglutinin and neuraminidase). A fully characterized influenza virus includes both descriptors, although only type A viruses are subtyped (e.g., influenza A H3N2, a common virus seen in seasonal epidemics). Although type B influenza viruses are composed of the same genetic material as type A viruses, they do not exhibit enough antigenic variation to warrant classification into subtypes.

When specimens from the two California cases were first tested, the results were unusual: influenza A, no recognizable subtype. The reason for this is that the RT-PCR test that was initially used to identify these cases included only avian (influenza A/H5) and seasonal (influenza A/H1 and A/H3) subtypes in its matching catalog. Because pH1N1 originated in swine, the RT-PCR test essentially could not recognize it. All human infections with influenza viruses of unknown subtypes are events of public health importance because these viruses all have pandemic potential. In fact, they are considered so important that they must be reported to the global public health community as a public health emergency of international concern (PHEIC) within 24 hours of identification.[14]

Human infections with swine flu viruses are rare and usually limited to people who have had contact with pigs (e.g., children who show pigs at a state fair). From 2005 until just before the start of the pandemic, only 11 sporadic cases of human infection with swine influenza (H1) had been reported to the CDC.[12] To ensure that these occasional cases did not become a bigger problem, the CDC was developing the ability to recognize swine viruses in its RT-PCR testing kits. In fact, they had a working model of this RT-PCR test ready just before the first two pandemic cases were reported.[15] Dr. Stephen Lindstrom, one of the CDC scientists who helped develop the new test, recalls its first application:

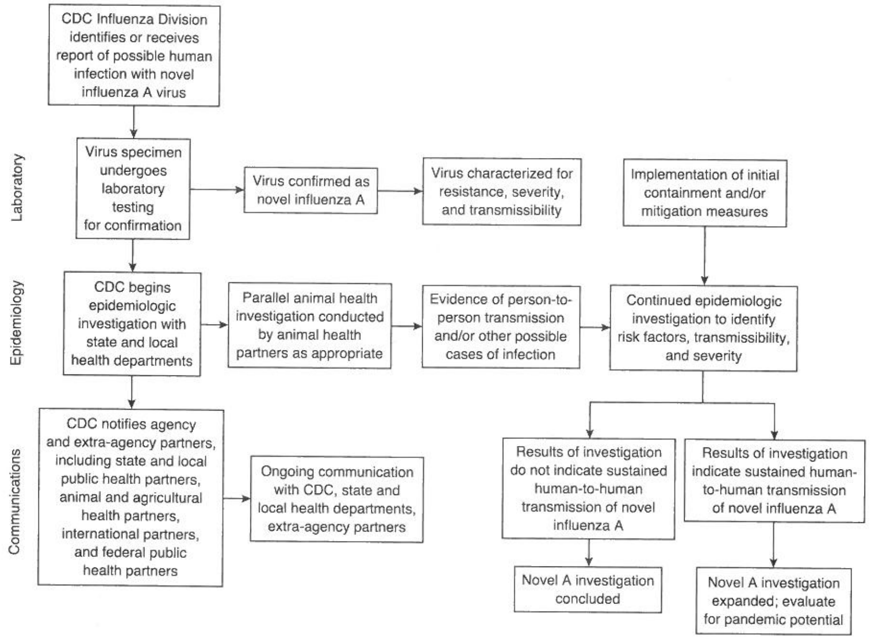
> It was very odd timing. Luckily, we had an assay almost ready, and it was designed to let us know if there was a novel virus emerging. This was a situation where our advanced work on swine really helped—if we had needed to start from scratch, it would have taken another two weeks to develop.[7]

At first it was not clear whether the California cases were just a few more isolated cases of swine flu. But what caught Lindstrom's attention (along with everybody else at the CDC) was the fact that neither California case had had any contact with pigs, or with each other. Lindstrom notes, "That was a pretty big red flag."

Over the next 2 weeks, additional cases of infection with this new virus were detected in Mexico, California, Texas, and other states.[16,17] When a case of human infection with novel A influenza is identified, the CDC undertakes a complex and comprehensive set of laboratory, epidemiologic, and communications measures to determine the extent and severity of each incident (see **Figure 13-2**).

Figure 13-2

Flow chart showing essential steps in an investigation of human infection with a novel A influenza virus.



At this point, the CDC still did not really know what it had—clearly *something* was happening, as there were multiple infections with a novel influenza A virus in people that were unlikely to have been exposed to the same animal. Dr. Lyn Finelli, the CDC lead epidemiologist during the response, puts it best:

> On April 15, when we heard about the first case, we thought that that this would be a typical swine flu investigation, and it wasn't obvious to me that it would be as unusual as it turned out to be. It wasn't until two days later, when we heard about the second case, that I realized this might be very different from the novel A investigations we had done before. Within a few days, the parents of both children in California had been interviewed many times, and we just couldn't link the kids to any swine exposure. Now, about three weeks before all this happened, we had started to hear about outbreaks of severe respiratory disease in villages and small towns in Mexico where some people were hospitalized. So when we heard about two cases in Texas, another state bordering Mexico, I became really alarmed. We thought that this was a big outbreak, potentially a very big one, involving multiple states and Mexico, but we weren't quite sure whether it was the pandemic or not. Over the next week, we very sincerely asked each other many times during the day—do you think this could be a pandemic? We really didn't know.[7]

FOURTEEN MONTHS IN THE SUBBASEMENT

By late April, however, there were dozens of confirmed cases in the United States, and the public health response had begun in earnest. The CDC quickly deployed six field investigation teams to California, Texas, Mexico, and other areas, and activated its Emergency Operations Center to help manage the rapidly increasing amount of data and requests for information that came pouring in.

What We Needed to Know #1

The public health questions surrounding pandemic influenza are not fundamentally different from those of seasonal influenza—at the beginning of the pandemic, we had the same two questions we ask during every influenza season: How big will this get (i.e., questions regarding geographic spread and burden of illness), and how bad will this be (i.e., questions regarding severity of illness)?

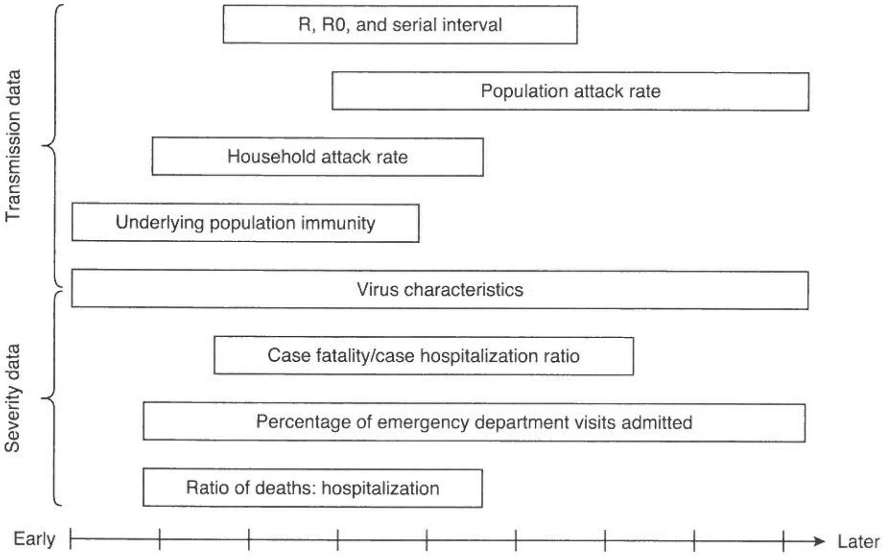
But the difference between pandemic and seasonal influenza is that a pandemic suggests widespread circulation of a *novel* virus, which means that pH1N1 characteristics such as its transmission properties, clinical spectrum, and antiviral resistance profile were largely unknown (see **Figure 13-3**). We also needed to know the answers to these questions quickly—much more quickly than for seasonal epidemics. Only certain pieces of information describing a new virus, however, are available early in its emergence, and this created tremendous tension between a need for careful and deliberate collection of information and the desire to take immediate action.

What We Needed to Know #2

It was also critical to describe the epidemiology and transmission of pH1N1 to make accurate recommendations to clinicians on how to protect themselves and treat their patients, and to make good

Figure 13-3

Diagram of surveillance data elements and relative timing of their availability in a pandemic.



decisions on nonpharmaceutical interventions such as restricting travel and closing schools.

Every year, the CDC's Advisory Committee on Immunization Practices (ACIP) makes recommendations about the use of influenza vaccine and antiviral medications to prevent and control influenza.[11,18] These recommendations include priority groups for whom vaccine is especially important due to increased risk of severe complications from infection. The literature describing the epidemiology of seasonal influenza is quite extensive, and this allows the ACIP to be confident in prioritizing certain persons (e.g., the very young, the elderly, and people with underlying medical conditions) for vaccination and antiviral treatment. But there was no guarantee that pH1N1 would affect the population in the same way as seasonal influenza viruses. It was therefore very important to describe the epidemiology of pH1N1 accurately and quickly in order to identify priority groups for H1N1 vaccine, which initially was available in limited supply. Martin Meltzer, a senior health economist at the CDC who was extensively involved in the response, describes it well:

> We knew vaccine production would take time. Who gets the first doses off the production line? Who goes to the front of the line? We've been discussing this for a number of years, and one of the most critical decisions was the ACIP recommendations about who should be vaccinated first. The ACIP as you know, gave a list of people who should be vaccinated first, but they also had another list within that list of what if there is a shortage of vaccine—who is the most important to vaccinate first? And that was the most critical decision in our response as far as I am concerned, because that then defined the whole nature of the vaccine-related response. The other critical decision was the use of antivirals. So those basic decisions upfront about what to do with the response resources in terms of vaccine and antivirals—who should get it—clearly defined the rest of the response. Everything about the response from then on led from this primary decision.[7]

WHAT WE DID

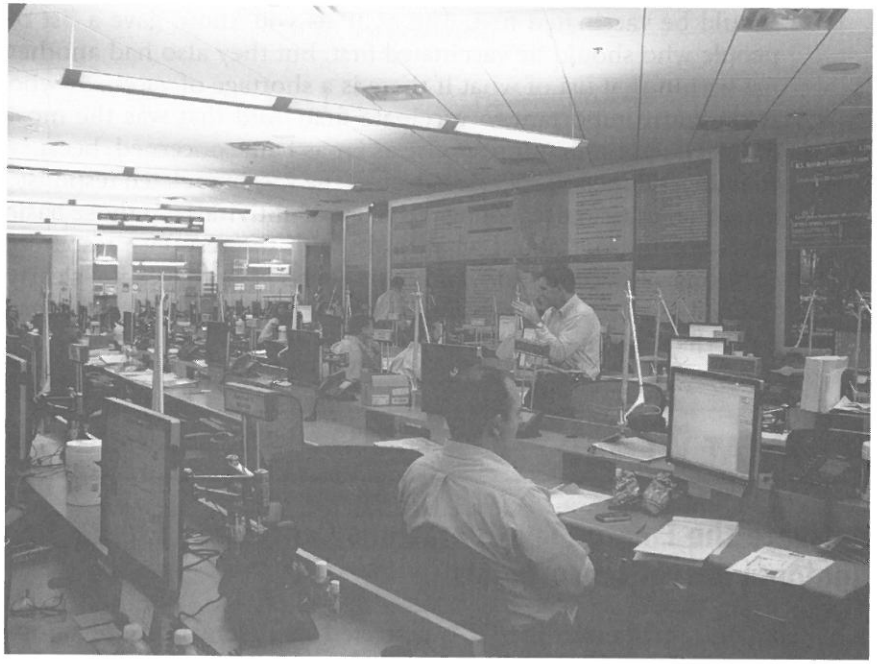
Activate the Emergency Operations Center and Create Regional Surveillance Teams

Almost immediately, the CDC activated its Emergency Operations Center (EOC) to help handle the increased information flow due to the pandemic response (see **Figure 13-4**). The EOC serves as the CDC's central public health incident management center for coordinating and supporting staff, information, communication, and security issues associated with a response to public health disasters, emergencies, disease outbreaks, and investigations. The EOC incident manager relies on a team of experts from across the CDC to staff the EOC during an event. This team determines the level of response required for each incident, depending on the information provided and analysis of each situation. The level of public health response also determines how many personnel will be needed to work in the CDC EOC during events. When asked how big the 2009 pandemic response was, Chief of Staff Toby Crafton had this to say:

> It ended up being close to $2 billion that we got from the federal government to respond to H1N1. At the end when it was all said and done here, there were a little over 3,000 people that had in some way participated in the response. So it started off as probably 20 people, and it grew from there.[7]

Figure 13-4

A typical day in the Centers for Disease Control and Prevention's Emergency Operations Center in Atlanta, GA during the 2009 H1N1 pandemic response.



Source: Mark Fletcher, CDC.

Throughout the pandemic, the EOC served as the information center of the response and provided a means to collect and disseminate data to the hundreds of international, federal, state, and local public health partners involved. In the United States, regional surveillance officers were based in the EOC to maintain daily contact with state and territorial public health departments in order to gather information, impressions, and concerns that were not reflected by formal surveillance systems (see **Figure 13-5**). The regular and frequent contact between this team and state responders provided an avenue for quick exchange of very specific information, and information from the regional surveillance team was used to identify patterns of influenza severity and distribution manifesting in individuals or small clusters. Under the structure of the CDC's pandemic epidemiology and surveillance team, regional surveillance officers were tasked with gathering information about unusual or particularly severe clinical presentations, institutional clusters (such as in prisons or schools), and cases in vulnerable groups such as pregnant women or healthcare workers. Regional officers were also identified as a primary point of contact for state and local health departments to exchange information with the CDC regarding diagnostic laboratory testing during the pandemic and for questions about other CDC surveillance systems. The information gathered by the regional surveillance team proved valuable for many reasons; notably, it was often the initial impetus for launching a field investigation, and it was also used to provide situational awareness of the pandemic to senior leadership at the CDC.

Figure 13-5

A team of regional surveillance officers at work in the Centers for Disease Control and Prevention's Emergency Operations Center in Atlanta, GA during the 2009 H1N1 pandemic response.

Source: Mark Fletcher, CDC.

What this meant for me was that the first "office" I had in my new position with the Influenza Division was a giant room I shared with 40 to 50 other people, the majority of whom rotated through about every 2 to 4 weeks. I spent the first 14 months of my new job in the CDC's secondary EOC (which happened to be in the subbasement of the oldest building on campus—not in the main EOC on the third

Figure 13-6

The author at work during the 2009 H1N1 pandemic response.

Source: Mark Fletcher, CDC.

floor of a brand new building), supervising the regional surveillance officers, managing one of our new influenza national surveillance systems, and sifting through incoming data for anomalies that would trigger a field investigation. I was often the first person in the building (usually before 6:00 AM), but was almost never the last to leave, even though I typically left after 7:00 PM every night—people in the Influenza Division were routinely working 12 to 16 hours a day, and everybody was focused on the pandemic (see **Figure 13-6**). Professionally, it was one of the most rewarding times of my life.

Rely on Existing Surveillance Systems

As pH1N1 activity accelerated throughout the United States, national influenza surveillance systems began to accumulate more data that confirmed findings from early investigations and case studies. In fact, the bulk of the robust epidemiologic data available during the 2009 pandemic were collected largely from preexisting local, state, and federal influenza surveillance systems. Influenza surveillance in the United States is composed of many systems that provide data on the location, timing, severity, and viral characteristics of influenza each season.[19] These systems have three primary goals: (1) to detect and characterize influenza viruses through determination of antigenic and genetic changes over time; (2) to determine the burden, epidemiology, and clinical characteristics of influenza and influenza-like illness (ILI); and (3) to detect the onset, duration, and geographic spread of disease caused by seasonal and other influenza viruses.

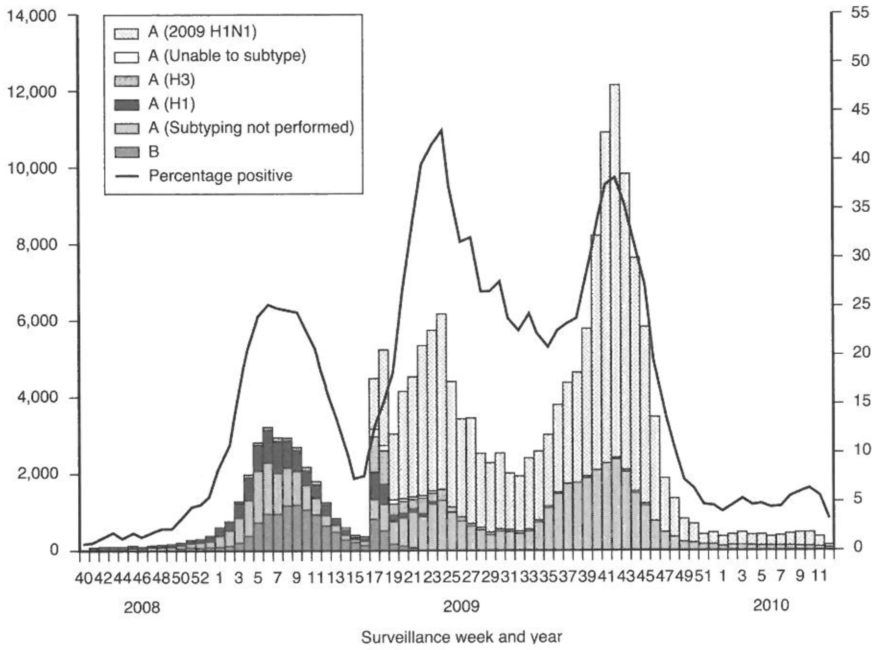
A fundamental responsibility of national influenza surveillance systems is to conduct laboratory surveillance for influenza viruses. In the United States, all state public health laboratories collaborate with the CDC and the World Health Organization (WHO) as do some county and city public health laboratories, as well as some large tertiary care or academic medical centers. This consists of approximately 80 laboratories that report the total number of human specimens received for respiratory virus testing and the number positive for influenza types A and B each week to the CDC; influenza A subtype, when known, is also reported. There are 70 National Respiratory and Enteric Virus Surveillance System (NREVSS) laboratories that report the total number of respiratory specimens tested and the number positive for influenza types A and B each week to the CDC. Most NREVSS laboratories participating in influenza surveillance are hospital laboratories; some have the ability to perform and report influenza A subtyping. During the 2009 pandemic, WHO/NREVSS laboratories provided influenza diagnostic test result data on more than 900,000 clinical specimens (see **Figure 13-7**).

In 2007, the Council of State and Territorial Epidemiologists (CSTE) and the CDC designated human infection with novel influenza A viruses as a nationally notifiable disease. Since that time, local, state, and territorial epidemiologists have worked alongside public health laboratories to report suspected novel influenza A infections in humans to the CDC Influenza Division. This arrangement worked as designed in April 2009 when the CDC Diagnostics and Strain Surveillance Branch rapidly confirmed the identification of two cases of pH1N1 infection in children from Southern California, marking the beginning of the 2009 pandemic.

Another component of U.S. national surveillance is responsible for influenza-associated hospitalizations. FluSurv-NET is a collaborative network with participants from the CDC, state and local health departments, and academic institutions. In 2004, surveillance for

Figure 13-7

Graph of laboratory specimens tested for influenza by WHO/NREVSS laboratories and at the Centers for Disease Control and Prevention.



Source: The Epidemiology and Prevention Branch, Centers for Disease Control and Prevention.

laboratory-confirmed influenza resulting in hospitalization among children less than 18 years of age was initiated in nine Emerging Infections Program (EIP) sites; surveillance was expanded in 2005 and 2006 to include hospitalized adults, and an additional site was included. In September 2009, six new sites were added to FluSurv-NET, and this network of population-based sites in 16 states now represents approximately 7 million children and 21 million adults. FluSurv-NET's main goals are to characterize the incidence of, and risk factors for, laboratory-confirmed influenza resulting in hospitalization. During the pandemic, FluSurv-NET collected detailed information describing the epidemiology of over 7,000 patients hospitalized with influenza and was critical in assessing the severity of illness associated with the pH1N1 virus.

The U.S. Outpatient Influenza-Like Illness Surveillance Network (ILINet) conducts surveillance for outpatient healthcare encounters for influenza-like illness (ILI is defined as fever [temperature > 100°F /37.8°C] with cough or sore throat). In this collaborative network, data regarding ILI among outpatients are collected by healthcare providers recruited and coordinated by local, state, and territorial health departments. Each week, the providers report directly to the CDC Influenza Division their total number of office visits and the number of visits for ILI. The integrated data provide regional and national views of current influenza activity. The network functions year-round and currently has approximately 4,000 providers enrolled in 50 states, covering approximately 30 million patient visits per year. Due in part to the relatively mild illness associated with many pH1N1 infections, most of the estimated 61 million pandemic cases in the United States did not result in hospitalization or death,[20] and the only opportunity to conduct surveillance for these cases was during an outpatient healthcare encounter. The CDC, therefore, relied upon ILINet to track the temporal and geographic distribution of the vast majority of all influenza activity during the pandemic, and the network rapidly became the most important routine surveillance system in use during the pandemic.

Two national surveillance systems monitor mortality related to influenza. The 122 Cities Mortality Reporting System collects reports each week from vital statistics offices representing 122 cities and metropolitan areas. This system identifies, by age group, the proportion of filed death certificates that include a diagnosis of pneumonia or influenza. These data are used to define a baseline and epidemic threshold for mortality due to pneumonia and influenza and provide a means to compare mortality from year to year. The Influenza-Associated Pediatric Mortality Reporting System was initiated in 2003, when the CDC began requesting voluntary reporting of all deaths among children less than 18 years of age due to laboratory-confirmed influenza. In 2004, the CSTE designated influenza-associated pediatric mortality a nationally notifiable disease for public health surveillance.

The final component of the national system is the State and Territorial Epidemiologists' Report, which is responsible for detecting the onset, duration, and geographic spread of disease caused by seasonal and other influenza viruses. Each week, the CDC receives reports from state, territorial, or regional epidemiologists estimating their region's overall level of influenza activity. The epidemiologists' estimates are based on data obtained from several surveillance sources within their jurisdictions, including ILINet, 122 Cities Mortality Reporting System, and local reports of school absenteeism.

Enhancements to existing influenza surveillance systems were ongoing prior to the 2009 pandemic and included activities such as increasing the number of ILINet providers, particularly the number of sites that could submit electronically gathered data; establishing electronic laboratory reporting between public health laboratories and the CDC; and encouraging electronic reporting of influenza-associated mortality. Existing influenza surveillance systems were further augmented early in the pandemic to improve timeliness and geographic coverage to meet the special needs of the response. These modifications included increasing the frequency of ILI, laboratory, and mortality reporting from a subset of surveillance sites as well as the addition of new sites collecting population-based hospitalization rates.

These systems were relied upon heavily during the pandemic, and they provided two important benefits for the response, in addition to the information they gathered during the course of the pandemic. First, because they had been in continuous operation and had long-standing infrastructure in place, they could accommodate a rapid surge in activity when the pandemic began. Second, they provided a seasonal influenza baseline against which to compare pandemic illness burden and clinical severity.

Although not dedicated solely to influenza surveillance, the CDC's national automated biosurveillance system, BioSense, was also used extensively during the pandemic. BioSense receives primarily syndromic health data from U.S. civilian hospitals, Department of Defense and Veterans Affairs hospitals, emergency departments, and outpatient clinics.[21] Since 2007, BioSense has included a special influenza module that summarizes data from three sources within the National Influenza Surveillance System: chief complaint and International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM) discharge diagnosis data from emergency departments, diagnosis data from outpatient clinics, and third-party payer electronic prescriptions for influenza antiviral medications.[22] The Distribute project was implemented in 2006 by the International Society for Disease Surveillance to assist with national monitoring of ILI reported from state and local health departments. The network was designed to aggregate ILI reports from existing emergency department syndromic surveillance systems and, as such, is closely related to the BioSense system in both purpose and operation. Distribute, in fact, incorporates some BioSense reports into its data stream. Originally developed as a proof-of-concept system, Distribute was rapidly expanded during the pandemic, and by November 2010, the systems participating in Distribute represented approximately one-third of the emergency department visits in the United States. Although syndromic surveillance likely overestimated influenza illness due to a nonspecific case definition, BioSense and Distribute generated reports on a daily basis, making them two of the most timely systems providing data to the CDC during the pandemic.

Outbreak Investigations and Special Studies

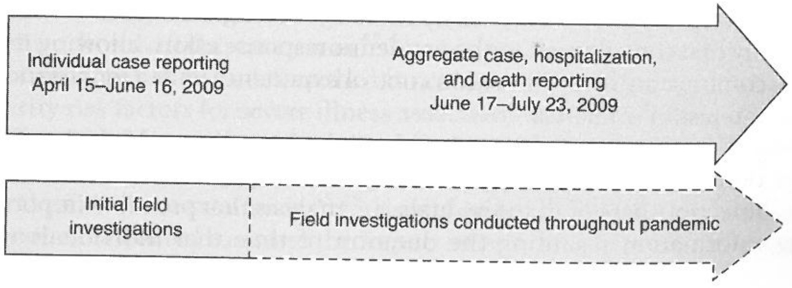
Early in the pandemic, case reports, field investigations, and case series were instrumental in answering several key questions surrounding the newly emerged pH1N1 virus (see **Figure 13-8**). Knowledge of community and household attack rates, reproductive rate, and generation time was crucial for understanding the epidemiology of the pandemic and informing control measures. Field investigations also provided critical data that helped shape early pandemic response efforts. Dr. David Swerdlow, one of the leads for the epidemiology and laboratory task force during the the response, tells us how these investigations got started:

> The epidemiologic investigations team was manned with EIS Officers or staff. When we heard about a cluster or an outbreak the team would send people or sometimes just give advice to the state epidemiologist and others at the state level. I actually called my friends in Foodborne Diseases who've had a lot of experience with this kind of outbreak, and they helped tremendously with investigations and with setting up a system for states to report cases to us. We were able to get that system up and running in 12 hours, and it was identical to systems that we had used for food-borne disease outbreaks. So that was one of the things that we did. It was sort of just nice that we had friends. I had come from Foodborne Diseases not that long ago, and we had friends there, and we were able to use their expertise.[7]

ILI attack rates were estimated in a household survey in a heavily affected Chicago community following an outbreak of

Figure 13-8

Surveillance at the beginning of the pandemic, showing an early transition from case-based reporting to aggregate surveillance for severe outcomes.



laboratory-confirmed pH1N1 at a neighborhood elementary school.[23,24] Attack rates, risk factors, and the effect of nonpharmaceutical interventions were the focus of an investigation of the first reported U.S. university pH1N1 outbreak, which occurred in Delaware during April 2009.[25,26] The secondary household attack rate following introduction by an index patient with influenza is an important indicator of the overall transmissibility of an newly emerged influenza virus.[27]

Secondary household ILI attack rates were estimated during field investigations in Texas, California, and New York City. In San Antonio, Texas, one of the first affected areas in the United States, transmission and the effect of nonpharmaceutical interventions was investigated in 77 households between April 15 and May 8, 2009, in which at least one person in the household had laboratory-confirmed pH1N1 infection.[28] In New York City, following the first large laboratory-confirmed pH1N1 school outbreak in the United States, 222 households of high school students with ILI were evaluated.[29] In San Diego County, California, 117 contacts in 38 households in which at least one person had laboratory-confirmed influenza were investigated at the onset of the pandemic (CDC unpublished data). Finally, 216 index cases with laboratory-confirmed pH1N1 and 600 household members reported to the CDC from April 2009 to June 11, 2009, were described in a study to estimate the secondary attack rate of pH1N1 to be at the lower range of that seen for seasonal influenza (10%–40%) and lower than that reported during previous pandemics.[30]

In May, the CDC investigated a cluster of approximately 50 cases of pH1N1 infections in a Chicago hospital in order to help characterize virus transmission.[31] At this time, the public health community was still struggling with personal protective equipment (PPE) recommendations, and it was thought that an outbreak in a healthcare facility might present a unique opportunity to determine whether surgical masks or N-95 respirators were needed to protect healthcare workers against pH1N1 transmission. Although results were inconclusive, this was an especially exciting investigation for me, as it was my first contribution to the pandemic response effort, allowing me to combine my recent infection control experience with a long-standing interest in influenza.

Data from seven focused epidemiologic studies and field investigations conducted from April through June 2009 were used to estimate infectiousness of ill individuals, an analysis that provided important information regarding the duration of time that individuals with ILI should remain isolated to reduce spread of the pH1N1 virus.[32] Finally, a description of an outbreak at an elementary school in rural Pennsylvania at the outset of the pandemic provided insight into the dynamics of school outbreaks and transmission within schools.[33,34]

Early field investigations also provided information used to determine the basic reproductive number and the generation time (serial interval) for pH1N1 infection. The basic reproductive number R_0 is defined as the average number of secondary cases per typical case in a susceptible population.[35] Data from early cases were used to estimate the reproductive number of pH1N1 to be between 2.2 and 2.3,[35] although estimates decreased to 1.7–1.8 after adjustment for increased case ascertainment during the initial pandemic period. In a sensitivity analysis making use of previous estimates of the mean serial interval, the reproductive number was estimated to be between 1.5 and 3.1.[35] Cases from the initial outbreak in Mexico were used to estimate R_0 in the range of 1.2–1.6,[36] and reported case clusters in the United States estimated R_0 to be 1.3–1.7.[37] Most estimates of R_0 for pH1N1, therefore, have indicated that the virus was at the low end of transmissibility compared with the strains that caused the 1918 pandemic, and comparable, or slightly lower than the 1957 and 1968 pandemics. The time period between successive generations of infected persons can be measured indirectly by using the serial interval (the time between onset of symptoms in successive generations) and incubation period (the time between exposure and onset of symptoms) associated with a disease.[38,39] The serial interval for pH1N1 was estimated to be between 2.2 and 3.2 days,[30,35,37] less than that of seasonal influenza,[40,41] possibly due to higher proportions of susceptible persons. The distribution of the serial interval determines, along with R_0, the rate at which an epidemic can spread and can inform recommendations for control measures such as school closure, isolation of infected persons, and use of other nonpharmaceutical interventions.[30,35]

Several case series were also initiated early in the pandemic to help define the clinical spectrum of pH1N1 illness, identify populations at risk for severe disease, and assess the overall burden of disease. Two hospitalized case series[42,43] and one death case series[44] were conducted to help define the clinical spectrum of illness and identify risk factors for severe illness associated with pH1N1. In addition, serological studies were conducted to assess the level of preexisting immunity in the population and estimate infection rates at the conclusion of the pandemic.[45,46] Finally, several focused investigations were conducted to assess the impact of pH1N1 on important groups thought to represent at-risk populations. These included pH1N1 among persons infected with HIV,[47] Alaskan Natives and Pacific Islanders,[48,49] and healthcare personnel in the United States.[50,51]

Through rapid response activities like these, public health practitioners were able to confirm quickly that human-to-human transmission of pH1N1 virus was sustainable, describe the efficiency of transmission as approximately equivalent to that of seasonal influenza, and identify a broad clinical spectrum of pH1N1 illness whose severity was largely less than previous pandemics and similar to that of seasonal influenza. This, of course, is not the whole story of the pandemic, and it was partly through the use of influenza surveillance systems described in the forthcoming sections that public health identified a key feature of pH1N1—the relative sparing of health impact on older adults compared to both seasonal influenza and prior pandemics, and its disproportionate impact on children.

Modify Existing Surveillance Systems and Create New Ones

New methods to track pH1N1 and better understand its epidemiology were employed during the pandemic to fill critical knowledge gaps. Case-based reporting by state health departments, as described in the previous section, allowed tracking of detailed data and trends in severe disease with greater geographic representativeness than would have been possible with existing systems alone. As the pandemic evolved, however, case-based reporting rapidly became unmanageable, and the CDC began to encourage aggregate reporting of severe influenza outcomes (see Figure 13-8). In September 2009, the CDC and the Council of State and Territorial Epidemiologists formalized this sentiment by implementing a new influenza surveillance system to supplement available data from established systems, improve surveillance timeliness, and expand geographic coverage to meet the needs of the pandemic response. The Aggregate Hospitalization and Death Reporting Activity (AHDRA) was part of an overall national influenza surveillance strategy that was intended to provide timely and representative notification of severe outcomes associated with pH1N1. Objectives of this new system included the ability to (1) track severe disease within states and territories in order to better capture the focal nature of the pandemic, (2) track disease trends over brief units of time in order to respond rapidly to changes in pH1N1 epidemiology, and (3) accommodate variation in resources by providing a simple, flexible method to allow reliable reporting by all states and territories without overwhelming health departments during the course of the pandemic response. From August 30, 2009, through April 6, 2010, the CDC requested weekly reporting of influenza-associated hospitalizations and deaths from all 50 states and 6 U.S. territories. States and territories were asked to identify hospitalizations and deaths in their jurisdictions according to either a laboratory-confirmed or syndromic surveillance definition and could use either definition to report hospitalizations or deaths. Jurisdictions were instructed to submit aggregate weekly counts, by age group, to a secure website. Laboratory-confirmed reports from AHDRA were used to estimate weekly ratios, which were age-group specific, of influenza-associated deaths relative to influenza—associated hospitalizations. These values were also incorporated into a model used to estimate the national illness burden of influenza-associated cases, hospitalizations, and deaths during the pandemic, accounting for variation in medical care–seeking, laboratory practice and detection capability, and underreporting of confirmed cases.[20] Data collected by AHDRA helped characterize the epidemiology of pH1N1-associated influenza hospitalizations and deaths in the United States, revealing a time course and illness distribution for pH1N1 that were substantially different from those seen in seasonal influenza epidemics.[9,52–54] Although the total AHDRA laboratory-confirmed hospitalization and death counts likely substantially underestimated the total number of pH1N1-associated hospitalizations and deaths, they were helpful in monitoring trends in the distribution of illness and age groups over time in specific jurisdictions. The AHDRA data helped define the beginning and end of the 2009–2010 influenza season and accurately depicted the second wave of pH1N1 illness seen in the fall of 2009; similar double-wave patterns have been seen in previous pandemics.[55–57] AHDRA was also instrumental in the detection of and response to a minor third wave of pH1N1 activity in the southeastern United States in early 2010.[58] Although also useful in monitoring trends within jurisdictions, the AHDRA syndromic reports were less effective, as these data were complicated by limited representativeness and a low specificity for detecting influenza-attributable hospitalizations and deaths among those associated with respiratory illness. Because the system was implemented within a few weeks, AHDRA may prove particularly useful as a model for a national influenza pandemic surveillance system that needs to be implemented quickly and efficiently.

Dr. Nancy Cox, Influenza Division director at the CDC, provides some important perspective on the work done at the CDC during the 14-month-long response:

> I think that the rewarding thing about the public health mission working on the H1N1 response is that every day mattered. What you did at work every day mattered. That's the way most of us feel who work at the CDC anyway. But this was a response where you knew that you were going to have to work very hard every single day of the response, and that you would be making decisions or helping make decisions that would make a difference in saving lives and helping people.[7]

I WISH THAT I KNEW THEN WHAT I KNOW NOW

Since the pandemic was declared over by the World Health Organization in June 2010, many in the public health community have reflected upon lessons learned from this first pandemic of the 21st century. In the United States, demands of the response were met using different public health systems, depending on the timing and nature of disease activity—as the course of the pandemic evolved, response efforts evolved as well. By its end, a tremendous amount of information was available to describe the scope, magnitude, and severity of the pandemic. In fact, more data describing the epidemiology of influenza was collected, analyzed (some are still being analyzed!), and disseminated during the pandemic than at any time previously. This information was collected by thousands of public health practitioners using a combination of existing influenza surveillance systems, enhancements to these existing systems, new influenza surveillance systems created to address pandemic needs, outbreak investigations, and special studies. As post-H1N1 assessments continue and preparations for the next pandemic begin, we would do well to remember some of the most important lessons learned during 2009 and 2010.

The Importance of Strong Public Health Partnerships

In planning for and responding to influenza pandemics and other public health emergencies, collaboration with public health partners is essential. The response to the 2009 pandemic was successful largely thanks to teamwork among public health partners in state and local health departments, schools, and businesses. The comprehensive public health response to the pandemic would not have been possible without creating, maintaining, and refining partnerships inside and outside the public health community. The design and implementation of measures to prevent and control disease transmission relied upon a similar network of partners to inform and engage communities. Vaccination and antiviral therapy, in particular, are effective interventions that are less useful without the infrastructure to distribute them and a public notion that they offer protection from infection and illness. Success in the control of pandemic influenza, as with any public health threat, required awareness of the necessary partnerships to make surveillance and interventions useful. The 2009 pandemic response also required active engagement of the public, and for that, collaboration between public health and community partners was essential.

The Value of Having a Wide Range of Resources Available

We were fortunate in that when the pandemic began in 2009, the CDC was already operating multiple surveillance systems for influenza, each of which added information to what we knew about pH1N1. Because many of these systems had been in operation for years, (decades for some), there was infrastructure and experience in place that allowed us to scale surveillance up or down as needed, depending on the severity and timing of the pandemic. While it was initially difficult to forecast the course or duration of this pandemic, we suspected that there would likely be defined periods between the onset of pandemic activity, the peak of disease transmission, and the resolution of disease (this turned out to be true). These time points would dictate which surveillance systems and response strategies would be appropriate. As communities, regions, territories, and states were affected by pandemic influenza at different levels of intensity and at different times, regional public health authorities were able to implement surveillance and response strategies asynchronously and focus efforts on communities as they were affected. The multiple influenza surveillance systems used during the response worked very well to provide a comprehensive picture of the pandemic. In addition, although the bulk of information came via long-standing disease surveillance systems, other "surveillance" activities such as outbreak investigations and case studies were important in understanding pH1N1 transmission, clinical severity, and risk groups for illness.

The Value of Preparedness Planning

Although the timing, nature, and severity of a pandemic may be difficult to predict, it is imperative that preparedness planning occur to mitigate the impact of influenza. Regardless of its extent and severity, a pandemic can be expected to strain local, state, and federal resources, and without suitable planning, it may overwhelm them. The pandemic influenza plan in the United States [5] includes aggressive surveillance for novel influenza virus strains, comprehensive seasonal influenza surveillance, and enhanced virologic and disease surveillance once sustained human-to-human transmission is documented.

Prior to the 2009 H1N1 pandemic, the Department of Health and Human Service (DHHS) and the CDC were engaged in a broad array of surveillance activities with multiple public health partners to prepare for an influenza pandemic. These included efforts to expand geographic coverage of sentinel disease-reporting sites, improve the timeliness of influenza-related reporting to public health officials, develop clinical and epidemiological assessment tools, and establish rapid outbreak identification for both domestic and international events. One of the most important surveillance modifications occurred in 2007 when human infection with a novel influenza A virus became a nationally notifiable health condition. This new reporting requirement was preceded by an increase in diagnostic capacity at state public health laboratories, improving their ability to detect unusual influenza viruses. Together these activities enhanced a system that in April 2009 did exactly what it was designed to do—identify and report novel influenza A infections with pandemic potential.

Finally, the importance of practicing should not be overlooked. In the 5 years prior to April 2009, the CDC had conducted five functional pandemic exercises, each designed to simulate the response to an actual influenza pandemic. Functional exercises are complex events, usually lasting several days, that allow participants to learn and practice response plans while facilitating review and refinement of response strategies. Toby Crafton, chief of staff during the 2009 pandemic, commented on the value of pandemic exercises:

> Instituting pandemic exercise programs was probably the best thing we ever did. People complained, but after about the first month or two of the actual response, you heard them say, "Well it was a good thing we did those exercises." It really, really helped. The exercises we did were against a completely different scenario, but it didn't matter. It was the processes and the procedures and the things that you learn, and how you interact and communicate during those exercises that I think was real important. And it doesn't matter what the disease is. It can be anything.[7]

Despite these achievements, there were some aspects of the response that should have gone better. Although years of pandemic planning left the United States with a public health infrastructure well-prepared to respond to the 2009 pandemic, there is no question that unanticipated gaps in the response existed.

THE ROAD AHEAD

Rapid and Ongoing Impact Assessment

One of the most-requested pieces of information about the pandemic revolved around the question of public health impact. Historically, the severity of influenza pandemics have been described using estimates of the case fatality ratio (CFR),[59] but this approach is limited because it does not account for the effect of virus transmissibility or for vulnerable population subgroups (e.g., children, the elderly, people with chronic medical conditions). Using the CFR to estimate severity was thought to be particularly ineffective in 2009 because information describing deaths from pH1N1 would not be available until weeks after the pandemic began, too late to inform recommendations for evidence-based public health interventions, and because initial reports suggested that this pandemic caused predominantly mild illness, resulting in too few fatalities to estimate an accurate CFR.

Rather than rely on the CFR as a sole measure of pandemic impact, the CDC developed an impact assessment framework based on five measures of transmission and three measures of severity, including community, school, and workplace attack rates; secondary household attack rates; the basic reproductive number (R_0); the case-hospitalization ratio; and a death-to-hospitalization ratio in addition to the CFR. Many of these measures will be available earlier in a pandemic than would data to estimate the CFR, and because the framework is designed to accept multiple inputs, it has flexibility to accommodate more (or fewer) measures as additional data become available (or if anticipated data are delayed). Although it has only been tested on historical data, this new approach shows promise for making pandemic impact assessment a more accurate and timely process.

A Nimble Way to Visualize and Access Data

Integrating, sharing, and disseminating information among public health partners were important parts of the pandemic that were moderately successful throughout the response. However, there are two groups in particular that would benefit from a more nimble way to visualize and access available data—decision makers and the public. Clear, concise, and easily accessible information would help speed decision making and facilitate a common understanding of issues among all contributing stakeholders.

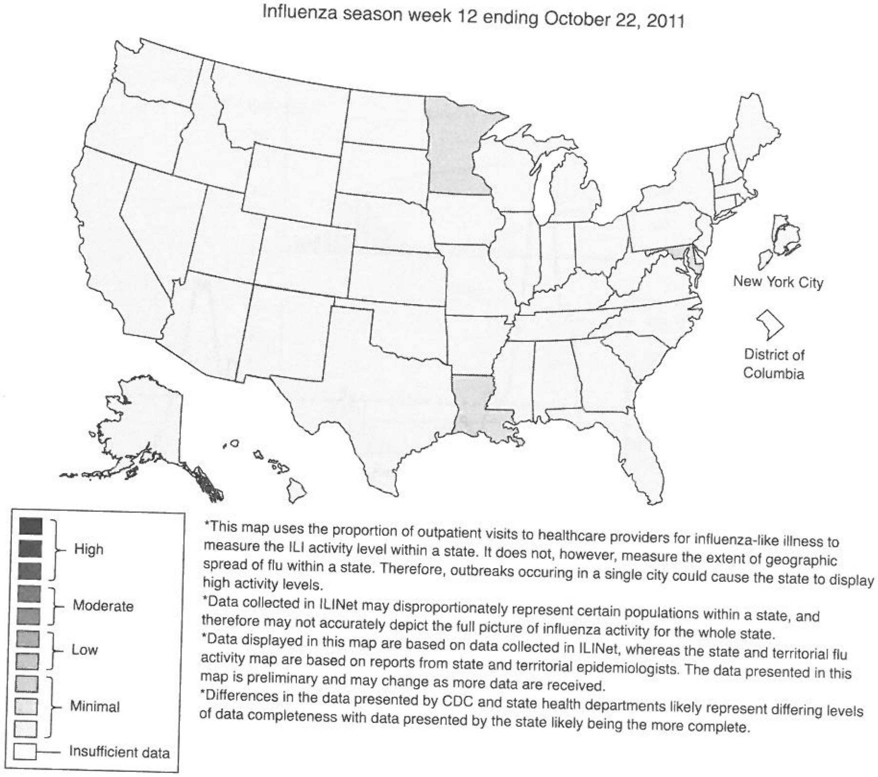
To address this issue, the DHHS/CDC is adopting a technique used by the military to visualize positions, identify emerging and existing threats, manage available resources, and command troops in battle. A common operating picture (COP) can be defined as a single identical display of relevant information describing an event. At its simplest level the COP identifies *what* is *where*, but as more information is compiled and portrayed, the COP can give stakeholders greater situational understanding and allow decision makers to be more proactive in application of resources. Because the COP approach is also used by many U.S. government sister agencies, it should help synchronize reporting and data sharing among the CDC's external partners.

Additionally, displaying information in a clear, intuitive, and accessible manner would allow the nonscientific public to better understand the scope and severity of the pandemic and make better personal decisions regarding vaccination, social distancing, and other prevention strategies. Easily accessible information also has the added benefit of alleviating some of the public health resource burden of trying to answer each request for information individually. During the pandemic, the CDC assessed its communication strategies for epidemiologic and surveillance data with a goal to improve visualization of important public health data at FluView, its main influenza information site (http://www.cdc.gov/flu/weekly/); two recent modifications have been made. The first is the addition of a state-specific activity level indicator to the U.S. Outpatient Influenza-Like Illness Surveillance Network to facilitate a better understanding of how much ILI is being treated in outpatient clinics and doctor's offices (see **Figure 13-9**).

The second is a change in the way FluSurv-NET influenza-associated hospitalization data are displayed (see **Figure 13-10**). Both of these changes incorporate an interactive element and allow the user to tailor the way data are displayed. FluView is updated every week during the normal influenza season and is a very useful tool for learning about influenza and its associated complications—if you have not accessed it yet, I encourage you to give it a try.

Figure 13-9a

Screenshot of FluView, showing recent modification allowing state-specific visualization of influenza-like illness each week.



*This map uses the proportion of outpatient visits to healthcare providers for influenza-like illness to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occuring in a single city could cause the state to display high activity levels.

*Data collected in ILINet may disproportionately represent certain populations within a state, and therefore may not accurately depict the full picture of influenza activity for the whole state.

*Data displayed in this map are based on data collected in ILINet, whereas the state and territorial flu activity map are based on reports from state and territorial epidemiologists. The data presented in this map is preliminary and may change as more data are received.

*Differences in the data presented by CDC and state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

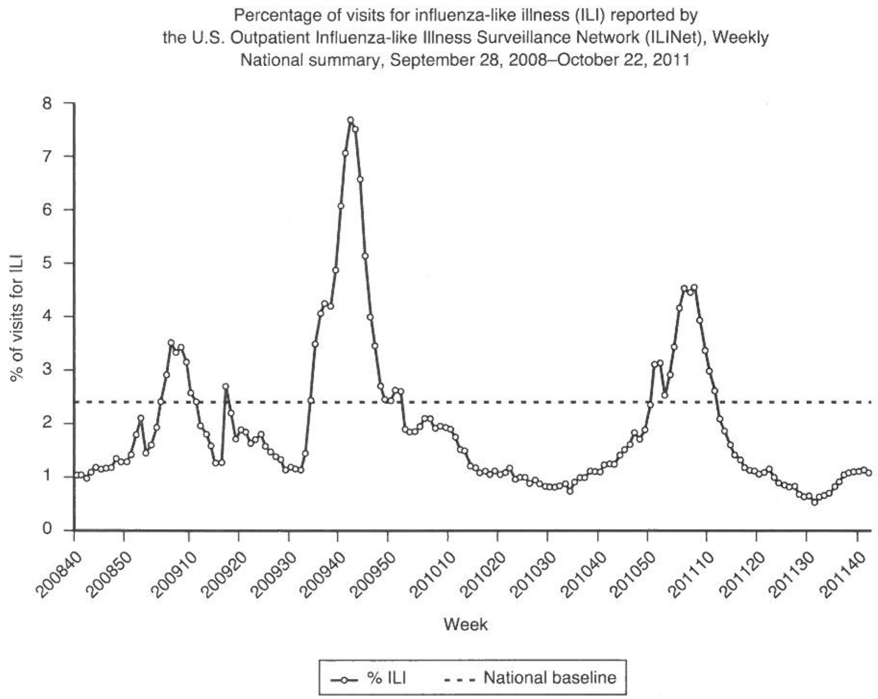
Source: CDC's FluView. Available at: http://www.cdc.gov/flu/weekly/. Accessed May 5, 2013.

Better Use of Electronic and Automated Data Sources

New electronic data sources for influenza surveillance were introduced during the pandemic to supplement existing national systems. These sources generally fell into one of three categories: (1) syndromic data that monitored aggregate ILI occurrence, (2) administrative data (e.g., ICD-9-CM discharge diagnosis codes), and (3) information from patient electronic medical records (EMRs) that provided deidentified patient-specific data from outpatient and inpatient healthcare encounters. Early in the pandemic, it was

Figure 13-9b

Screenshot of FluView, CDC's weekly online influenza information site showing percent of outpatient influenza-like illness each week.



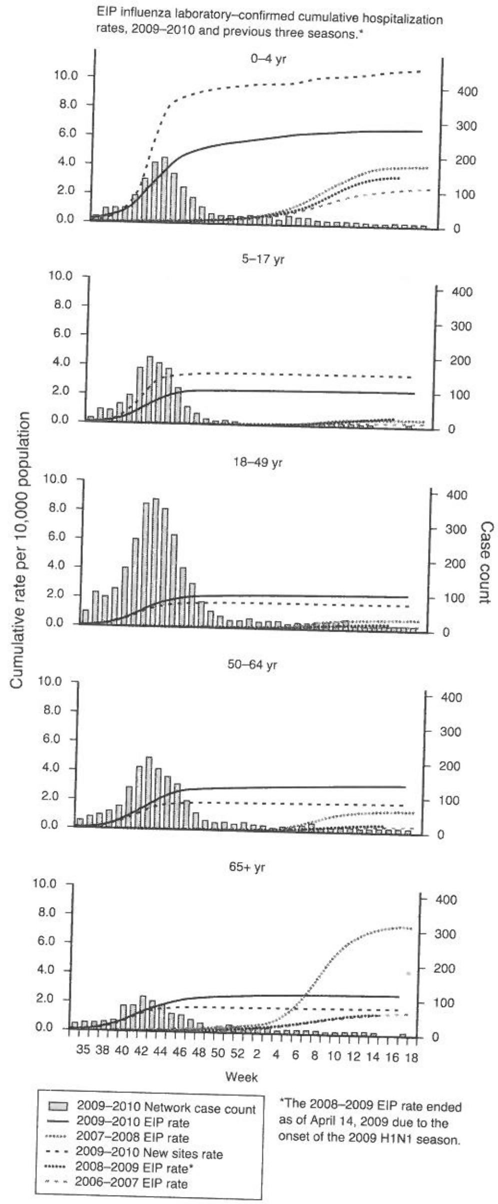
Source: CDC's FluView. Available at: http://www.cdc.gov/flu/weekly/. Accessed May 5, 2013.

thought that electronic data streams could be incorporated into national surveillance for influenza quickly and efficiently. By the end of the pandemic, however, it was clear that none of the available electronic data sources evaluated by the CDC could be utilized without additional substantial time and resource expenditures. Fundamentally, these data were encumbered by a lack of experience at the vendors supplying them and the infectious disease epidemiologists at the CDC trying to validate and incorporate them into traditional influenza surveillance reports.

Difficulties encountered with electronic surveillance data included a lack of timeliness in receiving reports, limited representativeness for some sources, and the inability to obtain consistently valid and

Figure 13-10a

Screenshots of FluView, showing old depiction of influenza-associated hospitalization rates (Figure 13-10a) and recent modification (Figure 13-10b), which allows user to change display modes.

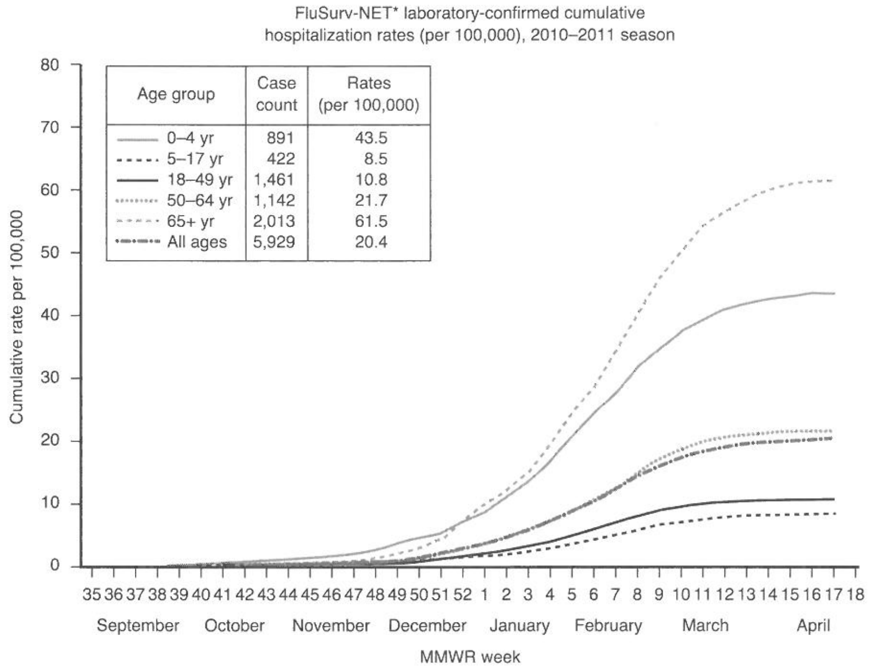


*The 2008–2009 EIP rate ended as of April 14, 2009 due to the onset of the 2009 H1N1 season.

Source: CDC's FluView. Available at: http://www.cdc.gov/flu/weekly/.

Figure 13-10b

Screenshots of Fluview, showing old depiction of influenza-associated hospitalization rates (Figure 13-10a) and recent modification (Figure 13-10b), which allows user to change display modes.



*FluSurv-NET results include surveillance at EP sites and at sites in six additional states (ID, MI, OH, OK, RI, UT)

Source: CDC's FluView. Available at: http://www.cdc.gov/flu/weekly/. Accessed May 5, 2013.

complete data. Of the three categories of data sources, syndromic data were the most timely and the easiest to implement. Although syndromic data streams did not provide much additional information over what was already being captured by existing surveillance systems, their application during the pandemic can be considered a success as they were indeed more timely and represented a higher volume of illness activity for the areas they covered. EMR data likely have the most potential for contributing to pandemic and influenza surveillance, and may prove to be a rich source of information for conducting scientific studies to describe influenza illness. However, issues of data storage and management and compatibility of data will need to be resolved before EMRs can be relied upon as an accurate and timely information source for surveillance purposes. The extent to which electronic data may eventually enhance traditional influenza surveillance remains to be seen, but limitations are likely to persist because administrative data and EMRs were not designed for surveillance purposes; instead, their primary roles lie in remuneration and provision of clinical care. Thus, system attributes such as data quality, representativeness, and sensitivity, which are critical to the successful operation of surveillance systems,[60] may not be priorities for vendors providing these data.

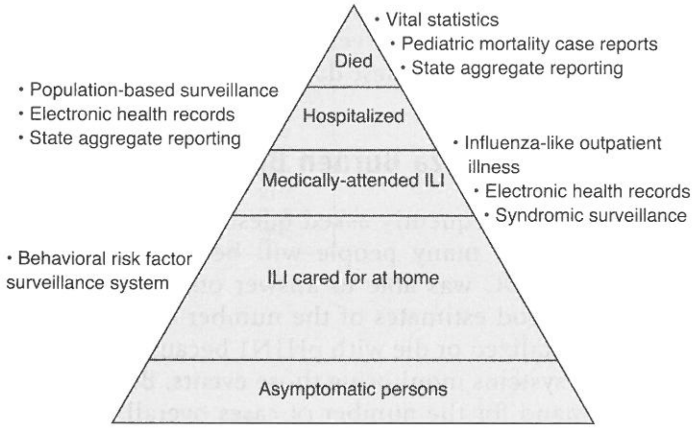
Estimating the Influenza Burden Better

One of the most frequently asked questions throughout the pandemic was, "How many people will become ill?" Early in the response, the CDC was able to answer only partially—we could provide very good estimates of the number of people who would become hospitalized or die with pH1N1 because we had very good surveillance systems monitoring those events. But that did not satisfy the demand for the number of cases overall, and we initially struggled to provide an estimate because (1) all of our established surveillance systems were set up such that they monitored people who had a healthcare encounter for influenza, and (2) most people who get influenza do not end up seeing a doctor for their illness. In other words, we were unable to capture as broad a spectrum of illness as we would have liked in order to estimate the burden of the pandemic—our surveillance was missing most of the people who get infected with influenza, and we needed some way to measure disease outside the healthcare system (see **Figure 13-11**).

During the pandemic, the CDC began surveillance of self-reported ILI using the Behavioral Risk Factor Surveillance System (BRFSS). BRFSS conducts population-based surveillance of health conditions and health risk behaviors in persons older than 18 years of age.[61] During the pandemic, BRFSS respondents were asked additional questions pertaining to ILI, even if they did not seek healthcare for their illness.[62] BRFSS data provided the only source of information describing ILI in persons outside the healthcare system during the pandemic in the United States. The CDC also expanded its existing surveillance systems for ambulatory and hospitalized cases, and when combined with the new BRFSS data, we were able to estimate the overall burden of pH1N1 illness in the population using a simple mathematical model.[20] The CDC is now working on enhancing its modeling capacity in order to improve burden estimation for future public health crises, including pandemics.

Figure 13-11

The influenza disease burden pyramid and surveillance inputs important to overall burden estimation.



CONCLUSION

In retrospect, it seems unlikely that some of the most valuable lessons learned during the response would have been discovered in any scenario other than an actual influenza pandemic. In this respect, experience might have been the best teacher, and the modern public health community can consider itself fortunate that 2009 H1N1 was a relatively mild influenza virus. As such, the experience of responding to the 2009 pandemic may provide the best lessons for preparing to respond to future public health crises. So, to conclude, let us hear from people involved in the response at many different levels about what they would have done differently, given the opportunity.

Dr. Joe Bresee, Chief of the Influenza Epidemiology and Prevention Branch at the CDC:

> I think that most of the things that the CDC did during the response were reasonable and appropriate given the information we had at the time. The quick changes to surveillance and data handling, the rapid development of critical policies, timely development of a national vaccination program, and the implementation of a broad and effective public communication campaign—all were remarkable achievements under the circumstances, and I would say that these accomplishments are typical of CDC work. For the next pandemic, we will do a better job of communicating—both to each other among the folks involved in the response, and to our partners in the public, the scientific colleagues and colleagues in public health. You can always do a better job of communicating.

Dr. Michael Shaw, Associate Director for Laboratory Science in the Influenza Division at the CDC:

> Actually, not much. I think it went very well at the beginning; extremely well. It would have been nice to have had an idea of what was going on in Mexico earlier than we did. If we had been able to get specimens a little earlier, we might have had the vaccine maybe a month earlier. We couldn't decide on a good vaccine strain to use until we had more information about the circulating viruses. And that just requires data, and data requires time. And that's something you can't speed up.[7]

Toby Crafton, Chief of Staff for the 2009 H1N1 Response at the CDC:

> Staffing was a huge problem, getting people. The CDC never has a problem getting people to respond to an event or to a catastrophe for about a month, and then after a month, people are like, "I got another job I have to do." To get people to give up what they're doing for three or four months is really asking a lot. But we learned early on that unless you get people for two months, then you are wasting their time and our time as well. Because by the time they get up to speed to what's going on, they're rotating off again unless they are there for a while.[7]

Joe Gregg, Deputy Team Lead for the Surveillance and Outbreak Response Team in the Influenza Division at the CDC:

> The amount of data coming in and the requests for information going out both increased exponentially within a few days of the response. To process and respond, we needed a lot of personnel with very specific skill sets. At first, we resorted to asking people we had worked with before and knew had the skills we needed. That worked for about three weeks and then we ran out of people. On top of that, we often needed to interpret the same data multiple times a day to meet information requests from different agencies. In hindsight we could have planned better by having a clear information cycle and standardized reports. We finally got there, but it wasn't until several months into the response.

Dr. David Sencer, CDC Director during the last swine influenza epidemic in 1976:

> Well, the advice I gave was basically to do what's right. If you have to take an unpopular stance, do that. But you need to expect the unexpected. Things are going to happen that you could not have anticipated. Make sure of your facts. Put heavy emphasis on the surveillance and then find a way to communicate this not just to the health professionals but to the public. And I think one of the outstanding successes of CDC in H1N1 was that they were able to take the scientific information and present it in such a fashion that the public could accept it, could understand it, and could realize that the CDC was playing right flat on the table. There were no hidden things going on.[7]

DISCUSSION QUESTIONS

1. Which of the competencies described in the Appendix does this case demonstrate?
2. Dwight D. Eisenhower once said: "Plans are nothing, planning is everything." Does this case illustrate this concept? If so, how?
3. What were the benefits of opening the CDC Emergency Operations Center?
4. What are the advantages of having a national surveillance system for influenza already in place before a pandemic?
5. How should the CDC handle the assignment of personnel during an emergency response?

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Mandatory Vaccination and H1N1: A Large Urban Hospital's Response

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